GRAS Notice for *Clostridium beijerinckii* ASCUSDY20 for Use as a Direct Fed Microbial in Dairy Cattle

June 1, 2020

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LIST OF ABBREVIATIONS

AAFCO	Association of American Feed Control Officials
ADF	Acid Detergent Fiber
ANI	Average Nucleotide Identity
AOAC	Association of Official Analytical Chemists
BAM	Bacteriological Analytical Manual
BLAST	Basic Local Alignment Search Tool
BUSCO	Benchmarking Universal Single-Copy Orthologs
CFR	Code of Federal Regulations
CFU	Colony Forming Units
cGMP	current Good Manufacturing Practices
CLSI	Clinical and Laboratory Standards Institute
CV	Coefficient of Variation
CVM	Center for Veterinary Medicine
DFM	Direct Fed Microbial
DM	Dry matter
DNA	DeoxyriboNucleic acid
EUCAST	European Committee on Antimicrobial Susceptibility Testing
FCC	Food Chemicals Codex
FDA	Food and Drug Administration
FFDCA	Federal Food, Drug and Cosmetic Act
FSMA	Food Safety Modernization Act
GC	Guanine-Cytosine
GRAS	Generally Recognized As Safe
HACCP	Hazards Analysis Critical Control Points
ITS	Internal Transcribed Spacer
MIC	Minimum Inhibitory Concentrations
NCBI	National Center for Biotechnology Information
ND	Not Detected
NDF	Neutral Detergent Fiber
NRRL	Agricultural Research Service Culture Collection
OP	Official Publication
QPS	Qualified Presumption of Safety
RNA	RiboNucleic acid
SD	Standard Deviation
SPC	Spiral Plate Count
TMR	Total Mixed Ration
USC	United States Code
USP	United States Pharmacopoeia
YPD	Yeast extract Peptone Dextrose

NOMENCLATURE

The notified substance is *Clostridium beijerinckii* ASCUSDY20. The spray dried powder comprises *C. beijerinckii* ASCUSDY20 cell concentrate on a starch carrier. The microbial strain is deposited in the NRRL culture collection as B-67248.

The microbial strain *Clostridium beijerinckii* ASCUSDY20 is often referred to in some appended reports as 'Dairy-20', which is the internal research name for *Clostridium beijerinckii* ASCUSDY20.

GRAS Notice for *Clostridium beijerinckii* ASCUSDY20 for Use as a Direct Fed Microbial in Dairy Cattle

PART 1 – SIGNED STATEMENTS AND CERTIFICATION

In accordance with 21 CFR §570 Subpart E consisting of §570.203 to 280, ASCUS Biosciences, Inc. hereby informs the U.S. Food and Drug Administration (FDA) that they are submitting a Generally Recognized As Safe (GRAS) notice for *Clostridium beijerinckii* ASCUSDY20.

1.1 Name and Address of Organization

ASCUS Biosciences, Inc.
6450 Lusk Blvd Suite E209
San Diego, CA 92121

1.2 Name of the Notified Substance

The notified substance is *Clostridium beijerinckii* ASCUSDY20 (microbial strain). The product comprises *C. beijerinckii* ASCUSDY20 cell concentrate on a starch carrier. This standardized product is referred to as '*Clostridium beijerinckii* ASCUSDY20 spray dried powder' or '*Clostridium beijerinckii* ASCUSDY20 SDP'. In addition, a number of the appended reports refer to *Clostridium beijerinckii* ASCUSDY20 or the spray dried powder product under the internal research name, Dairy-20.

1.3 Intended Conditions of Use

C. beijerinckii ASCUSDY20 spray dried powder is intended for use as a supplemental source of viable microorganisms in the feed of dairy cattle. The intended purpose of supplementation of the microorganism is to augment the digestion of feed in the rumen. The spray dried powder will be delivered to dairy cattle either alone or in combination with other microbial strains. Examples of the conditions under which direct fed microbial products containing *C. beijerinckii* ASCUSDY20 spray dried powder may be incorporated into the diet of dairy cattle include as part of the total mixed ration (TMR), as top-dressing to individual feeds or the daily ration, and as a component of a feed supplement. *C. beijerinckii* ASCUSDY20 spray dried powder will be incorporated into feed at a recommended level of $1x10^7$ CFU/cow/day.

1.4 Statutory Basis for the Conclusion of GRAS Status

Pursuant to 21 CFR §570.30(a) and (b), *C. beijerinckii* ASCUSDY20 spray dried powder manufactured by ASCUS Biosciences, has been concluded to have GRAS status for use as a direct fed microbial in dairy cattle, as described in Part 1.3, on the basis of scientific procedures.

1.5 Premarket Exception Status

ASCUS Biosciences hereby informs the U.S. FDA of the view that *C. beijerinckii* ASCUSDY20 spray dried powder is not subject to the premarket approval requirements of the Federal Food, Drug and Cosmetic Act (FFDCA) based on ASCUS Biosciences conclusion that the notified substance is GRAS under the conditions of intended use as described in Part 1.3 above.

1.6 Availability of Information

The data and information that serve as the basis for this GRAS notification will be made available to the U.S. FDA for review and copying upon request during customary business hours at the offices of:

ASCUS Biosciences, Inc.
6450 Lusk Blvd Suite E209
San Diego, CA 92121

In addition, upon request, ASCUS Biosciences will supply the U.S. FDA with a complete copy of the data and information either in an electronic format that is accessible for the Agency's evaluation or on paper.

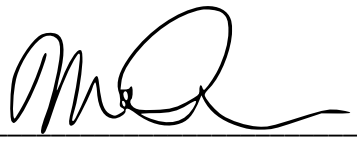
1.7 Freedom of Information Act, 5 U.S.C. 552

In ASCUS Biosciences view, all data and information presented in Parts 2 through 7 of this notice do not contain any trade secrets, commercial or financial information that is privileged or confidential, and therefore, all data and information presented herein are not exempt from the Freedom of Information Act, 5 U.S.C. Section 552 with the exception of Appendix 10 and 15, which is considered to contain proprietary commercial information which is confidential.

1.8 Certification

As required in 21 CFR 570.250(c)(2), ASCUS Biosciences, Inc. hereby certifies that to the best of their knowledge, all data and information presented in this notice constitutes a complete, representative and balanced submission, which includes all unfavorable as well as favorable information known to ASCUS Biosciences and pertinent to the evaluation of the safety and GRAS status of *Clostridium beijerinckii* ASCUSDY20 spray dried powder.

Signed,



Mallory Embree, PhD, Chief Scientific Officer

01JUN2020
Date

PART 2 – IDENTITY, METHOD OF MANUFACTURE, SPECIFICATIONS AND PHYSICAL OR TECHNICAL EFFECT

2.1 Identity

2.1.1 Taxonomic Classification

The current taxonomic classification of the microbial strain, *C. beijerinckii* ASCUSDY20, is provided in Table 2.1. In the past, *Clostridium* species were extensively used for the industrial production of butanol and acetone from starch-based substrates (Jones and Wood, 1986; Jones and Keis, 1995; Keis *et al*., 2001). The first strains isolated and developed for large scale production of these solvents were identified as *Clostridium acetobutylicum* but were later assigned to four distinct species, *C. acetobutylicum*, *C. beijerinckii*, *Clostridium saccharoperbutylacetonicum* and *Clostridium saccharobutylicum* (Johnson *et al*., 1997; Keis *et al*., 1995; Wilkinson and Young, 1995; Keis *et al*., 2001). Similarly, strains historically assigned to the species *Clostridium butylicum* have been subsequently shown to members of *C. beijerinckii* (George and Chen, 1983).

Table 2.1: Taxonomic Classification of *C. beijerinckii*

Kingdom	Bacteria
Phylum	Firmicutes
Class	Clostridia
Order	Clostridiales
Family	*Clostridiaceae*
Genus	*Clostridium*
Species	*beijerinckii*

2.1.2 Source of the Microorganism

C. beijerinckii ASCUSDY20 was identified and isolated to axenicity from a healthy, mid-lactation Holstein cow rumen sample obtained via cannula. The strain was isolated from sample DE03d9 received by ASCUS Biosciences on September 2, 2015. The isolate was deposited in the Agricultural Research Service Culture Collection (NRRL) and referenced as B-67248. A copy of the Certificate of Deposition is provided in Appendix 001.

2.1.3 Description of the Microorganism

C. beijerinckii ASCUSDY20 is an anaerobic, catalase and oxidase negative bacterium that readily sporulates. It is gram-positive and forms long chains of small cocci when cultured in liquid medium. When cultured on yeast extract peptone dextrose (YPD) agar, *C. beijerinckii* ASCUSDY20 forms large, translucent white colonies with undefined borders. Images of *C. beijerinckii* ASCUSDY20 colonies, vegetative cells and spores are presented in Figures 2.1 to 2.3, respectively.

Figure 2.1: ***C. beijerinckii*** **ASCUSDY20 Colonies on YPD Agar (Magnification 10x)**

Figure 2.2: ***C. beijerinckii*** **ASCUSDY20 Vegetative Cells (Magnification 1000x)**

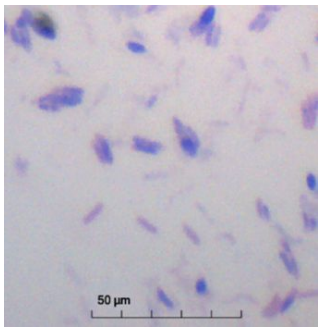


Figure 2.3: ***C. beijerinckii*** **ASCUSDY20 Spores (Magnification: 1000x)**

In vitro assays demonstrate that *C. beijerinckii* ASCUSDY20 grows on a variety of soluble and insoluble carbon sources and the results are summarized in Table 2.2. The strain was found to utilize various carbon sources, particularly monosaccharides such as glucose, fructose and xylose. The study report is provided in Appendix 002. Similar phenotypes are reported for other *C. beijerinckii* strains in the published literature (Keis *et al*., 2001).

Table 2.2: Growth of *C. beijerinckii* ASCUSDY20 on Different Carbon Sources

Carbon Source	Growth	Carbon Source	Growth
No carbon control	No growth	Fructose	Growth
Glucose	Growth	Acetate + Glucose	Growth
Lactose	Growth	Lactate	No growth
Maltose	Growth	Succinate	No growth
Sucrose	Growth	Glycerol	No growth
Cane Molasses	Growth	Acetate-Dextrose	Growth
Beet Molasses	Growth	Gluconate	No growth
Arabinose	Growth	Xylose	Growth
Ribose	No growth	Cellobiose	Growth
Mannitol	Growth	Starch	Growth
Sorbitol	Growth		

Metabolite production of *C. beijerinckii* ASCUSDY20 was measured at 48 hours elapsed fermentation time using an Agilent 1260 series HPLC with refractive index (RI) detector. The results are summarized in Table 2.3 and Appendix 002. Major fermentation products include acetate, butyrate, ethanol, and 1-butanol.

Table 2.3: Metabolite Production of *C. beijerinckii* ASCUSDY20 on Complex Media with Glucose

Metabolite	Production
Pyruvic acid	No growth
Succinic acid	No growth
Lactic acid	No growth
Glycerol	No growth
Acetic acid	Growth
Propionic acid	No growth
Butyric acid	Growth
Ethanol	Growth
1-Butanol	Growth

2.1.4 Identification of the Microorganism

2.1.4.1 16S rRNA Gene Sequencing

The 16S rRNA gene was amplified from the strain using 27F and 543R primers and paired end sequenced [2x2300 base pairs (bp)] using an Illumina Miseq (Stackebrandt and Goodfellow, 1991; Muyzer *et al*., 1993). The resulting sequence was quality trimmed and compared to National Center for Biotechnology Information (NCBI) databases using the Basic Local Alignment Search Tool (BLAST) to establish the identity of the strain. Details of the analysis including the BLAST output are provided in Appendix 003A and 003B. The results indicated that *C. beijerinckii* ASCUSDY20 was most closely related to *Clostridium*

saccharoperbutylacetonicum (100%), *Clostridium butyricum* (99%) and *Clostridium beijerinckii* (99%). Although the closest match is *C. saccharoperbutylacetonicum*, all three species fall within the minimum 98.7% sequence identity threshold typically used to define a species (Yarza *et al*., 2014). 16S rRNA sequence analysis is unable to discriminate between these closely related species on the basis that the interspecies percent similarity ranges are too high to apply the 97%, 98.7% or 99% limits classically proposed for species delineation within a genus (Bouvet *et al*., 2014). Thus, further genetic analyses including whole genome Average Nucleotide Identity (ANI) and sequence analysis of additional housekeeping genes were conducted to obtain species-level taxonomic resolution.

2.1.4.2 Whole Genome Sequence Assembly and Annotation

Genomic DNA was isolated from a pure culture of *C. beijerinckii* ASCUSDY20 and sequencing libraries were prepared using the Nextera XT kit (Illumina, San Diego, CA). The resulting libraries were paired-end sequenced (2x300bp) on an Illumina Miseq and in parallel, long-read libraries were prepared from the same extracted DNA using SQK-RAD004 kit (Oxford Nanopore Technologies, Oxford) following the protocol outlined by Jain *et al.* (2018) and 1D sequenced on the MinION (R9.4 flowcell; Oxford Nanopore, Oxford). The genome was assembled through hybrid methods utilizing both short and long reads. Read quality and genome coverage was evaluated using FASTQC for Illumina data and NanoStat for the Oxford Nanopore data. The complete genome sequence was assembled into one chromosome with a length of 5,984,367 bp and a GC content of 29.9%. Assembly statistics can be found in Table 2.4. The full details of the assembly are provided in Appendix 003C.

Protein coding genes were predicted through GLIMMER2 (Delcher *et al*., 1999) and through an iterative process of annotating putative genes using the FIGfams database (Meyer *et al*., 2009). To identify protein coding open reading frames of potential genes, contigs were first filtered of all potential tRNA coding genes (Lowe and Eddy, 1997) and rRNA genes (Aziz *et al*., 2008).

C. beijerinckii ASCUSDY20 contains 5,468 coding sequences which were subsequently built into a metabolic reconstruction describing 434 functional subsystems (DeJongh *et al*., 2007; Becker and Palsson, 2005). These subsystems include larger metabolic groups describing metabolism, virulence, plasmids, disease, defense metabolic products, stress response and dormancy.

The assembled genome has been deposited at NCBI under accession number CPO53893.

Table 2.4: Assembly Statistics for *C. beijerinckii* ASCUSDY20

# of Contigs	1
# of Contigs ≥ 5,000 bp	1
Longest Contig (bp)	5,984,367
Assembly Length	5,984,367
N50	5,984,367
N75	5,984,367
GC%	29.9

2.1.4.3 Whole Genome Sequence Comparison

To determine relatedness of *C. beijerinckii* ASCUSDY20 to other closely related species at a higher resolution, whole genomes were compared using ANI. All genomes used for the comparison were

closed with no gaps, with the exception of *Clostridium diolis* for which no closed genome was available. MUMmer was used to generate the alignments for ANI on the basis that this software is adept at aligning highly similar sequences and is more stringent than most other aligners such as BLAST (Kurtz *et al*., 2004). The results indicated that *C. beijerinckii* (ANI 98%, coverage 89%) was the most closely related species. Full details of the analysis are provided in Appendix 003A and C.

Table 2.5: Average Nucleotide Identity (ANI) of Related *Clostridium* Species to *C. beijerinckii* ASCUSDY20

Genus species (assembly)	ANI (%)	Coverage (%)	Comparison Genome Characteristics
Clostridium saccharoperbutylacetonicum (ASM200330v1)	86	20	Complete (1 chromosome, 1 plasmid)
Clostridium butyricum (ASM188687v1)	84	8	Complete (1 chromosome, 2 plasmids)
Clostridium beijerinckii (NCIMB 8052)	98	89	Complete
Clostridium diolis (NJP7)	97	86	Incomplete (58 contigs)

2.1.4.4 Housekeeping Gene Comparison

The comparison of housekeeping genes has been used successfully to distinguish *Clostridium* species (Udaondo *et al*., 2017). To further elucidate the taxonomy of the *C. beijerinckii* ASCUSDY20, DNA sequence comparison of the four housekeeping genes, ribonuclease P RNA (rnpB), ATP synthase alpha subunit (atpA), RNA polymerase alpha subunit (rpoA) and phenylalanyl-tRNA synthetase (pheS) was conducted. *C. beijerinckii, C. diolis, C. saccharoperbutylacetonicum,* and *C. butyricum* were compared. The closest match for all four housekeeping genes was to *C. beijerinckii* (≥98.8%) although a *C. diolis* was also a very close match. Full details of the analysis are provided in Appendix 003D.

2.1.4.5 Summary and Conclusions

16S rRNA analysis, whole genome sequence ANI analysis, and housekeeping gene comparisons have unambiguously confirmed the taxonomic identity of this commensal rumen microorganism to be *C. beijerinckii.*

2.1.5 Plasmid Analysis

To confirm the presence/absence of plasmids, the assembly graph for the *C. beijerinckii* ASCUSDY20 assembly was analyzed by Bandage (Wick *et al*., 2015). The assembly graph analysis confirmed that the *C. beijerinckii* ASCUSDY20 was contained in 1 circular chromosome with no unincorporated fragments, confirming the completeness of the assembly and indicating that the organism does not contain any plasmids. Image of the assembly graph can be found in Figure 2.4.

Figure 2.4: ***C. beijerinckii*** **ASCUSDY20 Assembly Graph as Generated by Bandage**

2.1.6 *In-vitro* and *In-silico* Analysis of Antibiotic Susceptibility

Phenotypic testing was conducted on *C. beijerinckii* ASCUSDY20 to determine the minimum inhibitory concentrations (MICs) against a selected group of antimicrobials of relevance to human and veterinary medicine. The full study report is provided in Appendix 004. The results were evaluated against the microbiological cut-off values reported by the European Food Safety Authority for "other gram positive bacteria" (EFSA, 2018), as well as the resistant breakpoints set by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) for "gram positive anaerobes" and the Clinical and Laboratory Standards Institute (CLSI) for "anaerobes" (where available). The MIC values reported for *C. beijerinckii* ASCUSDY20 were equal, or lower than, the cut-off values and break-points established by EFSA, EUCAST and/or CLSI for all antimicrobials except chloramphenicol, gentamycin and tetracycline. Results can be found in Table 2.6.

MIC testing revealed values above one or more breakpoints for three antimicrobial compounds; chloramphenicol, gentamicin, and tetracycline. For chloramphenicol , the MIC of 16 µg/mL exhibited by *C. beijerinckii* ASCUSDY20 is higher than the EFSA microbiological cut-off value (4 µg/mL) and the EUCAST resistant breakpoint value (8 µg/mL) but lower than the CLSI resistant breakpoint value (32 µg/mL). Resistance to aminoglycosides (gentamicin and streptomycin) is recognized to be intrinsic in anaerobic bacteria because the mechanism of uptake requires respiration (Bryan *et al.*, 1979). Consistent with this expectation, the MIC of >32 µg/mL for gentamicin exhibited by *C. beijerinckii* ASCUSDY20 is not considered a concern. However, streptomycin MIC for *C. beijerinckii* ASCUSDY20 was equal to EFSA cut-off value of 8 ug/mL and would be considered susceptible to streptomycin. The tetracycline MIC of 4 µg/mL reported for *C. beijerinckii* ASCUSDY20 is higher than the EFSA microbiological cut-off value (2 µg/mL) but lower than the CLSI resistant breakpoint value (16 µg/mL). Additionally, tetracycline resistance was observed to be relatively common among 68 livestock derived *Clostridium* strains analyzed by Dutta *et al.* (1983) with 17/68 (25%) strains displaying MIC values above the EFSA microbiological cut-off value.

Table 2.6: *C. beijerinckii* ASCUSDY20 Antimicrobial Susceptibility in Relation to EFSA, EUCAST, and CLSI Breakpoints					
Antimicrobial	**Tested Range (ug/mL)**	**MIC (ug/mL) of *C. beijerinckii* ASCUSDY20**	**2018 EFSA Microbiological Cut-off Values (ug/mL) for Other Gram +**	**EUCAST Resistant Breakpoints (ug/mL) Gram + Anaerobes**	**CLSI Resistant Breakpoints (ug/mL) Anaerobes**
Ampicillin	0.06-64	≤ 0.06	1	8	≥2
Chloramphenicol	2-32	16	4	8	≥32
Clindamycin	0.03-32	2	4	4	≥8
Erythromycin	0.25-8	1	1	Not Available	Not Available
Gentamicin	0.12-32	>32	4	Not Available	Not Available
Kanamycin	0.12-32	2	16	Not Available	Not Available
Streptomycin	0.12-32	8	8	Not Available	Not Available
Tetracycline	1-32	4	2	Not Available	≥16
Vancomycin	0.25-32	1	4	2	Not Available

To evaluate the presence of antimicrobial resistance genes in the *C. beijerinckii* ASCUSDY20 genome, amino acid sequences from coding regions identified in Part 2.1.4.3 were aligned to the PATRIC database. Included in the PATRIC database is the Comprehensive Antibiotics Resistance Database (CARD) and NCBI's National Database of Antibiotic Resistant Organisms (NDARO) for assessing antimicrobial resistance. In addition to the protein sequences from the databases, PATRIC has compiled protein hits to CARD and NDARO from 331,756 bacterial genomes and included those as redundant gene entries as a means to understand the global distribution of antimicrobial resistance proteins across diverse taxa isolated from a wide range of environments and hosts. Antimicrobial resistance was further explored using the ResFinder web server (Zankari *et al*. 2012) and BLASTp alignment to the NCBI AMR database as used by AMRFinder (Note: this database differs from NARDO used by PATRIC) (Feldgarden *et al*. 2019). Between these databases there are a total of 30,748 protein sequences, 773 sequences from Clostridia, 2 of which are from *C. beijerinckii*. Characteristics of each database can be found in Table 2.7.

Table 2.7: Characteristics of Databases Used to Assess Antimicrobial Resistance				
Database Name	**Number of Entries**	**Number of Clostridial Entries**	***C. beijerinckii* Entries**	**Contains Redundant Entries**
CARD (PATRIC)	17,559 (2,227 non redundant proteins	463 (14 non redundant proteins)	1, Chloramphenicol O-acetyltransferase (EC 2.3.1.28) => CatA15/A16 family	Yes
NDARO (PATRIC)	5,138 (4,004 non redundant proteins)	141 (20 non redundant proteins)	1, Chloramphenicol O-acetyltransferase (EC 2.3.1.28) => CatA15/A16 family	Yes
ResFinder	3,105	38	No	No
AMRFinder Plus	6,946	28	No	No

To ensure no hits were missed due to codon bias or sequencing error, protein alignments were considered a hit if they have greater than 80% identity over more than 70% query coverage. Results for *C. beijerinckii* ASCUSDY20 can be found in Tables 2.8 to 2.10.

Genetic analysis of *C. beijerinckii* ASCUSDY20 identified two potential resistance genes (see Tables 2.8 – 2.10).

- One of the proteins genes identified exhibits 84% sequence similarity to tetA(P) in the NDARO database and 86.67% similarity to the same gene in the NCBI AMR database. The other gene identified exhibits 85% sequence similarity to tetB(P) in NDARO and 85.43% similarity to the same protein in the NCBI AMR database. These two genes fall under the same operon in other Clostridia, with tetA acting as an efflux pump and tetB conferring ribosomal protection (Sloan *et al*., 1994). These genes are chromosomally located (see Part 2.1.5) indicative of natural rather than acquired resistance. Additionally, tetracycline resistance was observed to be relatively common among 68 livestock derived *Clostridium* strains analyzed by Dutta *et al*. (1983) with 17/68 (25%) strains displaying MIC values above the EFSA microbiological cut-off value.

A chloramphenicol acetyltransferase (catB) protein homologue in the *C. beijerinckii* ASCUSDY20 genome that was 97%, 97.73%, and 97.26% identical to genes found in the NDARO, ResFinder, and NCBI AMR databases respectively. Sebald (1994) reviewed the resistance of gram positive anaerobes in *Clostridium* species and noted that chloramphenicol resistance in two strains of *C. butyricum* (ATCC 19398 and NCIB 7423) was due to chromosomally located genes for chloramphenicol acetyltransferase. Considering that *C. beijerinckii* and *C. butyricum* are closely related and no plasmids were identified in *C. beijerinckii* ASCUSDY20 (see Part 2.1.5), potential chloramphenicol resistance is likely to be the result of the chromosomally located chloramphenicol acetyltransferase gene identified by genetic analysis and chance of horizontal transfer should be extremely low.

Table 2.8: *C. beijerinckii* ASCUSDY20 Antimicrobial Resistance by PATRIC

Source	Source Organism	Gene	Product	Function	Subject Coverage	Query Coverage	identity	E-Value
NDARO	*Clostridium perfringens*	tetB(P)	tetracycline resistance, ribosomal protection protein => TetB(P)	tetracycline resistance, ribosomal protection protein TetB(P); antibiotic target protection protein, tetracycline resistance gene	100	100	85	0.0
NDARO	*Clostridium butyricum*	catB	Chloramphenicol O-acetyltransferase (E.C. 2.3.1.28) => CatA15/A16 family	MULTISPECIES: class A beta-lactamase TEM-156; antibiotic inactivation enzyme, chloramphenicol resistance gene	100	100	97	1e-128
NDARO	*Clostridium perfringens*	tetA(P)	tetracycline resistance,MFS efflux pump => TetA(P)	efflux pump conferring antibiotic resistance	100	100	84	1e-201

Table 2.9: *C. beijerinckii* ASCUSDY20 Antimicrobial Resistance by ResFinder				
Gene	**Identity**	**Query Coverage**	**Function**	**Accession number**
catB	97.73	660/660(100%)	phenicol resistance	M93113

Table 2.10: *C. beijerinckii* ASCUSDY20 Antimicrobial Resistance by NCBI AMR BLASTp				
Gene	**e-value**	**Percent Identity**	**Query Coverage**	**Subject Coverage**
type A-15 chloramphenicol acetyltransferase	2.00E-158	97.26	100	100
tetracycline efflux MFS transporter TetA(P)	0.0	86.67	100	100
tetracycline resistance ribosomal protection protein TetB(P)	0.0	85.43	100	100

For comparative purposes, and to gauge the global pool of antimicrobial genes in *C. beijerinckii* and closely related species, sequences for *C. beijerinckii* (accession #GCA_000833105) and the closely related *C. butyricum* (accession #GCA_006742065) were downloaded from NCBI Genbank and analyzed for antimicrobial resistance by the same methods as *C. beijerinckii* ASCUSDY20.

Comparative analysis of *C. beijerinckii* (GCA_000833105) and *C. butyricum* (GCA_006742065) revealed no antimicrobial resistance genes. Results summary can be found in Table 2.11.

Table 2.11: Antimicrobial Resistance Summary for *C. beijerinckii* ASCUSDY20, *C. beijerinckii* (GCA_000833105), and *C. butyricum* (GCA_006742065)			
Organism	**Number of Antimicrobial Proteins Identified**	**Gene Names**	**Resistance conferred by Identified Proteins**
C. beijerinckii ASCUSDY20	3	tetA, tetB, catB	tetracycline, chloramphenicol
C. beijerinckii (GCA_000833105)	0	None	None
C. butyricum (GCA_006742065)	0	None	None

2.1.6.1 Section Summary

MIC testing for *C. beijerinckii* ASCUSDY20 reported values below or at established EUCAST and/or CLSI cutoffs for all antibiotics tested except for gentamicin. Genomic analysis indicates that *C. beijerinckii* ASCUSDY20 is potentially resistant to chloramphenicol and tetracycline, however, these were not confirmed through *in vitro* testing as the detected MIC was below the breakpoint for CLSI for both antibiotics. Together, these analyses suggest that should *C. beijerinckii* ASCUSDY20 cause an opportunistic infection in a human or animal, it can be readily treated using standard antibiotics.

2.1.7 Antimicrobial Production

C. beijerinckii ASCUSDY20 supernatant was tested for inhibitory activity against reference strains known to be susceptible to a range of antibiotics. No zones of inhibition were observed indicating that the strain is not an antimicrobial producer. Further details of the study are provided in Appendix 005.

2.1.8 Toxigenicity and Pathogenicity

To assess the presence of virulent and pathogenic genes, amino acid sequences from coding regions identified in Part 2.1.4.3 were aligned to several databases. All applicable, publicly available databases were used to identify potential pathogenic genes. The characteristics of these databases are described in Table 2.7. The PATRIC database has compiled relevant genes from external databases including Victors, Virulence Factors Database (VFDB), and the PATRIC_VF database. These genes represent 331,756 bacterial genomes. Redundant gene entries (e.g. the same toxin showing up in multiple microbial species) are included as a means to understand the global distribution of pathogenicity and virulence associated proteins across diverse taxa isolated from a wide range of environments and hosts. PathogenFInder and IslandViewer web servers (Cosentino *et al*. 2013; Bertelli *et al*. 2017) as well as BLASTp alignment to the Pathogen-Host Interaction Database (Phi-BASE) (Urban *et al*., 2015) were also utilized to assess the pathogenicity and virulence of *C. beijerinckii* ASCUSDY20. The total number of sequences in the PATRIC and Phi-BASE databases is 134,396 and includes 376 Clostridial sequences. IslandViewer contains 4,065 pathogenicity islands including 47 from Clostridia, and 3 pathogenicity islands from *C. beijerinckii.* The analysis in PathogenFinder is database independent and uses a model trained with protein sequences from 886 whole genome sequences. Twenty-six of these whole genome sequences are from pathogenic *Clostridium*. The PathogenFinder model predicts pathogenicity based on matches to proteins found differentially in pathogenic and non-pathogenic bacteria regardless of their annotated function. Therefore, a single hit to a protein found in pathogenic species does not necessarily suggest the query organism is virulent or pathogenic, but a collection of hits to proteins uniquely found in pathogens could be enough for PathogenFInder to deem the organism pathogenic, even if the proteins are not traditionally implicated in virulence or pathogenicity. The program allows the organism to be evaluated more holistically and enables the evaluation of proteins that are potentially involved in virulence and pathogenicity beyond well annotated virulence factors such as toxins. Characteristics of each database can be found in Table 2.12.

Table 2.12: Characteristics of Databases Used to Assess Virulence and Pathogenicity				
Database Name	**Number of Entries**	**Number of Clostridial Entries**	***C. beijerinckii* Entries**	**Contains Redundant Protein ID entries**
Victors (PATRIC)	67,914 (4,950 non-redundant proteins)	218 (23 non-redundant proteins)	No	Yes
VFDB (PATRIC)	20,911 (2,595 non-redundant proteins)	124 (28 non redundant proteins)	No	Yes
PATRIC_VF	38,791(1,570 non-redundant proteins)	2 (0 non-redundant proteins)	No	Yes
Phi-Base	6,780	32	No	No
IslandViewer4	4,065 pathogenicity islands	47 pathogenicity islands	Yes, 3 pathogenicity islands	No
PathogenFInder	N/A	N/A	N/A	N/A

The alignment process compares all identified *C. beijerinckii* ASCUSDY20 genes against all known pathogen-related genes that have been identified across the Bacterial and Fungal kingdoms. To ensure no hits are missed due to codon bias or sequencing error, protein alignments are considered a hit if they have greater than 80% identity over more than 70% query coverage. No genes involved in toxin synthesis, pathogenicity, or virulence were identified by PATRIC, PathogenFinder, or IslandViewer. Additionally, PathogenFinder deemed *C. beijerinckii* ASCUSDY20 to "not be predicted as a human pathogen". Results for these analyses can be found in Table 2.13 and Table 2.14.

Table 2.13: Significant Alignments Between the Victors Virulence Database and *C. beijerinckii* ASCUSDY20						
Organism	**Protein Hits to Victors**	**Protein Hits to VFDB**	**Protein Hits to PATRIC_VF**	**Protein Hits to Phi-Base**	**Pathogenicity Island Hits in IslandViewer**	**Hits to Proteins from Pathogens in PathogenFinder**
C. beijerinckii ASCUSDY20	0	0	0	0	0	0

Table 2.14: PathogenFinder Results *C. beijerinckii* ASCUSDY20 Virulence/Pathogenicity by PathogenFinder			
Gene_Matches	**Proteins from Pathogens Matched**	**Proteins from Non-Pathogens Matched**	**Predicted as Human Pathogen?**
131	0	131	No

For comparative purposes, and to better gauge the global pool of virulence factors in *C. beijerinckii* and related species, amino acid sequences for published genomes of *C. beijerinckii* (GCA_000833105) (Little *et al*. 2015) and *C. butyricum* (GCA_006742065) (NBRC Whole Genome Sequencing Project) were downloaded from NCBI Genbank and analyzed using the same method as *C. beijerinckii* ASCUSDY20.

Comparative analysis of *C. beijerinckii* (GCA_000833105) revealed no proteins involved in virulence or pathogenicity.

One protein from a pathogen was identified by the PathogenFinder web server in *C. butyricum* (GCA_006742065), a GNAT family acetyltransferase. GNAT family acetyltransferases comprise a large family of universally distributed enzymes which act to acetylate a wide variety of substrates (Vetting *et al.*, 2005). In prokaryotes a subset of GNAT family acetyltransferases (Aminoglycoside N-acetyltransferases) have been linked to aminoglycoside antibiotics (Ud-Din *et al.*, 2016). However, there is no evidence to suggest that this particular acetyltransferase is implicated in antibiotic resistance and the substrates which it acetylates are not fully elucidated. Ultimately, the organism was deemed non-pathogenic by PathogenFInder even though the GNAT family acetyltransferase was identified in the genome. This indicates that the genome didn't meet the profile generally identified in pathogens by PathogenFInder and that the acetyltransferase is likely unable to cause virulence or pathogenicity without the presence of other pathogenic features. Results can be found in Table 2.15, Table 2.16 and Table 2.17.

Table 2.15: Number of Alignments Between Pathogenicity and Virulence Databases and Publicly Available Genomes of Organisms Closely Related to *C. beijerinckii* ASCUSDY20

Organism	Victors	VFDB	PATRIC_VF	Phi-Base	Island Viewer	Pathogen Finder
C. beijerinckii (GCA_000833105)	0	0	0	0	0	0
C. butyricum (GCA_006742065)	0	0	0	0	0	1, *Clostridium botulinum* GNAT family acetyltransferase (Genbank ACD53758)

Table 2.16: PathogenFinder Results *C. beijerinckii* (GCA_000833105)

Gene_Matches	Proteins from Pathogens Matched	Proteins from Non-Pathogens Matched	The organisms is predicted as human pathogenic
49	0	49	No

Table 2.17: PathogenFinder Results *C. butyricum* (GCA_006742065)

Gene_Matches	Proteins from Pathogens Matched	Proteins from Non-Pathogens Matched	The organisms is predicted as human pathogenic
9	1	8	No

2.1.8.1 Section Summary

No genes directly involved in pathogenesis or toxin production were identified.

All publicly available pathogen and virulence-related databases were queried to determine the pathogenic potential of *C. beijerinckii* ASCUSDY20. In total, these databases encompass 138,461 known pathogen-related genes spanning all microbial taxonomies, of which 376 originated from *Clostridium*

species. Comprehensive alignment of the *C. beijerinckii* ASCUSDY20 genome to these databases yielded 0 hits at 80% identity, 70% query coverage. The analysis also included a search of 4,065 pathogenicity islands, 47 of which originated from *Clostridium* species, and 3 pathogenicity islands from *C. beijerinckii* by the IsandViewer web interface. Additionally, database independent analysis using the PathogenFinder web interface was conducted. IslandViewer did not identify any pathogenicity islands and *C. beijerinckii* ASCUSDY20 was deemed non-pathogenic by PathogenFinder.

To better assess the completeness of the analysis, genomes of publicly available *C. beijerinckii* (GCA_000833105) and close relative *C. butyricum* (GCA_006742065) were analyzed using the same methods to assess completeness of the analysis: 0 nonredundant genes aligned for *C. beijerinckii* (GCA_000833105) and 1 non-redundant gene aligned for *C. butyricum* (GCA_006742065). The gene identified in *C. butyricum* is a GNAT family acetyltransferase which could potentially be implicated in aminoglycoside antibiotic resistance but is not responsible for virulence or toxin production. No genes directly involved in pathogenesis or toxin production were identified in either genome.

2.1.9 Summary of Organism Safety Based on Genomics

C. beijerinckii ASCUSDY20 was unambiguously identified using 16S rRNA analysis and whole genome sequence ANI analysis. *C. beijerinckii* ASCUSDY20 is not resistant to clinically relevant any antimicrobial or antimycotic compounds, suggesting that should *C. beijerinckii* ASCUSDY20 cause an opportunistic infection in a human or animal, it can be readily treated using standard antibiotics. Additionally, phenotypic testing confirmed that no antimicrobials were produced during fermentation. Comparison of the *C. beijerinckii* ASCUSDY20 genome to several databases containing known pathogenic-related genes yielded 0 hits. No genes in the *C. beijerinckii* ASCUSDY20 genome were associated with toxin production, pathogenicity, or virulence. To better assess the completeness of the analysis, genomes of publicly available *C. beijerinckii* (GCA_000833105) and close relative *C. butyricum* (GCA_006742065) were analyzed using the same methods to assess completeness of the analysis: 0 non-redundant genes aligned for *C. beijerinckii* (GCA_000833105) and 1 non-redundant gene aligned for *C. butyricum* (GCA_006742065). No genes directly involved in pathogenesis or toxin production were identified. Based on these analyses, *C. beijerinckii* ASCUSDY20 is safe for use as direct fed microbial.

2.2 Method of Manufacture

2.2.1 Raw Materials and Processing Aids

The raw materials and processing aids used in the manufacture of starch encapsulated *C. beijerinckii* ASCUSDY20 are listed in Appendix 009. All raw materials used in the manufacture of *C. beijerinckii* ASCUSDY20 spray dried powder have a history of use in the industrial food and feed fermentation processes, and are considered by ASCUS Biosciences to be safe and suitable for use in the manufacture of feed ingredients in the U.S.

2.2.2 Manufacturing Process

A schematic overview of the manufacturing process of *C. beijerinckii* ASCUSDY20 spray dried powder is provided in Figure 2.5. *C. beijerinckii* ASCUSDY20 is produced through a standard anaerobic dextrose fed-batch fermentation process. A working cell culture stock is maintained by ASCUS Biosciences and used for the seed fermentation. (b) (4)

(b) (4)

(b) (4)

The resultant *C. beijerinckii* ASCUSDY20 spray dried powder is suitable for use as a direct fed microbial in feed. Further details on the manufacturing process are provided in Appendix 010.

Figure 2.5: Schematic Overview of the Manufacturing Process

2.2.3 Production Controls

Commercial manufacture of *C. beijerinckii* ASCUSDY20 spray dried powder will be in accordance with current Good Manufacturing Practices (cGMP) and a Hazards Analysis Critical Control Points (HACCP) plan is in place. The requirements of the Food Safety Modernization Act (FSMA) as laid down in 21 CFR §117 will be applied at all stages of the production, processing and distribution.

2.3 Product Specifications and Batch Analyses

2.3.1 Proposed Product Specifications for the Unstandardized Cell Concentrate

Appropriate feed-grade specifications have been established for the *C. beijerinckii* ASCUSDY20 cell concentrate and are presented in Table 2.18. Copies of the methods of analysis are provided in Appendices 007 and 012.

Table 2.18: *C. beijerinckii* ASCUSDY20 Concentrate Specifications		
Parameter	**Specification Limits**	**Analytical Method**
Spores	(b) (4)	Internal Method
Coliform		BAM-SPC
E. coli		BAM-SPC
Salmonella		AOAC 2013.01
Listeria		AOAC 2013.10
Botulinum toxins		FDA BAM

Abbreviations: CFU = colony forming units; BAM = Bacteriological Analytical Manual; AOAC = Association of Official Analytical Chemists. Internal Method; Appendix 012A

2.3.2 Batch Analyses for the Unstandardized Cell Concentrate

Three batches of *C. beijerinckii* ASCUSDY20 cell concentrate representative of the commercial material were analyzed to verify that the manufacturing process produces a consistent product that complies with the proposed specifications. The results are summarized in Table 2.19 and the Certificates of Analysis are provided in Appendix 013. Consistent with the findings of the WGS analysis (see Part 2.1), *C. beijerinckii* ASCUSDY20 does not harbor any genes encoding for toxin synthesis, and no botulinum toxins were identified in any of the batches (Appendix 008).

Table 2.19: Analytical Results for 3 Batches of *C. beijerinckii* ASCUSDY20 Concentrate					
			Analytical Results		
Parameter	**Unit**	**Specification**	**Lot 18-0202-041-P22**	**Lot 18-0202-001-P79**	**Lot 18-0202-001-P73**
Spores	Spores/g	(b) (4)			(b) (4)
Coliform	CFU/g				
E. coli	CFU/g				
Salmonella	Per 25 g				
Listeria	Per 25 g				
Botulinum toxins*	Per 2 g				

Abbreviations: CFU = colony forming units.* Testing done at end of fermentation process

2.3.3 Proposed Product Specifications for the Standardized *C. beijerinckii* ASCUSDY20 Spray Dried Powder

As mentioned in Part 2.2, *C. beijerinckii* ASCUSDY20 spore concentrate is stabilized and standardized by spray drying with starch (approximately 70% starch by weight) to yield a product suitable for use in dairy cattle feed (the notified substance). Appropriate feed-grade specifications have been established for *C. beijerinckii* ASCUSDY20 spray dried powder and are presented in Table 2.20. Copies of the methods of analysis are provided in Appendices 007 and 012.

Table 2.20: *C. beijerinckii* ASCUSDY20 Spray Dried Powder Product Specifications		
Parameter	**Specification Limits**	**Analytical Method**
Viable cells count	(b) (4)	Internal Method
Coliform		BAM-SPC
E. coli		BAM-SPC
Salmonella		AOAC 2013.01
Listeria		AOAC 2013.10

Abbreviations: CFU = colony forming units; BAM = Bacteriological Analytical Manual; AOAC = Association of Official Analytical Chemists. Internal Method Appendix 012

2.3.4 Batch Analyses for *C. beijerinckii* ASCUSDY20 Spray Dried Powder

Three batches of *C. beijerinckii* ASCUSDY20 spray dried powder representative of the commercial material were analyzed to verify that the manufacturing process produces a consistent product that complies with the proposed specifications. The results are summarized in Table 2.21 and the Certificates of Analysis are provided in Appendix 013.

Table 2.21: Analytical Results for 3 Batches of *C. beijerinckii* ASCUSDY20 Spray Dried Powder					
			Analytical Results		
Parameter	**Unit**	**Specification**	**Lot 18-0202-041-P22**	**Lot 18-0202-001-P79**	**Lot 18-0202-001-P73**
Viable cells count	CFU/g	(b) (4)			
Coliforms	CFU/g				
E. coli	CFU/g				
Salmonella	Per 25 g				
Listeria	Per 25 g				

Abbreviations: CFU = colony forming units.

2.3.5 Additional Analytical Data

The levels of heavy metals are also routinely monitored in batches of *C. beijerinckii* ASCUSDY20 spray dried powder. Three batches of *C. beijerinckii* ASCUSDY20 spray dried powder representative of the commercial material were analyzed to verify that the levels of these contaminants fall within acceptable ranges. The results are summarized in Table 2.22 and the Certificates of Analysis from analytical laboratories are provided in Appendix 14. On the basis of the analytical data, no specifications for heavy metals are considered necessary. Based on the level of use, there is no need to identify a specification on these heavy metals based on their insignificant levels and a safety assessment as provided in Part 6.

Table 2.22: Further Analytical Results for 3 Batches of *C. beijerinckii* ASCUSDY20 Spray Dried Powder					
		Analytical Results			Analytical Method
Parameter	Unit	Lot 18-0202-041-P22	Lot 18-0202-001-P79	Lot 18-0202-001-P73	
Arsenic	ppm	(b) (4)			AOAC 2015.01
Cadmium	ppm				AOAC 2015.01
Lead	ppm				AOAC 2015.01
Mercury	ppm				AOAC 2015.01

Abbreviations: AOAC = Association of Official Analytical Chemists.

2.4 Stability

2.4.1 Shelf-Life Stability Data

ASCUS Biosciences guarantees conformity of *C. beijerinckii* ASCUSDY20 spray dried powder to the proposed product specifications (see Table 2.21) for 12 months when stored in the original, unopened (sealed) packaging at temperatures of between 4 and 25°C. The proposed shelf-life is supported by ongoing stability studies in which 3 batches of *C. beijerinckii* ASCUSDY20 spray dried powder in packaging representative of the commercial material are stored at 5°C, 25°C and 40°C, respectively. Packaging information is provided in Appendix 008. Real-time data are available for 12 months for samples stored at 5°C, and the recommended 12 months shelf-life are based from the results of the stability studies conducted under accelerated conditions (25°C [12 months] and 40°C for 6 months).

2.4.1.1 Stability Study at 5°C

The results of the stability study conducted at 5°C for 12 months on *C. beijerinckii* ASCUSDY20 spray dried powder are summarized in Table 2.23 and the report is provided in Appendix 015A. Over the period evaluated to date, no significant changes in the viable cell count were observed and the values reported for the 3 batches of *C. beijerinckii* ASCUSDY20 spray dried powder comply with the proposed product specification (min. (b

Table 2.23: Results of a Stability Study on 3 Batches of *C. beijerinckii* ASCUSDY20 Stored at 5°C Spray Dried Powder							
		Analytical Results					
		Lot 18-0202-001-P73		Lot 18-0202-041-P22		Lot 18-202-001-P79	
Time (Months)	Unit	Viable Cells Count	SD	Viable Cells Count	SD	Viable Cells Count	SD
0	CFU/g	(b) (4)					
1	CFU/g						
2	CFU/g						
3	CFU/g						
6	CFU/g						
9	CFU/g						
12	CFU/g						

Abbreviations: CFU = colony forming units; SD = standard deviation.

2.4.1.2 Stability Study at 25°C

The results of the stability study conducted at 25°C for 12 months on *C. beijerinckii* ASCUSDY20 spray dried powder are summarized in Table 2.24 and the report is provided in Appendix 015B. Over the period evaluated to date, no significant changes in the viable cell count were observed and the values reported for the 3 batches of *C. beijerinckii* ASCUSDY20 spray dried powder comply with the proposed product specification (min. (b)

Table 2.24: Results of a Stability Study on 3 Batches of *C. beijerinckii* ASCUSDY20 Spray Dried Powder Stored at 25°C Spray Dried Powder

Time (Months)	Unit	Analytical Results					
		Lot 18-0202-001-P73		Lot 18-0202-041-P22		Lot 18-202-001-P79	
		Viable Cells Count	SD	Viable Cells Count	SD	Viable Cells Count	SD
0	CFU/g	(b) (4)					
1	CFU/g						
2	CFU/g						
3	CFU/g						
6	CFU/g						
9	CFU/g						
12	CFU/g						

Abbreviations: CFU = colony forming units; SD = standard deviation.

2.4.1.3 Stability Study at 40°C

The results of a stability study conducted at 40°C for 26 weeks on *C. beijerinckii* ASCUSDY20 spray dried powder are summarized in Table 2.25 and the report is provided in Appendix 015C. Over the period evaluated to date, no significant changes in the viable cell count were observed and the values reported for the 3 batches of *C. beijerinckii* ASCUSDY20 spray dried powder comply with the proposed product specification (min. (b)

Table 2.25: Results of a Stability Study on 3 Batches of *C. beijerinckii* ASCUSDY20 Spray Dried Powder Stored at 40°C

Time (Weeks)	Unit	Analytical Results					
		Lot 18-0202-001-P73		Lot 18-0202-041-P22		Lot 18-202-001-P79	
		Viable Cells Count	SD	Viable Cells Count	SD	Viable Cells Count	SD
0	CFU/g	(b) (4)					
1	CFU/g						
2	CFU/g						
3	CFU/g						
4	CFU/g						
26	CFU/g						

Abbreviations: CFU = colony forming units; SD = standard deviation.

2.4.2 In-Feed Stability

As mentioned in Part 1, *C. beijerinckii* ASCUSDY20 spray dried powder may be incorporated into the diet of dairy cattle as part of the TMR, as top-dressing to individual feeds or the daily ration, and as a component of a feed supplement. The strain is spray dried with starch to generate a stable product suitable for handling under practical commercial farming conditions in the U.S. The dry matter intake of dairy cattle is optimized by feeding fresh TMR on a twice daily basis. The forage content is typically adjusted to meet the nutrient requirements of the animals on a pen basis. Under the conditions of intended use, *C. beijerinckii* ASCUSDY20 spray dried powder may be mixed directly into the TMR or added as a top-dressing at the point of use. On this basis, long-term stability is not relevant, and an in-feed stability study was not conducted. Demonstration that *C. beijerinckii* ASCUSDY20 survives the mixing process in feed is provided by the homogeneity study (see below, Part 2.4.3).

2.4.3 Homogeneity Data

The ability of *C. beijerinckii* ASCUSDY20 spray dried powder to be mixed homogeneously into feed was evaluated. A direct fed microbial product containing *C. beijerinckii* ASCUSDY20 spray dried powder was incorporated into 3 samples of grain at 5 g/lb which is representative of practical conditions of use in feed. Ten sub-samples of grain were collected across the mixer and analyzed for *C. beijerinckii* viable cells count. The coefficients of variation (CV) in viable cells count for the 10 sub-samples was determined for each grain sample and the results are summarized in Table 2.26 and Appendix 015D. The CV reported for *C. beijerinckii* viable cells count varied from 39 to 62% among the 3 grain samples indicating that under the conditions of intended use, *C. beijerinckii* ASCUSDY20 (microbial strain) is distributed throughout the feed.

Table 2.26: Results of a Homogeneity Study on 3 Samples of Grain Containing *C. beijerinckii* ASCUSDY20 Spray Dried Powder

Grain Sample	Analytical Data			Calculations	
	Unit	Mean Viable Cells Count	SD	Unit	CV (%)
1	CFU/g	(b) (4)		%	33.4
2	CFU/g			%	61.8
3	CFU/g			%	42.7

Abbreviations: CFU = colony forming units; SD = standard deviation; CV = coefficient of variation.

2.4.4 Manufacturing Summary

ASCUS Biosciences will manufacture a safe stable product for dairy cattle meeting cGMP and FSMA compliance. This was demonstrated through batches of product meeting product specifications for contaminants, heavy metals and potency. The product is packaged in moisture protected barrier bags.

2.5 Effect of the Notified Substance

This portion of the notice addresses the requirements specified in 21 CFR 570.230(d):

> (d) When necessary to demonstrate safety, relevant data and information bearing on the physical or other technical effect the notified substance is intended to produce, including the quantity of the notified substance required to produce such effect.

The GRAS Final Rule (81 FR 54960) provides interpretation of this regulation specific to animal feed ingredients in response to comment 144: "We agree that data and information bearing on the physical or other technical effect the notified substance is intended to produce are only necessary when they bear on safety." A product like phytase would require data, however, the intended purpose of supplementation of *C. beijerinckii* ASCUSDY20 is to augment normal rumen digestion. As described below, ASCUS Biosciences has determined that the technical effect of *C. beijerinckii* ASCUSDY20 when fed to dairy cattle as a direct fed microbial under the conditions of intended use does not have a bearing on safety. Thus, data and information demonstrating the intended effect of *C. beijerinckii* ASCUSDY20 in the feed of dairy cattle are not required as part of this GRAS notice.

The use of this organism is to facilitate the digestion of various carbohydrates of animal feed within the rumen to volatile fatty acids such as butyrate and acetate. *C. beijerinckii* has been found in rumen and silage globally (Kameshwar *et al*., 2019; Avila and Carvaho, 2019; Thi Hoang *et al*., 2020; Seshadri *et al*., 2018) and has been assessed as a probiotic for monogastric animals (Vanbelle *et al*., 1990; Prosekov *et al*., 2015). The contribution of DFMs to the fermentation characteristics of the rumen has been extensively evaluated (Elghandour *et al*., 2015), and is further described below in context of technical effect and animal safety (Part 6.4 of this notice).

Crittenden *et al*., 2002 reported that *C. beijerinckii* is able to ferment important dietary fibers such as xylan and beta-glucan. Supplementation of dietary fibrolytic enzymes could improve DMI and milk production has also been reported (Rode *et al*., 1999). As a commensal microorganism, feeding *C. beijerinckii* would have no impacts on animal health. Should *C. beijerinckii* not act to ferment dietary fibers such as xylan and beta-glucan, there would be no safety impact, as the other rumen microorganism will continue fermentation, and the feed was formulated to assure nutrient requirements were met without consideration of the potential for increased digestion of less soluble carbohydrates.

2.5.1 Rumen Microbiome

The most recent authoritative text on the nutrition of major ruminants (NRC, 2016), states that the rumen is a "complex dynamic anaerobic ecosystem." The dynamics of the microbial community arises from variability introduced by feed source, the environment, and physiological state impacts the microbiome (Xue *et al*., 2018). Experts (NRC, 2016) note that diurnal shifts of a full pH unit are not uncommon, and this can significantly impact the microbial population. The rumen microbial population is well adapted to these standard diurnal shifts in the rumen environment and continue to serve the function of digestion of feed despite these changes (NRC, 2016). This ability to rapidly adapt is due in part to the rumen microbiome's ability to utilize specialized enzymes and enzyme complexes to convert feed components to end products of digestion and microbial cells (NRC, 2016). It is this specific understanding that ASCUS uses in their identification of existing, commensal microorganisms in the rumen of high producing ruminants. Particularly, understanding of their unique enzymatic properties and physiology support the selection and use of them as DFMs.

Several studies have linked the rumen microbiome profile to animal performance and digestibility (Lima *et al*., 2015; Jami *et al*., 2013; Kumar *et al*., 2015). The rumen microbiome is highly variable depending on several factors including age, breed, diet composition, time after feeding, season, stage of lactation, location, and farm management practices (Pitta *et al*., 2016; Furman *et al*., 2020; Henderson *et al*., 2015; Wallace *et al*., 2019). Additionally, there are groups of microorganisms that are unique to particular

breeds of cow (i.e., Jersey or Holstein), regions, and individual animals that further increase the inherent complexity of the microbial community native to the rumen. Diet, in particular, has been shown to be the main driver of microbiome composition (Ghaffari *et al*., 2014). To better study the microbiome in context of this variability, many studies have focused on identifying and characterizing the core rumen microbiome (Petri *et al*., 2013; Xue *et al*., 2018; Henderson *et al*., 2015; Wallace *et al*., 2019; Furman *et al*., 2020; Kumar *et al*., 2015; Jami *et al*., 2013; Kittleman *et al*., 2013; Lima *et al*., 2015; Fouts *et al*., 2012). The concept of core microbiome, a common assemblage of microorganisms that exists in or is associated with a specific habitat, was first introduced and applied to differentiate human microbiomes associated with healthy and diseased conditions (Turnbaugh *et al*., 2007; Turnbaugh and Gordon, 2009; Turnbaugh *et al*., 2009). Since then, core microbiomes have been identified in a broad spectrum of environments including agroecosystems, monogastric animals, and ruminants (Shade and Handelman, 2012; Yeoh *et al*., 2017; Toju *et al*., 2018; Lowe *et al*., 2012; Dougal *et al*., 2013).

There is a core microbiome that appears in the majority of dairy cows that provides the basal level of fermentation required for animal survival. Although the results are variable at times and defining a "normal healthy'' rumen is challenging, there are several phyla that tend to appear across all ruminants. Henderson *et al*. (2015) reported 32 different species of ruminants globally shared a core assembly of rumen bacteria. Xue *et al*. (2018) demonstrates that individual animals within a large cohort of dairy cattle with similar genetics, diet, environment, and management can have significant differences in their rumen microbiome species. The core microbiome identified included microorganisms from over 391 genera covering 26 phyla. The microorganisms unique to individual animals (termed "pan microbiome") along with the core microbiome dictated the variability in rumen fermentation and production. Consistent with other studies (Jami and Mizrahi, 2012; Lima, 2014; Deusch, 2017; Huws, 2018; Xue, 2018), members of Bacteroidetes, Firmicutes, Proteobacteria, and Fibrobacteres were among the topmost abundant bacteria identified regardless of animal origin and diet.

As more rumen microbiomes were studied, it became clear that diet was the major determinant of observed microbiome differences (Johnson and Johnson, 1995; Brulc *et al*., 2009; Carberry*et al*., 2014; Deusch *et al*., 2017; Belanche *et al*., 2019; Kumar, 2015; Mizrahi and Jami 2018). This indicates the direct impact of diet on rumen microbial populations. Hence, modifying either diet or microbiome could influence the rumen fermentation process (Morais and Mizrah, 2019; Wallace *et al*., 2019; Furman *et al*., 2020; Belanche *et al*., 2012). To better assess the impact of *C. beijerinckii* ASCUSDY20 on deleteriously impacting the existing microbiome. If the abundances of core microbiome members are within typically observed ranges, it is likely that rumen fermentation is also operating within normal ranges as well. These studies cover a variety of diets, as diet has the most impact on microbiome composition. In-house data corroborates that no large shifts in the core microbiome beyond observed thresholds are anticipated through feeding a native microorganism, and thus, no detrimental effects of rumen fermentation are expected (Appendix 018). The intent of feeding DFMs, particularly *C. beijerinckii* ASCUSDY20, is to improve the nutrient availability from feed. Feeding *C. beijerinckii* ASCUSDY20 to dairy cattle supplements the existing populations of *C. beijerinckii* ASCUSDY20 in the rumen, and ultimately provides additional nutrient availability to the animal. Should *C. beijerinckii* ASCUSDY20 fail, other members of the existing rumen microbiome will continue to ferment feed, thus supplying the animal with sufficient nutrients. This notice includes a more detailed discussion of the core microbiome and microbiome safety in Part 6.4 of this GRAS notice.

2.5.2 Impact of Failure of the Notified Substance

If this product fails, that is, the product fails to enhance feed digestibility in the rumen, there would not be a safety concern with respect to the animal's health or nutrition. The notified substance increases the digestion of carbohydrates by acting upon the existing feed within the rumen. The diet offered to the animal would be formulated to meet the existing nutritional needs of the animal (NRC, 2001). Should *C. beijerinckii* ASCUSDY20 fail, other members of the existing rumen microbiome will continue to ferment feed, thus supplying the animal with sufficient nutrients.

Several published experiments have directly investigated the impacts of DFMs by comparing groups of animals receiving a "dead" microbial against a variety of treatment conditions. Cunha, *et al*. (2019) compared heifers fed a basal diet against heifers fed the same basal diet containing a live yeast or inactive yeast supplement (2 different doses) in a 5x5 Latin square experimental design with 15-day periods. Live and dead yeasts were administered to the appropriate animals after each feeding through infusion directly into the rumen. No differences in digestibility were observed between the control, live yeast, or either of the inactive yeast doses. No differences were observed in feed intake nor animal behavior. Hence the inactive yeast did not alter the overall digestion of the feed, nor impact the health of the animals. Feeding inactive yeast did not decrease rumen function.

Muscato, *et al*. (2002) evaluated the feeding of fresh and inactivated rumen fluid to calves in a series of four experiments. The animals were dosed daily with 8 mL of either fresh or inactivated rumen fluid obtained from a cannulated Holstein cow from 0-6 weeks of age. In the first experiment, calves were either fed a typical basal ration or the same basal ration supplemented with fresh rumen fluid. In the second experiment, calves were fed the basal ration with either the cell pellet of fresh rumen fluid, supernatant of fresh rumen fluid, or no addition. In the third experiment, calves were fed a basal ration, or a basal ration supplemented with autoclaved rumen fluid. Autoclaving rumen fluid ensures microbial death, thus inactivating the biological component. The fourth experiment had a similar set-up to the third experiment, but rumen fluid was only fed for 5 days rather than 6 weeks. In the studies that evaluated autoclaved rumen fluid, the number of days of scouring were significantly decreased compared to the control. Similarly, the calves receiving autoclaved rumen fluid experienced higher gains in the first two weeks, but by the end of the experimental period there was no impact on growth. There were no differences in the outcomes of calves receiving fresh rumen fluid as compared to calves receiving autoclaved rumen fluid. This study suggests that the feeding of inactivated microorganisms does not decrease rumen function or create a safety concern when fed to animals.

The contribution of members of *Clostridium*, specifically, to the fermentations characteristics of the rumen has been evaluated in the published literature. Uyeno, *et al*. (2013) investigated the effects of *C. butyricum* and a prebiotic on the health and performance of Holstein calves. Forty calves were fed a milk replacer with either a prebiotic, *C. butyricum*, or no supplement for 46 days. Feeding *C. butyricum* found feed intake, daily gain, and occurrence of diarrhea of the calves were unaffected. No deleterious health effects were observed in calves fed *C. butyricum*, even though they did not demonstrate the intended performance response.

Philippeau, *et al.* (2017) fed multiple DFM treatments to investigate the effects of DFM on rumen fermentation characteristics and digestibility. Animals were assigned one of four treatment groups: control (CON), *Propionibacterium* P63 (P63), *Propionibacterium* P63 and *Lactobacillus plantarum* 115 (P63+Lp), or *Propionibacterium* P63 and *Lactobacillus rhamnosus* 32 (P63+Lr). Each strain was

administered at 10^{10} cfu/d. No change in ruminal VFA concentration was observed, and only P63 was found to impact the concentration of some milk fatty acids. pH increased on average 0.18 units in all DFM groups as compared to the control. Although the study did not demonstrate the positive response in performance as was expected, there was no negative change in the assessed parameters that may suggest a decrease in health. Similar results were observed in studies feeding *Lactobacillus acidophilus* (Raeth-Knight *et al*., 2007, Abu-Tarboush *et al*., 1996, Higginbotham *and Bath*., 1993, McGilliard and Stallings, 1997). In Weiss *et al*. (2008), dairy cows were supplemented with *Propionibacterium* P169 2 weeks before anticipated calving to 119 days in milk. Cows fed *Propionibacterium* P169 had lower concentrations of acetate and greater concentrations of propionate and butyrate compared to control cows. Treatment cows also produced similar amounts of milk with similar composition as cows fed the control diet and had similar body weights throughout the trial. Chiquette *et al*. (2008) fed *Prevotella bryantii* 25A to dairy cows in early lactation, and found that administration did not change milk yield, but tended to increase milk fat. This is in alignment with the increased acetate and butyrate concentrations observed in the rumen of treatment animals. In Chiquette *et al*. (2007), *Ruminococcus flavefaciens* NJ was fed to non-lactating dairy cows on either a high concentrate or a high forage diet daily. Cows fed *R. flavefaciens* NJ exhibited improved *in sacco* digestibility of hay in the rumen when fed as part of a high concentrate diet. Several experiments have fed *Megasphaera elsdenii* with various results on digestibility and performance, but no deleterious impacts were observed (Aikman *et al*., 2011; Hagg *et al*., 2010, Zebeli *et al*., 2012; Hagg , 2008, Kung and Hession, 1995). A *Lactobacillus*-based probiotic fed alone and in combination with *S .cerevisiae* showed no change in milk production or efficiency in early-lactation dairy cows (Boga and Gorgulu, 2007). In a meta-analysis conducted at INRA, 33 probiotic bacteria studies with or without yeast were evaluated for their impact on the production and health of dairy and beef cattle (Lettat et al., 2012). Variable performance and rument impacts were observed, however the study indicated no negative health consequences were reported. In the studies summarized above, even though the direct fed microbials did not achieve the performance response expected, there was no indication of a safety concern.

In these examples, failure of DFM supplementation or the DFM itself did not cause any harm to the fermentation characteristics of the rumen or animal well-being. In the case of *C. beijerinckii* ASCUSDY20, if the DFM failed to provide improved digestibility, rumen fermentation of treated cows would be identical to rumen fermentation of untreated cows. Since no alterations are made to the standard feeding regime when using this product, the value of the feed that would be digested and utilized for the nutrients required to sustain life is identical between the control and treated group. Animals would be fed rations that meet established nutrient requirements as recommended by the NRC for dairy cattle (NRC, 2001). Any non-performing *C. beijerinckii* ASCUSDY20 or deceased *C. beijerinckii* ASCUSDY20 would pass through the GI tract with the normal flow of digesta, providing nutrients for absorption by the animal (NRC, 2016).

In this respect, based on the results of published comparative studies, *C. beijerinckii* ASCUSDY20 will act only to support normal ruminal function of digestion of animal feed. Like other DFMs, while *C. beijerinckii* ASCUSDY20 may aid the digestion of feed, the effect is not required for the general well-being and normal performance of dairy cattle. Thus, the absence of the anticipated effect of *C. beijerinckii* ASCUSDY20 on feed digestion by dairy cattle would not have an impact on safety. ASCUS product labeling does not suggest a change in normal feeding regime, and its use would be specific for gaining additional nutritional value from a typical balanced ration. Animals would continue to be fed

rations that meet established nutrient requirements as recommended by the NRC for dairy cattle (NRC, 2001).

2.5.3 Summary

In summary it is ASCUS' understanding that the regulatory hurdle provided in §570.230(d), is not applicable to the conclusion of the generally recognized as safe substance *C. beijerinckii* ASCUSDY20, that is "failure" of the intended use will not raise a safety concern, as the intended use is to provide increased nutritive value from nutritionally adequate feeds. As such, failure would result in typical nutrient availability of the diets, as they have been formulated to meet the nutritional requirements of the animal. Should *C. beijerinckii* ASCUSDY20 fail, other members of the existing rumen microbiome will continue to ferment feed, thus supplying the animal with sufficient nutrients. Therefore, there is no regulatory requirement to provide specific utility data to support the intended use.

PART 3 – TARGET ANIMAL AND HUMAN EXPOSURE

3.1 Target Animal Exposure

3.1.1 Exposure to the Direct Fed Microbial Strain

As mentioned in Part 1, *C. beijerinckii* ASCUSDY20 spray dried powder is intended for use as a source of viable microorganisms in feed for dairy cattle. The microbial strain will be delivered as a spray dried product with starch (*C. beijerinckii* ASCUSDY20 spray dried powder, min. $4x10^6$ CFU/g) to dairy cattle either alone or in combination with other microbial strains. Examples of the conditions under which direct fed microbial products containing *C. beijerinckii* ASCUSDY20 spray dried powder may be incorporated into the diet of dairy cattle include as part of the TMR, as top-dressing to individual feeds or the daily ration, and as a component of a feed supplement. The spray dried powder will be incorporated into dairy cattle feed at the recommended use level of $1x10^7$ CFU of *C. beijerinckii* ASCUSDY20/cow/day. As mentioned in Part 2.2, the starch encapsulated product is comprised of approximately 70% modified food starch and 30% spray-dried unstandardized *C. beijerinckii* ASCUSDY20 (spore concentrate). Thus, under the conditions of intended use, dairy cattle will be exposed to around 0.75 g of the unstandardized *C. beijerinckii* ASCUSDY20 spore concentrate. No withdrawal period is considered necessary on the basis that *C. beijerinckii* ASCUSDY20 is native to the rumen of dairy cattle and as detailed in Part 6, is not expected to be pathogenic or toxigenic.

3.1.2 Exposure to the Other Components of the Starch Encapsulated Product

At the intended intake of $1x10^7$ CFU *C. beijerinckii* ASCUSDY20/cow/day, the animal will be exposed to up to 2.5 g of the spray dried powder (min. $4x10^6$ CFU/g). The spray dried powder is comprised of approximately 70% modified food starch and 30% unstandardized *C. beijerinckii* ASCUSDY20 (spore concentrate) (see Appendix 010). As mentioned in Part 2, the amount of modified food starch and spray-dried unstandardized *C. beijerinckii* ASCUSDY20 is adjusted for each batch to standardize the viable cells count. The modified food starch complies with the specifications laid down in 21 CFR §172.892 and these ingredients are generally accepted for use as starches in animal feed (see Appendix 009). At the recommended rate of incorporation of *C. beijerinckii* ASCUSDY20 spray dried powder in dairy cattle feed, animals will be exposed to approximately 1.75 g modified food starch and 0.75 g of *C. beijerinckii* ASCUSDY20 cell concentrate. Considering that the typical dry matter (DM) intake by dairy cattle will be approximately 25 kg/cow/day, the contribution of modified food starch to the daily ration of the animal will be negligible (<0.001% DM). Thus, the use of modified food starch or similar acceptable carbohydrate-based carrier, is not expected to significantly impact the nutrient intake by dairy cattle under the intended conditions of *C. beijerinckii* ASCUSDY20 spray dried powder as a source of viable microorganisms in feed.

3.1.3 Background Exposure to the Microorganism

As mentioned in Part 2, the strain was isolated from the rumen content of a healthy mid-lactation Holstein cow and in this respect, *C. beijerinckii* ASCUSDY20 spray dried powder will contribute to the native population of *Clostridium* species in the gut of the animal (see Part 6.4). *C. beijerinckii* is part of the rumen microflora and is routinely isolated from livestock feces, soil samples and silages (Sankar *et al*. 2003; Pan *et al*., 2008; Hussain and El Sanousi, 2011; Brandle *et al*., 2016; Driehuis *et al*., 2016). Thus,

while not present to a significant or intentional degree in feedstocks, background exposure by dairy cattle to *C. beijerinckii* from the environment is likely to be significant.

3.2 Human Exposure

C. beijerinckii ASCUSDY20 spray dried powder is intended for use as a supplemental source of viable microorganisms in the feed of dairy cattle. As mentioned in Part 2.1, the strain was isolated from the rumen content of a healthy mid-lactation Holstein cow and in this respect, *C. beijerinckii* ASCUSDY20 spray dried powder will contribute to the native ruminal population of *Clostridium* species (see Part 6). No transfer of viable *C. beijerinckii* ASCUSDY20 from the rumen to milk or other edible tissues is anticipated.

The strain has been unambiguously characterized as *C. beijerinckii* and whole genome sequence analysis indicates the absence of any genetic element sequences that code for virulence factors or protein toxins (see Part 2.1). As a consequence, there should be no transfer of pathogenicity or toxigenicity to milk or edible tissues through the use of *C. beijerinckii* ASCUSDY20 spray dried powder as a source of viable microorganisms in the feed of dairy cattle.

No withdrawal period is considered necessary on the basis that *C. beijerinckii* ASCUSDY20 should not impact the quality or composition of milk, or other edible tissues when used as a direct fed microbial in dairy cattle feed.

PART 4 – SELF-LIMITING LEVELS OF USE

No known self-limiting levels of use are associated with *C. beijerinckii* ASCUSDY20 spray dried powder.

PART 5 – EVIDENCE BASED ON COMMON USE BEFORE 1958

Not applicable.

PART 6 – NARRATIVE

The conclusion that *C. beijerinckii* ASCUSDY20 spray dried powder, as described herein, is GRAS under the conditions of intended use as a direct fed microbial in feed for dairy cattle is based on scientific procedures using product-specific characterization data on the microbial strain together with a body of published information on the prevalence and potential pathogenicity and toxigenicity of the *Clostridium* species.

As mentioned in Part 1.3, *C. beijerinckii* ASCUSDY20 will be provided to dairy cattle as a spray dried powder with starch, either alone or in combination with other direct fed microbials. The strain was isolated from the rumen content of a healthy mid-lactation Holstein cow and is intended as a source of commensal microorganisms. In this respect, *C. beijerinckii* ASCUSDY20 spray dried powder will contribute to the native microbial population in the rumen and the functionality of the direct fed microbial strain is considered in Part 6.1.

The safety of *C. beijerinckii* ASCUSDY20 for use as a direct fed microbial for dairy cattle is evaluated according to the guidelines developed by Pariza *et al.* (2015). These guidelines are widely accepted by the scientific community and regulatory agencies as criteria for assessing the safety of microbial cultures for consumption by humans and animals (AAFCO, 2019). In accordance with these guidelines, the safety of a microorganism without an extensive history of use in food or feed is primarily addressed by evaluating the pathogenic and toxigenic potential. In order to understand the pathogenic and toxigenic potential, the microbial strain must be fully characterized and the body of knowledge pertaining to safety based on its taxonomic unit considered. Full details of the characterization of *C. beijerinckii* ASCUSDY20 are detailed in Part 2. The microbial has been unambiguously characterized as *Clostridium beijerinckii* (see Part 2.1.4). Furthermore, whole genome sequence analysis indicates the absence of any genetic element sequences that code for virulence factors or protein toxins (see Part 2.1.8). Whole genome sequence analysis together with phenotypic testing indicate that *C. beijerinckii* ASCUSDY20 is susceptible to antimicrobials and should not increase the risk of transfer of resistance to other microorganisms (see Part 2.1.5 and 2.1.6). Testing also confirms *C. beijerinckii* ASCUSDY20 does not produce antimicrobial substances (see Part 2.1.7 and Appendix 005).

In addition to the characterization data, a body of information is available in the public domain pertaining to (a) the identity of *C. beijerinckii* (see Part 6.2); (b) the history of exposure of the species by animals and humans (see Parts 6.4 and 6.5); and (c) the potential for toxigenicity and pathogenicity (see Part 6.6). Following the decision tree established by Pariza *et al.* (2015), these data are pivotal to the safety evaluation of *C. beijerinckii* ASCUSDY20 spray dried powder and are summarized below. The Pariza *et al*. (2015) decision tree that outlines the safety evaluation is provided in Appendix 016.

6.1 Functionality

The microbial population of the rumen plays an important role in the utilization of feed by dairy cattle. Manipulation of rumen microbiota by dietary supplementation with sources of viable microorganisms is common practice in the dairy cattle industry in the U.S. in order to facilitate fermentation and contribute to the general digestive health of the animal (Yoon & Stern, 1995; Chaucheyras-Durand & Durand, 2010; El-Tawab *et al*., 2016). The contribution of bacteria to the fermentation characteristics of the rumen have been extensively evaluated in the published literature, with important functions

reported to be stabilization of the rumen pH, increase in volatile fatty acid production, reduction in ammonia concentrations, improved microbial protein synthesis and fiber digestibility(*e.g.*, McAllister et al., 2011, Nocek et al., 2002, Henning et al., 2010, Krehbiel et al., 2003, Qiao et al., 2009, Weinberg et al., 2007, Jeyanathan et al., 2019, Yoon & Stern, 1995). As mentioned in Part 2, *C. beijerinckii* ASCUSDY20 was isolated from the rumen content of a healthy mid-lactation Holstein and is expected to contribute in the same way as other bacteria to digestion and metabolism in the ruminal environment.

In particular, *C. beijerinckii* ASCUSDY20 was shown to utilize various carbon sources including simple carbohydrates (e.g., glucose and fructose) as well as reducing sugar derived from plant materials such as xylose and cellobiose (see Part 2.1). Similar phenotypes are reported in the published literature for other *C. beijerinckii* strains (*e.g.*, Zhang *et al.*, 2012; Ezeji *et al.*, 2007). Zhang et al (2012) found that *C. beijerinckii* NCIMB 8052 could ferment corncobs and produce butanol, acetone, ethanol, acetate, and butyrate. Ezeji et al. (2007) reported that *C. beijerinckii* BA101 was able to grow on major reducing sugars of lignocellulose (glucose, xylose, cellobiose, mannose, arabinose, galactose) and produce acetone, butanol, and ethanol. Thus, the microorganism has the potential to support digestion by aiding fermentation of forages and partially degraded digesta in the rumen.

Similar to other *Clostridium* species, *C. beijerinckii* ASCUSDY20 has been shown to utilize a range of monosaccharides including glucose, fructose and xylose to produce relatively high levels of butyric acid and acetic acid (Ho *et al.*, 2011). Volatile fatty acids (VFAs) are the main source of energy in ruminants and are produced predominantly through microbial fermentation of feed in the rumen (Bergman, 1990; NRC, 2001). The three major VFAs produced by anaerobic microbial fermentation in the rumen are acetate, propionate and butyrate with the relative ratios largely depending on the nature of the feed. The VFAs are readily absorbed and utilized by ruminants accounting for up to 80% of their maintenance energy requirements. Butyrate in particular acts as the major energy source for epithelial cells in ruminants and is recognized to play an important role in maintaining colonic health in the animal. Studies have also linked butyrate to the development of rumen papillary and calf gastrointestinal tracts (Weigand et al., 1975; Górka et al., 2018). Seymour *et al.* (2005) reviewed the results of 20 studies evaluating the relationship between VFAs and production-related variables in Holstein cows. The strongest associations identified were between rumen butyrate concentration, which displayed a significant positive linear regression relationship with dry matter intake, and milk yield. The authors concluded that butyrate indirectly supports the milk yield and production although the relationship is complex. Similarly, a number of other studies in the published literature indicate that butyrate can support the general production performance of the animals (Rook and Balch, 1961; Huhtanen *et al.*, 1993; Miettinen and Huhtanen, 1996). Similarly, acetate is considered essential for milk fat production and low levels of rumen acetate have been reported to lead to depressed milk fat content (Bergman, 1990; Gäbel *et al.*, 2002; Aluwong *et al.*, 2010). The role of VFAs as energy sources for dairy cattle also is supported by the existing food additive listing for the ammonium or calcium salts of isobutyric acid, iso-valeric acid, 2-methylbutyric acid and n-valeric acid as sources of energy in dairy cattle feeds under 21 CFR §573.914.

C. beijerinckii can also undergo mixotrophic growth to recapture carbon during fermentation processes. Sandoval-Espinola et al (2017) monitored biogas availability and the transcriptomes of *C. beijerinckii* in batch fermentation systems. The study found that in the presence of external electron sinks (eg.,

CO/CO2), the production of acetyl-coA along with the acetone-butanol-alcohol pathway in *C. beijerinckii* lead to better sugar utilization and could recover 17-27% more carbon. This suggests that *C. beijerinckii* may play a unique role in improving sugar utilization and carbon-energy recapture in rumen.

Taken together, these examples of the potential functionality of anaerobic *Clostridium* species in the rumen support the proposed role of *C. beijerinckii* ASCUSDY20 as a source of viable microorganisms in the diet to positively influence the production of VFAs and general colonic health of the animals. While *C. beijerinckii* ASCUSDY20 may contribute to the native population of *Clostridium* species in the gut of the animal, the technical function has no bearing on the safety when used as a direct fed microbial in feed for dairy cattle. Should *C. beijerinckii* ASCUSDY20 fail, other members of the existing rumen microbiome will continue to ferment feed, thus supplying the animal with sufficient nutrients. On this basis, no further demonstration of the technical effect (utility) of *C. beijerinckii* ASCUSDY20 was required for the safety evaluation (see Part 2.5).

6.2 Identity

The genus *Clostridium* consists of a heterogeneous set of species which are not phylogenetically coherent. Many species were assigned to the genus based only on their being gram positive anaerobic rods which are capable of endospore formation. Phylogenetic and comparative analyses indicate that of the >150 *Clostridium* species identified, fewer than half are part of cluster I, the distinct cluster in the 16S rRNA tree which are generally regarded as the true representatives of the genus *Clostridium* and which includes *C. beijerinckii* (Johnson & Francis, 1975; Collins *et al*., 1994; Stackebrandt *et al*., 1999; Gupta & Gao, 2009; Lawson & Rainey, 2016; Udaondo *et al*., 2017). *Clostridium* cluster I is recognized as *Clostridium sensu stricto* and includes the medically important *Clostridium botulinum* but not *Clostridium difficile*. The species assigned to *Clostridium* cluster I are metabolically and physiologically diverse species capable of utilizing carbohydrates and peptones to produce organic acids and alcohols. The G+C content of cluster I species varies from between 22 and 37 mol%, and the 16S rRNA gene sequence similarities range from 92 to 99% (Wiegel *et al*., 2006; Rainey *et al*., 1993).

In the past, *Clostridium* species were extensively used for the industrial production of butanol and acetone from starch-based substrates (Jones and Woods, 1986; Jones and Keis, 1995; Keis *et al*., 2001). The first strains isolated and developed for large scale production of these solvents were identified as *Clostridium acetobutylicum* but were later assigned to four species, *C. acetobutylicum*, *C. beijerinckii*, *Clostridium saccharoperbutylacetonicum* and *Clostridium saccharobutylicum* (Johnson *et al*., 1997; Keis *et al*., 1995; Wilkinson and Young, 1995; Keis *et al*., 2001). Similarly, strains historically assigned to the species *Clostridium butylicum* have been subsequently shown to members of *C. beijerinckii* (George and Chen, 1983).

Additionally, some strains originally designated as *C. butyricum* have been renamed *C. beijerinckii*. While challenging to distinguish phenotypically, these species can largely be (Cummins & Johnson, 1971; Ikeda *et al*., 1998) differentiated based on electrophoretic patterns of cellular proteins or by testing nutritional requirements (Brandle *et al*., 2016).

From the perspective of the safety assessment, it is therefore acknowledged that some strains of *C. beijerinckii* were formerly classified as *C. acetobutylicum*, *C. butylicum* and *C. butyricum* and all species were included in the literature search and subsequent review of published information.

6.3 Literature Search

A comprehensive literature search was conducted in order to identify all publicly available information pertaining to the safety of *C. beijerinckii* for the intended use as a source of viable cells for dairy cows. As mentioned in Part 6.2, all potential nomenclature was included in the literature search (*i.e.*, *Clostridium acetobutylicum*, *Clostridium butylicum, Clostridium butyricum* and *Clostridium beijerinckii*) and details of the search strategy are provided in Appendix 017.

6.4 Natural Occurrence

6.4.1 Prevalence in Animals

C. beijerinckii is ubiquitous in nature and routinely isolated from livestock feces and soil samples (Sankar *et al*. 2003; Pan *et al*., 2008; Hussain and El Sanousi, 2011; Brandle *et al*., 2016; Driehuis *et al*., 2016). It was one of the major populations of butyric acid bacteria isolated in 296 samples of soil, maize and grass silage, dairy cow feces and farm tank milk collected from dairy farms in the Netherlands (Driehuis *et al*., 2016). Similarly, in a study by Hussain *and El sanousi.,* 210 fecal samples were collected from 7 different animals (cattle, sheep, goats, camels, horses, donkeys, and chickens) to investigate the prevalence of *Clostridium*-like species. The prevalence of *C. beijerinckii* among these samples was 3.3%(Hussain and El Sanousi, 2011). Isolation and characterization of xylanolytic solventogenic bacteria from cow rumen fluid identified 5 strains of *C. beijerinckii* to be present, in combination with *C. acetobutylicum*, *C. butyricum* and *C. bifermentans* strains (Sankar *et al*., 2003). Dutta, et al. (1983) isolated members of Clostridia, Lactobacilli, and Streptococci from pigs, cattle, and poultry to investigate their antibiotic susceptibility. The group was able to isolate 3 *C. beijerinckii* strains, and found that all three did not possess any acquired antimicrobial resistance.

A total of 207 different strains of *C. beijerinckii* have been isolated, sequenced, and analyzed in the JGI genome portal to date (https://genome.jgi.doe.gov/portal/). Many strains within this database represent industrial fermentation strains, however, several of the isolates were obtained from rumen content as part of the Hungate1000 project (http://www.rmgnetwork.org/hungate1000.html; Seshadri *et al.,* 2018*)*. The Hungate1000 project attempted to isolate taxonomically diverse microorganisms from rumen content. In total, 410 bacteria and archaea were isolated, representing ~75% of the genera present in the rumen. Similarly, the Global Rumen Census found that Clostridiales were present in all ruminants surveyed, and were found to comprise 15.3% of the rumen microbial community on average (Henderson *et al.,* 2015). The *Clostridium* genus was found to comprise an average of 0.71% of the rumen microbial community. *Clostridium* was detected in 98% of the 742 samples from 32 animal species across 35 countries. The samples in which *Clostridium* was not detected were primarily male crossbreed cattle being fed 100% concentrate diets. Thus, *Clostridium* and *C. beijerinckii* are highly prevalent as a commensal organism of the rumen microbial ecosystem.

6.4.2 Microbiome Safety

The rumen microbiome is crucial for the digestion of feed and supplies necessary nutrients to ruminants (Faichney, 1996 ; Huws et al., 2018). The rumen hosts a diverse group of microorganisms that work closely to degrade plant materials. The fermentation process converts nearly all dietary carbohydrates to volatile fatty acids (VFA), predominantly butyrate, acetate, and propionate. It has been widely

recognized that the rumen VFAs are crucial for digestive system development and animal carbon and nitrogen needs [storm and Orskov, 1984; Wallace et al., 1997; Broudiscou and Jouany, 1995; Weigand et al., 1975; Górka et al., 2018; Leng et al., 1967; Young, 1977; Huws et al., 2018; Bach et al., 2005; Edwards et al., 2008.]. Direction infusion of VFAs into the rumen can also improve animal performances. For example, direct infusion of butyrate into the rumen increased milk fat production without changing milk yield (Huhtanen *et al*., 1993) and direct infusion of propionate into the rumen increased milk protein production (Rook and Balch, 1961).

The contribution of DFMs to the fermentation characteristics of the rumen has been extensively evaluated (Elghandour *et al*., 2015). Specific species within the genera *Lactobacillus, Bifidobacterium, Enterococcus, Streptococcus, Bacillus, Propionibacterium, Megasphaera and Prevotella* have been fed to animals (Nocek *et al*., 2002; Yoon and Stern, 1995; Ghorbani *et al*., 2002; Stein *et al*., 2006; Yang *et al*., 2004; Nagaraja *et al*., 1997; Chiquette *et al*., 2008; Mohammed *et al*., 2012; Weiss *et al*., 2008; Aikman *et al*., 2011). There are several studies, for example, that describe the fermentation patterns and feed digestibility of ruminants fed a standard diet supplemented with a DFM compared to ruminants only on a standard diet. Feeding of *Lactobacillus plantarum* via silage in Mohammed *et al*., (2012) showed no changes in production, but no deleterious effects on the animal. Similar results were observed in studies feeding *Lactobacillus acidophilus* (Raeth-Knight *et al*., 2007; Abu-Tarboush *et al*. 1996; Higginbotham and Bath, 1993; McGilliard and Stallings, 1997). In Weiss *et al*. (2008), dairy cows were supplemented with *Propionibacterium* P169 2 weeks before anticipated calving to 119 days in milk. Cows fed *Propionibacterium* P169 had lower concentrations of acetate and greater concentrations of propionate and butyrate compared to control cows. Treatment cows also produced similar amounts of milk with similar composition as cows fed the control diet and had similar body weights throughout the trial. Chiquette *et al*. (2008) fed *Prevotella bryantii* 25A to dairy cows in early lactation, and found that administration did not change milk yield, but tended to increase milk fat. This is in alignment with the increased acetate and butyrate concentrations observed in the rumen of treatment animals. In Chiquette *et al*. (2007), *Ruminococcus flavefaciens* NJ was fed to non-lactating dairy cows on either a high concentrate or a high forage diet daily. Cows fed *R. flavefaciens* NJ exhibited improved *in sacco* digestibility of hay in the rumen when fed as part of a high concentrate diet. Several experiments have fed *Megasphaera elsdenii* with various results on digestibility and performance, but no deleterious impacts were observed (Aikman *et al*., 2011; Hagg *et al*., 2010; Zebeli *et al*., 2012; Hagg , 2008; Kung and Hession, 1995).

Bacteria catabolism also plays an important role in animal nutrient cycling. Hoogenraad et al (1969) studied how model organisms of gram-negative bacterium (*Escherichia coli*) and gram-positive bacterium (*Bacillus subtilis*) were utilized in adult sheep digestive tract. The study found that the freeze-dried whole cells of either bacteria were quickly digested by rumen microbiome and cell carbons were incorporated into VFAs. A large amount of the bacterial carbon (70%) was captured by the host animal. Bacterial whole cells and cell components such as cell wall and content were also readily digested and metabolized in abomasum. Despite the common belief that gram-positive cells are more difficult to metabolize due to the presence of peptidoglycan, 73-86% of *B. subtilis* cell and cell component carbon was captured by the animal through lower gut digestion. In contrast, a smaller portion (66-78%) of *E. coli* carbon was captured by the host animal. Notably, although *B. subtilis* cells contain a greater amount of glucose than *E. coli*, a much greater amount of *E. coli* carbon was incorporated into the lower gut glucose pool. The findings suggest that bacteria turnover in ruminant digestive tract is an important process and supplying building blocks to support the host metabolism.

The rumen microbiome is dynamic. Moraïs and Mizrahi (2019) summarized that multiple microbial community states exist within the rumen depending on the rumen metabolic needs. The flow of metabolites and energy were passed on from one functional group to the next rather than from one group to another. Thus, microbial interactions could drive larger changes in overall fermentation patterns and identifying the optimal microbial interactions could improve digestibility (Weimer, 2015). Published studies showed that diet contributes to the greatest rumen microbiome shifts observed (Kumar et al., 2015; Deusch et al., 2017; Mizrahi and Jami, 2018; Belanche et al., 2019; Johnson and Johnson, 1995; Brulc et al., 2009; Carberry et al., 2014). Under the same diet, the addition of DFMs does not change the rumen microbiome significantly but can improve rumen digestibility. Westergaard (2015) fed a *Bacillus pumilus* DFM to 21 dairy cows and compared the composition of their rumen microbiomes to 22 control animals. The study reported an insignificant increase in Firmicutes from 14.1% to 15.8% and an insignificant decrease of Bacteroidetes from 64.1% to 62.3% in rumen fluid of animals received the DFM. Its companion study reported that the animals receiving the DFM were more efficient at feed conversion (ECM:DMI) than the control animals, although not significantly ($p = 0.06$) (Luan et al., 2015). Le and colleagues (2016) conducted a study comparing the growth performance of 4 week-old dairy calves with and without DFM *Bacillus amyloliquefaciens* in feed. *B. amyloliquefaciens* was administered daily for 9 weeks to 12 calves and another 12 calves were used as controls. The study found that dairy calves administered *B. amyloliquefaciens* gained 20% more weight and suffered less diarrhea than the control group. Notably, its companion study observed that *B. amyloliquefaciens* supplementation did not change the dairy calf rumen microbiomes significantly, despite confirmation of colonization of the DFM strain in rumen (Schofield et al., 2018). In another study, Fomenky and colleagues (2018) compared the rumen digesta microbiome of pre- (33 days old) and post-weaned calves (96 days old) fed with control diet alone and control diet supplemented with *S. cerevisiae* (SCB) or *L. acidophilus* (LA) (8 per treatment). The study found that supplementing DFMs did not significantly change the overall rumen microbial community structure, where the p-values for alpha diversity indices ranged from 0.051 to 0.992 and the p-value for beta diversity (PERMANOVA) was 0.512. The study also predicted that pathways involved in lipid and protein metabolism and cellular processes were more abundant in pre-weaned rumen administered DFMs. Once weaned, no predicted pathways in rumen digesta were significantly different between control and LA fed animals. Riboflavin metabolism was the only significantly more abundant pathway in SCB fed animal rumen digesta than control. These studies demonstrated that DFMs could promote better microbial interactions and improve the overall rumen feed digestibility without significantly changing microbial community structures.

The use of *C. beijerinckii* to facilitate the digestion of complex carbohydrates such as starch and lignocellulose of animal feed within the rumen utilizes enzymes related to amylase, xylanase, and beta-gulcanase. *C. beijerinckii* has been frequently isolated from hemicellulose rich environments (Jones and Woods, 1986; Trudeau *et al.,* 1992; Noparat *et al.,* 2011; Thi Hoang *et al.,* 2020). Studies conducted on different *C. beijerinckii* strains revealed a high level of amylase production when grown on starch (Qureshi and Blaschek, 2001; Taguchi *et al.,* 1993). Crittenden *et al*., 2002 also reported that *C. beijerinckii* is able to ferment important dietary fibers such as xylan and beta-glucan. These fibrolytic enzymes are important for plant material digestion (Rode *et al*., 1999; Beacuchemin *et al*., 2002). *C. beijerinckii* is frequently found in rumen content and silage globally (Kameshwar *et al*., 2019; Avila and Carvaho, 2019; Thi Hoang *et al*., 2020; Seshadri *et al*., 2018) and is also commonly found in monogastric animals (Vanbelle *et al.,* 1990, Prosekov*et et al.,* 2015). Although it has not been used as a DFM in ruminants, *C. beijerinckii* is a common commensal rumen microorganism.

ASCUS Biosciences conducted a series of experiments in order to obtain a representative sampling of the rumen microbial community in dairy cows under farm-like conditions in the U.S. The full study report is provided in Appendix 018. In two general survey experiments, animals were cannulated and sampling conducted across the different regions of the rumen over a number of days. In a third study, *C. beijerinckii* ASCUSDY20 along with another native rumen microorganism was administered to lactating dairy cows via injection and rumen sampling conducted over a number of days. In all of the experiments, the typical abundance of *C. beijerinckii* specifically, in the rumen of dairy cows was found to vary from approximately 0.0001% to 2% of the bacterial population. General observations indicated that all animals were in good health. *C. beijerinckii* ASCUSDY20 inoculation was not observed to have a significant impact on the ruminal microbial community. Taken together, these studies provide corroborative experimental evidence that *C. beijerinckii* is naturally abundant in the rumen of dairy cattle and not associated with any health concerns.

6.4.3 Environmental Occurrence

C. beijerinckii occurs extensively in nature. It can be found in a variety of environments, including soil (Wu *et al.,* 2019; Bhutada and Shrivastava, 2018; Dobbin *et al.,* 1999; Montoya *et al.,* 2000; Abd-Alla *et al.* 2015), insects (Taguchi *et al.,* 1993; Cruden *et al.,* 1987) wastewater (Fonesca *et al.,* 2019; Rosewarne *et al.,* 2013), manure (Ostling and Lindgren. 1991; Scott *et al.,* 2018; An *et al.,* 2014; Pandey *et al.,* 2009; Islas-Espinoza *et al.,* 2012; Lin *et al.,* 2013; Scott and Murano 2007), as well as anaerobic sludge (Fonesca *et al.*, 2016; Pan *et al.,* 2008; Scott and Murano, 2007; Zhao *et al.,* 2011). A *C. beijerinckii* that is capable of coupling dechlorination of pentachlorophenol with Fe(III) reduction has been isolated from rice paddy fields in Zhejiang, China (Xu *et al.,* 2013). Eighteen different strains of *C. beijerinckii* have been deposited in the open collection of the American Type Culture Collection (ATCC) to date. Similarly, a total of 207 different strains of *C. beijerinckii* have been isolated, sequenced, and analyzed in the JGI genome portal to date (https://genome.jgi.doe.gov/portal/). Many strains within this database represent industrial fermentation strains, however, several of the isolates were obtained from rumen content as part of the Hungate 1000 project (http://www.rmgnetwork.org/hungate1000.html; Seshadri *et al.,* 2018).

Clostridium species are extensively used for the industrial production of butanol and acetone from starch-based substrates (Jones and Woods, 1986; Jones and Keis, 1995; Keis *et al*., 2001; Valdez-Vazquez *et al*., 2015). The first strains isolated and developed for large scale production of these solvents were identified as *Clostridium acetobutylicum* but were later assigned to four species, *C. acetobutylicum*, *C. beijerinckii*, *Clostridium saccharoperbutylacetonicum* and *Clostridium saccharobutylicum* (Johnson *et al*., 1997; Keis *et al*., 1995; Wilkinson and Young, 1995; Keis *et al*., 2001). New strains of these species (including *C. beijerinckii*) capable of more efficient industrial production of solvents, particularly acetone, butanol, and ethanol, are still being screened for in environmental samples for industrial applications (Abd-Alla *et al.* 2015). Abd-Alla, *et al.*, for example, isolated 107 *Clostridium* isolates from agriculture soil, several of which were *C. beijerinckii*.

6.4.4 Section Summary

C. beijerinckii occurs widely in the environment and is prevalent as a commensal member of the rumen microbiome. Supplementation of the diet with *C. beijerinckii* ASCUSDY20 will not negatively impact the function of the rumen nor negatively impact the well-being of the animal.

6.5 History of Use in Manufacture of Food and Feed Ingredients

Along with *C. butyricum*, *C. sporogens* and *C. tyrobutyricum*, the species is one of the anaerobic spore forming, butyric acid bacteria reported to spoil foodstuffs, including dairy products, meat products, and fresh and canned vegetables (EFSA, 2005). These butyric acid bacteria have been frequently isolated from milk and cheeses, where *C. tyrobutyricum* is considered the primary cause of the late-blowing effect (Drouin and Lafreniere, 2012; Brandle *et al*., 2016). The expected exposure of Clostridial spores in milk is < 10^1 – 10^2 spores/gram (Pahlow *et al.* 2003, Queiroz *et al.,* 2018). *Clostridium* spp. are common livestock commensal microorganisms, and thus animal feces are the primary source of *Clostridium* contamination of milk as feces can readily contaminate the cow's udder leading to spores entering the milk (Pahlow *et al.* 2003). While these species are associated with spoilage, they are not generally considered to pose a safety concern to human health (Ghoddusi and Sherburn, 2010).

C. beijerinckii has been proposed as a downstream biorefinery process to follow fermentation of seaweed for animal feed (Bikker *et al*., 2016). *Ulva lactuca*, a type of green seaweed, can be fractionated and the subsequent liquid fraction can leverage *C. beijerinckii* for fermentative production of chemicals. Similarly, *C. beijerinckii* can also be found in silage. The presence of *Clostridium* spp. in silage is mainly from soil contamination or slurry application and this can lead to contamination of animal feeds and products. It has been reported that the central part of a corn silage bunker silo had less than 10^3 spores of *Clostridium* spp. per gram of silage, whereas the peripheral area had more than 10^6 spores per gram (Queiroz *et al.,* 2018).

Thus, although *C. beijerinckii* and other closely related members of *Clostridium* are typically associated with spoilage in feed and food, they are generally always present in these environments at low abundance (Queiroz *et al.,* 2018). Despite the continuous consumption of these low levels of spores, no deleterious impacts on health are observed (Ghoddusi and Sherburn, 2010).

6.6 Toxigenicity and Pathogenicity

The potential pathogenicity of *Clostridium*, including *C. beijerinckii*, is widely reported in the published literature. Unlike known pathogenic *Clostridium,* such as *C. difficile* and *C. perfringens, C. beijerinckii* is considered an opportunistic pathogen in humans and animals. The American Type Culture Collection (ATCC) lists *C. beijerinckii* as BSL-1, indicating that it is a low-risk microorganism that poses little to no threat of infection in healthy humans and animals. DSMZ also classifies *C. beijerinckii* as BSL-1.

Large scale genome analysis of both pathogenic and nonpathogenic *Clostridium* has revealed that there were only 169 orthologous gene groups shared by all *Clostridium* strains, and a pangenome of 22,668 genes (Zhou *et al.,* 2014). This finding suggests that *Clostridium* contains a diverse gene pool that enables adaptation to different environments. Many of the clostridia are ubiquitously found in soil and in the gastrointestinal tract of healthy animals, including humans. Clinical cases are only rarely seen (Moore, and Lacey, 2019). Disease generally occurs when there is some tissue damage to the skin or gastrointestinal tract that results in proliferation of *Clostridium*. This bimodal lifestyle, split between a free-living existence in the environment and host colonization and pathogenesis, is reflected in the genomes of the Clostridia. The spore-forming machinery encoded Clostridial genomes increases resilience and survival in the environment, and the wide array of toxins and degradative enzymes that are encoded assist in nutrient scavenging. Many of the toxins produced by Clostridia are encoded on

large plasmids (Moore,and Lacey, 2019). The genomes of *Clostridium* tends to be larger, suggesting that they are generalists that can survive in a range of ecological niches and use a wider variety of substrates for growth (Suen, *et al.* 2007). Different levels of genomic plasticity have been noted amongst clostridial species, with sequence variation being driven primarily by mobile elements, chromosomal rearrangement, deletions and insertions, and SNPs (Moore and Lacey, 2019). The genomes of true clostridia (cluster I), including *C. beijerinckii,* were found to be more stable than other clusters of clostridia, with plasmids playing a large role in determining strain variation. Large conjugative toxin gene carrying plasmids, in particular, often determine the virulence of *Clostridium* isolates (Moore and Lacey, 2019).

While *Clostridia* are part of the commensal microbiota, epidemiology studies have implicated some species with human disease. Reports of *C. beijerinckii* causing endophthalmitis secondary to an initial injury have been reported (Newton, *et al.* 1999)

Clostridium have also been implicated as one of the causative agents of necrotizing enterocolitis in premature infants (EFSA, 2014; Cassir *et al*., 2016; Schönherr-Hellec *et al*., 2018). No studies were identified in the published literature associating *C. beijerinckii* with necrotizing enterocolitis, but there are some rare instances of the closely related species, *C. butyricum*, causing human disease, including necrotizing enterocolitis in premature infants when associated with very specific risk factors (Howard *et al*., 1977; Sturm *et al*., 1980; Caya and Truant, 2000; Gardner *et al*., 2008; Morowitz *et al*., 2010; EFSA, 2014; Cassir *et al*., 2016). For example, Caya and Truant (2000) reported the diagnosis of 53 infant pediatric patients with *clostridial* bacteremia, of which 25.9% cases were identified as being associated with *C. butyricum*. Necrotizing enterocolitis-related lesions were also induced by *C. butyricum* in chicken and quail experimental models (Popoff and Dodin, 1985; Butel *et al*., 1998; Waligora-Dupriet *et al*., 2009). The toxigenic mechanism responsible for the pathogenesis of necrotizing enterocolitis is not fully understood but β -haemolysin production has been proposed as a primary virulence factor (Cassir *et al*., 2015). The ability of the host to ferment lactose and the production of high levels of butyric acid by intestinal *C. butyricum* are also suggested by other researchers in the development of necrotic lesions (Waligora-Dupriet *et al*., 2009; Azcarate-Peril *et al*., 2011; Cassir *et al*., 2016). Recently, a systematic characterization of necrotizing enterocolitis and control strains was conducted by Schönherr-Hellec *et al*., (2018) suggested the existence of a specific signature associated with pathogenicity and that a unifying causative mechanism for development of the disease may be activation of an innate immune response. The presence of neuraminidase was investigated in several *Clostridium* strains belonging to *C. butyricum, C. difficile,* and *C. beijerinckii* (Popoff and Dodin, 1985). Neurominidase-production has been implicated in the pathogenesis of neonatal necrotizing enterocolitis. Of the 98 strains tested, including 16 *C. beijerinckii*, only a few *C. butyricum* strains were found to produce neuraminidase.

The pathogenic Clostridial species with the greatest impacts on human and animal health are *C. difficile, C. perfringens, C. tetani, C. botulinum*, and other species that produce botulinum toxins (Moore and Lacey, 2019). The clostridial species that produce botulinum toxins are also well studied. Botulism, caused by botulinum neurotoxin (BoNT) is most frequently associated with *Clostridium botulinum* but can occasionally arise from *C. butyricum* (Peck, 2002; Cassir *et al*., 2016). The disease can occur when BoNT-producing *Clostridium* species colonize the intestine or wounds of animals or humans and subsequently produce the toxin, or alternatively, when contaminated foods are ingested in which the toxin has already been formed. No reports of BoNT-producing *C. beijerinckii* were identified in the published literature. However, as mentioned above, a minority of closely-related *C. butyricum* strains

harbor the *BoNT/E* gene and are capable of producing botulinum neurotoxin E (Hauser *et al*., 1992; Peck, 2002; Dupuy *et al*., 2006; Cassir *et al*., 2015; EFSA, 2011; Ghoddusi and Sherburn, 2010). The operon harboring the *BoNT/E* gene in *C. butyricum* is reportedly similar to that carried by type II E toxin-producing *C. botulinum* strains consistent with horizontal transfer events and recombinant events mediated by mobile genetic elements. Toxigenic *C. butyricum* have been responsible for a number of cases of infantile and infantile-like botulism arising from the production of the toxin in the intestine after germination and colonization of *C. butyricum* (*e.g*., Abe *et al*., 2008; Aureli *et al*., 1986; Fenicia *et al*., 1999 and Dykes *et al.,* 2015). The reports of infantile-like botulism are generally isolated cases (single or few cases) in immunocompromised individuals (*e.g*., following intestinal surgery). Likewise, cases of food-borne botulism from the ingestion of *C. butyricum*-derived toxin type E are rare (Anniballi *et al*., 2002; Peck, 2002). The first report of an outbreak of food-borne botulism caused by toxin type E produced by *C. butyricum* was in China in 1994, when 6 people became ill after consuming a home-made salted and fermented paste of soybeans and wax gourds (Meng *et al*., 1997 and 1999). Subsequently, *C. butyricum* has been implicated in two earlier outbreaks of botulism following the consumption of soybeans in China and an incident in which 34 students contracted botulism after eating gram-flour based crisps in India (Peck, 2002).

Overall, the available data indicate that *C. beijerinckii* strains are not associated with botulinum toxin type E production or with pathogenicity in humans or animals. These data are consistent with the whole genome analyses (see Part 2.1.8) which confirmed the absence of the botulinum toxin biosynthetic operon.

6.6.1 Summary

Overall, the available information indicates that *C. beijerinckii* is a prevalent organism in the environment and in the microbiome of animals. Although generally benign, it can be an opportunistic pathogen and has been associated with infections in immunocompromised humans and animals. Despite the wide prevalence and exposure to *C. beijerinckii* in the environment and food, the number of reported cases of invasive infection caused by *C. beijerinckii* is low (see Appendix 17). As indicated in Part 2.1.8, interrogation of the whole genome sequence of *C. beijerinckii* ASCUSDY20 did not reveal the presence of any genetic element sequences that code for virulence factors or protein toxins.

6.7 Studies in Target Animals

The determination that *C. beijerinckii* ASCUSDY20 is GRAS under the intended conditions is based on product-specific characterization data together with the body of information in the published literature. The organism is a commensal rumen organism.

Two investigative studies in which dairy cattle were inoculated with *C. beijerinckii* ASCUSDY20 were conducted by ASCUS Biosciences corroborate the target animal safety determination. These unpublished studies, summarized in turn below, were of short duration and were designed primarily to assess the potential value of *C. beijerinckii* ASCUSDY20 and other microorganisms as potential direct fed microbials. In both studies, *C. beijerinckii* ASCUSDY20 was administered via ruminal cannulation in combination with at least one other microorganism. Overall, the study findings provide corroborative evidence that *C. beijerinckii* ASCUSDY20 is well-tolerated and without adverse effects but are of limited relevance to the assessment of safety.

6.7.1 Study DUS1601 (Unpublished Study Report – Appendix 019)

In the first study, 16 multiparous Holstein cows were individually housed for a total of 52 days at DairyExperts (Tulare, CA). Animals underwent ruminal cannulation surgery followed by a 10-day recovery and adaptation period. After this time, the cows were allocated at random to one of 2 treatment groups (8 cows/treatment; 1 cow/replicate) and administered either buffer (control) or buffer containing a selection of microorganisms including *C. beijerinckii* ASCUSDY20 once daily via ruminal cannulation for 32 days. Cows were monitored for a further 10 days after the last inoculation day. Observations included feed intake, body weight, milk yield, rumen digesta microbial content and pH, and fecal analysis. No adverse effects were reported for any of the variables measured over the duration of the study. Overall, the findings of the study corroborate the safety of *C. beijerinckii* ASCUSDY20 for dairy cattle.

6.7.2 Study DUS1701 (Unpublished Study Report – Appendix 020)

In the second study, 32 Holstein cows approximately 100 days in milk were assigned to one of 3 treatment groups (8 cows/treatment; 1 cow/replicate; mean days in milk, approximately 100). Cows were administered a buffer containing either 2 (treatment group 1), 3 (treatment group 2) or no (treatment group 3; control) microorganisms once daily via direct injection into the rumen for 28 days. The microorganisms fed to the cows in treatment groups 1 and 2 included *C. beijerinckii* ASCUSDY20. Fecal samples were taken at Days 1, 8, 16, 24 and 28 and analyzed for neutral detergent fiber (NDF), acid detergent fiber (ADF) and DM content. Rumen contents also were sampled from each cow at Days 1, 8, 18, 24 and 28. From Day -7 to Day 38 of the study, observations included milk yield, general health and clinical udder evaluation.

Abnormal clinical udder findings and abnormal clinical health observations were considered minimal, incidental and not related to treatment for the duration of the study. No adverse effects were reported in any of the other variables measured for the duration of the study. Overall, the findings of the study corroborate the safety of *C. beijerinckii* ASCUSDY20 for dairy cattle.

6.8 Summary and Critical Evaluation of Target Animal Safety

C. beijerinckii is a commensal bacteria in the gut of humans and animals. It occurs widely in soil and is commonly found in food. No reports of toxigenicity or pathogenicity associated with *C. beijerinckii* were identified in the published literature. However, a minority of strains of the closely related species *C. butyricum* is capable of producing botulinum-type toxin, and there are occasional reports of toxigenicity and pathogenicity arising from the species. ASCUS Biosciences has conducted an assessment of *C. beijerinckii* ASCUSDY20 and confirmed the absence of any genes encoding for toxin production or other virulence factors known to be associated with pathogenicity (see Part 2.1.8). Furthermore, the susceptibility of *C. beijerinckii* ASCUSDY20 strains to antibiotics of veterinary and pharmaceutical relevance, and the absence of antimicrobial production has been demonstrated (see Parts 2.1.6 and 2.1.7, and Appendices 004 and 005). Collectively, these data indicate that *C. beijerinckii* ASCUSDY20 spray dried powder (the notified substance) should not be associated with any safety concerns for dairy cattle under the intended conditions of use as a direct fed microbial.

6.9 Summary and Critical Evaluation of Human Food Safety

As mentioned in Part 3.2, no transfer of viable *C. beijerinckii* ASCUSDY20 from the rumen to milk or other edible species is anticipated under the conditions of intended use as a direct fed microbial in the feed of dairy cattle. Furthermore, the strain has been unambiguously characterized as *C. beijerinckii* and whole genome sequence analysis indicates the absence of any genetic element sequences that code for virulence factors or protein toxins (see Part 2.1.8). The absence of pathogenicity or toxigenicity is supported by the ubiquitous nature of *C. beijerinckii* and its natural occurrence in the rumen and gastrointestinal tract of animals. Taken together, these data indicate that *C. beijerinckii* ASCUSDY20 spray dried powder should not be associated with any human food safety concerns under the intended conditions of use as a direct fed microbial in the feed of dairy cattle.

In this safety assessment we identified, discussed and placed into context data and information that are, or may appear to be inconsistent with the GRAS status (21 CFR 570.250(c)(1)). Based on the preponderance of evidence, ASCUS' conclusion of safety is scientifically justified.

PART 7 – LIST OF SUPPORTING DATA AND INFORMATION IN YOUR GRAS NOTICE

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To: Animalfood-premarket
Cc: Howard@ascusbiosciences.com
Subject: Appendices to ASCUS Clostridium beijerinckii AGRN
Attachments: Appendix 13.zip; App_012 Analytical Methods and Validation Reports.zip; App_003D_Housekeeping_gene_comparison-3 16Jan2020.zip; App_009 Raw Material Specifications Confidential.zip

Thank you for the discussion this morning on the appendices supporting the AGRN for Clostridium beijerinckii. It appears when I downloaded the appendices from the shared website, the download was not complete. I apologize for this inconvenience and I appreciate your permitting us to provide the missing information by email.

This email contains appendix 13, appendix 12, appendix 9, and appendix 3D.

I will send a few emails with the needed information.

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Appendix 003D

Appendix 003E: Housekeeping Gene Comparison for *Clostridium beijerinckii* ASCUSDY20

To further elucidate the taxonomy of *Clostridium beijerinckii* ASCUSDY20, DNA sequence comparison between four housekeeping genes was conducted for the related species. The four genes in the comparison were ribonuclease P RNA (rnpB), ATP synthase alpha subunit (atpA), RNA polymerase alpha subunit (rpoA), and phenylalanyl-tRNA synthetase (pheS). Gene sequences were downloaded from the NCBI database. MUMmer was used to generate the sequence alignments for the gene comparison (Kurtz et al. 2004). The results are summarized in Table 1.

Table 1: Comparison of Housekeeping Genes in Dairy-20 and related *Clostridia* species.

	Housekeeping genes							
Related species	pheS Identity	Coverage	rnpB Identity	coverage	rpoA Identity	Coverage	atpA Identity	Coverage
C. beijerinckii	98.8	99.9	100.0	99.7	100.0	99.9	99.8	99.9
C. diolis	98.7	99.9	100.0	99.7	99.8	99.9	99.7	99.9
C. saccharoperbutyl-acetonicum	89.9	99.9	91.2	63.0	96.3	99.9	88.0	99.9
C. butyricum	0	0	0	0	92.3	98.2	83.7	99.9

Comparison of all four housekeeping genes gave the best match for *C. beijerinckii*, with greater than 98.8% identity.A very close match was also obtained for *Clostridium diolis*, which based on the limited evidence may be a strain of *C. beijerinckii.*

Kurtz S, A Phillippy, AL Delcher, M Smoot, M Shumway, C Antonescu and SL Salzberg. 2004.Versatile and open software for comparing large genomes. *Genome Biology*, 5(2), p.R12

Appendix 009 (all)

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Personalized PDF Catalog
Catalogue Generated March 27, 2019

Acetic acid glacial 99.7-100.5% USP, FCC, ACS,

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Danger

Synonyms: Ethanoic acid, Glacial acetic acid, Methanecarboxylic acid, Vinegar acid

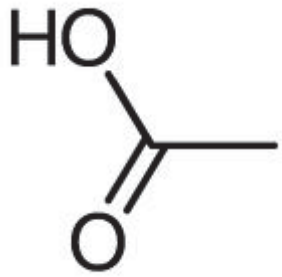
Only Class 3 Solvents are likely to be present. Residual concentration of all Class 3 Solvents is <0.5%.

Elemental Impurities (USP 232, EP 5.20) - Information on elemental impurities for this product is available the associated Product Regulatory Data Sheet and elemental impurity profile report.

Caution: Preserve in tight containers, and store at room temperature

Formula: H_3CCOOH
MW: 60,05 g/mol
Boiling Pt: 118 °C (1013 hPa)
Melting Pt: 17 °C
Density: 1,05 g/cm³ (20 °C)
Flash Pt: 39,4 °C (closed cup)
Storage Temperature: Ambient

MDL Number: MFCD00036152
CAS Number: 64-19-7
EINECS: 200-580-7
UN: 2789
ADR: 8,II
REACH: 01-2119475328-30



Specification Test Results

USP - Assay (CH_3COOH)	99.7 - 100.5 %
USP - Chloride (Cl) (USP)	Passes Test
USP - Congealing Temperature	>= 15.6 °C
USP - Heavy Metals (as Pb)	<= 0.5 ppm
USP - Identification A	Passes Test
USP - Identification B	Passes Test
USP - Readily Oxidizable Substances	Passes Test
USP - Sulfate (USP)(SO_4)	Passes Test
USP - Limit of Nonvolatile Residue	<= 0.005 %
FCC - Assay (CH_3COOH)	99.7 - 100.5 %
FCC - Identification A	Passes Test
FCC - Identification B	Passes Test
FCC - Lead (Pb)	<= 0.5 mg/kg
FCC - Limit of Nonvolatile Residue	<= 0.005 %
FCC - Readily Oxidizable Substances	Passes Test

FCC - Solidification Point	>= 15.6 °C
ACS - Assay (by GC, corrected for water)	>= 99.7 %
ACS - Acetic Anhydride ($(CH_3CO)_2O$)	<= 0.01 %
ACS - Chloride (Cl)	<= 1 ppm
ACS - Color (APHA)	<= 10
Dilution Test	Passes Test
ACS - Iron (Fe)	<= 0.2 ppm
ACS - Heavy Metals (as Pb)	<= 0.5 ppm
ACS - Substances Reducing Dichromate	Passes Test
ACS - Substances Reducing Permanganate	Passes Test
ACS - Sulfate (SO_4)	<= 1 ppm
ACS - Titrable Base (meq/g)	<= 0.0004
Copper (Cu)	<= 0.00001 %
Nickel (Ni)	<= 0.00001 %
Residue after Evaporation	<= 0.001 %

ORDER

VWR Catalog Number	Unit	Price	Quantity	Size	Packaging	Supplier No.
(b) (4) (b) (4)	Case of 6 (500ml)	(b) (4)		500 mL	Clear Glass Bottle, PVC Coated	(b) (4)
(b) (4) (b) (4)	Case of 6 (2,500 ,ml)	(b) (4)		2.5 L	Clear Glass Bottle, PVC Coated	(b) (4)
	Each(2,500,ml)	(b) (4)				

In order to process your orders without delay, we request that you provide the required business documentation to purchase this product.

To order chemicals, medical devices, or other restricted products please provide identification that includes your business name and shipping addr (b) (4) referencing your (b) (4) account number . Acceptable forms of identification are:

State issued document with your organization's Federal Tax ID Number

State issued document with your organization's Resale Tax ID Number

City or County issued Business License

State Department of Health Services License

Any other ID issued by the State that includes the business name and address

* Please note if your account is within the State of California two of these pieces of identification will be required.

(b) (4) will not lift restrictions for residential shipping addresses.

(b) (4)

Specification for Ammonium Chloride, Granular, FCC (A1167)

Item Number	A1167
Item	Ammonium Chloride, Granular, FCC
CAS Number	12125-02-9
Molecular Formula	NH_4Cl
Molecular Weight	53.49
MDL Number	
Synonyms	

Test	Specification	
	Min	Max
ASSAY (DRIED BASIS)	99.0 %	
LEAD (Pb)		4 mg/kg
LOSS ON DRYING		0.5 %
IDENTIFICATION	TO PASS TEST	
RETEST DATE		

(b) (4)

Ammonia Solution

(b) (4)

PRODUCT INFORMATION

AMMONIA SOLUTION FG

PRODUCT DESCRIPTION

Ammonia Solution FG is a water white solution of anhydrous ammonia in water that meets food grade requirements and reference 21 CFR 184.1139.

CAS No. 1336-21-6

SYNONYMS

Ammonium hydrate

USES AND APPLICATIONS

Ammonia Solution FG may be used to replace anhydrous ammonia in most applications.

Product is designed for use in food and fermentation applications.

TYPICAL VALUES

Appearance:	Clear, Colorless Liquid
Odor:	Ammonia
Ammonia as NH_3 (wt.%):	27.0 – 30.0
Lead (ppm):	0.5 max
Nonvolatile Reside (wt.%):	0.02 max
Readily Oxidizable Substances:	Passes FCC Test

SHELF LIFE: Shelf life stability is dependent on temperature. At room temperature, the shelf life is 90 days.

PRECAUTIONS

Product safety information and handling precautions are contained on the product label and Safety Data Sheet (SDS).

READ AND UNDERSTAND LABEL AND SAFETY DATA SHEET BEFORE PRODUCT USE.

NH0028
8/1/2018
Rev: 21

(b) (4)

Biotin

(b) (4)

Specification for Biotin, Powder, FCC (BI115)

Item Number	BI115
Item	Biotin, Powder, FCC
CAS Number	58-85-5
Molecular Formula	$C_{10}H_{16}N_2O_3S$
Molecular Weight	244.31
MDL Number	
Synonyms	Vitamin H

Test	Specification	
	Min	Max
ASSAY ($C_{10}H_{16}N_2O_3S$)	97.5-100.5 %	
MELTING RANGE	229 - 232 C (dec	
OPTICAL ROTATION	+89 to+93	
LEAD (Pb)		2 mg/kg
IDENTIFICATION		TO PASS TEST
RETEST DATE		

(b) (4)

(b) (4)

SPECIFICATIONS

Ref: (b) (4)

SOLULYS® 095K

DEFINITION :

Spray-dried Corn Steep Liquor
CAS no.: 66071-94-1
EINECS : 266-113-4

SPECIFICATIONS :

LOSS ON DRYING (%)	5.5 max.
REDUCING SUGARS (% d.b. Bertrand)	1.5 max.
pH	3.5 - 4.5
ASH (% d.b.)	22.0 max.
PROTEIN (% d.b.)	43.0 - 54.0
NITROGEN (% d.b.)	7.0 - 8.5
AMINO NITROGEN (% d.b.)	1.5 - 3.5
ACIDITY as LACTIC ACID (% d.b.)	14.0 min.
PHOSPHOROUS (total, % d.b.)	2.4 min.

COMMENTS :

SOLULYS 095K is a spray-dried version of the Roquette SOLULYS 048K corn steep liquor. SOLULYS is a high quality corn steep liquor that is produced to a very consistent quality from batch to batch. It may be used effectively as a nutrient source in a wide variety of fermentations.

(b) (4)

QUALITY ASSURANCE / INDUSTRY February 10, 2016

(b) (4)

Cerelose® Dextrose M Non-GMO

technical specification

(b) (4)

CERELOSE® Dextrose M NON-GMO IP 02001090

CERELOSE® Dextrose 02001090 is a general purpose crystalline monohydrate dextrose suitable for most food, beverage, and industrial uses. This product is produced under (b) (4)

Chemical and Physical Properties

	Min.	Max.
Moisture %	8.0	9.0
Dextrose Equivalent	99.5	-
SO_2, ppm	-	<10
Dextrose, % d.b.	99.5	-
Ash, % d.b.	-	0.1
Solution Color		Passes test
Apparent Starch		Passes test

Physical Appearance

	Typical
Color	White
Form	Powder

Screen Test

	Typical
On USS 20 mesh, %	<1
On USS 100 mesh, %	<60

Microbiological Limits

	Max.
Standard Plate Count, cfu/g	100
Yeast, cfu/g	25
Mold, cfu/g	25
Salmonella/10 g	Negative
Coliforms, MPN/g	3

Nutritional Data/ 100g

	Typical
Calories	362
Calories from Fat	0
Total Fat, g	0
Cholesterol, mg	0
Sodium, mg	0
Total Carbohydrate, g	90.5
Dietary Fiber, g	0
Total Sugars**, g	90.5
Added Sugars, g	0
Other Carbohydrate, g	0
Protein, g	0
Vitamin D, mcg	0
Calcium mg	0
Iron, mg	0
Potassium, mg	0
Ash, g	<0.1*

* Not present at level of quantification.
** "Total Sugars" in this product may contribute to "Added Sugars" for nutrition labeling purposes in the final consumer product.

Certification

Kosher Pareve
Halal

Packaging and Storage

Bags
Product should be stored in a clean, dry area, not exposed to prolonged high (> 90°F / 32°C) temperature.

Shelf Life

3 years, provided product is stored the original container, well-closed in a cool, dried place free from humidity, dust, or foreign contamination.

Regulatory Data

Source	Corn (IP-TrueTrace™)
CAS No.	50-99-7

United States

Meets FCC (Food Chemical Codex) requirements.

Standard of Identity	21 CFR 168.111
GRAS Affirmation	21 CFR 184.1857
Labeling	Dextrose or Dextrose monohydrate

Canada

Standard Food	CFDA Regulation
Standard of Identity	B.18.015
Labeling	Dextrose or Dextrose monohydrate

Features and Benefits

TrueTrace™ certified non-GM.
Dry crystalline powder, Free flowing,
Mild sweetness
Bulking, Carrying
Highly fermentable

(b) (4)

Dipotassium Phosphate

[redacted] (b) (4)

[redacted] (b) (4)

DIPOTASSIUM PHOSPHATE
FOOD GRADE - EC/FCC

DESCRIPTION	Dipotassium Phosphate is a white, granular or milled product, which is essentially odorless. It is deliquescent with exposure to moist air.
USES	Food √ Buffering agent for processing foods √ Stabilizer for non-dairy coffee creamers Pharmaceuticals √ Nutrient for antibiotic production √ Humectant
NOMENCLATURE	Potassium Phosphate, Dibasic Dipotassium Monohydrogen Orthophosphate
FORMULA	K_2HPO_4
FORMULA WEIGHT	174.2
REFERENCE NUMBERS	CAS# 7758-11-4, E-340(ii)
CAS INDEX NAME	Phosphoric Acid, Dipotassium Salt
STORAGE	Store at Room Temperature
RE-TEST DATE	24 months after the date of manufacture
CERTIFICATES	Includes Kosher, NAFTA, NSF, HALAL and others.
LABEL DECLARATION	Potassium Phosphate
GRADE	**COMPLIES WITH FOOD CHEMICALS CODEX AND EUROPEAN COMMUNITY REQUIREMENTS.**

[redacted] (b) (4)

(b) (4)

(b) (4)

DIPOTASSIUM PHOSPHATE
FOOD GRADE EC/FCC GRADE

SHIPPING POINTS (b) (4)

CONTAINERS 50-pound net weight plastic bags (40 bags per pallet)
25-kg net weight plastic bags (40 bags per pallet)

SPECIFICATIONS

Assay (K_2HPO_4, dry basis)	98.0% min.
Phosphate as P_2O_5	40.3 – 41.5 %
pH, 1 % solution	8.7 – 9.4
Loss on drying	2.0 % max.
Water insoluble	0.2 % max.
Fluoride as F	10 ppm max.
Arsenic as As	1 ppm max.
Lead as Pb	1 ppm max.
Cadmium as Cd	1 ppm max.
Mercury as Hg	1 ppm max.
Identification Phosphate	Pass
Identification Potassium	Pass

TYPICAL PROPERTIES

Sieving	Available as granular or milled product
On 10 mesh	Trace
Bulk Density (g/cc)	1.03
Solubility	Approx. 63 grams per 100 grams saturated solution in 25°C.

2/3/15

(b) (4)

Ferrous Sulfate Heptahydrate, Dried

GENERAL

(b) (4) Dried Ferrous Sulfate Heptahydrate ($FeSO_4 \cdot 7H_2O$) is also called iron sulfate, green vitriol, or copperas. Ferrous Sulfate Heptahydrate is derived from the processing of ilmenite ore in the manufacture of the paint pigment Titanium Dioxide, or as a co-product from the pickling of steel. At QC Corporation, we evaporate all exterior moisture from each crystal, via rotary dryers, to produce a free-flowing Dried Ferrous Sulfate Heptahydrate, containing no exterior free water.

APPLICATIONS

(b) (4) Ferrous Sulfate products are used as a reducing agent in the treatment of hazardous wastes and as a coagulant and flocculent in the treatment of sewage waste, industrial effluents, raw drinking water and other wastewater sources. In addition, it is used as a reducing agent in the removal of phosphates and odor causing hydrogen sulfide from various waste sources.

The Agricultural, Lawn and Garden, and Turf Management industries use (b) (4) Ferrous Sulfate to correct iron chlorosis or deficiencies in plants and soils, to eliminate moss, to reduce alkalinity, and as a trace element or micronutrient in fertilizers. In addition, it is used in the diets of swine, poultry and other animals as a feed supplement, to prevent anemia caused by iron deficiencies.

PHYSICAL PROPERTIES

Dried Ferrous Sulfate Heptahydrate is free-flowing, has consistent iron, sulfur, water and oxygen contents, and goes into solution rapidly. Dried Ferrous Sulfate Heptahydrate has the tendency to compact and/or cake (becomes hard) under various shipping and storage conditions, particularly in extremely hot environments that exceed 75° F. QC Corporation can add up to 2% Calcium Carbonate as an anti-caking agent.

Appearance	**Blue-Green Monoclinic Crystalline Water-Soluble Salt**
Bulk Density	**65 Lbs./Cu. Ft.**
Sieve Analysis	**95% -16/+100**
Please note that up to 2% of Calcium Carbonate can be added to this product as an anti-caking agent upon request. Calcium Carbonate is insoluble in water and can potentially clog filters or pumps.	

Information regarding the contents and levels of metals in this product is available on the Internet at (b) (4) or (b) (4)

CHEMICAL PROPERTIES

Iron	20% ± 0.5%
Sulfur	12%
Oxygen	22%
Water	45%

PACKAGING AND TRANSPORT MODES

- 50 Lb. Bags Via Truck Or Rail
- 2,000 Lb. Super-Sacks Via Truck Or Rail
- Bulk Via Truck Or Rail
- Custom Valve Pack Bags Are Available Upon Request

TRACE MATERIALS (MAXIMUM PPM)

Shipping Point:	(b) (4)		
Raw Material Source:			
Arsenic	**1**	**1**	**1**
Cadmium	**2**	**2**	**5**
Chromium	**50**	**11**	**30**
Copper	**6**	**11**	**15**
Lead	**12**	**11**	**17**
Magnesium	**500**	**6,400**	**127**
Manganese	**950**	**1,350**	**2,200**
Nickel	**123**	**55**	**121**
Zinc	**160**	**500**	**900**

(b) (4) Ferrous (Iron) Sulfate products are registered in Canada as a Pest Control Product (PCP) under the Canadian PCP Act.

(b) (4)

(b) (4)

Specification for Folic Acid, Powder, FCC (F1079)

Item Number	F1079
Item	Folic Acid, Powder, FCC
CAS Number	59-30-3
Molecular Formula	$C_{19}H_{19}N_7O_6$
Molecular Weight	441.40
MDL Number	
Synonyms	N-[4-(2-Amino-4-hydroxypteridin-6-ylmethylamino)benzoyl]-L(+)-glutamic Acid ; Folacin ;

Test	Specification	
	Min	Max
ASSAY (ANHYDROUS BASIS)	95.0	102.0 %
LEAD (Pb)		2 mg/kg
RESIDUE ON IGNITION		0.3 %
WATER		8.5 %
IDENTIFICATION		TO PASS TEST
APPEARANCE		
EXPIRATION DATE		
DATE OF MANUFACTURE		

(b) (4)

Specification Sheet

(b) (4)

Product Name	L-Cysteine hydrochloride, FG, product of (b) (4)
Product Number	W778567
Product Brand	(b) (4)
CAS Number	52-89-1
Molecular Weight	157.62

TEST	SPECIFICATION
APPEARANCE (COLOR)	White to Off White
APPEARANCE (FORM)	Powder or Crystals
ASSAY	98.5 - 101.0 %
OPTICAL ROTATION	6.2 ± 0.5 Degrees
CONCENTRATION	C=8, IN HCL, 20 DEG C
SOLUBILITY (COLOR)	Colorless
SOLUBILITY (TURBIDITY)	Clear
SOLUBILITY (METHOD)	250MG/10ML WATER
LOSS ON DRYING	≤ 2.0 %
RESIDUE ON IGNITION	≤ 0.1 %
INFRARED SPECTRUM	CONFORMS TO STRUCTURE
HEAVY METALS	≤ 10 ppm
ARSENIC (ICP)	≤ 1 ppm
CADMIUM (ICP)	≤ 1 ppm
MERCURY (ICP)	≤ 1 ppm
LEAD (ICP)	≤ 5 ppm
AMMONIUM (NH4+)	≤ 200 PPM
EXPIRATION DATE PERIOD	60 MONTH

Magnesium Sulfate Heptahydrate

(b) (4)

(b) (4)

SALES SPECIFICATIONS FOR
MAGNESIUM SULFATE CRYSTALS, USP
DECEMBER 1ST, 2018

CHARACTERISTICS

The material shall be colorless, solid at ambient temperatures, formed in small needle-like rhombic crystals and free of solid or fibrous foreign matter that will require the dissolved material to be filtered before being used.
Epsom salt is one of the most common forms of magnesium sulfate heptahydrate. EPSOM SALT is a hydrated salt with seven molecules of water, so caking or bridging can occur. Care should be taken to protect the material if it is stored in the granular form for long periods of time. EPSOM SALT is readily soluble in water.

PROPERTIES	Identification	Test of Magnesium	Positive
		Test of Sulfate	Positive
		Consistently Free of Volatile Organic Impurities	
	Chemical	pH	5.0 – 9.2
		Loss of ignition	40.0% - 52.0%
		Chloride, maximum, ppm	140
		Arsenic, maximum, ppm	3
		Heavy Metals, maximum, ppm	10
		Iron, maximum, ppm	20
		Selenium, maximum, ppm	30
		Assay	99%–100.5%
	Physical	Color	Colorless
		Crystal Form	Rhombic (monoclinic)

QUALITY ASSURANCE PROVISION

GENERAL:
The material specified herein shall be manufactured using acceptable industrial practices.
The material shall be guaranteed to meet chemical and physical properties specified herein.

RESPONSIBILITIES FOR TESTS & INSPECTIONS:
Unless otherwise specified by purchaser, the supplier is responsible for providing a lot analysis on the material. Except as otherwise specified, the supplier may utilize his own facilities or any commercial laboratory. Analysis' are available for each lot at an additional charge.

PACKAGING & SHIPPING

PACKAGING:
Shall be accomplished in accordance with acceptable commercial practices for domestic or foreign shipments unless otherwise indicated by the purchaser. It shall be the vendor's responsibility to determine that packaging, as done, is adequate to assure that all materials shall arrive at destination in an uncontaminated condition and ready for intended use.

SHIPPING:
Shall be accomplished in accordance with acceptable commercial practices for domestic or foreign shipment for this type of product unless otherwise indicated by the purchaser.

(b) (4)

Manganese Sulfate, Monohydrate

(b) (4)

Product Specification

Product Name:
Manganese sulfate monohydrate - meets USP testing specifications

Product Number:	**M8179**
CAS Number:	10034-96-5
MDL:	MFCD00149159
Formula:	MnO4S · H2O
Formula Weight:	169.02 g/mol

$MnSO_4 \cdot xH_2O$

TEST	Specification
Assay	98.0 - 102.0 %
Identity	Pass
Loss on Ignition	10.0 - 13.0 %
Substances not ppt. by (NH4)2S	≤ 0.5 %
Residual Solvents USP 467	Meets Requirements
Recommended Retest Period 6 Years	----------

Specification: PRD.0.ZQ5.10000033488

(b) (4)

Section 1 - PRODUCT AND COMPANY IDENTIFICATION

Material Name
CAPSUL® 06670103

Synonyms
Modified Food Starch

Product Description
Manufacture of food products

Details of the supplier of the safety data sheet

(b) (4)

Section 2 - HAZARDS IDENTIFICATION

Classification in accordance with paragraph (d) of 29 CFR 1910.1200.
- Combustible Dust

GHS Label Elements

Symbol(s)
None needed according to classification criteria

Signal Word
WARNING!

Hazard Statement(s)
May form combustible dust concentrations in air.

Precautionary Statement(s)

Prevention
None needed according to classification criteria.

Response
None needed according to classification criteria.

Storage
None needed according to classification criteria.

Disposal
Dispose of contents/container in accordance with local/regional/national/international regulations.

Section 3 - COMPOSITION / INFORMATION ON INGREDIENTS

CAS	Component Name	Percent
Trade Secret	Trade Secret	Trade Secret

Component Related Regulatory Information
ACGIH TLVs, as Particulates Not Otherwise Classified: 10 mg/m³ (inhalable fraction) 3 mg/m3 (respirable fraction). OSHA PELs, as Particulates Not Otherwise Regulated: 15 mg/m³ (total dust) 5 mg/m³ (respirable fraction).

Section 4 - FIRST AID MEASURES

Inhalation
Remove to fresh air and keep at rest in a position comfortable for breathing. Obtain medical attention if breathing difficulty persists.

Skin
After contact with skin, take off immediately all contaminated clothing, and wash immediately with plenty of water and soap If skin irritation occurs: Get medical advice/attention.

Eyes
Rinse cautiously with water for several minutes. If eye irritation persists: Get medical advice/attention.

Ingestion
If a large amount is swallowed, get medical attention.

Most Important Symptoms/Effects

Acute
None.

Delayed
None.

Section 5 - FIRE FIGHTING MEASURES

Extinguishing Media

Suitable Extinguishing Media
Carbon dioxide. Water spray. Foam.

Unsuitable Extinguishing Media
None.

Special Hazards Arising from the Chemical
May form combustible dust concentrations in air. This material can be ignited by heat, sparks, flames, or other sources of ignition (e.g., static electricity, pilot lights, mechanical/electrical equipment, and electronic devices such as cell phones, computers, calculators, and pagers which have not been certified as intrinsically safe). Use explosion-proof electrical equipment. Contact with combustible material may cause fire.

Fire Fighting Measures
Remove product from area of fire. Wet the material with water to limit dust emission or explosion. Suitable extinguishing media. Avoid inhalation of the product. Stay upwind/keep distance from source.

Special Protective Equipment and Precautions for Firefighters
In case of fire: Wear self-contained breathing apparatus. Wear suitable protective clothing.

Section 6 - ACCIDENTAL RELEASE MEASURES

Personal Precautions, Protective Equipment and Emergency Procedures
See protective measures under point 7 and 8.

Methods and Materials for Containment and Cleaning Up
Avoid dust formation. Remove all sources of ignition. Ensure that the equipment is adequately grounded. Dispose of contents/container in accordance with local/regional/national/international regulations.

Section 7 - HANDLING AND STORAGE

Precautions for Safe Handling
Keep away from heat, hot surfaces, sparks, open flames and other ignition sources. No smoking. Take care for general good hygiene and housekeeping.

Conditions for Safe Storage, Including any Incompatibilities
None needed according to classification criteria.
Store in accordance with local/regional/national/international regulations. Store in a well-ventilated place. Keep container tightly closed. Store in a dry place. Avoid dust formation.

Incompatible Materials
Oxidizing agents. Combustible substance.

Section 8 - EXPOSURE CONTROLS / PERSONAL PROTECTION

Component Exposure Limits

ACGIH, NIOSH, EU, OSHA (US) and Mexico have not developed exposure limits for any of this product's components

EU - Occupational Exposure (98/24/EC) - Binding Biological Limit Values and Health Surveillance Measures
There are no biological limit values for any of this product's components.

ACGIH - Threshold Limit Values - Biological Exposure Indices (BEI)
There are no biological limit values for any of this product's components.

Engineering Controls
Ventilation equipment should be explosion-resistant if explosive concentrations of material are present. Provide local exhaust ventilation system. Ensure compliance with applicable exposure limits. Ensure that dust-handling systems (such as exhaust ducts, dust collectors, vessels, and processing equipment) are designed in a manner to prevent the escape of dust into the work area (i.e., there is no leakage from the equipment).

Individual Protection Measures, such as Personal Protective Equipment

Eye/face protection
If eye contact is likely, wear chemical resistant safety goggles.

Skin Protection
Protective clothing is not required under normal conditions.

Respiratory Protection
Respiratory protection is not required under normal conditions of use. If respirable dusts are generated, respiratory protection may be needed.

Glove Recommendations
Protective gloves are not required under normal conditions.

Section 9 - PHYSICAL AND CHEMICAL PROPERTIES

Appearance	Fine Powder	**Physical State**	solid
Odor	Not available	**Color**	White to Off-white
Odor Threshold	Not available	**pH**	3
Melting Point	Not available	**Boiling Point**	Not available
Freezing point	Not available	**Evaporation Rate**	Not available
Boiling Point Range	Not available	**Flammability (solid, gas)**	Not available
Autoignition	Not available	**Flash Point**	Not available
Lower Explosive Limit	Not available	**Decomposition**	Not available
Upper Explosive Limit	Not available	**Vapor Pressure**	Not available
Vapor Density (air=1)	Not available	**Specific Gravity (water=1)**	Not available
Water Solubility	90 %	**Partition coefficient: n-octanol/water**	Not available
Viscosity	Not available	**Solubility (Other)**	Not available
Density	Not available		

Section 10 - STABILITY AND REACTIVITY

Reactivity
No known hazardous reactions.

Chemical Stability
The product is stable under storage at normal ambient temperatures.

Possibility of Hazardous Reactions
None.

Conditions to Avoid
Avoid dust formation. Remove all sources of ignition.

Incompatible Materials
Oxidizing agents. Combustible substance.

Hazardous decomposition products
Carbon dioxide. Carbon monoxide.

Section 11 - TOXICOLOGICAL INFORMATION

Information on Likely Routes of Exposure

Inhalation
May cause respiratory irritation.

Skin Contact
No data available.

Eye Contact
Irritation to eyes. Corneal opacity.

Ingestion
No data available.

Acute and Chronic Toxicity

Component Analysis - LD50/LC50
The components of this material have been reviewed in various sources and no selected endpoints have been identified

Immediate Effects
No data available.

Delayed Effects
No data available.

Irritation/Corrosivity Data
No data available.

Respiratory Sensitization
No data available.

Dermal Sensitization
No data available.

Component Carcinogenicity
None of this product's components are listed by ACGIH, IARC, NTP, DFG or OSHA

Germ Cell Mutagenicity
No data available.

Reproductive Toxicity
No data available.

Specific Target Organ Toxicity - Single Exposure
No data available.

Specific Target Organ Toxicity - Repeated Exposure
No data available.

Aspiration hazard
No data available.

Medical Conditions Aggravated by Exposure
No data available.

Section 12 - ECOLOGICAL INFORMATION

Ecotoxicity
Avoid release to the environment.

Component Analysis - Aquatic Toxicity
No LOLI ecotoxicity data are available for this product's components

Persistence and Degradability
Biodegradable.

Bioaccumulative Potential
No data available.

Mobility
No data available.

Section 13 - DISPOSAL CONSIDERATIONS

Disposal Methods
Contain and dispose of waste according to local regulations.

Component Waste Numbers
The U.S. EPA has not published waste numbers for this product's components

Section 14 - TRANSPORT INFORMATION

US DOT Information:
Additional information: Not regulated as a hazardous material

TDG Information:
Additional information: Not regulated as a hazardous material

Section 15 - REGULATORY INFORMATION

U.S. Federal Regulations
None of this products components are listed under SARA Sections 302/304 (40 CFR 355 Appendix A), SARA Section 313 (40 CFR 372.65), CERCLA (40 CFR 302.4), TSCA 12(b), or require an OSHA process safety plan.

FDA - Direct Food Additive
No components of this material are listed.

FDA - Food additives Generally Recognized as Safe(GRAS)
No components of this material are listed.

FDA - Food additives Generally Recognized as Safe(GRAS) –Select Committee on GRAS Substances(SCOGS)
No components of this material are listed.

FDA - Food additives Permitted in Food on an Interim Basis
No components of this material are listed.

FDA - Substances Prohibited from use in human food
No components of this material are listed.

U.S. State Regulations
None of this product's components are listed on the state lists from CA, MA, MN, NJ or PA

Not listed under California Proposition 65

Canada Regulations
Components of this material have been checked against the Canadian WHMIS Ingredients Disclosure List. The List is composed of chemicals which must be identified on MSDSs if they are included in products which meet WHMIS criteria specified in the Controlled Products Regulations and are present above the threshold limits listed on the IDL.

Component Analysis - Inventory
Trade Secret (Trade Secret)

US	CA	EU	AU	PH	JP - ENCS	JP - ISHL	KR - KECI/KECL	KR - TCCA	CN	NZ	MX
Yes	DSL	No	No	No	No	No	Yes	No	Yes	Yes	No

Section 16 - OTHER INFORMATION

Key / Legend

ACGIH - American Conference of Governmental Industrial Hygienists; ADR - European Road Transport; AU - Australia; BOD - Biochemical Oxygen Demand; C - Celsius; CA - Canada; CA/MA/MN/NJ/PA - California/Massachusetts/Minnesota/New Jersey/Pennsylvania*; CAS - Chemical Abstracts Service; CFR - Code of Federal Regulations (US); CERCLA - Comprehensive Environmental Response, Compensation, and Liability Act; CLP - Classification, Labelling, and Packaging; CN - China; CPR - Controlled Products Regulations; DFG - Deutsche Forschungsgemeinschaft; DOT - Department of Transportation; DSD - Dangerous Substance Directive; DSL - Domestic Substances List; EC – European Commission; EEC - European Economic Community; EIN - European Inventory of (Existing Commercial Chemical Substances); EINECS - European Inventory of Existing Commercial Chemical Substances; ENCS - Japan Existing and New Chemical Substance Inventory; EPA - Environmental Protection Agency; EU - European Union; F - Fahrenheit; IARC - International Agency for Research on Cancer; IATA - International Air Transport Association; ICAO - International Civil Aviation Organization; IDL - Ingredient Disclosure List; IDLH - Immediately Dangerous to Life and Health; IMDG - International Maritime Dangerous Goods; ISHL - Japan Industrial Safety and Health Law; IUCLID - International Uniform Chemical Information Database; JP - Japan; Kow - Octanol/water partition coefficient; KECI - Korea Existing Chemicals Inventory; KECL – Korea Existing Chemicals List; KR - Korea; LD50/LC50 - Lethal Dose/ Lethal Concentration; LEL - Lower Explosive Limit; LLV - Level Limit Value; LOLI - List Of LIsts™ - ChemADVISOR's Regulatory Database; MAK - Maximum Concentration Value in the Workplace; MEL - Maximum Exposure Limits; MX – Mexico; NDSL – Non-Domestic Substance List (Canada); NFPA - National Fire Protection Agency; NIOSH - National Institute for Occupational Safety and Health; NJTSR - New Jersey Trade Secret Registry; NTP - National Toxicology Program; NZ - New Zealand; OSHA - Occupational Safety and Health Administration; PEL- Permissible Exposure Limit; PH - Philippines; RCRA - Resource Conservation and Recovery Act; REACH- Registration, Evaluation, Authorisation, and restriction of Chemicals; RID - European Rail Transport; SARA - Superfund Amendments and Reauthorization Act; STEL - Short-term Exposure Limit; TCCA – Korea Toxic Chemicals Control Act; TDG - Transportation of Dangerous Goods; TLV - Threshold Limit Value; TSCA - Toxic Substances Control Act; TW – Taiwan; TWA - Time Weighted Average; UEL - Upper Explosive Limit; UN/NA - United Nations /North American; US - United States; VLE - Exposure Limit Value (Mexico); WHMIS - Workplace Hazardous Materials Information System (Canada).

Other Information

Disclaimer:

The attached data has been compiled from sources which (b) (4) (b) (4) believe to be dependable and, to our knowledge and belief is accurate. However, (b) (4) (b) (4) cannot make any warranty or representation respecting the accuracy or completeness of the data. We assume no responsibility for any liability or damages relating thereto, or for advising you regarding the protection of your employees, customers, or others. You should make your own tests to determine the applicability of such information to, or the suitability of any products for your specific use. (b) (4) expressly disclaims all warranties, expressed or implied, including but not limited to, warranties of merchantability, accuracy, fitness for use or for a particular purpose, and noninfringement. The United Nations Convention on Contracts for the International Sale of Goods shall not apply to sales of products by (b) (4) (b) (4) The (b) (4) mark and logo are trademarks of the (b) (4) group of companies.

Monopotassium phosphate (MKP)

(b) (4)

(b) (4)

MONOPOTASSIUM PHOSPHATE (MKP)

GRADE: FCC
Complies with the specifications of the current edition of the Food Chemicals Codex

DESCRIPTION: White, odorless, crystalline material

NOMENCLATURE: Potassium Dihydrogen Phosphate
Potassium Phosphate, Monobasic

FORMULA: KH_2PO_4

FORMULA WEIGHT: 136.1

CAS NUMBER: 7778-77-0

E/INS NUMBER: 340(i)

SPECIFICATIONS[1]:

FCC Specifications		
Assay (KH_2PO_4)	NLT* 98.0	%
Arsenic (As)	NMT** 3 (Max 3)†	mg/kg (ppm)
Fluoride (F)	NMT 10 (Max 10)	mg/kg (ppm)
Lead (Pb)	NMT 2 (Max 2)	mg/kg (ppm)
Insoluble Substances	NMT 0.2	%
Loss on Drying	NMT 1	%
(b) (4) **Specifications**		
Assay - P_2O_5 Content	51.0 – 53.0	%
pH (1% solution)	4.2 – 4.7	
Sieving On 10 mesh	0 max	%
Sieving On 100 mesh	80 min	%

*not less than **not more than † values in parenthesis are in format as they appear on the Certificate of Analysis (COA)

[1] These specifications may not all be reported values on Certificates of Analysis for this product. In addition, some specifications and values reported on Certificates of Analysis may be based on periodic testing, not lot release testing. Microbial testing is not performed on this product. It is manufactured according to good manufacturing practices meeting food regulations in the place of manufacture, including physical, chemical and microbial hazard assessments

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(b) (4)

MONOPOTASSIUM PHOSPHATE (MKP)

ADDITIONAL INFORMATION[2]

pH (1% solution)	4.5
Bulk Density (lbs / ft3)	74

USES: Sports beverages, coffee creamers, process cheese products, fortification in food products, etc.

FUNCTION: Nutritional source of potassium and phosphorus
Buffer in foodstuffs
Ingredients in emulsifying salts for processed cheese products
Culture nutrients in pharmaceutical manufacture

CERTIFICATIONS: Kosher, NAFTA

MANUFACTURING LOCATION:

(b) (4)

SHIPPING POINTS:

STANDARD CONTAINERS: 50-lb net weight plastic bags (40 bags per pallet)

STORAGE CONDITIONS: Store at room temperature

RETEST DATE: 730 days from the date of manufacture

2 This section, "Additional Information," is provided for educational purposes only. These values are not reported on the product's Certificate of Analysis.

(b) (4)

Safety Evaluation of Monopotassium Phosphate for Use as Mineral Substance for Use in the Production of Direct-Fed Microbials for Use in Animal Feed

ASCUS Biosciences, Inc.

November, 2018

Safety Evaluation of Monopotassium Phosphate for Use as Mineral Substance for Use in the Production of Direct-Fed Microbials for Use in Animal Feed

TABLE OF CONTENTS

LIST OF TABLES

Safety Evaluation of Monopotassium Phosphate for Use as Mineral Substance for Use in the Production of Direct-Fed Microbials for Use in Animal Feed

1. INTRODUCTION

ASCUS Biosciences, Inc. (hereafter referred to as "ASCUS") develops direct-fed microbial (DFM) products for use as supplementary feeds for poultry and cattle in the United States (U.S.). One of the raw materials used to charge the fermenter for the production of the DFM strains is monopotassium phosphate. While dipotassium phosphate is permitted for use as a sequestrant in feed in accordance with good manufacturing or feeding practice under 21 CFR §582.6282[1], monopotassium phosphate is currently not currently acceptable for feeding to animals in the U.S. Considering that all raw materials used in the production of DFM products should be accepted feed substances in the U.S., ASCUS has conducted a safety evaluation to confirm the suitability of monopotassium phosphate for the intended use as a processing aid in the fermentation of its microbial strains.

2. REGULATORY STATUS

2.1 Regulatory Status in Animal Feed in the U.S.

A number of related phosphate salts are acceptable for use in animal feed in the U.S. and are summarized in Table 2.1.

Table 2.1: Examples of Related Phosphate Salts Accepted for Use in Animal Feed in the U.S.

Mineral Substance	Function in Feed	Regulatory Status
Diammonium phosphate	Mineral product and general purpose food additive	21 CFR §582.1141 and AAFCO ingredient definition 57.16
Dicalcium phosphate	Mineral product and general purpose food additive	21 CFR §582.1217, 21 CFR §582.5217 and AAFCO ingredient definition 57.71
Disodium phosphate	Mineral product and general purpose food additive	21 CFR §582.1778, 21 CFR §582.5778 and AAFCO ingredient definition 57.32
Monoammonium phosphate	Mineral product and general purpose food additive	21 CFR §582.1141 and AAFCO ingredient definition 57.33
Monocalcium phosphate	Mineral product and general purpose food additive	21 CFR §582.1217, 21 CFR §582.5217 and AAFCO ingredient definition 57.98
Monosodium phosphate	Mineral product and general purpose food additive	21 CFR §582.1778, 21 CFR §582.5778 and AAFCO ingredient definition 57.99
Phosphoric acid	Mineral product and general purpose food additive	21 CFR §582.1073 and AAFCO ingredient definition 57.19
Dipotassium phosphate	Sequestrant	21 CFR §582.6282

[1] https://www.accessdata.fda.gov/scripts/cdrh/cfdocs/cfcfr/CFRSearch.cfm?fr=582.6285&SearchTerm=dipotassium%20phosphate

2.2 Regulatory Status in Animal Feed in Canada

Monopotassium phosphate is permitted for use in animal feed as in Canada as a Class 6 – Mineral Product under Schedule IV, Part I of the Feed Regulations (1983). The substance must be labeled with guarantees for minimum percent potassium, minimum percent phosphorus and maximum milligrams fluorine, arsenic and iron per kilogram

2.3 Regulatory Status in Animal Feed in the European Union (EU)

Monopotassium phosphate is a recognized feed material in the EU and listed in the Feed Materials Catalogue laid down under Commission Regulation (EU) No 68/2013 (European Commission, 2013). The substance must be labeled with total phosphorus, potassium and, where greater than 10%, the content of phosphorus insoluble in citric acid.

2.4 Regulatory Status in Human Food in the U.S.

Monopotassium phosphate is generally recognized as safe as a food additive in frozen eggs at levels of less than 0.5% in accordance with 21 CFR §160.110.

3. SAFETY EVALUATION FOR TARGET ANIMALS

3.1 History of Use

As mentioned in Section 2, monopotassium phosphate has a long and established history of use as a mineral substance for use in animal feed in Canada and the EU. The levels of monopotassium phosphate as a source of phosphorus in feed is expected to be higher than the residues arising from carry-over of the fermentation process in DFM products. On this basis, the history of safe use of monopotassium phosphate in Canada and the EU for use in animal feed supports the suitability of the additive for use as a raw material in the fermentation of microbial strains by ASCUS.

3.2 Natural Occurrence

Potassium is present in most feedstuffs with the highest levels typically reported in protein sources such as soybean meal. Thus, deficiencies in animals, particularly non ruminants are rare (NRC, 2005). Where diets contain high levels of industrial by-products such as brewer's grains or corn gluten, supplementation can be required.

Likewise, phosphates are widely available from the feed, with oilseed meals and other plant-based materials, mineral feeds, and meat and marine animal feeds serving as major sources in the diet of animals. Availability of phosphorus from the diet can vary with the source and is generally taken into account in the formulation of livestock diets (NRC, 2005).

It is reasonable to assume that these background sources will provide potassium and phosphorus as significantly higher levels in the diet of poultry and cattle than will be carried over from the use as a fermentation aid in the production of microbial strains by ASCUS.

3.3 Metabolic Fate

On ingestion by animals, monopotassium phosphate will dissociate to the respective potassium, hydrogen and phosphate ions. Equivalent behavior in the gastrointestinal tract is observed on ingestion

of related salts such as mono- and di-sodium phosphate and dipotassium phosphate. Thus, the use of monopotassium phosphate will result in exposure by animals to ions commonly consumed in animal feed. On this basis, the available safety data on sodium, calcium and ammonium phosphate salts as well as dipotassium phosphate may be extrapolated to support the safety of monopotassium phosphate (see Section 3.3 and 3.4).

3.4 Mineral Tolerances

Both potassium and phosphorus are required nutrients for poultry and cattle and are considered by the National Research Council (NRC) to be of medium concern for animal health. The NRC has set maximum tolerable levels for potassium of 1% in the diet of poultry and cattle on a dry matter basis, and for phosphorus of 1% for growing birds, 0.8% for laying hens and 0.7% for cattle on a dry matter basis (NRC, 2005). Any carry-over in the diet of monopotassium phosphate from the production of microbial strains for use as DFM products will contribute to the levels of these minerals in the feed but the overall impact on the daily intakes by animals is expected to be low.

3.5 Evaluations by Scientific Bodies

3.5.1 JECFA Evaluation

The Joint FAO/WHO Committee on Food Additives (JECFA) has evaluated the safety of phosphoric acid and phosphate salts as a group, including within the scope of the review, mono-, di- and tri-potassium phosphate (JECFA, 1982). In the latest evaluation conducted in 1982, JECFA concluded that:

"*Metabolically, the phosphate salts provide a source of the various cations and phosphate ion. Of the greatest concern is the toxicity arising from calcium, magnesium and phosphate imbalance in the diet. Phosphate salts were not mutagenic in a number of test systems. Teratogenic effects have not been observed in mammalian test systems.*

Numerous animal studies have shown that excessive dietary phosphorus causes an increase of plasma phosphorus and a decrease in serum calcium. The resulting hypocalcemia stimulates excretion of PTH which in turn increases the rate of bone resorption and decreases calcium excretion. These homeostatic adjustment to high dietary phosphorus may result in bone loss and calcification of soft tissues in animals.

The dose levels of phosphate producing nephrocalcinosis were not consistent among the various rat feeding studies. However, the rat is exquisitely susceptible to calcification and hydronephrosis upon exposure to acids forming calcium chelates or complexes. The lowest dose levels that produce nephrocalcinosis overlap the higher dose levels failing to do so. However, this may be related to other dietary imbalances, such as the level of magnesium in the diet. There is still uncertainty on the optimal Ca:P ratio and whether this ratio is of any dietary significance in man.

The lowest level of phosphate that produced nephrocalcinosis in the rat (1% P in the diet) is used as the basis for the evaluation and, by extrapolation based on the daily food intake of 2800 calories, this give a dose level of 6600 mg P per day as the best estimate of the lowest level that might conceivably cause nephrocalcinosis in man. The usual calculation for provision of a margin of safety is probably not suitable for food additives which are also nutrients. Ingested phosphates from natural sources should be considered together with that from food additive sources. Since phosphorus (as phosphates) is an

essential nutrient and an unavoidable constituent of food, it is not feasible or appropriate to give a range of values from zero to maximum."

On the basis of the above, the maximum tolerable daily intake for man was estimated to be 70 mg/kg body weight.

3.5.2 SCF Evaluation

The Scientific Committee on Food (SCF) in the European Union (EU) evaluated the group of phosphate salts used as food additives in 1990 and agreed with the JECFA estimate of 70 mg/kg body weight for man, calculated as phosphorus (SCF, 1990).

3.5.3 Summary

Taken together the body of available data indicate that the safety of monopotassium phosphate can be considered from the available data on phosphoric acid and phosphate, which have been previously evaluated by JECFA and the SCF for use as food additives. These evaluations highlighted the role of phosphate salts to provide a metabolic source of cations and the phosphate ion. Safety was primarily based on the absence of any genotoxicity and the requirement to provide nutritionally balanced levels in the diet which do not exceed the maximum that can be tolerated by the body.

4. SUMMARY AND CONCLUSIONS

Monopotassium phosphate has an established history of safe use as a mineral substance for use in animal feed in Canada and in the EU. On ingestion by poultry or cattle, monopotassium phosphate will dissociated into the potassium, hydrogen and phosphate ions. For this reason, and consistent with the evaluations of the additive for use in food by JECFA and the SCF, the safety can be primarily derived from the body of available data on phosphoric acid and phosphate salts. Potassium and phosphate are both essential nutrients for animals and present naturally in the feed as well as being added in the form of supplemental salts. The carry-over of potassium and phosphate from its use as a salt in the fermentation of microbial strains for use as DFMs in poultry and cattle feed are not expected to make any significant contribution to the levels present in the diet from natural and supplemental sources. Together, it may be concluded that there are no safety concerns associated with the use of monopotassium phosphate by ASCUS as a fermentation aid under the conditions of intended use.

5. REFERENCES

CIR, 2016. Cosmetic Ingredient Review. Phosphoric acid and simple salts as used in cosmetics. Available at: https://www.cir-safety.org/

JECFA, 1982. Joint FAO/WHO Expert Committee on Food Additives. Toxicological Monograph: Phosphoric acid and phosphate salts. Available at: http://www.inchem.org/documents/jecfa/jecmono/v17je22.htm

NRC, 1990. National Research Council. Mineral Tolerances of Animals. The National Academies Press.

SCF, 1990. Scientific Committee on Food. Report, 25th Series. Food additives of various technological functions. Available at: https://ec.europa.eu/food/sites/food/files/safety/docs/sci-com_scf_reports_25.pdf

(b) (4)

KFO-402 Antifoam

(b) (4)

KFO™ 402

Product Type	**FOOD GRADE – GENERAL PURPOSE PROCESS AID DEFOAMER**
Product Description	KFO™ 402 is a defoamer designated to control foam in many processes. KFO™ 402 is especially effective when used in fermentation processes where a certain degree of foam control is needed without affecting oxygen transfer for optimum product yield. This product is made with food grade ingredients under our Good Manufacturing Practices Program. The components of KFO™ 402 meet FDA requirement for use in egg washing, potato processing defoamers as a dispersing aid for mineral oil at a limit of 10 ppm in the processing water followed by a potable water rinse. This product also contains ingredients for which the FDA has provided the Enzyme Technical Association with a "no objection" letter acknowledging that they are used as defoaming agents in the manufacture of enzyme preparations used in food in accordance with the principles of GMPs. Other uses in the processing and manufacture of food ingredients may also qualify for GRAS status. KFO™ 402 also is composed of ingredients that meet the current requirements of the FDA for food contact applications when used in accordance with the requirements and limitations of 21CFR 176.210(d)(3). Consideration for other FDA permitted uses would require further evaluation.

Typical Properties

Appearance	Clear Liquid
Viscosity @ 100°F, Kinematic	185 – 210 Cst
Odor	Sweet
Weight per gallon	8.5 Lbs
Flash Point (°C)	> 216°C PMCC (Min)
Specific Gravity	1.02

Typical Applications	Typical applications for KFO™ 402 include: • Fermentation • Egg washing
Incorporation	KFO™ 402 should be added, as received, early in the processing to prevent foam before it forms. KFO™ 402 should be evaluated in the process to determine the optimum dosage and legal limits allowed.
Shelf Life	2 years from date of manufacture when properly stored in the original container following proper storage and handling.
Storage & Handling	Keep from freezing. Store product between 40 and 100°F. Keep containers tightly closed when not in use.
Responsible Care	For complete safety, health, personnel protection and first aid information, refer to the Safety Data Sheet (SDS) that can be ordered through the numbers below.

Updated January 16, 2017

(b) (4)

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

Food and Drug Administration
Washington DC 20204

September 11, 2003

Mr. Gary Yingling
Kirkpatrick & Lockhart LLP
1800 Massachusetts Avenue, NW
Second Floor
Washington, DC 20036-1221

Dear Mr. Yingling:

You requested, on behalf of the Enzyme Technical Association, that OFAS review the use of certain defoaming and flocculating agents in the manufacture of enzyme preparations used in food. You provided information related to these compounds in your letters of December 20, 1996 (to Dr. Alan Rulis), 4-24-1998 (to Dr. Zofia Olempska-Beer), and 11-30-99 (to Dr. Zofia Olempska-Beer). You also arranged for a teleconference between ETA members and OFAS representatives, facilitated telephone contacts with technical experts from ETA member companies, and responded to numerous requests for clarification. We appreciate your and ETA's cooperation.

We reviewed the information on defoaming and flocculating agents that you submitted as well as the information provided in GRAS affirmation petitions and GRAS notices for enzyme preparations. The enclosed attachment provides a brief overview of our evaluation and itemizes the evaluated defoamers (Table 1) and flocculants (Table 2). We conclude that these compounds are used by enzyme manufacturers in accordance with the principles of good manufacturing practice (GMP).

Sincerely yours,

Laura M. Tarantino, Ph.D.
Acting Director
Office of Food Additive Safety, HFS-200
Center for Food Safety and Applied Nutrition

Defoaming and Flocculating Agents Used in the Manufacture of Enzyme Preparations Used in Food

Enzyme Preparations

Most enzymes currently used in food are derived from microorganisms. The manufacturing process of such enzymes includes three major steps: fermentation, enzyme recovery, and enzyme formulation. The formulated products are generally referred to as enzyme preparations. In addition to the enzymes of interest, enzyme preparations contain added substances such as diluents, preservatives, and stabilizers. They may also contain metabolites derived from the production microorganism and the residues of substances used in the manufacturing process, such as components of the fermentation medium or defoaming and flocculating agents used during fermentation and recovery. When FDA reviews safety data on enzyme preparations, it considers all components of the preparation.

Defoaming Agents

Defoaming agents (defoamers) are used by enzyme manufacturers to reduce or prevent foaming during fermentation and recovery. They are formulated with ancillary ingredients such as surface-active agents or carriers. Defoamers currently used in the manufacture of food enzymes are listed in Table 1. The Table includes five major defoamers that are identified by a double asterisk and several compounds that are used either as secondary defoamers or ancillary ingredients in defoamer formulations.

The major defoamers are added to the fermentation broth at levels within the range of 0.05-1% on a weight basis. Some of these defoamers, for example, polyoxyethylene-polyoxypropylene block copolymer, may contain trace levels of ethylene oxide, propylene oxide, and 1,4-dioxane which are known to cause cancer in laboratory animals. The Office of Food Additive Safety (OFAS) has evaluated the use of defoamers listed in Table 1 and determined that human exposure to the residues of these defoamers in enzyme preparations does not present human safety concern.

Flocculating Agents

Flocculating agents (flocculants) are used in the enzyme recovery step to separate microbial cells and cell debris from the fermentation broth containing the dissolved enzyme. The flocculation typically consists of two steps - primary flocculation and secondary flocculation. In the primary flocculation, inorganic salts (such as calcium chloride or aluminum sulfate) or "low molecular weight" polymers (such as polyamines) are used to agglomerate the cellular debris. The primary flocculation is usually followed by the secondary flocculation in which "high molecular weight" polymers are used to aid the formation of larger agglomerates that are subsequently removed by centrifugation or filtration. The polymers used as flocculants can be either cationic or anionic. The cationic polymers are added to the fermentation broth at levels not higher than 1% on a

weight basis. The anionic polymers are used at levels at or below 0.025%.

The flocculants used in the manufacture of food enzymes are listed in Table 2. They include inorganic salts, polyamines, and polyacrylamides. Several of these compounds are regulated in 21 CFR either as food additives or GRAS substances. Certain polyamines may contain traces of epichlorohydrin and 1,3-dichloro-2-propanol. Polyacrylamides usually contain very low levels of acrylamide. These contaminants of polyamines and polyacrylamides are known to cause cancer in laboratory animals. OFAS has evaluated all polymers included in Table 2 and determined that human exposure to the residues of these flocculants in enzyme preparations does not present human safety concern.

Sources of Information on Defoamers and Flocculants

OFAS compiled data on defoamers and flocculants listed in Tables 1 and 2 using information voluntarily submitted by the Enzyme Technical Association. OFAS also relied on the information provided in GRAS affirmation petitions and GRAS notices for enzyme preparations. Other sources of information included published articles, computer searches, and Material Safety Data Sheets issued by manufacturers of defoamers and flocculants.

Table 1. Defoamers Used in the Manufacture of Food Enzymes

Compound	CAS Reg. No.	Supplemental Information
Polypropylene glycol**	25322-69-4	Average MW: 2000
Polyglycerol polyethylene-polypropylene glycol ether oleate**	78041-14-2	
Polyoxyethylene-polyoxypropylene block copolymer**	9003-11-6	Average MW: 2000
Polypropylene glycol monobutyl ether**	9003-13-8	
Polydimethylsiloxane**	63148-62-9 68083-18-1	
Silica	7631-86-9 63231-67-4	
Stearic acid	57-11-4	
Sorbitan sesquioleate	8007-43-0	
Glycerol monostearate	123-94-4	
Polysorbates (polyoxyethylene sorbitan fatty acid esters)		Polysorbate 60 (CAS No. 9005-67-8), Polysorbate 65 (CAS No. 9005-71-4), and polysorbate 80 (CAS No. 9005-65-6) are regulated as food additives and components of defoamer formulations
Rape oil mono- and diglycerides	93763-31-6	
White mineral oil	64742-47-8	

Table 2. Flocculants Used in the Manufacture of Food Enzymes

Compound	CAS Reg. No.	Supplemental Information
Dimethylamine-epichlorohydrin copolymer	25988-97-0	Cationic polyamine
Methylamine-epichlorohydrin copolymer	31568-35-1	Cationic polyamine
Dimethylamine-epichlorohydrin-ethylenediamine terpolymer	42751-79-1	Cationic polyamine
Polyacrylamide modified by condensation with formaldehyde and dimethylamine	67953-80-4	Cationic polyacrylamide
Acrylamide-acryloxyethyl-trimethyl-ammonium chloride copolymer	69418-26-4	Cationic polyacrylamide
Acrylamide-acrylic acid copolymer	25987-30-8 9003-06-9	Anionic polyacrylamide
Aluminum sulfate	10043-01-3	
Calcium chloride	10035-04-8 10043-52-4	

ASCUS BIOSCIENCES

Specifications for Salt

Ingredient:	Sodium Chloride
Chemical Nomenclature:	NaCl
Specifications:	Feed/Food Grade or FCC
Moisture:	≤ 1.5% by LOD
Purity:	≥ 95%

Thiamine Hydrochloride

(b) (4)

Specification for Thiamine Hydrochloride, FCC (T1053)

Item Number	T1053
Item	Thiamine Hydrochloride, FCC
CAS Number	67-03-8
Molecular Formula	$C_{12}H_{17}ClN_4OS.HCl$
Molecular Weight	337.27
MDL Number	
Synonyms	3-(4-Amino-2-methylpyrimidin-5-ylmethyl)-5-(2-hydroxyethyl)-4-methylthiazolium Chloride

Test	Specification	
	Min	Max
ASSAY ($C_{12}H_{17}ClN_4OS$•HCl)	98.0 - 102.0 %	
COLOR OF SOLUTION		TO PASS TEST
pH OF A 1 IN 100 SOLUTION	2.7 - 3.4	
LEAD (Pb)		2 mg/kg
NITRATE (NO_3)		TO PASS TEST
RESIDUE ON IGNITION		0.2 %
WATER		5.0 %
IDENTIFICATION		TO PASS TEST
EXPIRATION DATE		

(b) (4)

(b) (4)

Technical Data Sheet

Revision Date: 8/14/2017 Version: 8

Product Code: AX1003-40-AG

Product Name: AMBEREX 1003 AG 40 LB BAG

Company Name: (b) (4)

General Information

All raw materials from which this product is produced meet appropriate food grade specifications. The processing, packaging, and storage of the finished product and the raw materials from which it is produced are consistent with current Good Manufacturing Practices (cGMP) and current industry practices. All information presented herein is in accordance to the regulation of country of manufacture USA.

Application (Dosage, Application, Usage)

Not Available

Processing Information: An excellent source of peptides, free amino nitrogen, vitamins, minerals and trace elements.

North America Ingredient List

Yeast Extract

FEMA/GRAS

All ingredients contained in this product conform in every respect to the United States Food & Drug Regulations and all flavor components are FEMA GRAS approved.

Quality Specification (Version number 4.00)

Sensorial Test	Min	Max	Target	UoM	Method
Physical State:			Solid		
Appearance:			Powder		Visual
Odor			Slightly Meaty, Slightly Beerish	2% Solution	
Color			Medium Brown, Yellow Tones	2% Solution	
Flavor:			Beefy, Bitter, Beerish, Roasted	2% Solution	

Analytical Test	Min	Max	Target	UoM	Method
Flash Point			201 °F		
Moisture		6		%	AOAC 930.15
pH	5.3	6.3		%	AOAC 930.30
Salt (as Chlorides)		1.5		%	AOAC 971.27

Microbiological Test	Min	Max	Target	UoM	Method
Standard Plate Count / Compte Sur Plaque Standard			<10,000	cfu/g	AOAC 990.12
Yeast & Mold		100		cfu/g	AOAC 121301

Coliform	10	/ gram	AOAC 966.24
E. coli	Non Detected	/ gram	AOAC 966.24
Salmonella	Negative	/750g	AOAC RI 100201
Listeria	Negative	/25g	AOACRI030502 AOAC2003.12

Allergen Properties

US Allergen Name	Status	Notes
Milk and Milk Products	Free	
Egg and Egg Products	Free	
Fish - Anchovy	Free	
Fish - Bonito	Free	
Fish - Cod	Free	
Fish - Menhaden	Free	
Fish - Salmon	Free	
Fish - Tuna	Free	
Crustacean shellfish - Crab	Free	
Crustacean shellfish - Lobster	Free	
Crustacean shellfish - Shrimp	Free	
Tree Nuts - Almond	Free	
Tree Nuts - Brazil nut	Free	
Tree Nuts - Cashew	Free	
Tree Nuts - Chestnut	Free	
Tree Nuts - Coconut	Free	
Tree Nuts - Ginko nut	Free	
Tree Nuts - Hazelnut	Free	
Tree Nuts - Lichee nut	Free	
Tree Nuts - Macadamia	Free	
Tree Nuts - Pecan	Free	
Tree Nuts - Pistachio	Free	
Tree Nuts - Walnut	Free	
Wheat	Free	
Peanuts and Peanut Products	Free	
Soybeans and Soybean Products	Free	

US Sensitizers Name	Status	Notes
Aspartame	Free	
Celery	Free	
Corn and Corn Products	Free	
FD&C Blue #1	Free	
FD&C Blue #2	Free	
FD&C Green #3	Free	
FD&C Red #2	Free	
FD&C Red #3	Free	
FD&C Red #40	Free	
FD&C Yellow #5	Free	
FD&C Yellow #6	Free	
Barley from the brewing process	Present	
Gluten (Barley)	Present	
Gluten (Oats)	Free	
Gluten (Rye)	Free	
Gluten (Wheat)	Free	
MSG	Free	
Naturally occurring Glutamic Acid	Free	
Mustard and Mustard Products	Free	
RBD Oils (Coconut)	Free	
RBD Oils (Canola)	Free	
RBD Oils (Cottonseed)	Free	
RBD Oils (Palm)	Free	
RBD Oils (Rice Bran)	Free	
RBD Oils (Safflower)	Free	
RBD Oils (Soy)	Free	
RBD Oils (Sunflower)	Free	
RBD Oils (Vegetable)	Free	

Sesame and Sesame Products	Free
Sulfites	Free

Nutritional - Average Nutritional Values per 100g

Nutrient	Qty	UM
Energy	326.0	kcal
Energy from fat	1.0	kcal
Fat	0.0	g
of which		
-saturated	0.0	g
Trans fatty acids	0.01	g
Cholesterol	1.0	mg
Sodium	2000.0	mg
Carbohydrate	24.3	g
of which		
-sugars	0.1	g
of which		
-Added Sugar	0.00	g
Fibre, Total Dietary	4.1	g
Protein	57.3	g
Potassium	2470.0	mg
Vitamin D (Calciferol)	0.00	µg
VITAMIN A - RAE	Not Available	
Vitamin A (Retinol)	Not Available	
Vitamin C (Ascorbic Acid)	0.00	mg
Calcium	194.00	mg
Iron	6.00	mg
Moisture	6.2	g
Ash	12.20	g

Religious Status

Kosher:
This product is Kosher suitable and has a status of Pareve. Contact (b) (4) for a Rabbinical Certificate, subject to availability.

Halal:
This product is Halal suitable. Contact (b) (4) for a Halal Certificate, subject to availability.

MUI:
This product is not MUI suitable.

Dietary Status

This product is suitable for Vegan.

GMO Status

This product is not derived from genetically modified source.

Organic Status

This product is not Organic.

Shelf Life, Temperature, Storage Condition

Shelf life	Temperature	Condition
24 months	Store Ambient	This product is hygroscopic and storage under cool and dry conditions is recommended. Packages should not be in direct contact with floors or walls. Stock should be used in a first-in-first-out rotation.

Packaging Configuration

Packaging Configuration

Net Weight	UoM	Packaging
40.000000	lbs	

Disclaimer

This specification, which is computer generated & does not carry a signature, is correct at the time of issue but may be subject to alteration.

The information on this specification, which remains the property of [redacted] (b) (4) is to the best of their knowledge and it should not be construed as a warranty.

Users should conduct their own tests to determine the suitability of this product/ data for their purposes.
Technical information and proposed formulations, including any production procedures, are believed to be correct.
While we believe materials supplied by our organization are legal in the country of use, we do not warrant or guarantee their legality and highly recommend the user confers with local authorities before use.

(b) (4)

DESCRIPTION

(b) (4) **is a primary yeast extract obtained by the autolysis of a selected strain of *Saccharomyces cerevisiae* yeast, especially grown on a molasses based media.**

CERTIFICATION

This product is guaranteed to be Non-GM, free of animal origin ingredient and Kosher.

APPLICATIONS

Recommended for most fermentation processes and laboratory media formulations :
High quality source of readily available soluble, amino acids, peptides, vitamins and essential elements.

PHYSICO-CHEMICAL CHARACTERISTICS

Solubility	Totally soluble
Colour of commercial product	Light beige
Colour in 10 % solution	Light clear yellow

Composition
in g per 100 g of product as is

Dry matter	**94.0**	**-**	**98.0**
Total nitrogen	**10.0**	**-**	**11.8**
Amino nitrogen	**4.5**	**-**	**5.8**
pH	**6.8**	**-**	**7.2**
Sodium chloride		**<**	**0.5**
Proteins (Nitrogen x 6.25)	62.5	-	73.8
Total carbohydrates	7.0	-	13.0
Ash	11.5	-	16.0

MICROBIOLOGICAL CHARACTERISTICS

CFU per g of product

Total plate count	**<**	**5 000**
Coliforms	**<**	**5**
Spores of Clostridium perfringens	**<**	**10**
Yeasts	**<**	**50**
Moulds	**<**	**50**
Salmonella *(per 25 g)*	**Negative**	
E.coli	**Negative**	
Staphylococcus aureus	**Negative**	

(Guaranteed values are listed in bold ; other values are given for indication only)

(b) (4)

AVERAGE AMINO ACID COMPOSITION

expressed in 100 g of raw proteins

Alanine	8.8	Lysine	8.0
Arginine	5.1	Methionine	1.4
Aspartic acid	9.9	Phenylalanine	3.7
Cystine	0.9	Proline	4.0
Glutamic acid	16.3	Serine	4.6
Glycine	4.8	Threonine	4.6
Histidine	2.1	Tyrosine	2.4
Isoleucine	5.5	Tryptophan	1.3
Leucine	7.6	Valine	5.9

AVERAGE VITAMIN COMPOSITION

in mg per kg (ppm)
(dry matter)

B1 (Thiamine)	15	-	110
B2 (Riboflavin)	80	-	130
B5 (Calcium Pantothenate)	200	-	400
B6 (Pyridoxine)	30	-	100
B8 (Biotin)	3	-	10
B9 (folic acid)	15	-	60
B12 (Cyanocobalamine) *(µg/kg)*	1	-	5
PP (Niacin)	600	-	1000

MINERALS

in g per 100 g of product as is

Sodium		<	0.5
Potassium	4.5	-	6.3
Phosphorus	1.0	-	2.7
Calcium *(ppm)*	100	-	300
Magnesium *(ppm)*	150	-	800
Selenium *(ppm)*		<	0.1
Zinc *(ppm)*		<	90

HEAVY METALS

in mg per kg (ppm)

Arsenic	<	0.5
Cadmium	<	0.1
Mercury	<	0.05
Lead	<	0.2

PACKAGING

Powder :
- 25 kg sealed paper bags with polyethylene liner / pallets of 750 or 1000 kg,
- 25 kg carboard boxes with polyethylene liner / pallets of 900 kg,
- 500 kg big bags.

Micrograniulated powder :
- 25 kg sealed paper bags with polyethylene liner / pallets of 500 or 600 kg,
- 25 kg carboard boxes with polyethylene liner / pallets of 720 kg,
- 500 or 700 kg big bags.

SHELF LIFE & STORAGE

3 years in their original packaging, stored in a cool and dry place protected from direct sun-light.

0.75 mg/mL to another conical flask. Add 1 mL of *Fehling's Solution A* and of *Fehling's Solution B* (see *Cupric Tartrate TS, Alkaline*, under *Solutions and Indicators*) to each flask, heat to boiling, and cool. The sample solution is less turbid than the dextrose solution, which forms a red-brown precipitate.

Residue on Ignition Determine as directed under *Residue on Ignition*, Appendix IIC, igniting a 2-g sample.

Water Determine as directed under *Water Determination*, Appendix IIB.

Packaging and Storage Store in well-closed containers in a dry place.

Yeast, Autolyzed

Autolyzed Yeast

DESCRIPTION

Yeast, Autolyzed, occurs in granular, powdered, flake, or paste form. It is the concentrated, nonextracted, partially soluble digest obtained from food-grade yeasts. Solubilization is accomplished by enzyme hydrolysis or autolysis of yeast cells. Food-grade salts and enzymes may be added. Yeast, Autolyzed contains both soluble and insoluble components derived from the whole yeast cell. It is composed primarily of amino acids, peptides, proteins, carbohydrates, fats, and salts.

Function Flavoring agent; flavor enhancer; protein source; binder.

REQUIREMENTS

Note: Perform all analyses after drying. Liquid and paste samples should be evaporated to dryness on a steam bath, then, as for the powdered and granular forms, dried to constant weight at 65° (see *General Provisions*).

Assay Not less than 6.1% total nitrogen, which is equivalent to not less than 38.1% protein (%N × 6.25), calculated on the sodium chloride-free basis.

α-Amino Nitrogen/Total Nitrogen (AN/TN) Percent Ratio Not less than 5.0%.

Ammonia Nitrogen Not more than 1.0%, calculated on the sodium chloride-free basis.

Glutamic Acid Not more than 13.0% of glutamic acid ($C_4H_7NO_4$), calculated on the sodium chloride-free basis, and not more than 24.0% of the total amino acids.

Insoluble Matter Between 20.0% and 60.0%.

Lead Not more than 2 mg/kg.

Mercury Not more than 3 mg/kg.

Microbial Limits:

Aerobic Plate Count Not more than 50,000 CFU per gram.

Coliforms Not more than 10 CFU per gram.

Salmonella Negative in 25 g.

Yeasts and Molds Not more than 50 CFU per gram.

Potassium Not more than 13.0%.

Sodium Chloride Not more than 43.0%.

TESTS

Assay Determine as directed under *Nitrogen Determination*, Appendix IIIC. Calculate the percent protein (*P*) by the formula

$$P = 6.25N,$$

in which *N* is the percent nitrogen.

α-Amino Nitrogen/Total Nitrogen (AN/TN) Percent Ratio Determine *α-Amino Nitrogen* as directed under *α-Amino Nitrogen Determination*, Appendix IIIC. Determine *Total Nitrogen* as directed under *Nitrogen Determination*, Appendix IIIC. Calculate the AN/TN percent ratio by dividing the percent α-amino nitrogen (*AN*) by the percent total nitrogen (*TN*) as corrected for ammonia nitrogen (NH_3-*N*) according to the formula

$$100[(AN - NH_3\text{-}N)/(TN - NH_3\text{-}N)].$$

Ammonia Nitrogen Determine as directed under *Ammonia Nitrogen*, Appendix IIIC.

Glutamic Acid Determine as directed under *Glutamic Acid*, Appendix IIIC.

Insoluble Matter Transfer about 5 g of sample, accurately weighed, into a 250-mL Erlenmeyer flask. Add 75 mL of water, cover the flask with a watch glass, and boil gently for 2 min. Filter the solution through a tared filtering crucible, dry at 105° for 1 h, cool, and weigh.

Lead Determine as directed in the *Flame Atomic Absorption Spectrophotometric Method* under *Lead Limit Test*, Appendix IIIB, using a 10-g sample.

Mercury Determine as directed under *Mercury Limit Test*, Appendix IIIB.

Microbial Limits (**Note:** Current methods for the following tests may be found online at <www.cfsan.fda.gov/~ebam/bam-toc.html>):

Aerobic Plate Count

Coliforms

Salmonella

Yeasts and Molds

Potassium

Spectrophotometer Use any suitable atomic absorption spectrophotometer.

Standard Solution Transfer 38.20 mg of reagent-grade potassium chloride, accurately weighed, into a 100-mL volumetric flask, dissolve in and dilute to volume with deionized water, and mix. Transfer 5.0 mL of this solution to a 1000-mL volumetric flask, dilute to volume with deionized water, and mix. Each milliliter contains 1.0 μg of potassium (K).

Sample Solution Transfer 2.33 g of a previously dried sample, accurately weighed, into a silica or porcelain dish. Ash in a muffle furnace at 550° for 2 to 4 h. Allow the ash to cool, and dissolve it in 5 mL of 20% hydrochloric acid, warming the solution if necessary to complete solution of the residue. Filter the solution through acid-washed filter paper into a 1000-mL volumetric flask. Wash the filter paper with hot water, dilute the solution to volume, and mix. Prepare a 1:300 dilution of this solution in water to obtain the final *Sample Solution*.

Procedure Determine the absorbance of each solution at 766.5 nm, following the manufacturer's instructions for optimum operation of the spectrophotometer. The absorbance of the *Sample Solution* does not exceed that of the *Standard Solution*.

Sodium Chloride

Spectrophotometer Use any suitable atomic absorption spectrophotometer.

Standard Solution Transfer 43.0 mg of reagent-grade sodium chloride, accurately weighed, into a 100-mL volumetric flask, dissolve in and dilute to volume with deionized water, and mix. Using water as the solvent, prepare a 1:100 dilution of this solution to obtain the final working *Standard Solution*. Each milliliter contains 4.3 μg of sodium chloride (NaCl).

Sample Solution Transfer 1.00 ± 0.05 g of a previously dried sample, accurately weighed, into a silica or porcelain dish. Ash in a muffle furnace at 550° for 2 to 4 h. Allow the ash to cool, and dissolve it in 5 mL of 20% hydrochloric acid, warming the solution if necessary to complete solution of the residue. Filter the solution through acid-washed filter paper into a 100-mL volumetric flask. Wash the filter paper with hot water, dilute the solution to volume, and mix. Using water as the solvent, prepare a 1:100 dilution of this solution to obtain the final *Sample Solution*.

Procedure Determine the absorbance of each solution at 589.0 nm, following the manufacturer's instructions for optimum operation of the spectrophotometer. The absorbance produced by the *Sample Solution* does not exceed that of the *Standard Solution*.

Packaging and Storage Store in well-closed containers.

Yeast, Dried

Brewer's Yeast; Dried Yeast; Torula Yeast

DESCRIPTION

Yeast, Dried, occurs as a light brown to buff powder, granules, or flakes. It is the comminuted, washed, dried, and pasteurized cell walls from *Saccharomyces cerevisiae*, *Saccharomyces fragilis*, or *Torula utilis*. It contains no added substances.

Function Carrier; flavor enhancer.

REQUIREMENTS

Identification When examined under a microscope, a sample exhibits numerous irregular masses and isolated yeast cells—the latter ovate, elliptical, spheroidal, or elliptic-elongate in shape, some with one or more attached buds—up to 12 μm in length and up to 7.5 μm in width. Each has a wall of cellulose surrounding a protoplast containing refractile glycogen vacuoles and oil globules.

Assay Not less than 45.0% protein.

Ash (Total) Not more than 8.0%.

Folic Acid Not more than 0.04 mg/g.

Lead Not more than 1 mg/kg.

Loss on Drying Not more than 7.0%.

Microbial Limits:

Aerobic Plate Count Not more than 7500 CFU per gram.

Coliforms Not more than 10 CFU per gram.

Salmonella Negative in 25 g.

TESTS

Assay Determine the percent nitrogen as directed under *Nitrogen Determination*, Appendix IIIC, and multiply by 6.25 to obtain the percent protein.

Ash (Total) Determine as directed under *Ash (Total)*, Appendix IIC.

Folic Acid (**Note**: In the microbiological assay of folic acid, the microorganism is highly sensitive to minute amounts of growth factors and to many cleansing agents. Meticulously cleanse 20- × 150-mm test tubes and other necessary glassware with a suitable detergent, sodium lauryl sulfate, or an equivalent substitute. Follow cleansing by heating for 1 to 2 h at approximately 250°.) This method is based on AOAC method 960.46.

Vitamin-Free, Acid-Hydrolyzed Casein Solution Prepare the solution by mixing 400 g of vitamin-free casein with 2 L of boiling 5 *N* hydrochloric acid. Autoclave for 10 h at 121°. Concentrate the mixture by distillation under reduced pressure until a thick paste remains. Redissolve the paste in water, adjust the solution to pH 3.5 ± 0.1 with a 10% solution of sodium hydroxide, and dilute with water to a final volume of 4 L. Add 80 g of activated charcoal, stir for 1 h, and filter. Repeat the treatment with activated charcoal. Filter the solution if a precipitate forms on storage.

Adenine–Guanine–Uracil Solution Dissolve 1.0 g each of adenine sulfate, guanine hydrochloride, and uracil in 50 mL of warm 1:2 hydrochloric acid, cool, and dilute with water to 1 L.

Asparagine Solution Dissolve 10 g of L-asparagine monohydrate in approximately 500 mL of water, and dilute with water to 1 L.

Manganese Sulfate Solution Dissolve 2.0 g of manganese sulfate monohydrate in water, and dilute with water to 200 mL.

Polysorbate 80 Solution Dissolve 25 g of polysorbate 80 (polyoxyethylene sorbitan monooleate) in ethyl alcohol, and dilute with ethyl alcohol to make 250 mL.

Salt Solution Dissolve 20 g of magnesium sulfate heptahydrate, 1 g of sodium chloride, 1 g of ferrous sulfate heptahydrate, and 1 g of manganese sulfate monohydrate in water, dilute with water to 1 L, add 10 drops of hydrochloric acid, and mix.

Tryptophan Solution Suspend 2.0 g of L-tryptophan in 800 mL of water, heat to 80°, and add, dropwise and while stirring, 1:2 hydrochloric acid until the suspension dissolves. Cool, and dilute with water to 1 L.

Vitamin Solution Dissolve 10 mg of *p*-aminobenzoic acid, 8 mg of calcium pantothenate, 40 mg of pyridoxine hydrochloride, 4 mg of thiamine hydrochloride, 8 mg of niacin, and 0.2 mg of biotin in approximately 300 mL of water. Add 10 mg of riboflavin dissolved in approximately 200 mL of 0.02 *N* acetic acid. Add a solution containing 1.9 g of anhydrous sodium acetate and 1.6 mL of glacial acetic acid in approximately 40 mL of water. Dilute the solution with water to a final volume of 2 L.

Xanthine Solution Suspend 1.0 g of xanthine in 200 mL of water, heat to approximately 70°, add 30 mL of 2:5 ammonium hydroxide, and stir until the suspension dissolves. Cool, and dilute with water to 1 L.

Basal Medium Stock Solution Prepare the solution by adding, with mixing, in the following order, 25 mL of the *Vitamin-Free, Acid-Hydrolyzed Casein Solution*, 25 mL of the *Tryptophan Solution*, 2.5 mL of the *Adenine–Guanine–Uracil Solution*, 5 mL of the *Xanthine Solution*, 15 mL of the *Asparagine Solution*, 50 mL of the *Vitamin Solution*, and 5 mL of the *Salt Solution*. Add approximately 50 mL of water, and add, with mixing, 0.19 g of L-cysteine monohydrochloride monohydrate, 10 g of anhydrous glucose, 13 g of sodium citrate dihydrate, 1.6 g of anhydrous dipotassium hydrogen phosphate, and 0.0013 g of glutathione. When solution is complete, adjust to pH 6.8 with 10% sodium hydroxide solution, and add, with mixing, 0.25 mL of the *Polysorbate 80 Solution* and 5 mL of the *Manganese Sulfate Solution*. Dilute to a final volume of 250 mL with water.

Liquid Culture Medium Dissolve 15 g of peptonized milk, 5 g of water-soluble yeast extract, 10 g of anhydrous glucose, and 2 g of anhydrous potassium dihydrogen phosphate in about 600 mL of water. Add 100 mL of filtered tomato juice (filtered through Whatman No. 1 filter paper, or equivalent), and adjust to pH 6.5 by the dropwise addition of 1.0 *N* sodium hydroxide. Add, with mixing, 10 mL of the *Polysorbate 80 Solution*. Dilute with water to a final volume of 1000 mL. Add 10-mL portions of this *Liquid Culture Medium* to test tubes, cover to prevent contamination, and sterilize by heating in an autoclave at 121° for 15 min. Cool the tubes rapidly to keep color formation to a minimum, and store at 10° in the dark.

Agar Culture Medium Add 6.0 g of agar to 500 mL of *Liquid Culture Medium*, and heat with stirring on a steam bath until the agar dissolves. Add approximately 10-mL portions of the hot solution to test tubes, cover to prevent contamination, sterilize by heating in an autoclave at 121° for 15 min, and cool tubes in an upright position to keep color formation to a minimum. Store at 10° in the dark.

Suspension Medium Dilute an appropriate volume of the *Basal Medium Stock Solution* with an equal volume of water. Distribute 10-mL portions of this *Suspension Medium* to test tubes, cover to prevent contamination, sterilize by heating in an autoclave at 121° for 15 min, and cool tubes rapidly to keep color formation to a minimum. Store at 10° in the dark.

Assay Organism Maintain *Enterococcus* (*Streptococcus*) *faecalis* ATCC 8043 by subculturing in stab cultures of *Agar Culture Medium* and incubating at 37° for 24 h. Stab cultures may be stored in the dark at 10° for a maximum of 7 days until use. Prepare fresh stab cultures at least on a weekly basis. Before using a new culture in the assay, make several successive transfers of the culture over a 1- to 2-week period. Transfer cells from the stab culture of *Assay Organism* to a sterile tube containing 10 mL of *Liquid Culture Medium*. Incubate for 18 h at 37°. Under aseptic conditions, centrifuge the culture, and decant the supernate. Wash the cells with three 10-mL portions of sterile *Suspension Medium*. Resuspend cells in 10 mL of sterile *Suspension Medium*—these cells serve as the inoculum.

Folic Acid Stock Solutions Accurately weigh, in a closed system, 50 to 60 mg of USP Folic Acid Reference Standard that has been dried to constant weight and stored in the dark over phosphorus pentoxide in a desiccator. Dissolve in approximately 30 mL of 0.01 *N* sodium hydroxide, add approximately 300 mL of water, adjust to pH 7.5 with 1:2 hydrochloric acid, and dilute with additional water to a final folic acid concentration of exactly 100 µg/mL. Store under toluene in the dark at 10°.

Prepare an intermediate *Folic Acid Stock Solution* containing 1 µg/mL by placing 10 mL of the 100 µg/mL *Folic Acid Stock Solution* in a flask, adding approximately 500 mL of water, adjusting to pH 7.5 with dilute hydrochloric acid or sodium hydroxide as necessary, and diluting with additional water to a final volume of 1 L. Store under toluene in the dark at 10°.

Prepare the final *Folic Acid Stock Solution* by taking 100 mL of the intermediate *Folic Acid Stock Solution*, adding approximately 500 mL of water, adjusting to pH 7.5 with dilute hydrochloric acid or sodium hydroxide as necessary, and diluting with additional water to a final volume of 1 L. Store under toluene in the dark at 10°. This final *Folic Acid Stock Solution* has a concentration of 100 ng/mL.

Preparation of the Standard Curve Dilute the *Folic Acid Stock Solution* with water to a measured volume such that after incubation, as described below, response at the 5.0-mL level of this solution is equivalent to a titration volume of 8 to 12 mL. This concentration is usually 1 to 4 ng of folic acid per mL but can vary with the culture used in the assay. Designate this solution as the *Folic Acid Working Standard Solution*. To duplicate test tubes, add 0.0 (for uninoculated blanks), 0.0 (for inoculated blanks), 1.0, 2.0, 3.0, 4.0, and 5.0 mL, respectively, of the *Folic Acid Working Standard Solution*. Add water to each tube to make a final volume of 5.0 mL. Add 5.0 mL of the *Basal Medium Stock Solution* to each tube, and mix. Cover the tubes suitably to prevent bacterial contamination, and sterilize by heating in an autoclave at 121° for 10 min. Cool tubes rapidly to keep color formation to a minimum.

Note: Sterilizing and cooling conditions must be kept uniform to obtain reproducible results.

Aseptically inoculate each tube with 1 drop of the *Assay Organism* inoculum, except for one set of duplicate tubes containing 0.0 mL of the *Folic Acid Working Standard Solution*, which serve as the uninoculated blanks. Incubate the tubes for 72 h at 37°.

Note: Contamination of assay tubes with any foreign organism invalidates the assay.

Titrate the contents of each tube with 0.1 *N* sodium hydroxide, using bromothymol blue as the indicator. Disregard the results of the assay if the titration volume for the inoculated blank is more than 1.5 mL greater than that for the uninoculated blank. The titration volume for the 5.0-mL level of the *Folic Acid Working Standard Solution* should be approximately 8 to 12 mL. Prepare a standard curve by plotting the titration values, expressed in milliliters of 0.1 *N* sodium hydroxide for each level of the *Folic Acid Working Standard Solution* used, against the amount of folic acid contained in that tube.

Assay Solution Weigh and suspend 1.0 g of sample in 100 mL of water. Add 2 mL of 2:5 ammonium hydroxide. If the sample is not readily soluble, comminute to disperse it evenly in the liquid, then agitate vigorously and wash down the sides of the flask with 0.1 *N* ammonium hydroxide. Heat the mixture in an autoclave at 121° for 15 min. If lumping occurs, agitate the sample until the particles are evenly dispersed. Dilute the mixture with water to 200 mL. Filter through Whatman No. 1 filter paper, or equivalent, if necessary, to remove any undissolved particles. Adjust the filtered mixture to pH 6.8 and dilute to 1000 mL with water. Prepare the final *Assay Solution* by diluting 1.0 mL of the intermediate solution with water to a final volume of 50.0 mL.

Procedure To duplicate test tubes, add 0.0 (for uninoculated blanks), 0.0 (for inoculated blanks), 1.0, 2.0, 3.0, 4.0, and 5.0 mL, respectively, of the *Assay Solution*. Add water to each tube to make a final volume of 5.0 mL. Proceed as directed above for *Preparation of the Standard Curve*. Determine the amount of folic acid for each level of the *Assay Solution* by interpolation from the standard curve. Discard any observed titration values equivalent to less than 0.5 mL or more than 4.5 mL of the *Folic Acid Working Standard Solution*. If necessary, the *Assay Solution* can be diluted to achieve the ideal concentration range of folic acid. For each level of *Assay Solution* used, calculate the vitamin content per milliliter of *Assay Solution*. Calculate the average vitamin content of values obtained from tubes that do not vary by greater than 10% from this average. More than two-thirds of the original number of tubes must be within 10% of the average folic acid value, or the data cannot be used to calculate the folic acid concentration in the sample. If the data are acceptable, determine the folic acid concentration in the sample by multiplying the average folic acid concentration, in nanograms per milliliter, of the *Assay Solution* by 0.025 to give the milligrams of folic acid per gram of sample.

Lead Determine as directed for *Method II* in the *Atomic Absorption Spectrophotometric Graphite Furnace Method* under *Lead Limit Test*, Appendix IIIB.

Loss on Drying Determine as directed under *Loss on Drying*, Appendix IIC, drying a 1-g sample at 105° for 4 h.

Microbial Limits (**Note:** Current methods for the following tests may be found online at <www.cfsan.fda.gov/~ebam/bam-toc.html>):

Aerobic Plate Count
Coliforms
Salmonella

Packaging and Storage Store in tight containers in a cool, dry place.

Yeast Extract

Autolyzed Yeast Extract

DESCRIPTION

Yeast Extract occurs as a liquid, paste, powder, or granular substance. It comprises the water-soluble components of the yeast cell, the composition of which is primarily amino acids, peptides, carbohydrates, and salts. Yeast Extract is produced through the hydrolysis of peptide bonds by the naturally occurring enzymes present in edible yeasts or by the addition of food-grade enzymes. Food-grade salts may be added during processing.

Function Flavoring agent; flavor enhancer.

REQUIREMENTS

Note: Perform all calculations on the dried basis. In a suitable tared container, evaporate liquid and paste samples to dryness on a steam bath, then, as for the powdered and granular forms, dry to constant weight at 105° (see *General Provisions*).

Assay (Protein) Not less than 42.0% protein.
α-Amino Nitrogen/Total Nitrogen (AN/TN) Percent Ratio Not less than 15.0% or more than 55.0%.
Ammonia Nitrogen Not more than 2.0%, calculated on a dry, sodium chloride-free basis.
Glutamic Acid Not more than 12.0% as $C_5H_9NO_4$ and not more than 28.0% of the total amino acids.
Insoluble Matter Not more than 2%.
Lead Not more than 2 mg/kg.
Mercury Not more than 3 mg/kg.
Microbial Limits:
Aerobic Plate Count Not more than 50,000 CFU per gram.
Coliforms Not more than 10 CFU per gram.
Salmonella Negative in 25 g.
Yeasts and Molds Not more than 50 CFU per gram.
Potassium Not more than 13.0%.
Sodium Chloride Not more than 50.0%.

TESTS

Assay (Protein) Determine as directed under *Nitrogen Determination*, Appendix IIIC. Calculate the percent protein (*P*) by the equation

$$P = 6.25N,$$

in which *N* is the percent nitrogen.

α-Amino Nitrogen/Total Nitrogen (AN/TN) Percent Ratio Determine *α-Amino Nitrogen* as directed under *α-Amino Nitrogen Determination*, Appendix IIIC. Determine *Total Nitrogen* as directed under *Nitrogen Determination*, Appendix IIIC. Calculate the *AN/TN* percent ratio, in which *AN* is the percent of α-amino nitrogen and *TN* is the percent of total nitrogen.

Ammonia Nitrogen Determine as directed under *Ammonia Nitrogen*, Appendix IIIC.

Glutamic Acid Determine as directed under *Glutamic Acid*, Appendix IIIC.

Insoluble Matter Transfer about 5 g of sample, accurately weighed, into a 250-mL Erlenmeyer flask, add 75 mL of water, cover the flask with a watch glass, and boil gently for 2 min. Filter the solution through a tared filtering crucible, dry at 105° for 1 h, cool, and weigh.

Lead Determine as directed in the *Flame Atomic Absorption Spectrophotometric Method* under *Lead Limit Test*, Appendix IIIB, using a 10-g sample.

Mercury Determine as directed under *Mercury Limit Test*, Appendix IIIB.

Microbial Limits (**Note:** Current methods for the following tests may be found online at <www.cfsan.fda.gov/~ebam/bam-toc.html>):

Aerobic Plate Count
Coliforms
Salmonella
Yeasts and Molds

Potassium Proceed as directed in the monograph for *Yeast, Autolyzed*.

Sodium Chloride Proceed as directed in the monograph for *Yeast, Autolyzed*, except to use 50.0 mg of reagent-grade sodium chloride to prepare the *Standard Solution*.

Packaging and Storage Store in well-closed containers.

Zein

CAS: [9010-66-6]

DESCRIPTION

Zein occurs as a very light yellow to tan colored, granular or fine powder. It comprises the prolamine protein component of corn (*Zea mays* Linne'). It is produced commercially by extraction from corn gluten with alkaline aqueous isopropyl alcohol. The extract is then cooled, which causes the Zein to precipitate. It is insoluble in water.

Function Surface-finishing agent; texturizing agent.

REQUIREMENTS

Identification

A. Dissolve about 0.1 g of sample in 10 mL of 0.1 *N* sodium hydroxide, and add a few drops of cupric sulfate TS. Warm in a water bath. A purple color appears.

B. Add 1 mL of nitric acid to a test tube containing 25 mg of sample. Agitate vigorously. The solution turns light yellow. Further addition of about 10 mL of 6 *N* ammonium hydroxide produces an orange color.

Assay Not less than 88.0% and not more than 96.0% protein, calculated on the dried basis.

Lead Not more than 2 mg/kg.

Loss on Drying Not more than 8.0%.

Loss on Ignition Not more than 2%.

TESTS

Assay Determine as directed under *Nitrogen Determination*, Appendix IIIC. Calculate the percent protein (*P*) by the equation

$$P = 6.25N,$$

in which *N* is the percent nitrogen.

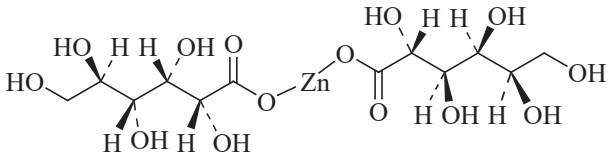
Lead Determine as directed in the *Flame Atomic Absorption Spectrophotometric Method* under *Lead Limit Test*, Appendix IIIB, using a 10-g sample.

Loss on Drying Determine as directed under *Loss on Drying*, Appendix IIC, drying a 2-g sample in an air oven at 105° for 2 h.

Loss on Ignition Determine as directed under *Ash (Total)*, Appendix IIC, using a 2-g sample.

Packaging and Storage Store in well-closed containers.

Zinc Gluconate



$C_{12}H_{22}O_{14}Zn$ Formula wt 455.68

CAS: [4468-02-4]

DESCRIPTION

Zinc Gluconate occurs as a white or nearly white, granular or crystalline powder and as a mixture of various states of

Appendix 012 (all)

ASCUS BIOSCIENCES

Method

Title	**Spore Counting**
Version	**02**
Effective Date	**16Jan2020**
Author	**Rich La**
Approver (Signature & Date)	DocuSigned by: Martin Maylew D1605F1B4C3E49A... 1/15/2020 **Martin Maynew** **Vice President - Process Development and Manufacturing**

Scope

The purpose of this method is to determine the number of viable spores in a sample by counting them in a Petroff-Hausser Haemocytometer.

Safety

Consult the Safety Data Sheet for all reagents prior to handling. Wear appropriate personal protective equipment (safety glasses and gloves) at all times.

Materials

N/A

Equipment

Petroff-Hausser Haemocytometer (Hausser Scientific Cat #3900) with supplied coverslip
Phase Contrast Microscope

Media and Reagents

95% Ethanol
Phosphate-Buffered Saline + 0.05% Tween-20 (PBST)

Component	Amount per 1.0L
(b) (4)	

Method

(b) (4)

(b) (4)

Re

1. Remove organism name from the method title so the method may be used for any spore-forming organisms.

ASCUS BIOSCIENCES

Spore Counting of *Clostridium butyricum* Method Validation Summary Report

Objective

The objective of this validation protocol was to demonstrate the accuracy and repeatability of the method "Spore Counting of *Clostridium butyricum*. used to quantify the amount of *Clostridium butyricum* in a sample.

Results

The following parameters were tested in this validation.

Repeatability – closeness of results obtained on the same sample (18-0202-001-P73) when assayed multiple times by the same person with the same reagents and equipment.

Robustness – reliability of the method to withstand small variations such as different technicians and reagent preparations on 3 lots of DY20-SDP (18-0202-001-P48-1 and 18-0202-001-P37-2).

A summary of the Spores results is shown in the table below. All samples fit the criteria for validation with a Coefficient of Variation of 35% or less.

Table 1. Spores/g results for Dairy-20-SDP

Analyst	Lot #	Sample ID	AVG Spores/g	STD DEV	CV
1	18-0202-001-P73	Sample 1A	(b) (4)		
		Sample 1B			
		Sample 1C			
	18-0202-041-P22	Sample 2			
	18-0202-001-P79	Sample 3			
2	18-0202-001-P73	Sample 1A			
		Sample 1B			
		Sample 1C			
	18-0202-041-P22	Sample 2			
	18-0202-001-P79	Sample 3			

Repeatability

From Analyst 1, the average of sample 1A, 1B, and 1C is 7.39E+11 Spores/g with a standard deviation of 1.18E+10 Spores/g. The coefficient of variation from these samples is 1.59%. From Analyst 2, the average of sample 1A, 1B, and 1C is 6.48E+11 Spores/g with a standard deviation of 2.06E+10 Spores/g. The coefficient of variation from these samples is 3.18%. This shows that there is a very small variation with the same analyst testing the same sample multiple times.

Robustness

Three samples were assayed by both analysts and the low CVs indicate that the assay is robust and there is little difference between the results on the same samples.

Conclusion

There were no changes or deviations from the protocol.

Raw data can be found on the Ascus Biosciences Google Drive /Lab/Process Development/ Spore counting of *Clostridium butyricum.*

Repeatability and robustness were tested on three samples of DY20-SDP and in all parameters this method validation has passed. The method is validated for the detection of *Clostridium butyricum* spores in any sample that can be prepared according to the method.

Summary Report Approvals:

Printed Name & Title	**Signature**	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AE21D1C745C...	1/2/2019
Patricia A. Williams – Quality	DocuSigned by: Patricia A Williams 5B301285A10643D...	12/27/2018

ASCUS BIOSCIENCES

Method

Title	DY20-SDP Microbe Enumeration
Version	07
Effective Date	15May2020
Author	Miranda Striluk
Approver (Signature & Date)	DocuSigned by: Martin Maylew D1605F1R4C3F49A 5/8/2020 Martin Maylew VP – Process Development & Manufacturing

Scope

The purpose of this assay is to determine the number of viable spores of Dairy-20 in Dairy-20 Spray Dried Powder (DY20-SDP) by counting colony forming units (CFU) on solid media.

Safety

Consult the Safety Data Sheet for all reagents prior to handling. Use caution in working with a hot water bath and hot liquids. Wear appropriate personal protective equipment (safety glasses and gloves) at all times.

Materials

BD GasPak™ EZ large incubation container (BD 260672)
BD GasPak™ EZ anaerobe container system sachets (BD 260678
Corning® 15mL Polypropylene Centrifuge Tubes (Corning 430052)
Test tubes, 13x100 mm, sterile
Test tube cap, 16 mm, polypropylene
1.5 mL polypropylene microcentrifuge tube with snap cap
1000 µL Pipette
200 µL Pipette
1000 µL pipette tips, sterile
200 µL pipette tips, sterile
Glass beads, 3 mm, sterile, new

Equipment

Water bath set to 50°C
Laboratory Vortexer
Class I/II Biosafety Cabinet
pH meter
Magnet Stir Plate

Media & Reagents

NOTE: *Comparable quality ingredients (Laboratory, NF, USP, Reagent, or ACS grade) from different suppliers may be used.*

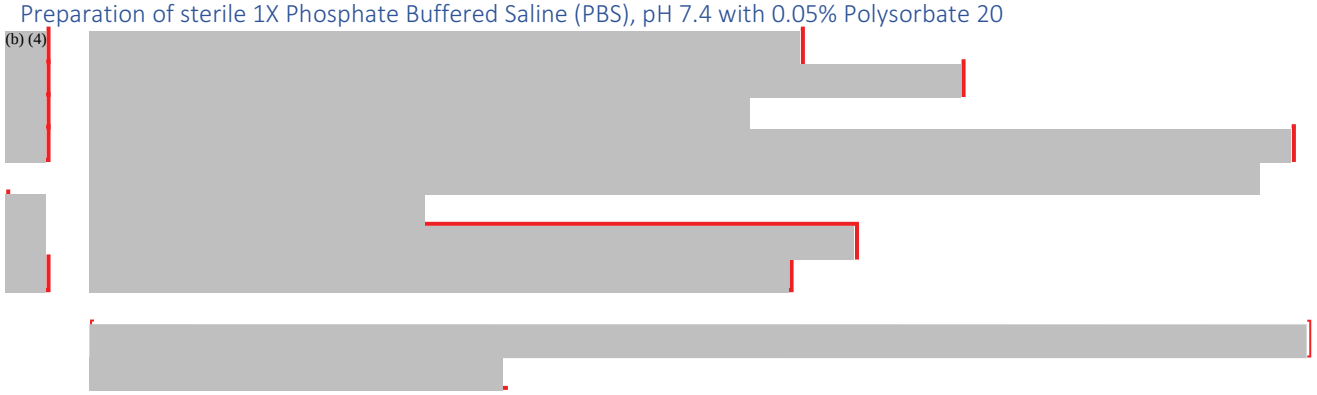
Growcells 10X Phosphate Buffered Saline pH 7.4 (PBS), sterile (Growcells MRGF-6235)
Growcells 1X Phosphate Buffered Saline with 0.05% TWEEN pH 7.4, sterile (Growcells MRGF-6275)
TSB+FAC plates
Reagent grade 95% Ethanol
1N Hydrochloric Acid
1N Sodium Hydroxide

DY20-SDP Microbe Enumeration

Method

1. Preparation of sterile 1X Phosphate Buffered Saline (PBS), pH 7.4 with 0.05% Polysorbate 20

(b) (4)



2. Prepare the Primary Dilution Mix

(b) (4)

3. DY20-SDP Heat Shock Anaerobic Plating

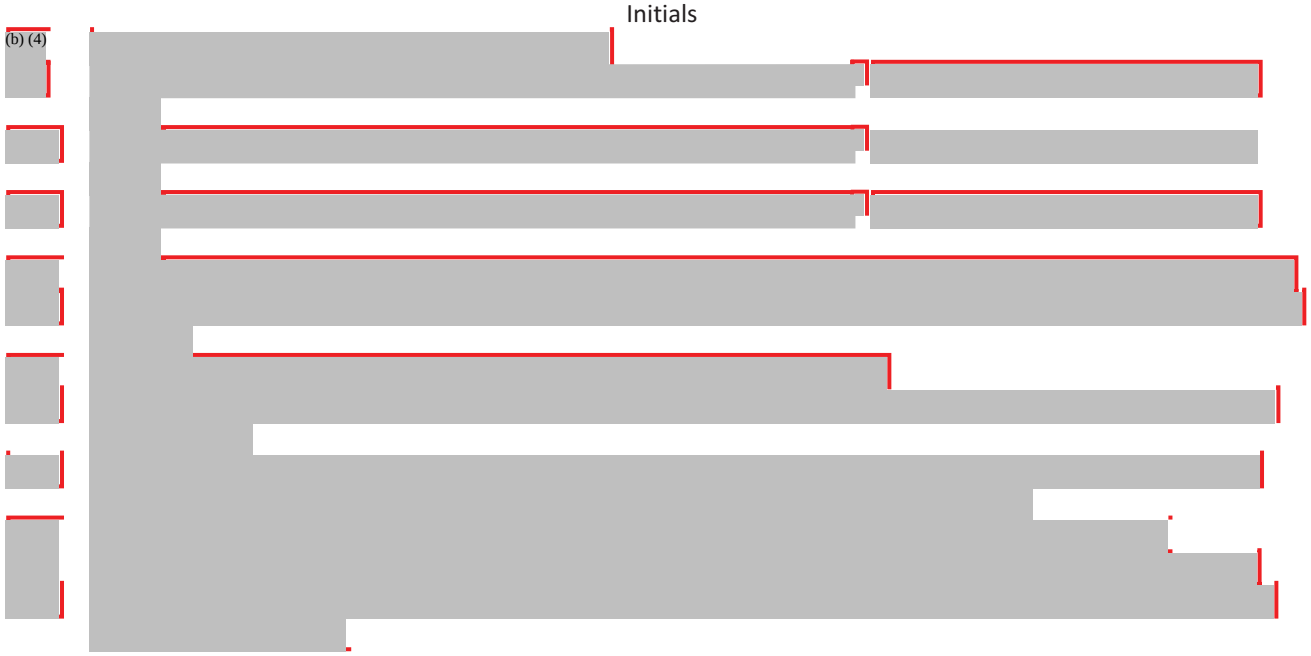
(b) (4)

(b) (4)

DY20-SDP Microbe Enumeration

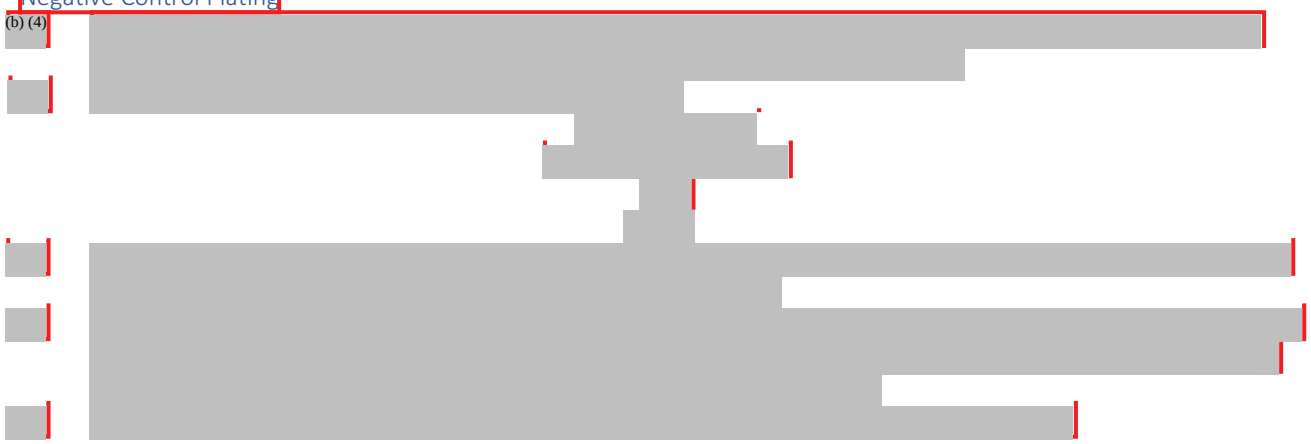
Date
Dilution
Initials

(b) (4)



4. Negative Control Plating

(b) (4)

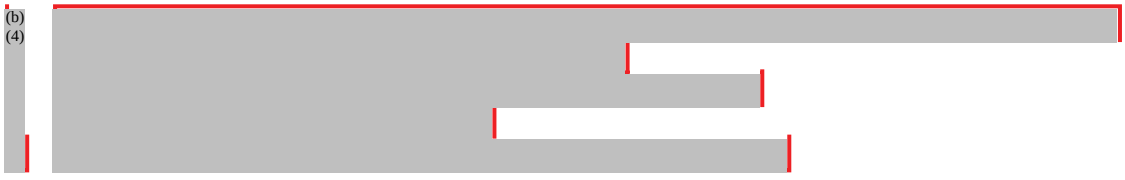


5. Plate Counting

(b) (4)

DY20-SDP Microbe Enumeration

Reasons for Revision



Methods
DY20-SDP Microbe Enumeration, V1

Objective
The objective of this validation protocol was to demonstrate the repeatability, robustness, and linearity of the method "DY20-SDP Microbe Enumeration". The method quantifies the amount of Dairy-20 (*Clostridium butyricum*) in the intermediate Dairy-20 Spray Dried Powder (DY20-SDP). This was the initial validation of this method.

Repeatability was tested by determining the closeness of results obtained on the same sample (18-0202-001-P40-3) when assayed multiple times by the same person with the same reagents and equipment.

Robustness was tested by determining the reliability of the method to withstand small variations such as different technicians and reagent preparations on 2 lots of DY20-SDP (18-0202-001-P40-3 and 18-0202-001-P43-1).

Linearity was tested by assessing the generation of reliable results over a range of concentrations on 2 lots of DY20-SDP (18-0202-001-P40-3 and 18-0202-001-P43-1)

Results
Repeatability
The average of sample 1-1, 1-2, and 1-3 is 1.84E+10 CFU/g with a standard deviation of 2.13E+09 CFU/g. The coefficient of variation from these samples is 12%. This shows that there is a small variation with the same analyst testing the same sample multiple times. See Table 1.

Robustness
Samples 1-6 were performed by another analyst and results show that the assay is robust by having all CVs below the limit of 75%. See Table 2

Table 1. CFU results for DY20-SDP

	Analyst 1			Analyst 2		
Sample Description	**Avg. CFU/g**	**Std. Dev.**	**CV**	**Avg. CFU/g**	**Std. Dev.**	**CV**
Sample 1-1	(b) (4)					
Sample 1-2						
Sample 1-3						
Sample 2						
Sample 3						
Sample 4						
Sample 5						
Sample 6						

Table 2. Summary of Analyst 1 and 2 testing two different samples of DY20-SDP.

Analyst	Lot#	Sample	Average DY20 (CFU/g)	STD Dev.	DY20 CV
1	18-0202-001-40-3	Sample 1-1	(b) (4)		
		Sample 1-2			
		Sample 1-3			
		Sample 2			
		Sample 3			
	18-0202-001-43-1	Sample 4			
		Sample 5			
		Sample 6			
2	18-0202-001-40-3	Sample 1			
		Sample 2			
		Sample 3			
	18-0202-001-43-1	Sample 4			
		Sample 5			
		Sample 6			

Linearity

The following table and corresponding graphs show the gram/mL of DY20-SDP plotted against the CFU/mL. For 18-0202-001-P43-1 the R^2 value for Analyst 1 was 0.9996 (Fig.1) and for Analyst 2 was 0.9692 (Fig.2). For 18-0202-001-P43-1 the R^2 value for Analyst 1was 0.8419 (Fig. 3) and for Analyst 2 was 0.9557 (Fig.4). This shows that the CFU/mL of each microbe in the product is linearly dependent on the amount of microbe added in the sample.

Table 3. Summary of Average g/mL and Average CFU/mL for linearity of DY20-SDP.

	18-0202-001-P40-3				18-0202-001-P43-1			
Analyst	Average (g/mL)	Average (CFU/mL)	STD Dev.	CV	Average (g/mL)	Average (CFU/g)	STD Dev.	CV
1	(b) (4)							
2								

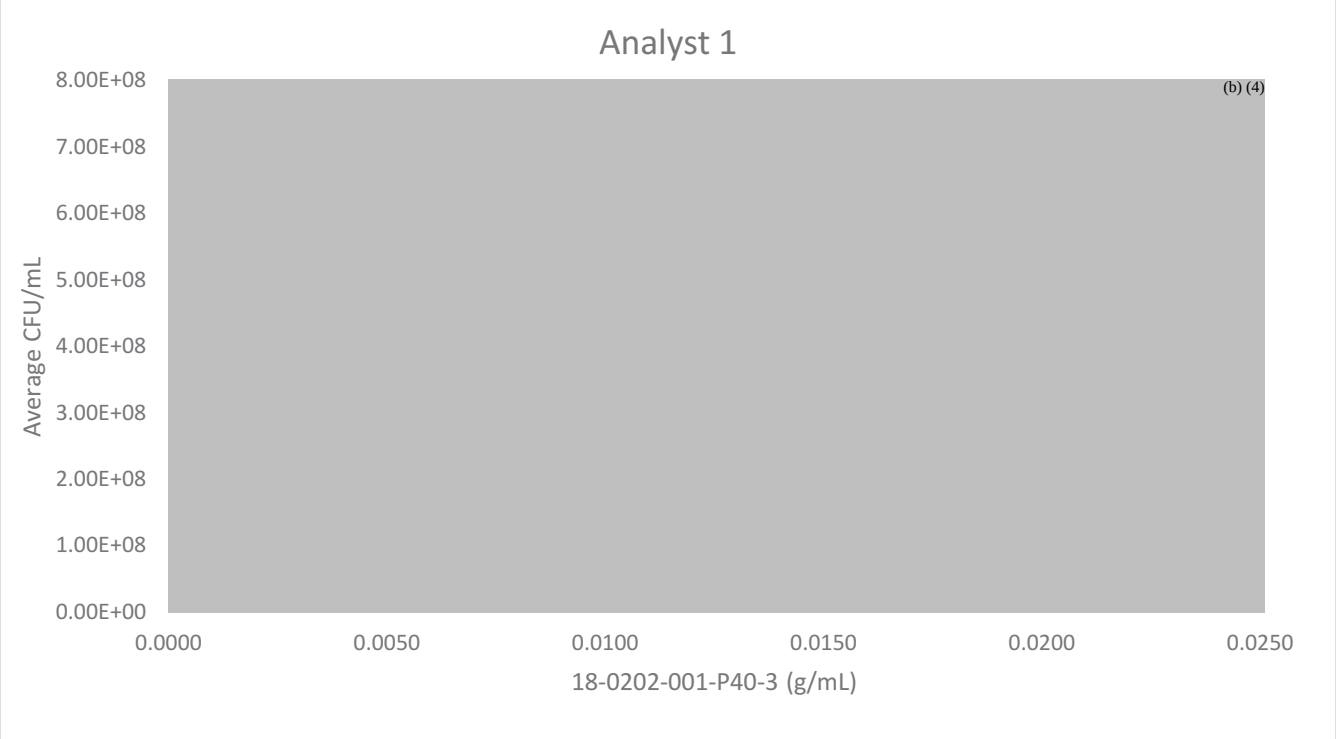


Figure 1. Dairy-20-SDP are plotted with g/mL of microbe from sample 18-0202-001-P40-3 vs CFU/mL. Analyst 1 is plotted in blue (R^2 = 0.9996).

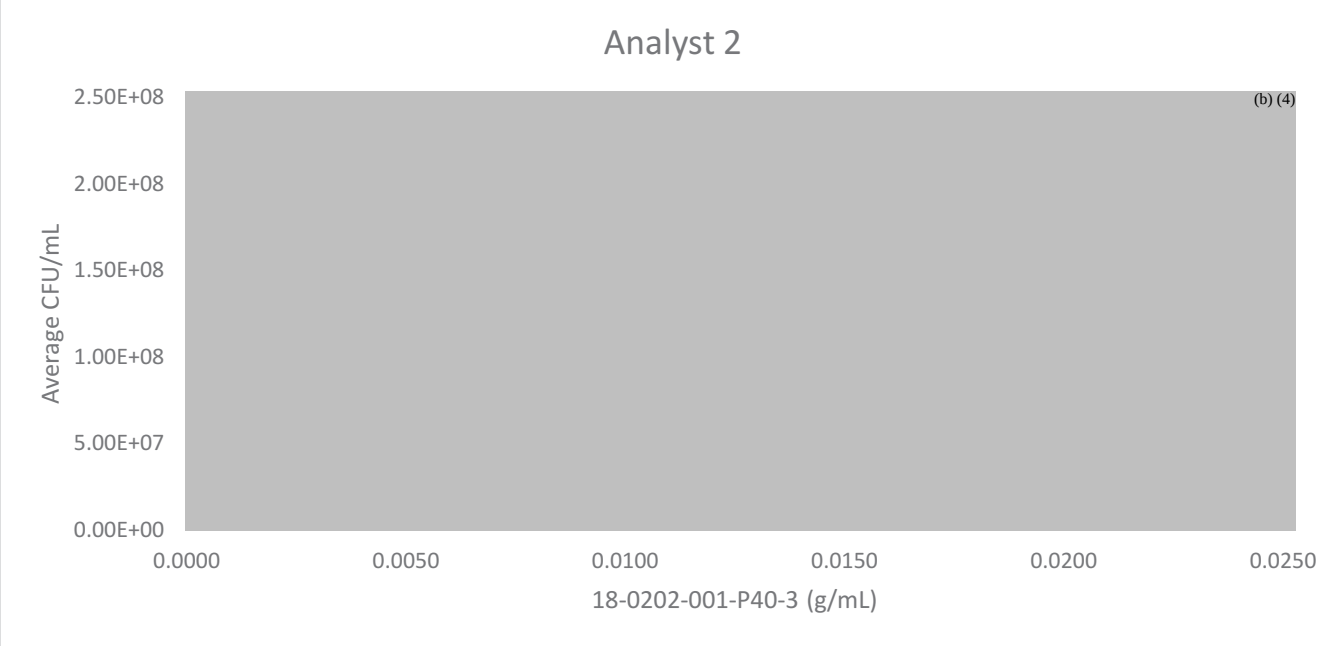


Figure 2. Dairy-20-SDP are plotted with g/mL of microbe from sample 18-0202-001-P40-3 vs CFU/g. Analyst 2 is plotted in blue ($R^2 = 0.9692$).

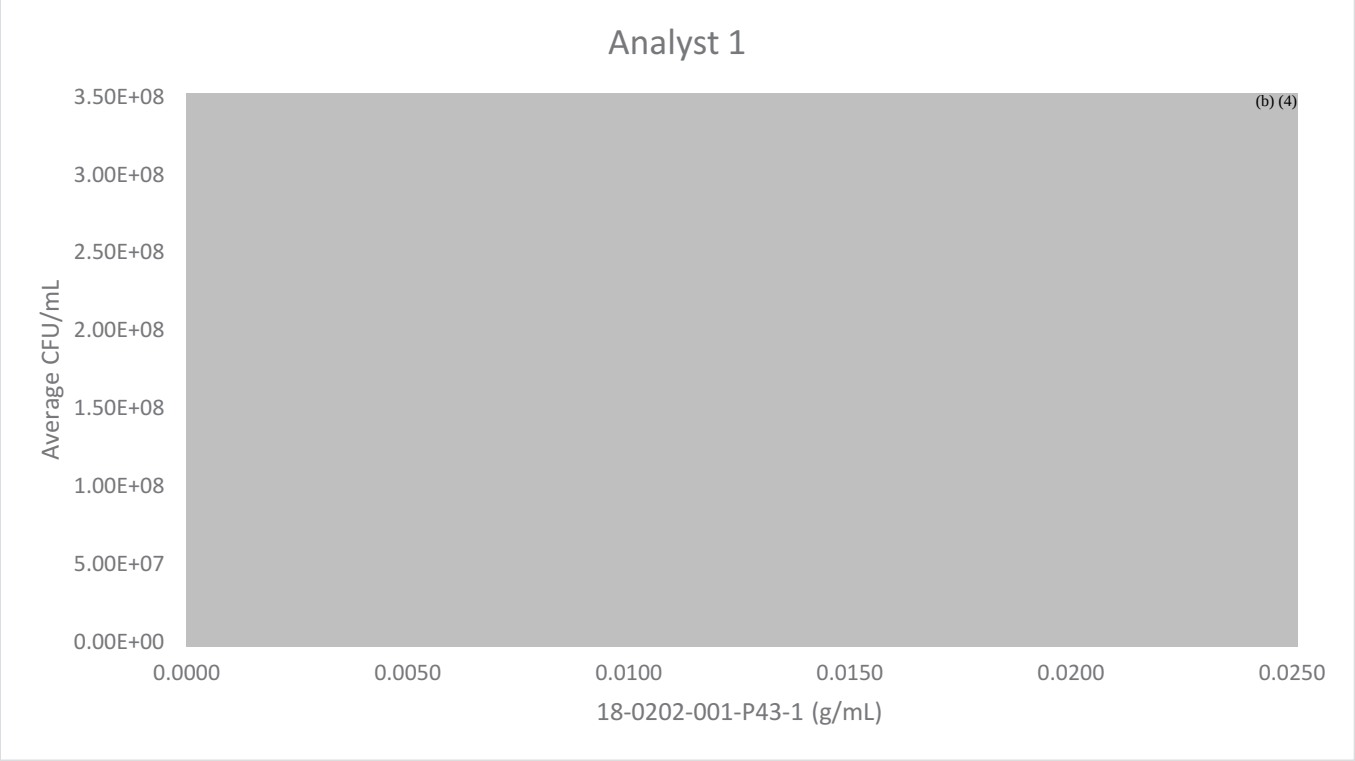


Figure 3. Dairy-20-SDP are plotted with g/mL of microbe from sample 18-0202-001-P43-1 vs CFU/g. Analyst 1 is plotted in blue ($R^2 = 0.8419$).

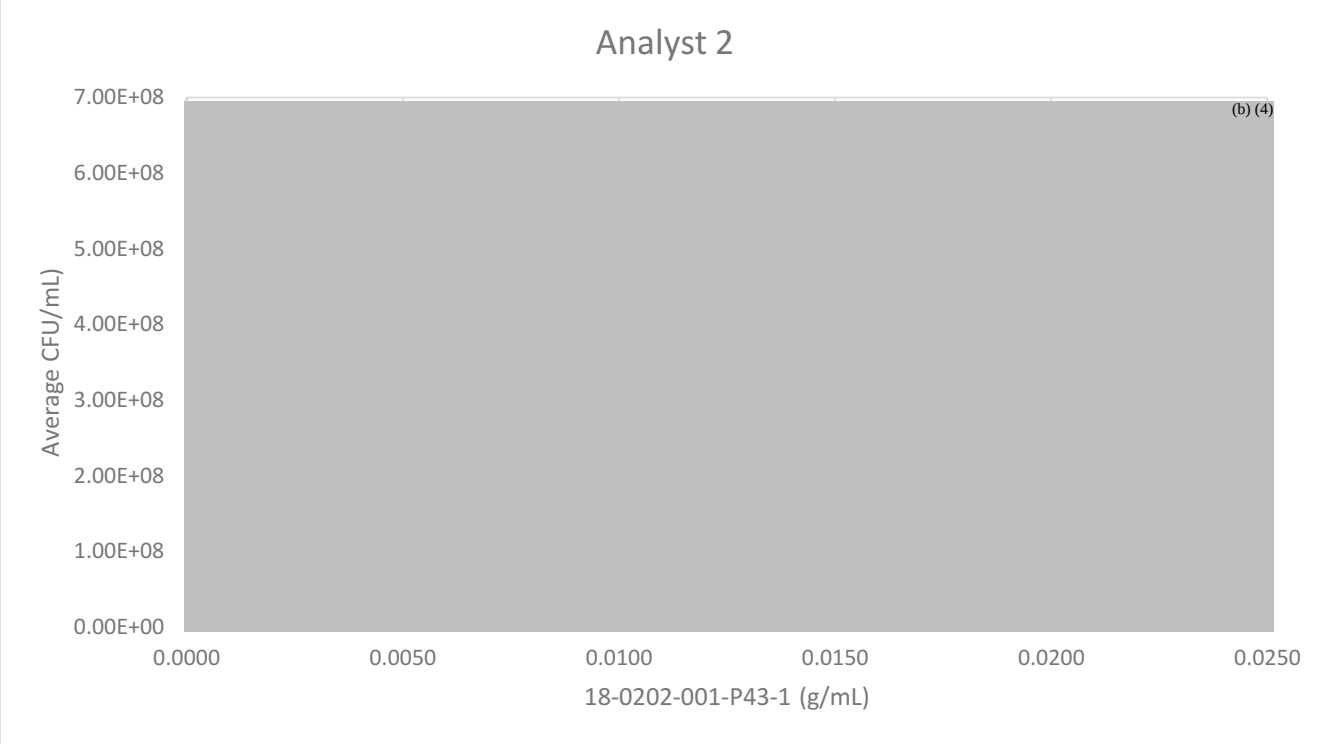


Figure 4. Dairy-20-SDP are plotted with g/mL of microbe from sample 18-0202-001-P43-1 vs CFU/g. Analyst 2 is plotted in blue ($R^2 = 0.9557$).

Conclusion

The protocol was executed as written with no deviations or changes to the protocol during execution.

Repeatability, robustness, and linearity was tested on two samples of DY20-SDP and in all three parameters this method validation has passed.

This was the first attempt of "DY20-SDP Microbe Enumeration" methods. Within this validation a new section was added into the method to complete negative control plating of the beads and buffer used for each sample processed. Analyst 1 had zero account of contamination on negative control plating of beads and buffer. Analyst 2 had no account of contamination from negative control plating of beads but had accounts of contamination reported on negative plating of buffer aliquots. Upon investigation of contamination, the contamination visually matches colony appearance of Dairy-20 (*Clostridium butyricum*, white and slightly opaque, with undefined borders that may resemble small stars and may vary in size). Due to aliquoting of buffer solutions in a clean Biological Safety Cabinet with no DY20 present and lack of contamination in additional platings of randomly selected buffer solution tubes, the source of this contamination is determined to be technique error and has been addressed. No outliers were observed within the data, and so this contamination did not impact the results.

Location of all raw data can be found on the Ascus Biosciences Google Drive /Lab/Process Development/ DY20-SDP Microbe Enumeration.

Summary Report Approvals:

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AE21D1C745C...	7/18/2018 8:36:35 AM PDT
Patricia A. Williams – Quality	Patricia A. Williams 5B3C1285A...0643D...	7/18/2018 8:15:43 AM PDT

Appendix 013 (all)

ASCUS BIOSCIENCES

Product Certificate of Analysis

Product Name	DY20 SDP
Batch Number	18-0202-001-P73
Date of Manufacture	07Nov2018
Expiration Date	07Nov2019
Retest Date	N/A
Storage Conditions	20-25 °C

Analytical Property	**Specification**	**Result**
DY20-SDP Microbe Enumeration	>4.0E6 CFU/g	(b) (4)
Coliform	<10 CFU/g	
E. coli	<10 CFU/g	
Salmonella	Negative/25g	
Listeria	Negative/25g	
Spore Count	5.0E10 spores/g	

Approval (Name, Title, Signature, and Date)

This batch was manufactured and tested according to the product registration and regulatory agency requirements.

Patricia A. Williams
Quality

DocuSigned by:
Patricia Williams
5B301285A10643D...

9/19/2019

ASCUS BIOSCIENCES

Product Certificate of Analysis

Product Name	DY20 SDP
Batch Number	18-0202-001-P79
Date of Manufacture	17Dec2018
Expiration Date	17Dec2019
Retest Date	N/A
Storage Conditions	20-25 °C

Analytical Property	**Specification**	**Result**
DY20-SDP Microbe Enumeration	>4.0E6 CFU/g	(b) (4)
Coliform	<10 CFU/g	
E. coli	<10 CFU/g	
Salmonella	Negative/25g	
Listeria	Negative/25g	
Spore Count	5.0E10 spores/g	

Approval (Name, Title, Signature, and Date)

This batch was manufactured and tested according to the product registration and regulatory agency requirements.

Patricia A. Williams
Quality

DocuSigned by:
Patricia Williams
5B301285A10643D...

9/19/2019

ASCUS BIOSCIENCES

Product Certificate of Analysis

Product Name	DY20 SDP
Batch Number	18-0202-041-P22
Date of Manufacture	27Nov2018
Expiration Date	27Nov2019
Retest Date	N/A
Storage Conditions	20-25 °C

Analytical Property	**Specification**	**Result**
DY20-SDP Microbe Enumeration	>4.0E6 CFU/g	(b) (4)
Coliform	<10 CFU/g	
E. coli	<10 CFU/g	
Salmonella	Negative/25g	
Listeria	Negative/25g	
Spore Count	5.0E10 spores/g	

Approval (Name, Title, Signature, and Date)

This batch was manufactured and tested according to the product registration and regulatory agency requirements.

Patricia A. Williams
Quality

DocuSigned by:
Patricia A Williams
5B301285A10643D...

1/8/2019

Appendix 015 (all)

Cerrito, Chelsea

From: Kristi Smedley <smedley@cfr-services.com>
Sent: Wednesday, August 05, 2020 10:50 AM
To: Animalfood-premarket
Cc: Howard@ascusbiosciences.com
Subject: RE: Appendices to ASCUS Clostridium beijerinckii AGRN
Attachments: App_15A_B Clostridium beijerinckii 5C 12 month Summary Report.zip

Appendix 15 A and B.

This is the second of 3 emails on appendices.

Kristi O. Smedley, Ph.D.

Center for Regulatory Services, Inc.
5200 Wolf Run Shoals Rd.
Woodbridge, VA 22192

Ph. 703-590-7337
Cell (b) (4)
Fax 703-580-8637

From: Kristi Smedley [mailto:smedley@cfr-services.com]
Sent: Wednesday, August 05, 2020 10:40 AM
To: Animalfood-premarket (Animalfood-premarket@fda.hhs.gov)
Cc: Howard@ascusbiosciences.com
Subject: Appendices to ASCUS Clostridium beijerinckii AGRN

Thank you for the discussion this morning on the appendices supporting the AGRN for Clostridium beijerinckii. It appears when I downloaded the appendices from the shared website, the download was not complete. I apologize for this inconvenience and I appreciate your permitting us to provide the missing information by email.

This email contains appendix 13, appendix 12, appendix 9, and appendix 3D.

I will send a few emails with the needed information.

Kristi O. Smedley, Ph.D.

Center for Regulatory Services, Inc.
5200 Wolf Run Shoals Rd.
Woodbridge, VA 22192

Ph. 703-590-7337
Cell (b) (4)
Fax 703-580-8637

Clostridium beijerinckii ASCUSDY20 Spray-Dried Powder 5. C: 12-Month Stability Summary Report

Approvers:

DocuSigned by:
Martin Mayhew
D1605F1B4C3E49A...

5/12/2020

Martin Mayhew
Vice President – Product Development & Manufacturing

Date

DocuSigned by:
Patricia A Williams
5B301285A10643D...

5/6/2020

Patricia A. Williams
Quality

Date

DocuSigned by:
Howard B Green
0FAA38037D49453...

5/8/2020

Howard B. Green
Regulatory

Date

Prepared by
Ascus Biosciences
San Diego, CA

April 2020

Table of Contents

Clostridium beijerinckii ASCUSDY20 Spray-Dried Powder 5°C – 12-Month Stability Summary Report

Organism: ***Clostridium beijerinckii* ASCUSDY20**

Testing Condition: 5°C ± 3°C

Purpose: To support temperature excursions during shipping and storage and potential long-term refrigerated storage.

Study Numbers: DUS1804 (Lot# 18-0202-001-P73)
DUS1807 (Lot# 18-0202-041-P22)
DUS1810 (Lot# 18-0202-001-P79)

Acceptance Criteria: Not Less Than 4.0 X 10^6 CFU/g

1 Results

Table 1. Results for Each Lot at Each Time Point

Note: Results are reported in average colony forming units (CFU)/gram of *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder.

	Avg. CFU/g			Std. Dev.		
Time (mo)	DUS1804	DUS1807	DUS1810	DUS1804	DUS1807	DUS1810
0	(b) (4)					
1						
2						
3						
6						
9						
12						

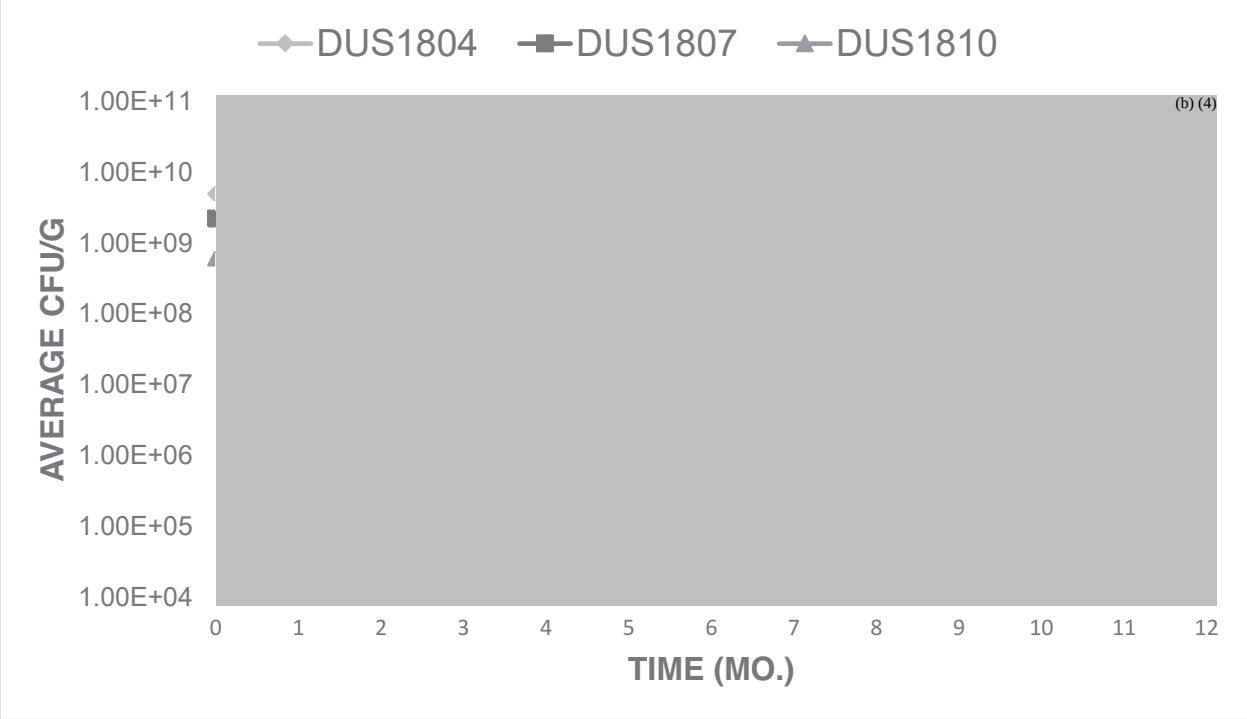


Figure 1. Graph of Results for Each Lot at Each Time Point

Note: Results are reported in average colony forming units (CFU)/gram of *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder.

2 Discussion

The stability study of *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder on three separate lots conducted at 5°C ± 3°C for 12 months resulted in no degradation of the material below the original acceptance criteria of 4.00 X 10^6 CFU/g and the revised acceptance criteria of 5.00 X 10^8 CFU/g (Table 1, Figure 1).

Viability of the 3 lots remained above 5.00 X 10^8 CFU/g for the duration of this stability study, indicating *Clostridium beijerinckii* ASCUSDY20 will remain above the acceptance criteria during shipping and storage and potential long term refrigerated storage for up to 12 months at 5°C ± 3°C.

3 Deviations

Deviations from the *Clostridium beijerinckii* ASCUSDY20 SDP Microbe Enumeration method V3 that were considered minor were the following:

1. Media was prepared in 1000 L volumes (Step 1.8) instead of in 500mL volumes due to high demand of media production.

2. Hot water bath temperature ranged from 65 - 80°C (Step 1.10) instead of 80°C to reduce condensation in the bottle while cooling the media prior to additional media additions.

One deviation investigated further was the preparation and storage instructions for the vitamin solution in Step 1.2. A comparison study was performed to confirm that the vitamin preparation did not impact the assay results. The corrected method was used for subsequent time points.

4 Changes

No significant changes occurred during the stability study.

5 Appendices

Appendix 1. *Clostridium beijerinckii* ASCUSDY20 SDP 5°C Stability Protocol

Appendix 2. Lot# 18-0202-041-P22 Master Production Record

Appendix 3. Lot# 18-0202-001-P73 Master Production Record

Appendix 4. Lot# 18-0202-001-P79 Master Production Record

Appendix 5. *Clostridium beijerinckii* ASCUSDY20 SDP Stability Data for Tables & Graphs

Appendix 6. D2019-005: Wrong Vitamin Concentration Used in Galaxis / Altius and *Clostridium beijerinckii* ASCUSDY20 SDP Assays

Appendix 1. *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder 5°C Stability Protocol

ASCUS BIOSCIENCES

Stability Protocol Title:	DY20 SDP 5°C
Organism:	*Clostridium butyricum*
Purpose:	To support temperature excursions during shipping and storage and potential long term refrigerated storage
Number of Samples to Place on Stability:	9 (allows for retesting, when needed)
Sample Storage Container:	Heat sealed 48-gauge silver metalized PET / 2.5 mil LLDPE bags made from commercial bags
Temperature Conditions:	2-8°C
Acceptance Criteria:	>4 x 10^6 cfu/g

Tests and Timepoints:

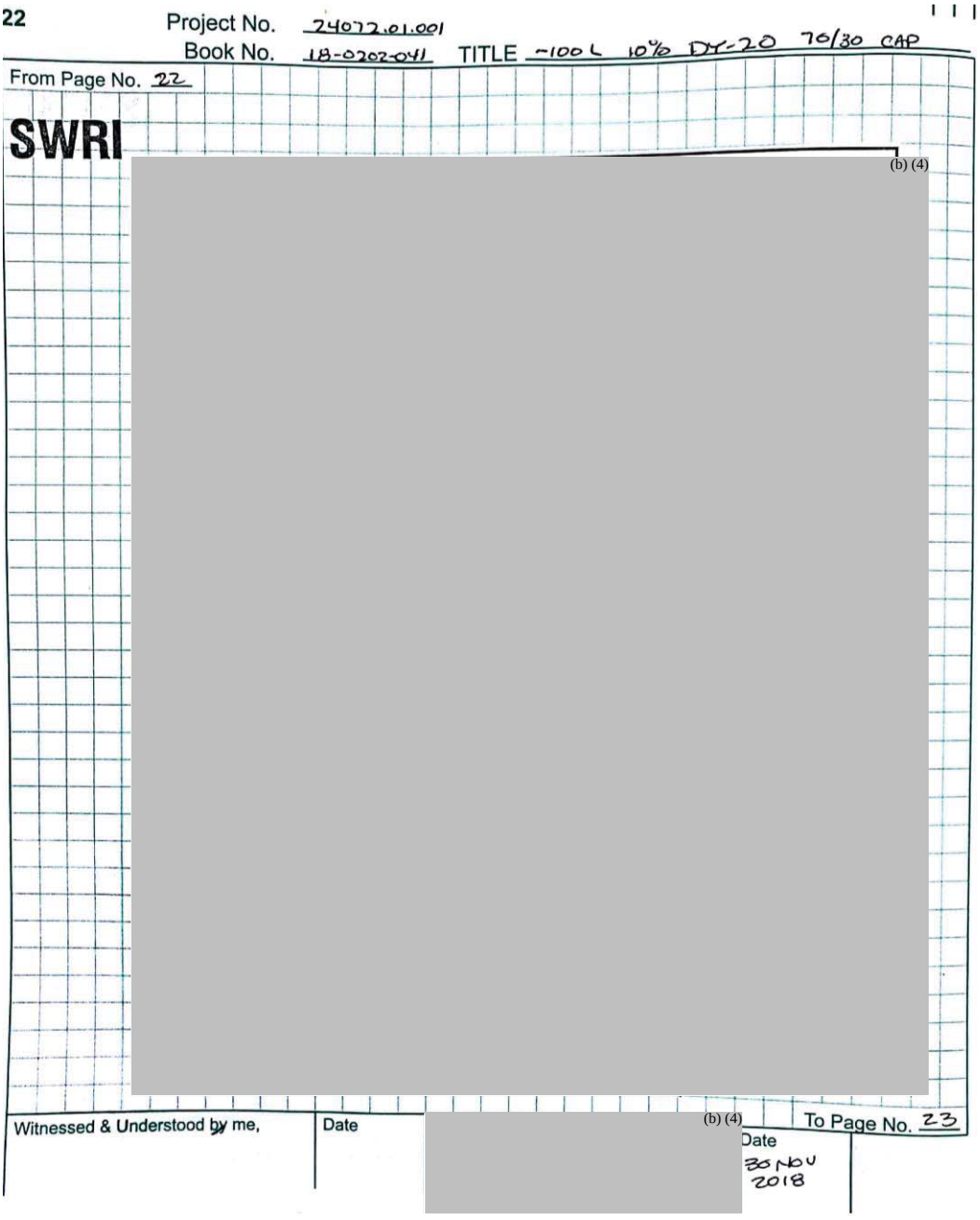
Assay	T_0	1 month	2 months	3 months	6 months	9 months	12 months
Microbe Enumeration*	X	X	X	X	X	X	X

*DY20-SDP Microbe Enumeration method

Approvals:

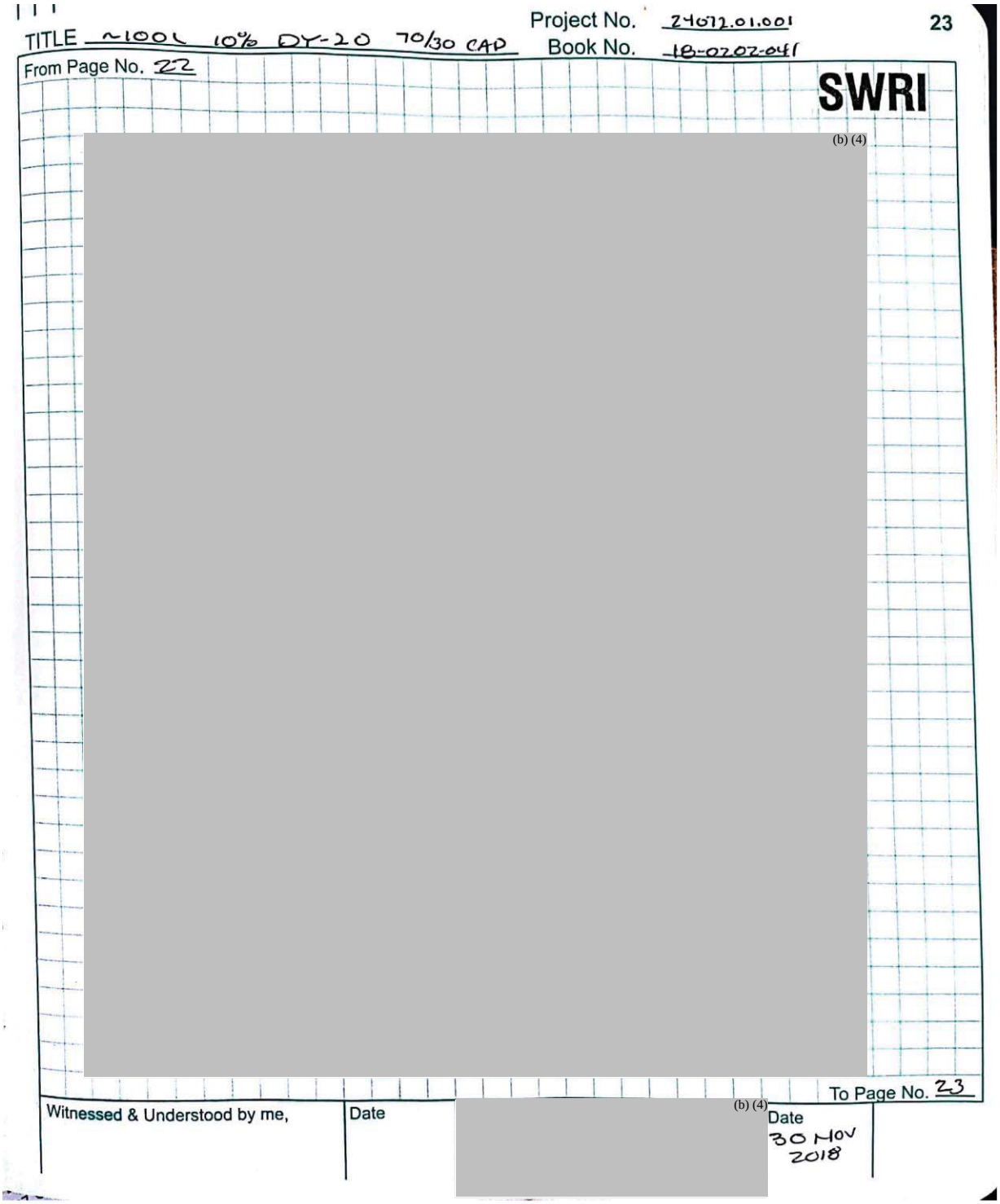
Howard Green Regulatory	DocuSigned by: Howard B Green 12/5/2018 9:23:46 AM PST
Corey Dodge Process Development	DocuSigned by: Corey Dodge 12/5/2018 8:16:36 AM PST
Patricia A. Williams Quality	DocuSigned by: Patricia A Williams 12/4/2018 7:05:27 PM PST

Appendix 2. Lot# 18-0202-041-P22 Master Production Records



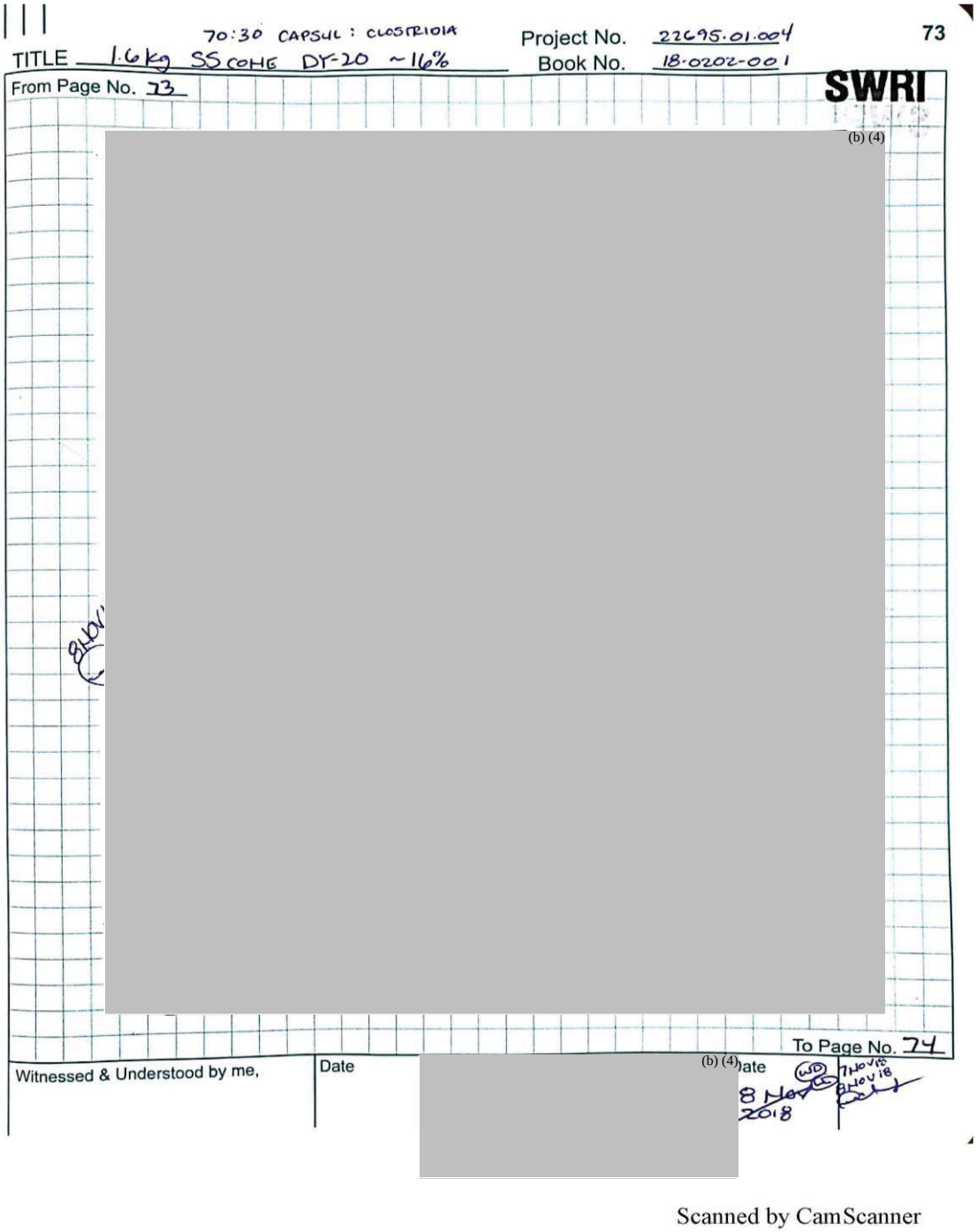
22 Project No. 24072.01.001
Book No. 18-0202-041 TITLE ~100 L 10% DY-20 70/30 CAP
From Page No. 22
SWRI
(b) (4)
Witnessed & Understood by me, Date (b) (4) Date 30 NOV 2018
To Page No. 23

Scanned by CamScanner

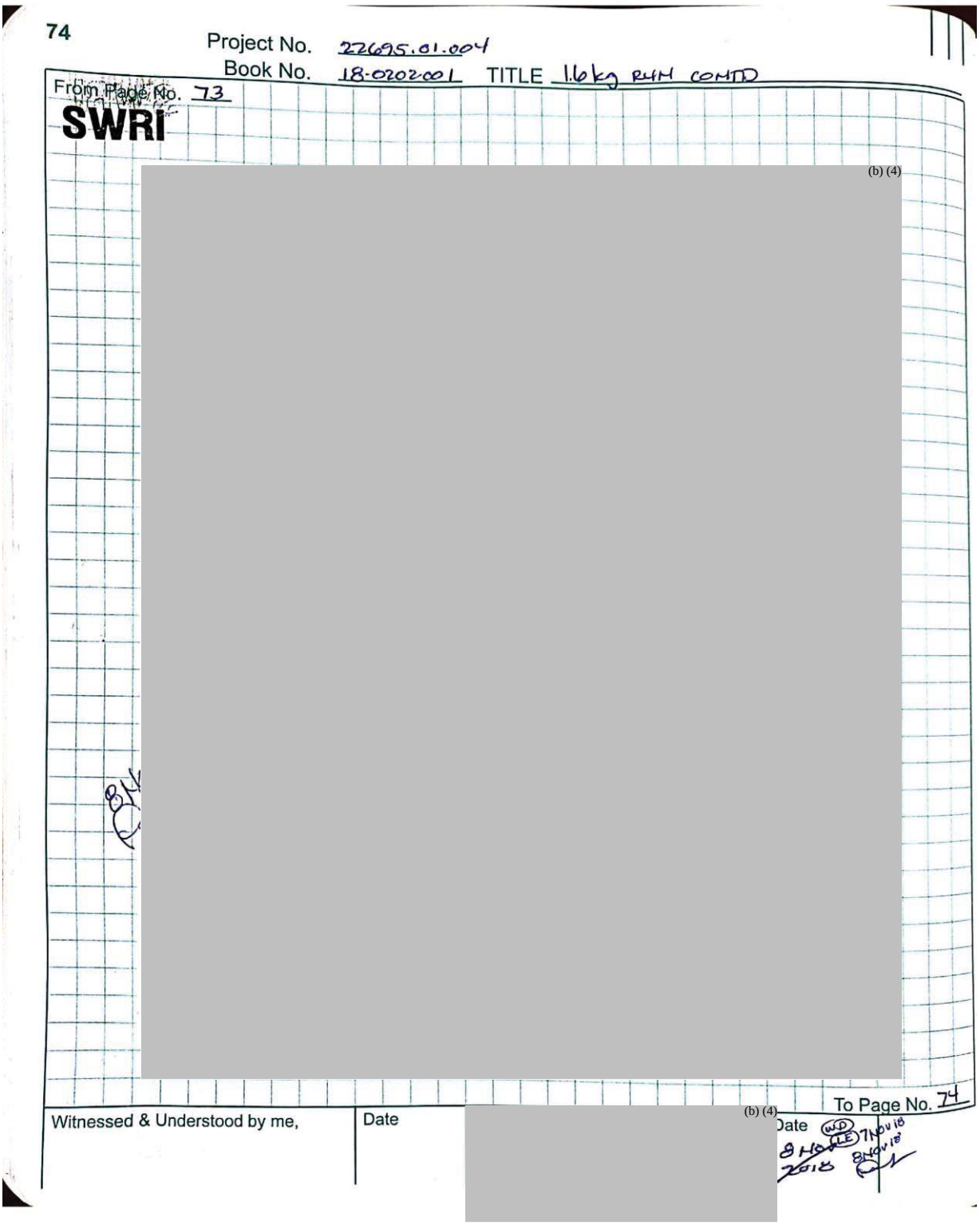


TITLE ~100L 10% DY-20 70/30 CAP
Project No. 24072.01.001
Book No. 18-0202-041
23
From Page No. 22
SWRI
(b) (4)
To Page No. 23
Witnessed & Understood by me,
Date
(b) (4)
Date
30 NOV 2018

Appendix 3. Lot# 18-0202-001-P73 Master Production Record



70:30 CAPSUL : CLOSTRIDIA
TITLE 1.6kg SS COHE DT-20 ~16%
Project No. 22695.01.004
Book No. 18-0202-001
73
From Page No. 73
SWRI
(b) (4)
To Page No. 74
Witnessed & Understood by me,
Date
(b) (4)ate
8 Nov 2018
7 NOV 18
8 NOV 18
Scanned by CamScanner



74

Project No. 22695.01.004
Book No. 18-0202-001 TITLE 1.6kg RHM CONTD

From Page No. 73

SWRI

(b) (4)

(b) (4)

To Page No. 74

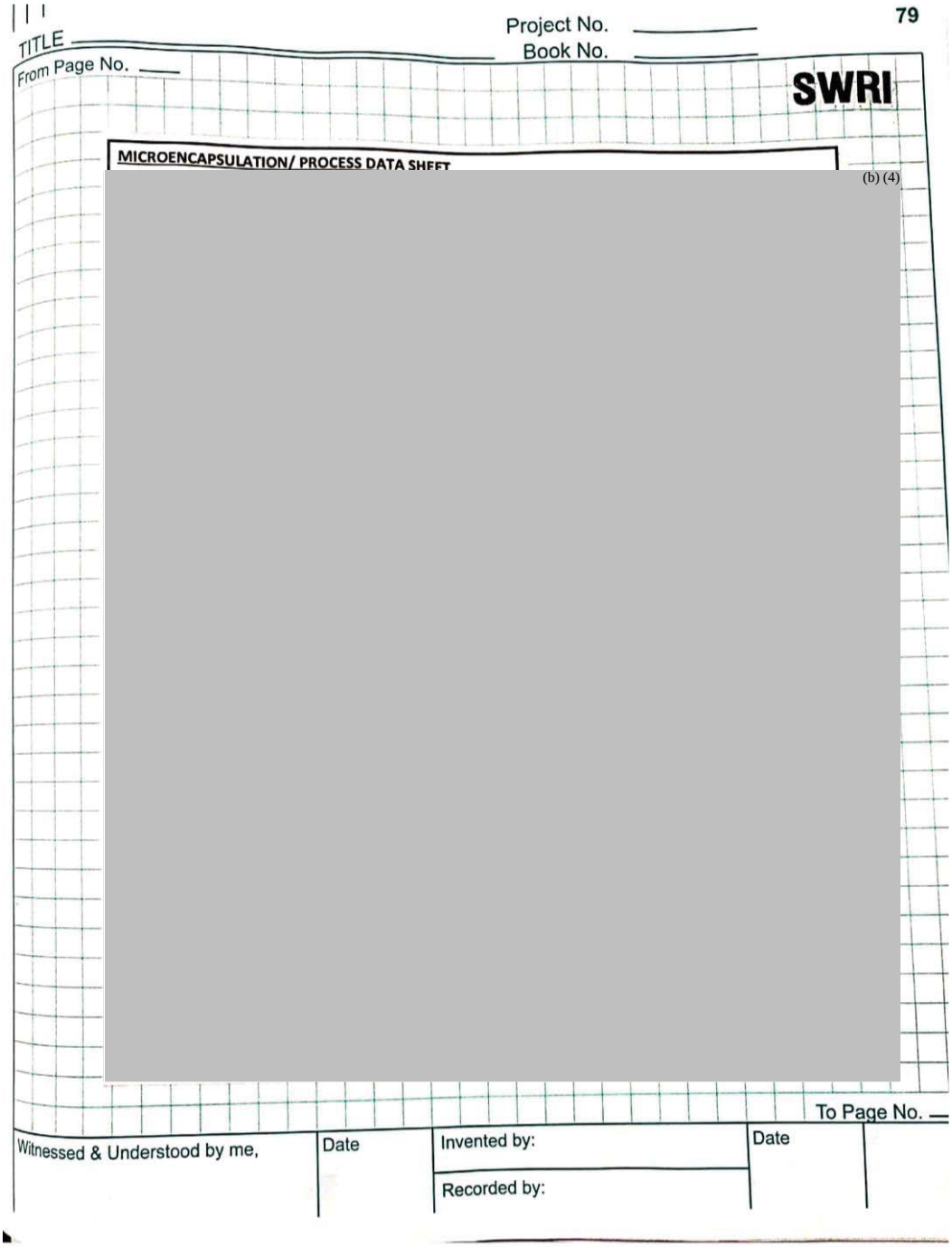
Witnessed & Understood by me,

Date

Date

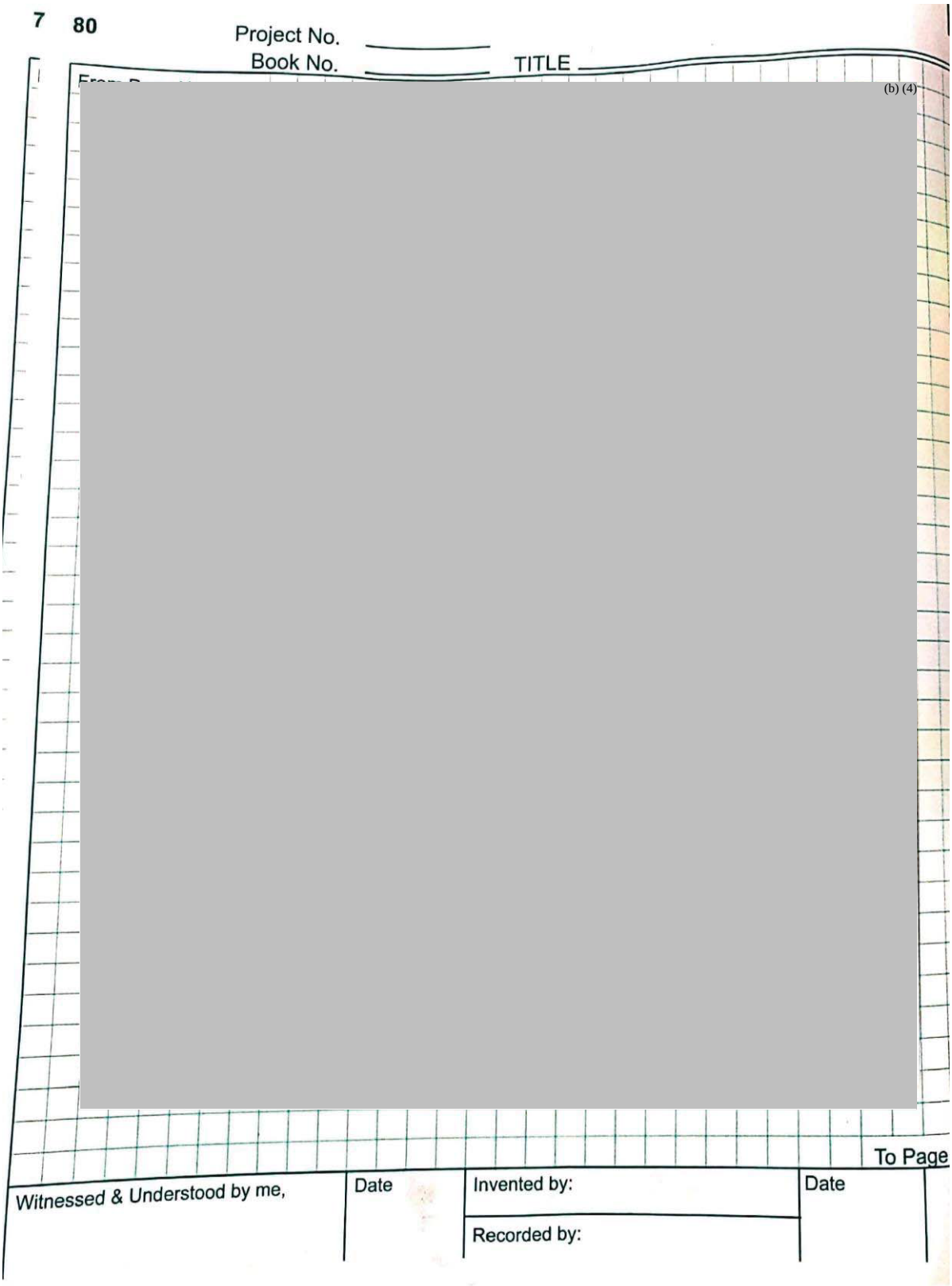
Scanned by CamScanner

Appendix 4. Lot# 18-0202-001-P79 Master Production Record



TITLE
From Page No.
Project No.
Book No.
79
SWRI
MICROENCAPSULATION/ PROCESS DATA SHEET
(b) (4)
To Page No.
Witnessed & Understood by me,
Date
Invented by:
Recorded by:
Date

Scanned by CamScanner



Appendix 5. *Clostridium beijerinckii* ASCUSDY20 SDP Stability Data for Tables & Graphs

Study Number	Scheduled Pull Date	Date Sample Was Pulled	Testing Condition	Timepoint	Batch Number	Lot Number	Analyst Initials	Sample	Mass (g)	Volume 1X PBST (mL)	DY20 Plating CFU Counts, CFU/100uL: 1E-04 A	1E-04 B	1E-04 C	1E-05 A	1E-05 B	1E-05 C	1E-06 A	1E-06 B	1E-06 C	DY 20: CFU/mL A	CFU/mL B	CFU/mL C	CFU/g A	CFU/g B	CFU/g C	Ave. CFU/g	Std. Dev.	CV
DUS1804	13-Jan-19	11-Jan-19	5C	1 month	1	18-0202-001-P73	SM/MS	5_1	0.1010	10																		
								5_2	0.1000	10																		
								5_3	0.1010	10																		
	13-Feb-19	13-Feb-19	5C	2 month	1	18-0202-001-P73	SM	6-1	0.1008	10																		
								6-2	0.1007	10																		
								6-3	0.1018	10																		
	13-Mar-19	10-Mar-19	5C	3 month	1	18-0202-001-P73	RL	2-1	0.1083	10																		
								2-2	0.1089	10																		
								2-3	0.1039	10																		
	13-Jun-19	11-Jun-19	5C	6 month	1	18-0202-001-P73	RL	1-1	0.1060	10																		
								1-2	0.1020	10																		
								1-3	0.1020	10																		
	13-Sep-19	11-Sep-19	5C	9 month	1	18-0202-001-P73	RL	3-1	0.1040	10																		
								3-2	0.1030	10																		
								3-3	0.1010	10																		
	13-Dec-19	12-Dec-19	5C	12 month	1	18-0202-001-P73	AT	4-1	0.1020	10																		
								4-2	0.0970	10																		
								4-3	0.0980	10																		
DUS1807	13-Jan-19	11-Jan-19	5C	1 month	2	18-0202-041-P22	SM/MS	30-1	0.1010	10																		
								30-2	0.1020	10																		
								30-3	0.1000	10																		
	13-Feb-19	13-Feb-19	5C	2 month	2	18-0202-041-P22	SM	31-1	0.1014	10																		
								31-2	0.1015	10																		
								31-3	0.1006	10																		
	13-Mar-19	10-Mar-19	5C	3 month	2	18-0202-041-P22	RL	27-1	0.1022	10																		
								27-2	0.1038	10																		
								27-3	0.1024	10																		
	13-Jun-19	11-Jun-19	5C	6 month	2	18-0202-041-P22	RL	26-1	0.1060	10																		
								26-2	0.1040	10																		
								26-3	0.1040	10																		
	13-Sep-19	11-Sep-19	5C	9 month	2	18-0202-041-P22	RL	28-1	0.1000	10																		
								28-2	0.1020	10																		
								28-3	0.1060	10																		
	13-Dec-19	12-Dec-19	5C	12 month	2	18-0202-041-P22	AT	29-1	0.0980	10																		
								29-2	0.1000	10																		
								29-3	0.1010	10																		
DUS1810	20-Jan-19	1/17/2019	5C	1 month	3	18-0202-001-P79	AT	56-1	0.1000	10																		
								56-2	0.1040	10																		
								56-3	0.0990	10																		
	20-Feb-19	2/20/2019	5C	2 month	3	18-0202-001-P79	RL	51-1	0.1019	10																		
								51-2	0.1011	10																		
								51-3	0.1039	10																		
	20-Mar-19	3/19/2019	5C	3 month	3	18-0202-001-P78	AT	65-1	0.1074	10																		
								65-2	0.1041	10																		
								65-3	0.1000	10																		
	20-Jun-19	6/18/2019	5C	6 month	3	18-0202-001-P79	AT	53-1	0.1020	10																		
								53-2	0.1010	10																		
								53-3	0.1040	10																		
	20-Sep-19	9/19/2019	5C	9 month	3	18-0202-001-P78	AT	54-1	0.1000	10																		
								54-2	0.0980	10																		
								54-3	0.1010	10																		
	20-Dec-19	12/18/2019	5C	12 month	3	18-0202-001-P78	AT	55-1	0.1010	10																		
								55-2	0.1080	10																		
								55-3	0.1060	10																		

(b) (4)

(b) (4)

Date of creation	Date of assay	Timepoint	Batch Number	Lot Number	Analyst Initials	Sample	Mass (g)	Volume 1X PBST (mL)
8-Nov-18	10-Dec-18	T=0	1	18-0202-001-P73	MS	Batch 1-1	0.1024	10
						Batch 1-2	0.1009	10
						Batch 1-3	0.1020	10
7-Dec-18	12-Dec-18	T=0	2	18-0202-041-P22	AT	P22-1	0.1008	10
						P22-2	0.1006	10
						P22-3	0.1007	10
17-Dec-18	20-Dec-18	T=0	3	18-0202-001-P79	SM	P79-1	0.1002	10
						P79-2	0.1000	10
						P-79-3	0.1015	10

Appendix 6. D2019-005: Wrong Vitamin Concentration Used in Galaxis / Altius and *Clostridium beijerinckii* ASCUSDY20 SDP Assays

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Deviation Number: D2019-005

Deviation Title: Wrong Vitamin Concentration Used for in Galaxis/Alitus and DY20 SDP Assays

Deviation Investigator: Adam Taylor

Description of the Deviation:
In April 2019 (b) (4) informed Ascus of problems in execution of Vitamin Mix section of the Galaxis/Altius Microbe Enumeration methods. The issue was that the solids did not fully dissolve into solution.

Investigation:
The methods used at (b) (4) (Microbe Enumeration of Galaxis 100 V5 and Microbe Enumeration of Altius and Galaxis 5 V8) were compared to methods used at Ascus for the preparation of the 0.1% Vitamin mix. The (b) (4) (b) (4) labs followed the methods as written. However, Ascus personnel were deviating from the methods by increasing the solvent/solute ratio by 10X. This allowed the solutes to readily dissolve, but resulted in an incorrect amount of vitamins in the media.

Further investigation indicated that Ascus personnel have been preparing the vitamin solution this way since August 2017 due to unclear wording in the method. In addition, all methods were validated with the lower amount of vitamins in the media.

Impacted results since 2017 include:

- Stability studies involving Galaxis 100, Galaxis 5, Altius, and DY20SDP
- Product release results for DY20SDP.

Impacted methods used since 2017 include:

- Microbe Enumeration for Galaxis 100
- Microbe Enumeration for Altius and Galaxis 5
- DY20 SDP Microbe Enumeration V3

Confidential T203A – Deviation Template Page 1 of 3

Deviation Number: D2019-005

Impacted commercial cell banks:

- DY20 Master Cell Bank 15Aug2018
- DY20 Working Cell Bank 1
- DY20 Working Cell Bank PCC1
- DY20 Working Cell Bank PCC5
- DY20 Working Cell Bank 3

To determine if the different vitamin preparation impacted the assay results, a comparison study was conducted with 2 analysts, 2 samples, and both preparation methods. See the attachment. The comparison study confirmed that the vitamin preparation method did not impact the assay results. Therefore, all the results generated at Ascus are valid. Methods will not be re-validated and cell banks will not be re-tested.

To ensure that the methods are executed correctly from now on, they will be revised to more clearly state how to prepare the vitamin mixture.

Immediate Corrections:

Action	Completed by	Date Completed	Comments
None			

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Deviation Number: D2019-005

CAPA:

CAPA Log #	Action	Assigned to	Due Date	Comments
CA2019-005	Clarify the section on vitamin mix preparation for the following methods: DY20SDP, Galaxis 5/Altius, and Galaxis 100	Pat Williams	08May2019	
CA2019-006	Send revised methods to (b) (4)	Adam Taylor	09May2019	
CA2019-007	Clarify the section on vitamin mix preparation for the following cell bank protocols: DY20 Working Cell Bank, DY20 Master Cell Bank, DY20 Cell Bank Retesting	Pat Williams	15May2019	

Approvers:

Printed Name & Title	Signature
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AF21D1C745C 5/3/2019
Patricia A. Williams – Quality	DocuSigned by: Patricia Williams 5B301285A10843D... 5/3/2019
Howard Green – Regulatory	DocuSigned by: Howard B Green 5/3/2019

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Comparison of Vitamin Concentrations in DY20 SDP Method Enumeration

Method Titles and Versions

Title	DY20-SDP Microbe Enumeration
Version	03

Lab Performing the Comparison: Ascus Biosciences Inc.

Pre-Execution Approval:

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AE21D1C745C...	4/22/2019

Post Execution Approval (includes Summary Report):

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AE21D1C745C...	5/3/2019
Patricia A. Williams – Quality	DocuSigned by: Patricia Williams 5B301285A10643D...	4/30/2019

Personnel Executing the Comparison:
Your signature indicates that you have read and understand this protocol.

Printed Name	Signature	Tasks Performed
Rich La		Analyst 1
Adam Taylor		Analyst 2
Samantha Marroquin		Media preparation

Purpose:
Deviation D2019-005 documents issues with execution of the DY20-SDP Microbe Enumeration method. Specifically, some analysts were using a 1000X less of the vitamin solution than what the method requires. See the deviation for details of the investigation.

This protocol will determine if a 1000X concentration difference in the Vitamin Solution has an impact on the results obtained from the DY20-SDP Microbe Enumeration method. The method

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will be run by 2 analysts, using 3 different lots of DY20 SDP, and the high and low concentration of vitamins. This will provide enough data to determine if the vitamin concentration impacts the results.

The intent is to use the validated method with the high concentration of vitamins going forward; therefore, this is not a method validation protocol. The method will be run as validated, with the exception of changing the vitamin concentration. Raw data will be recorded as listed in the method. The full method is retained in the Ascus Google Drive/Commercial Documents/Analytical Documents.

Directions for preparation of the 2 different vitamin concentrations are attached to this protocol.

The closeness of results from both vitamin concentrations will be assessed to determine if there is an impact on results.

Acceptance Criteria and Summary:
If the CVs between the vitamin solutions are ≤75% then the concentration of vitamins does not impact the results. (For example, if the CV between analyst 1, sample 1, for both vitamin concentrations is ≤75%, then there is no impact.)

A summary of the study and copy of Plate Count Data will be written after execution and approved by the Director of Product Development and Quality.

Analyst 1 Sample 1 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0702-041-P22				

(b) (4)

Analyst 1 Sample 2 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0202 041-726				

(b) (4)

[redacted]

Analyst 1 Sample 3 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0702-041-P30				

(b) (4)

[redacted]

Entered into database by (initial and date): AT 23 Apr 2019
Verification of database entries (initial and date): RL 24 Apr 2019

ASCUS BIOSCIENCES

Analyst 2 Sample 1 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0202-041 -P22				

(b) (4)

[redacted]

Verification of database entries (initial and date): RL 24 Apr 2019

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Analyst 2 Sample 2 Data						
Study Number	Date & Time	Lot Number				
	22Apr2019 11:00AM	18-0202-041 -P26				

(b) (4)

[redacted]

Entered into database by (initial and date): AH 23Apr 2019
Verification of database entries (initial and date): ZL 24 Apr 2019

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Analyst 2 Sample 3 Data						
Study Number	Date & Time	Lot Number				
	22Apr2019 11:00AM	18-0202-041 -P30				

(b) (4)

[redacted]

Verification of database entries (initial and date): RL 24 Apr 2019

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Sample Information

Analyst 1

Sample ID	DY20 SDP Lot Number	Initials and Date
P22 (1,2,3)	18-0202-041-P22	RL 24 Apr 2019
P26(4,5,6,7①)	18-0202-041-P26	RL 24 Apr 2019
P30(7,8,9)	18-0202-041-P30	RL 24 Apr 2019

① RL 24 Apr 2019 Entry Error

Analyst 2

Sample ID	DY20 SDP Lot Number	Initials and Date
P22	18-0202-041-P22	AT 24 Apr 2019
P26	18-0202-041-P26	AT 24 Apr 2019
P30	18-0202-041-P30	AT 24 Apr 2019

Comparison of Results

Analyst	Sample	Low Conc. Result (CFU/g)	High Conc. Result (CFU/g)	CV between samples	Pass/Fail	Initials & Date
RL	P22	(b) (4)			Pass	RL 24 Apr 2019
RL	P26				Pass	RL 24 Apr 2019
RL	P30				Pass	RL 24 Apr 2019
AT	P22				Pass	AT 24 Apr 2019
AT	P26				Pass	AT 24 Apr 2019
AT	P30				Pass	AT 24 Apr 2019

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Attachment

1000X Wolf's Vitamin Solution

Ingredient	Catalog Number	Amount/ liter	Amount Added
Pyridoxine Hydrochloride	Spectrum PY103	(b) (4)	
p- Aminobenzoic Acid	Spectrum AM150		
Alpha Lipoic Acid	Spectrum L1506		
Nicotinic acid	Spectrum NI100		
Riboflavin	Spectrum RI103		
Thiamine Hydrochloride	Spectrum T1053		
Calcium Pantothenate	Spectrum CA159		
Biotin, Powder	Spectrum B1103		
Folic Acid, Powder	Spectrum FO105		
Vitamin B12	Spectrum C1454		
diH2O			

(b) (4)

pH (initial): 3.60

pH (adjusted): 6.77

Note Acid/Base Concentration used: 1.9 mL of 1N NaOH

Initials and date: SM 19 Apr 2019

0.1% Wolf's Vitamin Solution

(b) (4)

Initials and date: S.M 19 Apr 2019

Comparison of Vitamin Concentrations in DY20 SDP Method Enumeration – Summary Report

Organism: *Clostridium butyricum*

Tested Lots: 18-0202-041-P22, 18-0202-041-P26, 18-0202-041-P30

Purpose: To determine effects, if any, of using high or low concentrations of vitamins with the DY20 enumeration method.

Acceptance Criteria: If the CVs between vitamin solutions are ≤75% then the concentration of vitamins does not impact the results.

Results

Table 1. Analyst 1 vitamin concentration comparison results.

Analyst 1 Results					
Lot Number	Low Conc CFU/g	High Conc CFU/g	Avg. CFU/g	Std. Dev.	CV
18-0202-041-P22	(b) (4)				
18-0202-041-P26					
18-0202-041-P30					

Table 2. Analyst 2 vitamin concentration comparison results

Analyst 2 Results					
Lot Number	Low Conc CFU/g	High Conc CFU/g	Avg. CFU/g	Std. Dev.	CV
18-0202-041-P22	(b) (4)				
18-0202-041-P26					
18-0202-041-P30					

Discussion

The vitamin concentration effect was tested on DY20-SDP on three separate lots by two analysts. Results between the vitamin concentrations were comparable and indicate that the vitamin concentration does not impact the growth of DY20.

Variability (CV) of the 3 lots remained less than 75% across 6 replicates comparing the different vitamin concentrations. There is no significant effect of vitamin concentration on the growth of DY20.

Deviations from the Protocol: None.

Changes from the protocol: None

Location of raw data: Executed protocol (attached)

Clostridium beijerinckii ASCUSDY20 Spray-Dried Powder 25°C: 12-Month Stability Summary Report

Approvers:

DocuSigned by:
Martin Mayhew
D1605F1B4C3E49A...

5/12/2020

Martin Mayhew
Vice President – Product Development & Manufacturing

Date

DocuSigned by:
Patricia A Williams
5B301285A10643D...

5/6/2020

Patricia A. Williams
Quality

Date

DocuSigned by:
Howard B Green
0FAA38037D49453...

5/8/2020

Howard B. Green
Regulatory

Date

Prepared by
Ascus Biosciences
San Diego, CA

April 2020

Table of Contents

Clostridium beijerinckii ASCUSDY20 Spray-Dried Powder 25°C: 12-Month Stability Summary Report

Organism: ***Clostridium beijerinckii*** **ASCUSDY20**

Testing Condition: 25°C ± 3°C

Purpose: To support registered expiration dating and storage conditions for 20 - 25°C for 12 months.

Study Numbers: DUS1805 (Lot# 18-0202-001-P73)
DUS1808 (Lot# 18-0202-041-P22)
DUS1811 (Lot# 18-0202-001-P79)

Acceptance Criteria: Not Less Than 4.0 X 10^6 CFU/g

1 Results

Table 1. Results for Each Lot at Each Time Point

Note: Results are reported in average colony forming units (CFU)/gram *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder.

	Avg. CFU/g			Std. Dev.		
Time (mo)	**DUS1805**	**DUS1808**	**DUS1811**	**DUS1805**	**DUS1808**	**DUS1811**
0	(b) (4)					
1						
2						
3						
6						
9						
12						

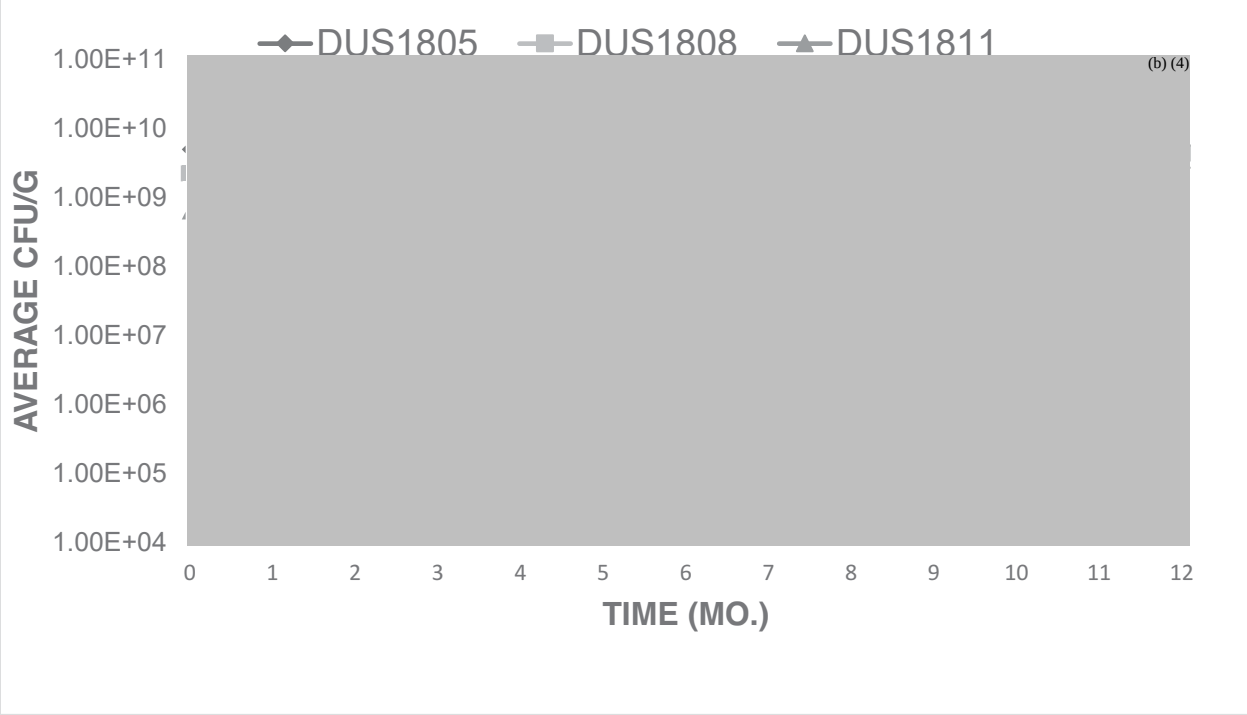


Figure 1. Graph of Results for Each Lot at Each Time Point

Note: Results are reported in average colony forming units (CFU)/gram *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder.

2 Discussion

The stability study of *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder on three separate lots conducted at 25°C ± 3°C for 12 months resulted in no degradation of the material below the original acceptance criteria of 4.00 X 10^6 CFU/g and the revised acceptance criteria of 5.00 X 10^8 CFU/g (Table 1, Figure 1).

Viability of the 3 lots remained above 5.00 X 10^8 CFU/g for the duration of this stability study, indicating *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder will remain above the acceptance criteria for up to 12 months at 25°C ± 3°C.

3 Deviations

Deviations from the *Clostridium beijerinckii* ASCUSDY20 SDP Microbe Enumeration method that were considered minor were the following:

1. Media was prepared in 1000 L volumes (Step 1.8) instead of in 500mL volumes due to high demand of media production.

2. Hot water bath temperature ranged from 65 - 80°C (Step 1.10) instead of 80°C to reduce condensation in the bottle while cooling the media prior to additional media additions.

One deviation investigated further was the preparation and storage instructions for the vitamin solution in Step 1.2. A comparison study was performed to confirm that the vitamin preparation did not impact the assay results. The corrected method was used for subsequent time points.

4 Changes

No significant changes occurred during the stability study.

5 Appendices

Appendix 1. *Clostridium beijerinckii* ASCUSDY20 SDP 25°C Stability Protocol

Appendix 2. Lot# 18-0202-041-P22 Master Production Record

Appendix 3. Lot# 18-0202-001-P73 Master Production Record

Appendix 4. Lot# 18-0202-001-P79 Master Production Record

Appendix 5. *Clostridium beijerinckii* ASCUSDY20 SDP Stability Data for Tables & Graphs

Appendix 6. D2019-005: Wrong Vitamin Concentration Used in Galaxis/Altius and *Clostridium beijerinckii* ASCUSDY20 SDP Assays

Appendix 1. *Clostridium beijerinckii* ASCUSDY20 SDP 25°C Stability Protocol

ASCUS BIOSCIENCES

Stability Protocol Title:	**DY20 SDP 25°C**
Organism:	***Clostridium butyricum***
Purpose:	**To support the registered expiration dating and storage conditions of 20-25°C for 12 months**
Number of Samples to Place on Stability:	**9 (allows for retesting, when needed)**
Sample Storage Container:	Heat sealed 48-gauge silver metalized PET / 2.5 mil LLDPE bags made from commercial bags
Temperature Conditions:	**20 - 25°C**
Acceptance Criteria:	**>4 x 10^6 cfu/g**

Tests and Timepoints:

Assay	T_0	1 month	2 months	3 months	6 months	9 months	12 months
Microbe Enumeration*	X	X	X	X	X	X	X

***DY20-SDP Microbe Enumeration method**

Approvals:

Howard Green Regulatory	DocuSigned by: Howard B Green 12/5/2018 9:23:46 AM PST
Corey Dodge Process Development	DocuSigned by: Corey Dodge 12/5/2018 8:16:36 AM PST
Patricia A. Williams Quality	DocuSigned by: Patricia A Williams 12/4/2018 7:05:27 PM PST

Appendix 2. Lot# 18-0202-041-P22 Master Production Record

22

Project No. 24072.01.001

Book No. 18-0202-041 TITLE ~100 L 10% DX-20 70/30 CAP

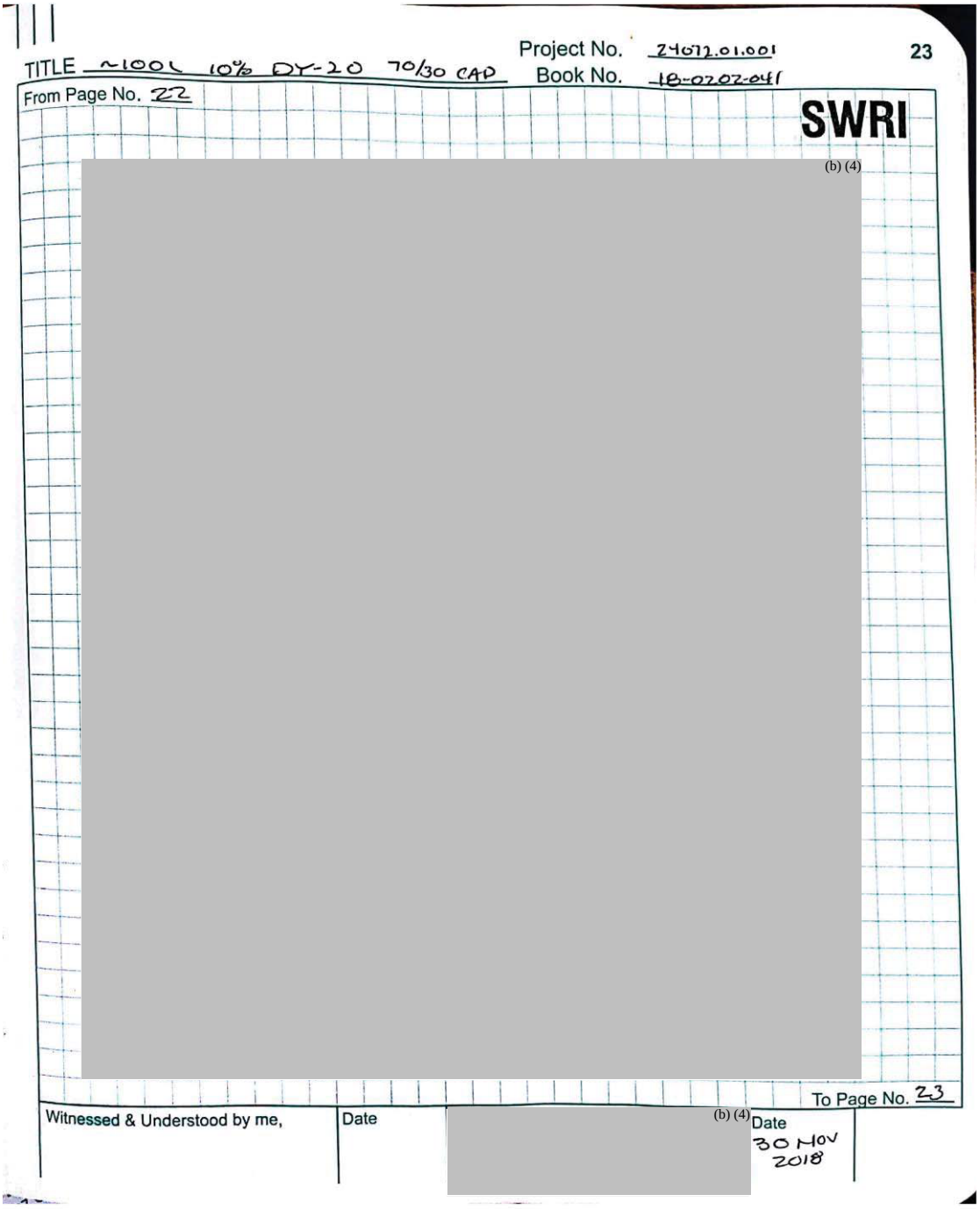
From Page No. 22

SWRI

MICROENCAPSULATION/ PROCESS DATA SHEET

(b) (4)

Witnessed & U



TITLE ~100L 10% DY-20 70/30 CAP
Project No. 24072.01.001
Book No. 18-0202-041
23
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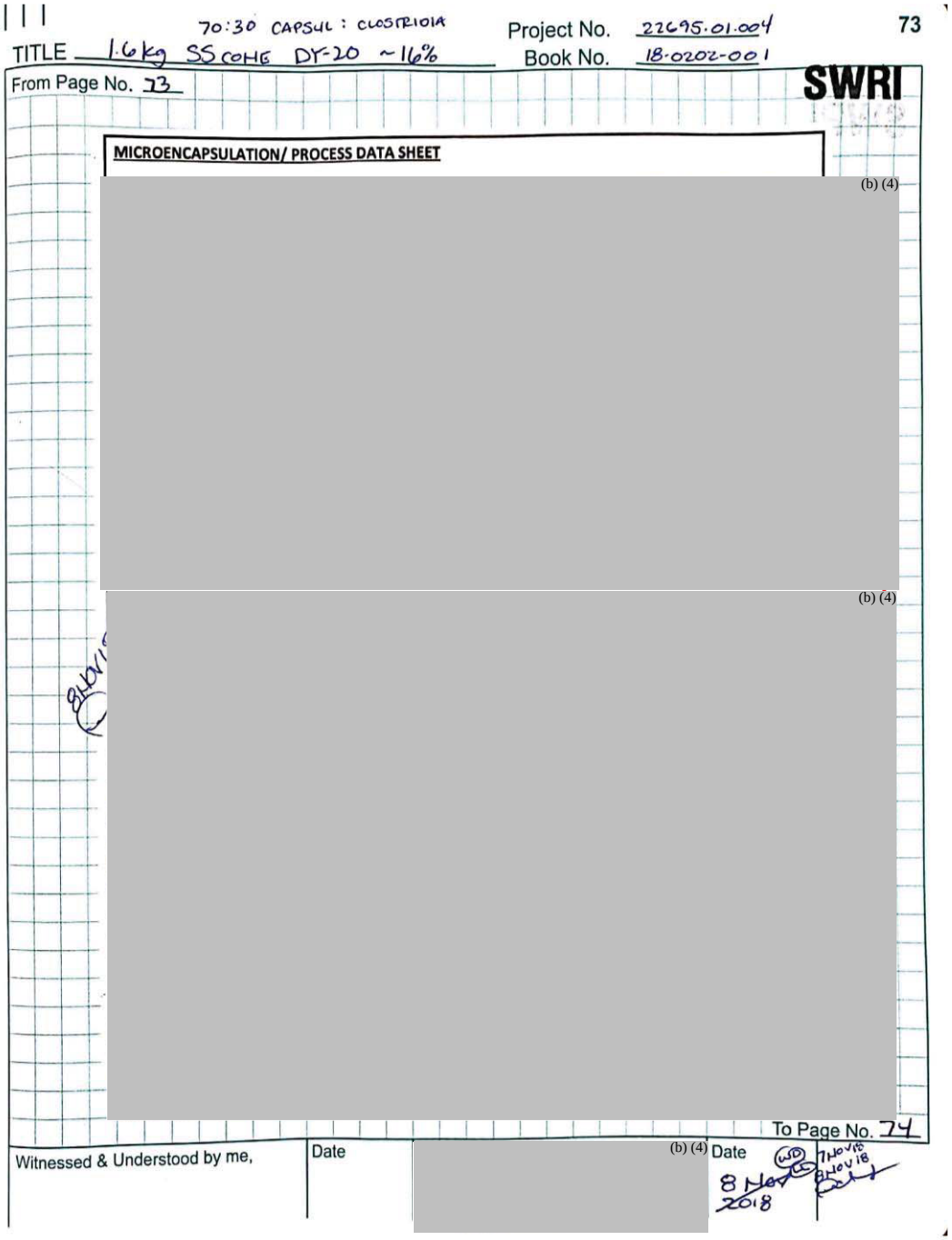
To Page No. 23
Witnessed & Understood by me,
Date
(b) (4)
Date
30 NOV 2018

Appendix 3. Lot# 18-0202-001-P73 Master Production Record



70:30 CAPSUL : CLOSTRIDIA
TITLE 1.6kg SS COHE DY-20 ~16%
Project No. 22695.01.004
Book No. 18-0202-001
73
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Witnessed & Understood by me,
Date
(b) (4)
Date
8 Nov 2018

74

Project No. 22695.01.004
Book No. 18-0202-001 TITLE 1.6kg R4H CONTD
From Page No. 73
SWRI

(b) (4)

[redacted]

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Witnessed & Understood by me, | Date | (b) (4) [redacted] | Date 7Nov18 8 Nov 2018 8Nov18

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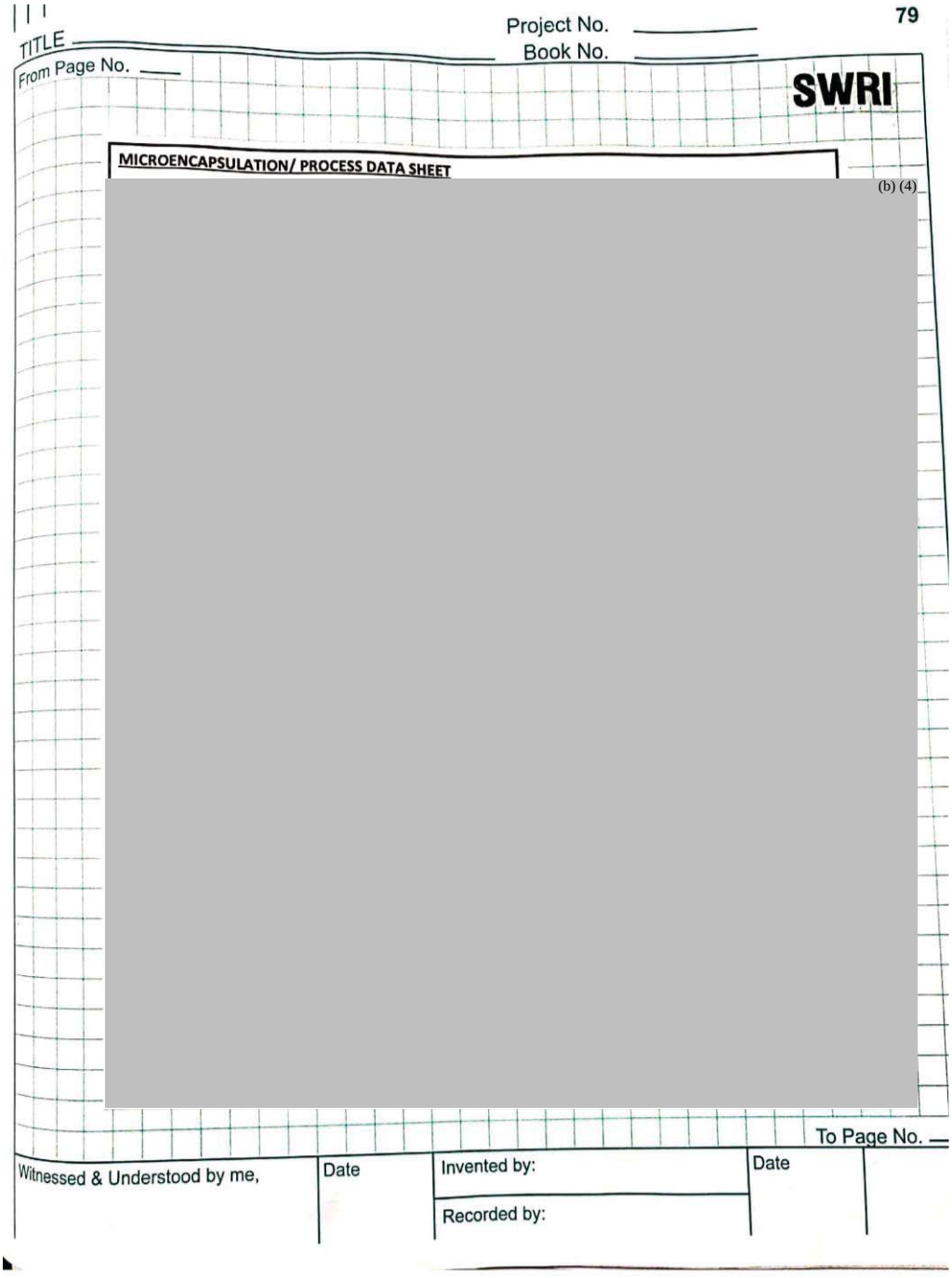
Appendix 4. Lot# 18-0202-001-P79 Master Production Record



TITLE
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Project No.
Book No.
79
SWRI
MICROENCAPSULATION/ PROCESS DATA SHEET
(b) (4)
To Page No.
Witnessed & Understood by me,
Date
Invented by:
Recorded by:
Date

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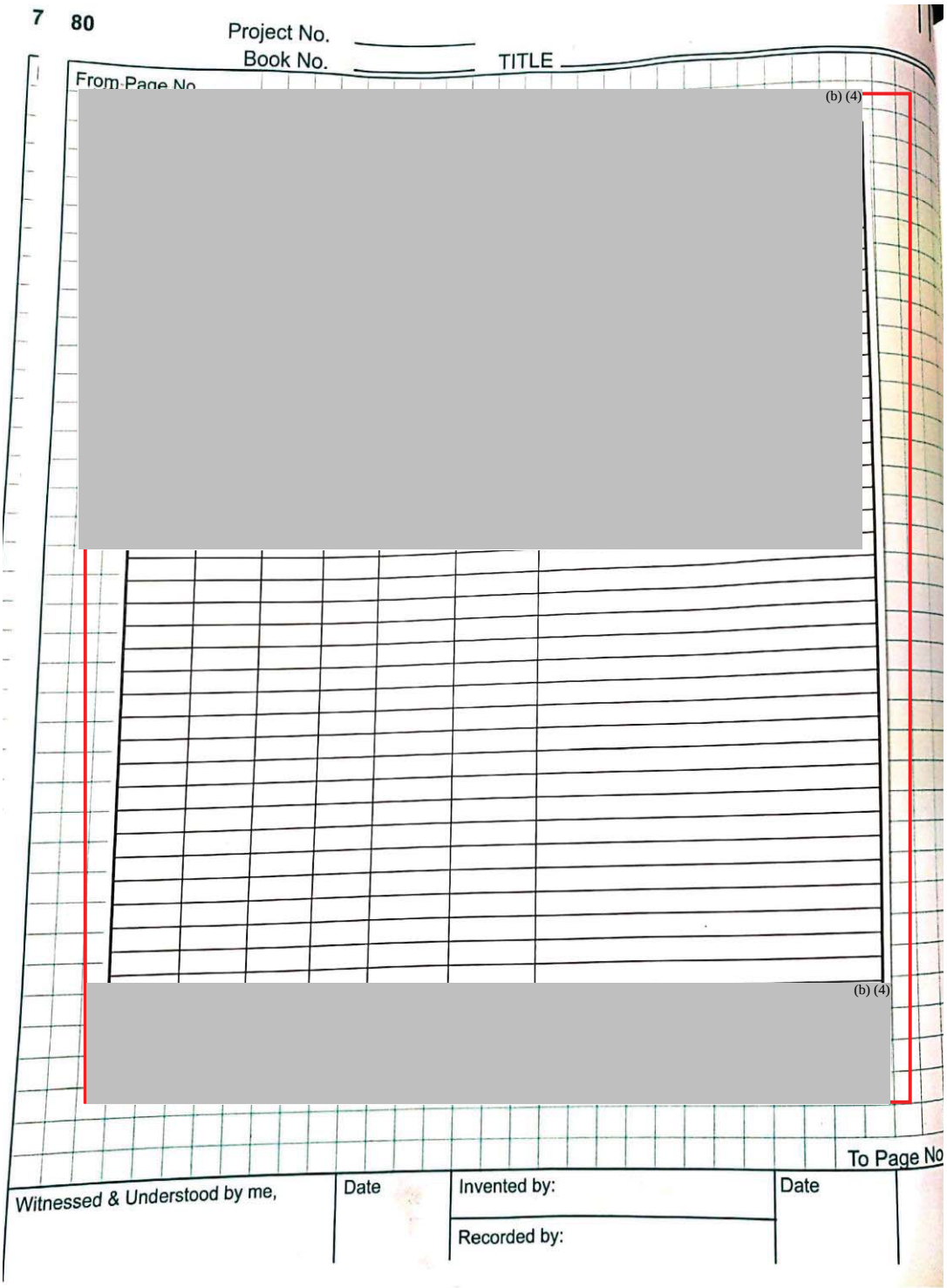

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Appendix 5. *Clostridium beijerinckii* ASCUSDY20 SDP Stability Data for Tables & Graphs

Study Number	Scheduled Pull Date	Date Sample Was Pulled	Testing Condition	Timepoint	Batch Number	Lot Number	Analyst Initials	Sample	Mass (g)	Volume 1X PBST (mL)	DY20 Plating CFU Counts, CFU/100uL 1E-04 A	1E-04 B	1E-04 C	1E-05 A	1E-05 B	1E-05 C	1E-06 A	1E-06 B	1E-06 C	DY 20 CFU/mL A	CFU/mL B	CFU/mL C	CFU/g A	CFU/g B	CFU/g C	Avg. CFU/g	Std. Dev.	CV
DUS1805	13-Jan-19	1/11/2019	25C	1 month	1	18-0202-001-P73	MS	15-1	0.1010	10	TMTC	TMTC	TMTC	92	78	118	8	8	7	9.20E+07	7.80E+07	1.18E+08	9.20E+09	7.80E+09	1.17E+10			
								15-2	0.1000	10	TMTC	TMTC	TMTC	100	76	77	6	3	5	1.00E+08	7.60E+07	7.70E+07	1.00E+10	7.60E+09	7.70E+09			
								15-3	0.1060	10	TMTC	TMTC	TMTC	122	97	111	3	7	6	1.22E+08	9.70E+07	1.11E+08	1.15E+10	9.15E+09	1.05E+10	9.64E+09	1.05E+09	11%
	13-Feb-19	2/13/2019	25C	2 month	1	18-0202-001-P73	SM	12-1	0.1016	10	168	124	168	15	5	5	1	0	0	1.68E+07	1.24E+07	1.68E+07	1.65E+09	1.22E+09	1.65E+09			
								12-2	0.1005	10	160	137	89	6	11	10	0	2	0	1.60E+07	1.37E+07	8.90E+06	1.59E+09	1.36E+09	8.86E+08			
								12-3	0.1015	10	65	75	87	10	5	5	0	0	1	6.50E+06	7.50E+06	8.70E+06	6.40E+08	7.39E+08	8.57E+08	1.18E+09	3.92E+08	33%
	13-Mar-19	3/10/2019	25C	3 month	1	18-0202-001-P73	RL	11-1	0.1084	10	TMTC	TMTC	TMTC	51	25	62	3	7	3	5.10E+07	2.50E+07	6.20E+07	4.70E+09	2.31E+09	5.72E+09			
								11-2	0.1050	10	TMTC	TMTC	TMTC	86	125	97	11	8	6	8.60E+07	1.25E+08	9.70E+07	8.19E+09	1.19E+10	9.24E+09			
								11-3	0.1058	10	TMTC	TMTC	TMTC	76	141	86	14	7	9	7.60E+07	1.41E+08	8.60E+07	7.18E+09	1.33E+10	8.13E+09	7.86E+09	3.13E+09	40%
	13-Jun-19	6/11/2019	25C	6 month	1	18-0202-001-P73	RL	10-1	0.1000	10	193	260	TMTC	36	47	37	7	4	4	1.93E+07	2.60E+07	N/A	1.93E+09	2.60E+09	N/A			
								10-2	0.1050	10	TMTC	227	151	67	50	40	2	1	14	N/A	2.27E+07	1.51E+07	N/A	2.16E+09	1.44E+09			
								10-3	0.1090	10	53	42	187	41	53	55	5	9	0	5.30E+06	4.20E+06	1.87E+07	4.86E+08	3.85E+08	1.72E+09	1.53E+09	7.14E+08	47%
	13-Sep-19	9/11/2019	25C	9 month	1	18-0202-001-P73	RL	14-1	0.1020	10	TMTC	273	157	20	22	24	2	2	4	2.00E+07	2.20E+07	2.40E+07	1.96E+09	2.16E+09	2.35E+09			
								14-2	0.1000	10	TMTC	TMTC	271	22	38	15	3	5	1	2.20E+07	3.80E+07	1.50E+07	2.20E+09	3.80E+09	1.50E+09			
								14-3	0.1040	10	TMTC	293	281	23	28	28	4	2	5	2.30E+07	2.80E+07	2.80E+07	2.21E+09	2.69E+09	2.69E+09	2.40E+09	2.08E+08	9%
	13-Dec-19	12/12/2019	25C	12 month	1	18-0202-001-P73	AT	13-1	0.0990	10	TMTC	TMTC	TMTC	83	61	62	6	7	14	8.30E+07	6.10E+07	6.20E+07	8.38E+09	6.16E+09	6.26E+09			
								13-2	0.0990	10	TMTC	TMTC	TMTC	46	41	34	0	4	2	4.60E+07	4.10E+07	3.40E+07	4.65E+09	4.14E+09	3.43E+09			
								13-3	0.0980	10	TMTC	TMTC	TMTC	56	59	58	8	5	2	5.60E+07	5.90E+07	5.80E+07	5.71E+09	6.02E+09	5.92E+09	5.63E+09	1.45E+09	26%
DUS1808	13-Jan-19	11-Jan-19	25C	1 month	2	18-0202-041-P22	MS	40-1	0.1000	10	TMTC	TMTC	TMTC	89	130	126	4	4	0	8.90E+07	1.30E+08	1.26E+08	8.90E+09	1.30E+10	1.26E+10			
								40-2	0.1010	10	TMTC	TMTC	TMTC	51	52	45	4	2	3	5.10E+07	5.20E+07	4.50E+07	5.05E+09	5.15E+09	4.46E+09			
								40-3	0.1010	10	TMTC	TMTC	TMTC	67	92	90	4	1	5	6.70E+07	9.20E+07	9.00E+07	6.63E+09	9.11E+09	8.91E+09	8.20E+09	3.31E+09	40%
	13-Feb-19	13-Feb-19	25C	2 month	2	18-0202-041-P22	SM	37-1	0.1004	10	189	156	134	4	8	4	0	0	0	1.89E+07	1.56E+07	1.34E+07	1.88E+09	1.55E+09	1.33E+09			
								37-2	0.1005	10	87	75	50	4	4	9	1	1	0	8.70E+06	7.50E+06	5.00E+06	8.66E+08	7.46E+08	4.98E+08			
								37-3	0.1011	10	195	193	169	3	6	6	0	0	0	1.95E+07	1.83E+07	1.69E+07	1.93E+09	1.81E+09	1.67E+09	1.37E+09	5.84E+08	43%
	13-Mar-19	13-Mar-19	25C	3 month	2	18-0202-041-P22	RL	36-1	0.1028	10	TMTC	TMTC	TMTC	47	68	49	14	9	10	4.70E+07	6.80E+07	4.90E+07	4.57E+09	6.61E+09	4.77E+09			
								36-2	0.1036	10	TMTC	TMTC	TMTC	57	31	33	6	5	4	5.70E+07	3.10E+07	3.30E+07	5.50E+09	2.99E+09	3.19E+09			
								36-3	0.1096	10	TMTC	TMTC	TMTC	104	161	107	16	6	4	1.04E+08	1.61E+08	1.07E+08	9.49E+09	1.47E+10	9.76E+09	6.84E+09	3.94E+09	58%
	13-Jun-19	11-Jun-19	25C	6 month	2	18-0202-041-P22	RL	35-1	0.1010	10	206	261	TMTC	74	72	58	3	4	5	7.40E+07	7.20E+07	5.80E+07	7.33E+09	7.13E+09	5.74E+09			
								35-2	0.1060	10	270	TMTC	TMTC	68	57	57	7	5	4	6.80E+07	5.70E+07	5.70E+07	6.42E+09	5.38E+09	5.38E+09			
								35-3	0.1030	10	199	223	TMTC	55	78	59	8	6	4	5.50E+07	7.80E+07	5.90E+07	5.34E+09	7.57E+09	5.73E+09	6.22E+09	5.05E+08	8%
	13-Sep-19	11-Sep-19	25C	9 month	2	18-0202-041-P22	RL	39-1	0.1070	10	TMTC	TMTC	TMTC	38	33	24	1	3	0	3.80E+07	3.30E+07	2.40E+07	3.55E+09	3.08E+09	2.24E+09			
								39-2	0.1010	10	TMTC	TMTC	TMTC	17	39	31	2	0	0	1.70E+07	3.90E+07	3.10E+07	1.68E+09	3.86E+09	3.07E+09			
								39-3	0.1010	10	TMTC	280	TMTC	34	25	28	3	3	0	3.40E+07	2.50E+07	2.80E+07	3.37E+09	2.48E+09	2.77E+09	2.90E+09	5.09E+07	2%
	13-Dec-19	12-Dec-19	25C	12 month	2	18-0202-041-P22	AT	38-1	0.0990	10	TMTC	TMTC	TMTC	59	48	52	3	6	2	5.90E+07	4.80E+07	5.20E+07	5.96E+09	4.85E+09	5.25E+09			
								38-2	0.0980	10	TMTC	TMTC	TMTC	41	55	32	1	6	3	4.10E+07	5.50E+07	3.20E+07	4.18E+09	5.61E+09	3.27E+09			
								38-3	0.1050	10	TMTC	TMTC	TMTC	38	31	45	2	3	3	3.80E+07	3.10E+07	4.50E+07	3.62E+09	2.95E+09	4.29E+09	4.44E+09	8.71E+08	20%
DUS1811	20-Jan-19	1/17/2019	25C	1 month	3	18-0202-001-P79	AT	60-1	0.0990	10	83	121	92	21	11	25	1	2	2	8.30E+06	1.21E+07	9.20E+06	8.38E+08	1.22E+09	9.29E+08			
								60-2	0.1020	10	276	231	139	5	11	13	2	1	1	2.76E+07	2.31E+07	1.39E+07	2.71E+09	2.26E+09	1.36E+09			
								60-3	0.1010	10	282	TMTC	228	14	17	18	6	2	2	2.82E+07	N/A	2.28E+07	2.79E+09	N/A	2.26E+09	1.80E+09	7.90E+08	44%
	20-Feb-19	2/20/2019	25C	2 month	3	18-0202-001-P79	RL	61-1	0.1024	10	45	43	77	12	19	18	1	2	2	4.50E+06	4.30E+06	7.70E+06	4.39E+08	4.20E+08	7.52E+08			
								61-2	0.1068	10	44	77	118	20	26	25	0	1	0	4.40E+06	7.70E+06	1.18E+07	4.12E+08	7.21E+08	1.10E+09			
								61-3	0.1038	10	19	41	48	6	12	10	1	4	2	1.90E+06	4.10E+06	4.80E+06	1.83E+08	3.95E+08	4.62E+08	5.43E+08	2.00E+08	37%
	20-Mar-19	3/19/2019	25C	3 month	3	18-0202-001-P79	AT	65-1	0.1013	10	TMTC	TMTC	TMTC	54	57	43	8	7	2	5.40E+07	5.70E+07	4.30E+07	5.33E+09	5.63E+09	4.24E+09			
								65-2	0.1053	10	TMTC	TMTC	TMTC	57	55	50	6	4	2	5.70E+07	5.50E+07	5.00E+07	5.41E+09	5.22E+09	4.75E+09			
								65-3	0.1068	10	TMTC	TMTC	TMTC	74	89	82	5	11	6	7.40E+07	8.90E+07	8.20E+07	6.93E+09	8.33E+09	7.68E+09	5.95E+09	1.47E+09	25%
	20-Jun-19	6/18/2019	25C	6 month	3	18-0202-001-P79	AT	62-1	0.1030	10	47	38	29	2	2	2	0	0	1	4.70E+06	3.80E+06	2.90E+06	4.56E+08	3.69E+08	2.82E+08			
								62-2	0.0990	10	99	88	90	12	7	9	1	0	0	9.90E+06	8.80E+06	9.00E+06	1.00E+09	8.89E+08	9.09E+08			
								62-3	0.0980	10	50	36	26	6	8	11	0	0	0	5.00E+06	3.60E+06	2.60E+06	5.10E+08	3.67E+08	2.65E+08	5.61E+08	3.22E+08	57%
	20-Sep-19	6/19/2019	25C	9 month	3	18-0202-001-P79	AT	64-1	0.1010	10	90	145	69	20	15	7	1	0	0	9.00E+06	1.45E+07	6.90E+06	8.91E+08	1.44E+09	6.83E+08			
								64-2	0.1010	10	133	112	78	12	6	1	1	0	0	1.33E+07	1.12E+07	7.80E+06	1.32E+09	1.11E+09	7.72E+08			
								64-3	0.1020	10	121	104	129	18	19	18	2	0	0	1.21E+07	1.04E+07	1.29E+07	1.19E+09	1.02E+09	1.26E+09	1.08E+09	7.72E+07	7%
	20-Dec-19	12/18/2019	25C	12 month	3	18-0202-001-P79	AT	63-1	0.1000	10	TMTC	TMTC	TMTC	37	31	33	2	12	1	3.70E+07	3.10E+07	3.30E+07	3.70E+09	3.10E+09	3.30E+09			
								63-2	0.0980	10	TMTC	TMTC	TMTC	37	35	30	8	5	0	3.70E+07	3.50E+07	3.00E+07	3.78E+09	3.57E+09	3.06E+09			
								63-3	0.1010	10	TMTC	TMTC	TMTC	43	33	37	3	6	1	4.30E+07	3.30E+07	3.70E+07	4.26E+09	3.27E+09	3.66E+09	3.52E+09	1.87E+08	5%

Date of creation	Date of assay	Timepoint	Batch Number	Lot Number	Analyst Initials	Sample	Mass (g)	Volume 1X PBST (mL)	DY20 Plating CFU Counts, CFU/100uL 1E-04 A	1E-04 B	1E-04 C	1E-05 A	1E-05 B	1E-05 C	1E-06 A	1E-06 B	1E-06 C	DY 20 CFU/mL A	CFU/mL B	CFU/mL C	CFU/g A	CFU/g B	CFU/g C	Avg. CFU/g	Std. Dev.	CV
8-Nov-18	10-Dec-18	T=0	1	18-0202-001-P73	MS	Batch 1-1	0.1024	10	TMTC	TMTC	TMTC	57	49	95	7	4	2	5.70E+07	4.90E+07	9.50E+07	5.57E+09	4.79E+09	9.28E+09			
						Batch 1-2	0.1009	10	TMTC	TMTC	TMTC	33	47	37	3	3	4	3.10E+07	4.70E+07	3.70E+07	3.07E+09	4.66E+09	3.67E+09			
						Batch 1-3	0.1020	10	TMTC	TMTC	TMTC	52	49	40	5	6	9	5.20E+07	4.90E+07	4.00E+07	5.10E+09	4.80E+09	3.92E+09	4.98E+09	1.41E+09	28%
7-Dec-18	12-Dec-18	T=0	2	18-0202-041-P22	AT	P22-1	0.1008	10	TMTC	212	256	41	47	48	3	4	0	N/A	2.12E+07	2.56E+07	N/A	2.10E+09	2.54E+09			
						P22-2	0.1006	10	255	296	TMTC	20	55	43	2	1	1	2.55E+07	2.96E+07	N/A	2.53E+09	2.94E+09	N/A			
						P22-3	0.1007	10	195	203	162	17	40	19	10	5	1	1.95E+07	2.03E+07	1.62E+07	1.94E+09	2.02E+09	1.61E+09	2.24E+09	4.43E+08	20%
17-Dec-18	20-Dec-18	T=0	3	18-0202-001-P79	SM	P79-1	0.1002	10	36	33	64	1	6	10	0	1	3	3.60E+06	3.30E+06	6.40E+06	3.59E+08	3.29E+08	6.39E+08			
						P79-2	0.1000	10	61	51	35	21	8	9	0	0	0	6.10E+06	5.10E+06	3.50E+06	6.10E+08	5.10E+08	3.50E+08			
						P-79-3	0.1015	10	111	100	83	5	13	11	2	0	0	1.11E+07	1.00E+07	8.30E+06	1.09E+09	9.85E+08	8.18E+08	6.33E+08	2.89E+08	46%

Appendix 6. D2019-005: Wrong Vitamin Concentration Used in Galaxis/Altius and *Clostridium beijerinckii* ASCUSDY20 SDP Assays

ASCUS BIOSCIENCES

Deviation Number: D2019-005

Deviation Title: Wrong Vitamin Concentration Used for in Galaxis/Alitus and DY20 SDP Assays

Deviation Investigator: Adam Taylor

Description of the Deviation:
In April 2019 DetectLab, Mexico and CKC, Argentina informed Ascus of problems in execution of Vitamin Mix section of the Galaxis/Altius Microbe Enumeration methods. The issue was that the solids did not fully dissolve into solution.

Investigation:
The methods used at DetectLab, Mexico and CKC, Argentina (Microbe Enumeration of Galaxis 100 V5 and Microbe Enumeration of Altius and Galaxis 5 V8) were compared to methods used at Ascus for the preparation of the 0.1% Vitamin mix. The Mexican and Argentinian labs followed the methods as written. However, Ascus personnel were deviating from the methods by increasing the solvent/solute ratio by 10X. This allowed the solutes to readily dissolve, but resulted in an incorrect amount of vitamins in the media.

Further investigation indicated that Ascus personnel have been preparing the vitamin solution this way since August 2017 due to unclear wording in the method. In addition, all methods were validated with the lower amount of vitamins in the media.

Impacted results since 2017 include:

- Stability studies involving Galaxis 100, Galaxis 5, Altius, and DY20SDP
- Product release results for DY20SDP.

Impacted methods used since 2017 include:

- Microbe Enumeration for Galaxis 100
- Microbe Enumeration for Altius and Galaxis 5
- DY20 SDP Microbe Enumeration V3

Confidential T203A – Deviation Template Page 1 of 3

Deviation Number: D2019-005

Impacted commercial cell banks:

- DY20 Master Cell Bank 15Aug2018
- DY20 Working Cell Bank 1
- DY20 Working Cell Bank PCC1
- DY20 Working Cell Bank PCC5
- DY20 Working Cell Bank 3

To determine if the different vitamin preparation impacted the assay results, a comparison study was conducted with 2 analysts, 2 samples, and both preparation methods. See the attachment. The comparison study confirmed that the vitamin preparation method did not impact the assay results. Therefore, all the results generated at Ascus are valid. Methods will not be re-validated and cell banks will not be re-tested.

To ensure that the methods are executed correctly from now on, they will be revised to more clearly state how to prepare the vitamin mixture.

Immediate Corrections:

Action	Completed by	Date Completed	Comments
None			

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Deviation Number: D2019-005

CAPA:

CAPA Log #	Action	Assigned to	Due Date	Comments
CA2019-005	Clarify the section on vitamin mix preparation for the following methods: DY20SDP, Galaxis 5/Altius, and Galaxis 100	Pat Williams	08May2019	
CA2019-006	Send revised methods to [redacted]	Adam Taylor	09May2019	
CA2019-007	Clarify the section on vitamin mix preparation for the following cell bank protocols: DY20 Working Cell Bank, DY20 Master Cell Bank, DY20 Cell Bank Retesting	Pat Williams	15May2019	

Approvers:

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AF21D1C745C	5/3/2019
Patricia A. Williams – Quality	DocuSigned by: Patricia Williams 5B301285A10843D...	5/3/2019
Howard Green – Regulatory	DocuSigned by: Howard B Green	5/3/2019

ASCUS BIOSCIENCES

Comparison of Vitamin Concentrations in DY20 SDP Method Enumeration

Method Titles and Versions

Title	DY20-SDP Microbe Enumeration
Version	03

Lab Performing the Comparison: Ascus Biosciences Inc.

Pre-Execution Approval:

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AE21D1C745C...	4/22/2019

Post Execution Approval (includes Summary Report):

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AE21D1C745C...	5/3/2019
Patricia A. Williams – Quality	DocuSigned by: Patricia Williams 5B301285A10643D...	4/30/2019

Personnel Executing the Comparison:
Your signature indicates that you have read and understand this protocol.

Printed Name	Signature	Tasks Performed
Rich La		Analyst 1
Adam Taylor		Analyst 2
Samantha Marroquin		Media preparation

Purpose:
Deviation D2019-005 documents issues with execution of the DY20-SDP Microbe Enumeration method. Specifically, some analysts were using a 1000X less of the vitamin solution than what the method requires. See the deviation for details of the investigation.

This protocol will determine if a 1000X concentration difference in the Vitamin Solution has an impact on the results obtained from the DY20-SDP Microbe Enumeration method. The method

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will be run by 2 analysts, using 3 different lots of DY20 SDP, and the high and low concentration of vitamins. This will provide enough data to determine if the vitamin concentration impacts the results.

The intent is to use the validated method with the high concentration of vitamins going forward; therefore, this is not a method validation protocol. The method will be run as validated, with the exception of changing the vitamin concentration. Raw data will be recorded as listed in the method. The full method is retained in the Ascus Google Drive/Commercial Documents/Analytical Documents.

Directions for preparation of the 2 different vitamin concentrations are attached to this protocol.

The closeness of results from both vitamin concentrations will be assessed to determine if there is an impact on results.

Acceptance Criteria and Summary:
If the CVs between the vitamin solutions are ≤75% then the concentration of vitamins does not impact the results. (For example, if the CV between analyst 1, sample 1, for both vitamin concentrations is ≤75%, then there is no impact.)

A summary of the study and copy of Plate Count Data will be written after execution and approved by the Director of Product Development and Quality.

Analyst 1 Sample 1 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0202-041-P22				

(b) (4)

[redacted]

Analyst 1 Sample 2 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0202 041-726				

(b) (4)

[redacted]

Analyst 1 Sample 3 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0702-041-P30				

(b) (4)

[redacted]

Entered into database by (initial and date): AT 23 Apr 2019
Verification of database entries (initial and date): RL 24 Apr 2019

ASCUS BIOSCIENCES

Analyst 2 Sample 1 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0202-041 -P22				

(b) (4)

[redacted]

Verification of database entries (initial and date): RL 24 Apr 2019

Confidential

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Analyst 2 Sample 2 Data						
Study Number	Date & Time	Lot Number				
	22Apr2019 11:00AM	18-0202-041 -P26				

(b) (4)

[redacted]

Entered into database by (initial and date): AH 23Apr 2019
Verification of database entries (initial and date): RL 24 Apr 2019

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Analyst 2 Sample 3 Data						
Study Number	Date & Time	Lot Number				
	22Apr2019 11:00AM	18-0202-041 -P30				

(b) (4)

[redacted]

Verification of database entries (initial and date): RL 24 Apr 2019

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Sample Information

Analyst 1

Sample ID	DY20 SDP Lot Number	Initials and Date
P22 (1,2,3)	18-0202-041-P22	RL 24 Apr 2019
P26(4,5,6,X①)	18-0202-041-P26	RL 24 Apr 2019
P30(7,8,9)	18-0202-041-P30	RL 24 Apr 2019

① RL 24 Apr 2019 Entry Error

Analyst 2

Sample ID	DY20 SDP Lot Number	Initials and Date
P22	18-0202-041-P22	AT 24 Apr 2019
P26	18-0202-041-P26	AT 24 Apr 2019
P30	18-0202-041-P30	AT 24 Apr 2019

Comparison of Results

Analyst	Sample	Low Conc. Result (CFU/g)	High Conc. Result (CFU/g)	CV between samples	Pass/Fail	Initials & Date
RL	P22	(b) (4)			Pass	RL 24 Apr 2019
RL	P26				Pass	RL 24 Apr 2019
RL	P30				Pass	RL 24 Apr 2019
AT	P22				Pass	AT 24 Apr 2019
AT	P26				Pass	AT 24 Apr 2019
AT	P30				Pass	AT 24 Apr 2019

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Attachment

1000X Wolf's Vitamin Solution

Ingredient	Catalog Number	Amount/ liter	Amount Added
Pyridoxine Hydrochloride	Spectrum PY103	(b) (4)	
p- Aminobenzoic Acid	Spectrum AM150		
Alpha Lipoic Acid	Spectrum L1506		
Nicotinic acid	Spectrum NI100		
Riboflavin	Spectrum RI103		
Thiamine Hydrochloride	Spectrum T1053		
Calcium Pantothenate	Spectrum CA159		
Biotin, Powder	Spectrum B1103		
Folic Acid, Powder	Spectrum FO105		
Vitamin B12	Spectrum C1454		
diH2O			

(b) (4)

pH (initial): 3.60

pH (adjusted): 6.77

Note Acid/Base Concentration used: 1.9 mL of 1N NaOH

Initials and date: SM 19 Apr 2019

0.1% Wolf's Vitamin Solution

(b) (4)

Initials and date: S.M 19 Apr 2019

Comparison of Vitamin Concentrations in DY20 SDP Method Enumeration – Summary Report

Organism: *Clostridium butyricum*

Tested Lots: 18-0202-041-P22, 18-0202-041-P26, 18-0202-041-P30

Purpose: To determine effects, if any, of using high or low concentrations of vitamins with the DY20 enumeration method.

Acceptance Criteria: If the CVs between vitamin solutions are ≤75% then the concentration of vitamins does not impact the results.

Results

Table 1. Analyst 1 vitamin concentration comparison results.

Analyst 1 Results					
Lot Number	Low Conc CFU/g	High Conc CFU/g	Avg. CFU/g	Std. Dev.	CV
18-0202-041-P22	(b) (4)				
18-0202-041-P26					
18-0202-041-P30					

Table 2. Analyst 2 vitamin concentration comparison results

Analyst 2 Results					
Lot Number	Low Conc CFU/g	High Conc CFU/g	Avg. CFU/g	Std. Dev.	CV
18-0202-041-P22	(b) (4)				
18-0202-041-P26					
18-0202-041-P30					

Discussion

The vitamin concentration effect was tested on DY20-SDP on three separate lots by two analysts. Results between the vitamin concentrations were comparable and indicate that the vitamin concentration does not impact the growth of DY20.

Variability (CV) of the 3 lots remained less than 75% across 6 replicates comparing the different vitamin concentrations. There is no significant effect of vitamin concentration on the growth of DY20.

Deviations from the Protocol: None.

Changes from the protocol: None

Location of raw data: Executed protocol (attached)

Cerrito, Chelsea

From: Kristi Smedley <smedley@cfr-services.com>
Sent: Wednesday, August 05, 2020 10:50 AM
To: Animalfood-premarket
Cc: Howard@ascusbiosciences.com
Subject: RE: Appendices to ASCUS Clostridium beijerinckii AGRN
Attachments: App_15C_D Clostridium beijerinckii 40C 6 month Summary_Report_-_DY20SDP_6_mo_40C_12Dec2019_v2.zip

Appendix 15 C and D.

This is the third of the 3 appendices emails.

Kristi O. Smedley, Ph.D.

Center for Regulatory Services, Inc.
5200 Wolf Run Shoals Rd.
Woodbridge, VA 22192

Ph. 703-590-7337
Cell (b) (4)
Fax 703-580-8637

From: Kristi Smedley [mailto:smedley@cfr-services.com]
Sent: Wednesday, August 05, 2020 10:40 AM
To: Animalfood-premarket (Animalfood-premarket@fda.hhs.gov)
Cc: Howard@ascusbiosciences.com
Subject: Appendices to ASCUS Clostridium beijerinckii AGRN

Thank you for the discussion this morning on the appendices supporting the AGRN for Clostridium beijerinckii. It appears when I downloaded the appendices from the shared website, the download was not complete. I apologize for this inconvenience and I appreciate your permitting us to provide the missing information by email.

This email contains appendix 13, appendix 12, appendix 9, and appendix 3D.

I will send a few emails with the needed information.

Kristi O. Smedley, Ph.D.

Center for Regulatory Services, Inc.
5200 Wolf Run Shoals Rd.
Woodbridge, VA 22192

Ph. 703-590-7337
Cell (b) (4)
Fax 703-580-8637

Clostridium beijerinckii ASCUSDY20 Spray-Dried Powder 40°C: Six-Month Stability Summary Report

Approvers:

DocuSigned by:
Martin Mayhew
D1605F1B4C3E49A...

12/13/2019

Martin Mayhew
Vice President – Product Development & Manufacturing

Date

DocuSigned by:
Patricia A Williams
5B301285A10643D...

12/13/2019

Patricia A. Williams
Quality

Date

DocuSigned by:
Howard B Green
0FAA38037D49453...

12/13/2019

Howard B. Green
Regulatory

Date

Prepared by
Ascus Biosciences
San Diego, CA

December 2019

Table of Contents

Clostridium beijerinckii ASCUSDY20 Spray-Dried Powder 40°C: Six-Month Stability Summary Report

Organism: *Clostridium beijerinckii* ASCUSDY20

Testing Condition: 40°C ± 3°C

Purpose: To support temperature excursions during shipping and storing.

Study Numbers: DUS1806 (Lot# 18-0202-001-P73)
DUS1809 (Lot# 18-0202-041-P22)
DUS1812 (Lot# 18-0202-001-P79)

Acceptance Criteria: Not Less Than 4.0 X 10^6 CFU/g

1 Results

Table 1. Results for Each Lot at Each Time Point

Note: Results are reported in average colony forming units (CFU)/gram of *Clostridium beijerinckii* ASCUSDY20 Spray dry powder.

	Avg. CFU/g	Std. Dev.
Time (wk)	(b) (4)	
0		
1		
2		
3		
4		
26		

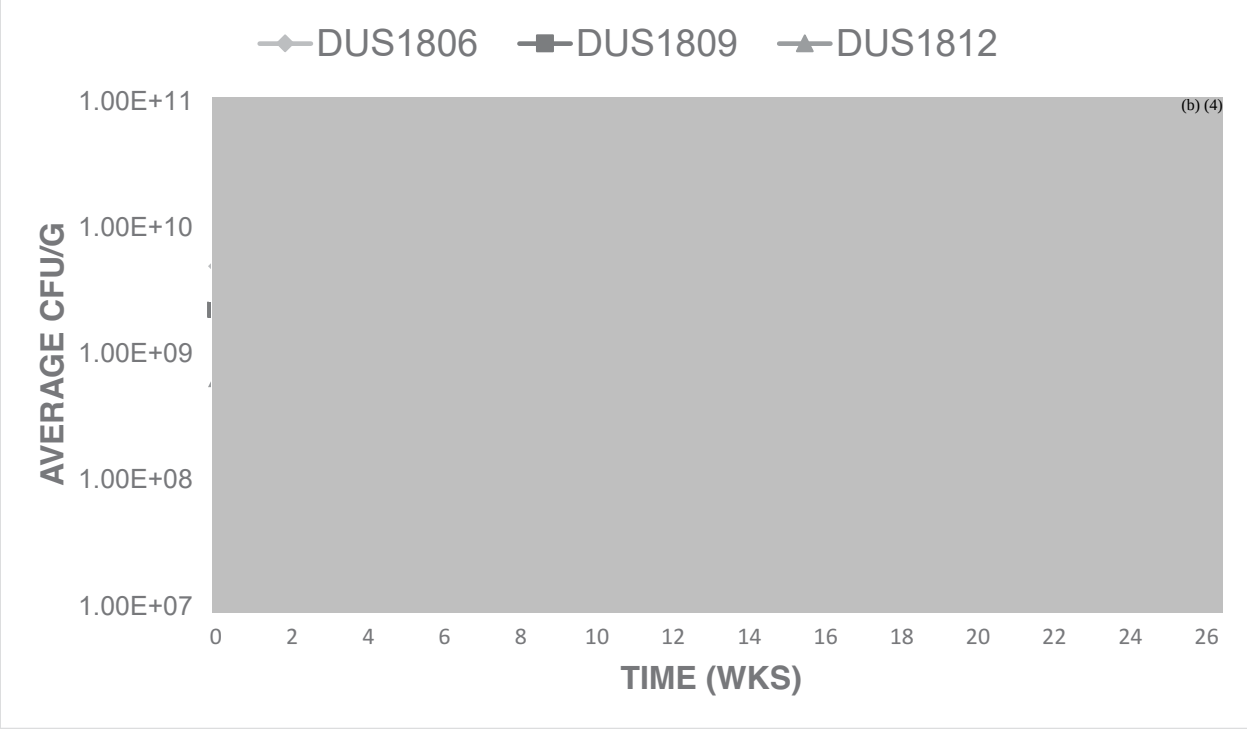


Figure 1. Graph of Results for Each Lot at Each Time Point

Note: Results are reported in average colony forming units (CFU)/gram *Clostridium beijerinckii* ASCUSDY20 Spray dry powder.

2 Discussion

The stability study of *Clostridium beijerinckii* ASCUSDY20 Spray dry powder on three separate lots conducted at 40°C ± 3°C for 6 months resulted in no degradation of the material below the acceptance criteria of 4.00 X 10^6 CFU/g (Table 1, Figure 1).

Viability of the 3 lots remained above 1.00 X 10^8 CFU/g for the duration of this stability study, indicating *Clostridium beijerinckii* ASCUSDY20 Spray dry powder will remain above the acceptance criteria during shipping and storage excursions at 40°C ± 3°C.

3 Deviations

Deviations in conduct with the *Clostridium beijerinckii* ASCUSDY20 Spray dry powder Microbe Enumeration Protocol V3 that were considered minor were the following:

1. Media was prepared in 1000 L volumes (Step 1.8) instead of in 500mL volumes due to high demand of media production.
2. Hot water bath temperature ranged from 65 - 80°C (Step 1.10) instead of 80°C to reduce condensation in the bottle while cooling the media prior to additional media additions.

One deviation investigated further was the preparation and storage instructions for the vitamin solution in Step 1.2. A comparison study was performed to confirm that the vitamin preparation did not impact the assay results.

Moving forward the *Clostridium beijerinckii* ASCUSDY20 Spray dry powder Microbe Enumeration Method V4 will be the method, which addresses these deviations.

4 Changes

No significant changes occurred during the stability study.

5 Appendices

Appendix 1. *Clostridium beijerinckii* ASCUSDY20 Spray Dry Powder 40°C Stability Protocol
Appendix 2. Lot# 18-0202-041-P22 Master Production Record
Appendix 3. Lot# 18-0202-001-P73 Master Production Record
Appendix 4. Lot# 18-0202-001-P79 Master Production Record
Appendix 5. *Clostridium beijerinckii* ASCUSDY20 Spray Dry Powder Microbe Enumeration Method V4
Appendix 6. *Clostridium beijerinckii* ASCUSDY20 Microbe Enumeration Method V3
Appendix 7. *Clostridium beijerinckii* ASCUSDY20 Spray Dry Powder 40°C Data for Tables & Graphs
Appendix 8. D2019-005: Wrong Vitamin Concentration used for in Galaxis / Altius and *Clostridium beijerinckii* ASCUSDY20 Spray Dry Powder Assays

Appendix 1. *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder 40°C Stability Protocol

ASCUS BIOSCIENCES

Stability Protocol Title:	DY20 SDP 40°C
Organism:	*Clostridium butyricum*
Purpose:	To support temperature excursions during shipping and storage
Number of Samples to Place on Stability:	10 (allows for retesting, when needed)
Sample Storage Container:	Heat sealed 48-gauge silver metalized PET / 2.5 mil LLDPE bags made from commercial bags
Temperature Conditions:	37-43°C
Acceptance Criteria:	>4 x 10^6 cfu/g

Tests and Timepoints:

Assay	T_0	1 week	2 weeks	3 weeks	4 weeks	3 months	6 months
Microbe Enumeration*	X	X	X	X	X	X	X

*DY20-SDP Microbe Enumeration method

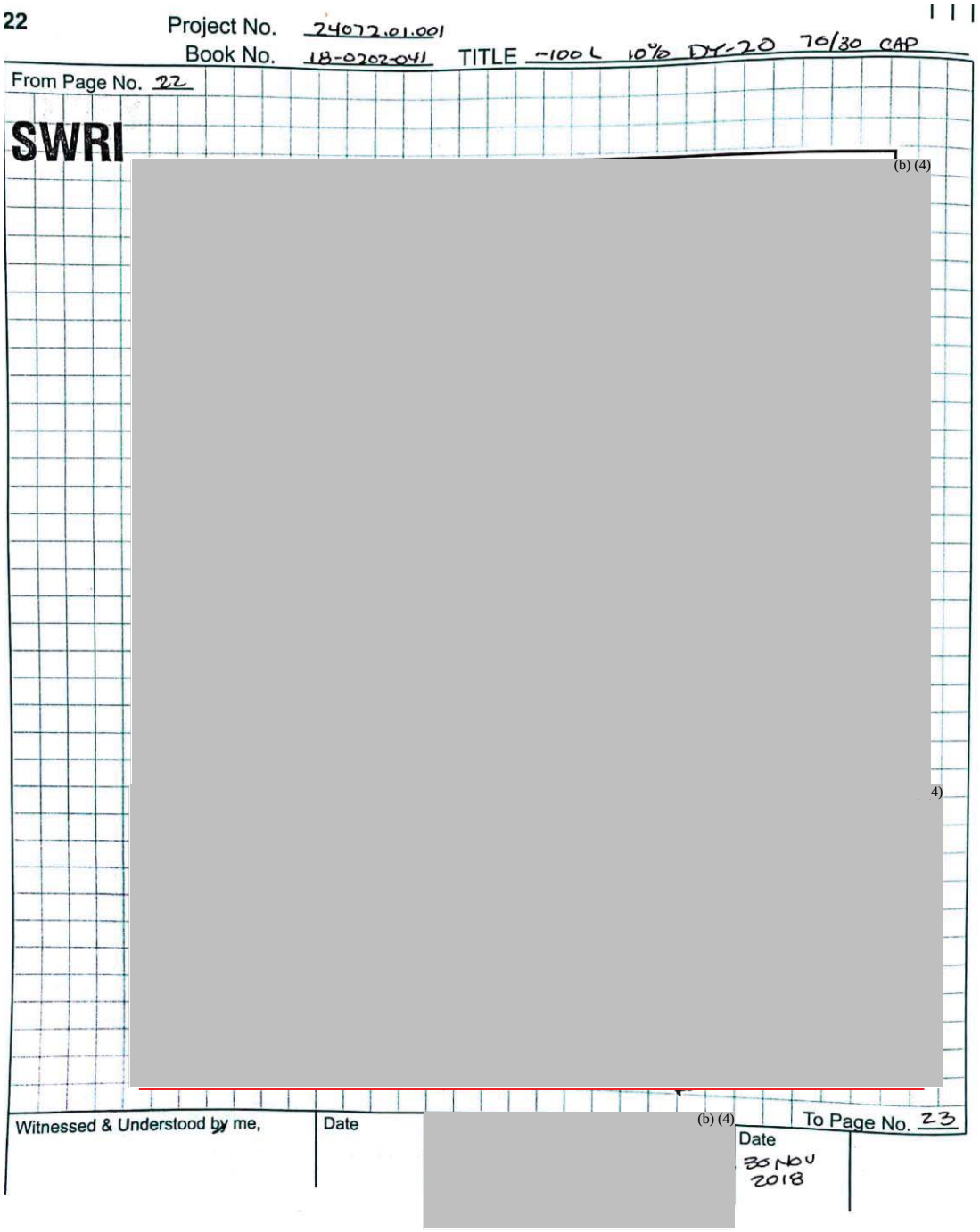
Reasons for Revisions:

Version 2	Add time points for 3 & 6 months. Update number of samples needed.

Approvals:

Howard Green Regulatory	DocuSigned by: Howard B Green 0FAA38037D49453...	5/10/2019
Corey Dodge Process Development	DocuSigned by: Corey Dodge	5/10/2019
Patricia A. Williams Quality	DocuSigned by: Patricia Williams 5B301285A10643D...	5/10/2019

Appendix 2. Lot# 18-0202-041-P22 Master Production Record



22

Project No. 24072.01.001

Book No. 18-0202-041 TITLE ~100 L 10% DY-20 70/30 CAP

From Page No. 22

SWRI

(b) (4)

(b) (4)

Witnessed & Understood by me,

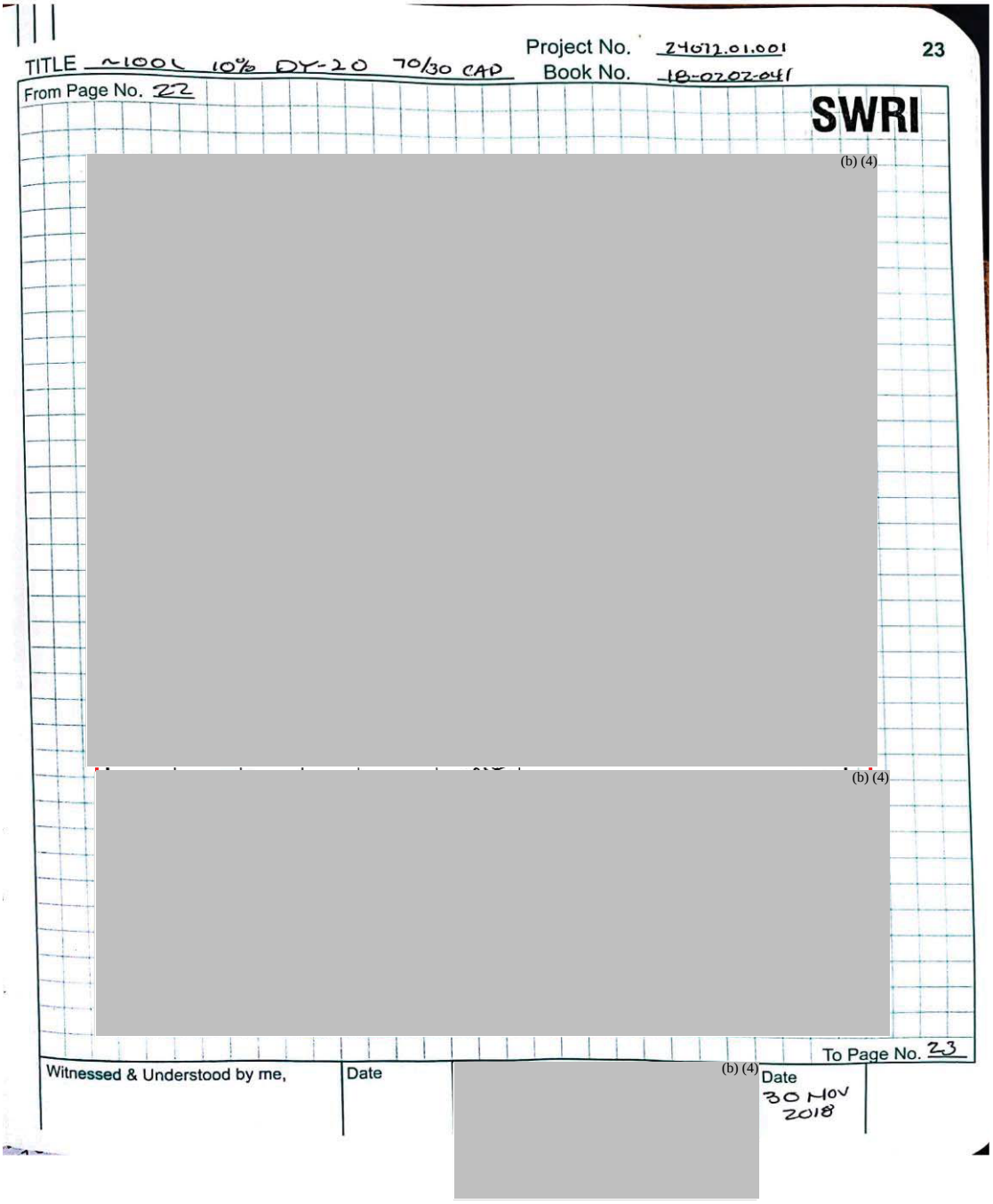
Date

(b) (4)

Date 30 NOV 2018

To Page No. 23

Scanned by CamScanner



TITLE ~100L 10% DY-20 70/30 CAD

Project No. 24072.01.001

Book No. 18-07202-041

23

From Page No. 22

SWRI

(b) (4)

(b) (4)

To Page No. 23

Witnessed & Understood by me,

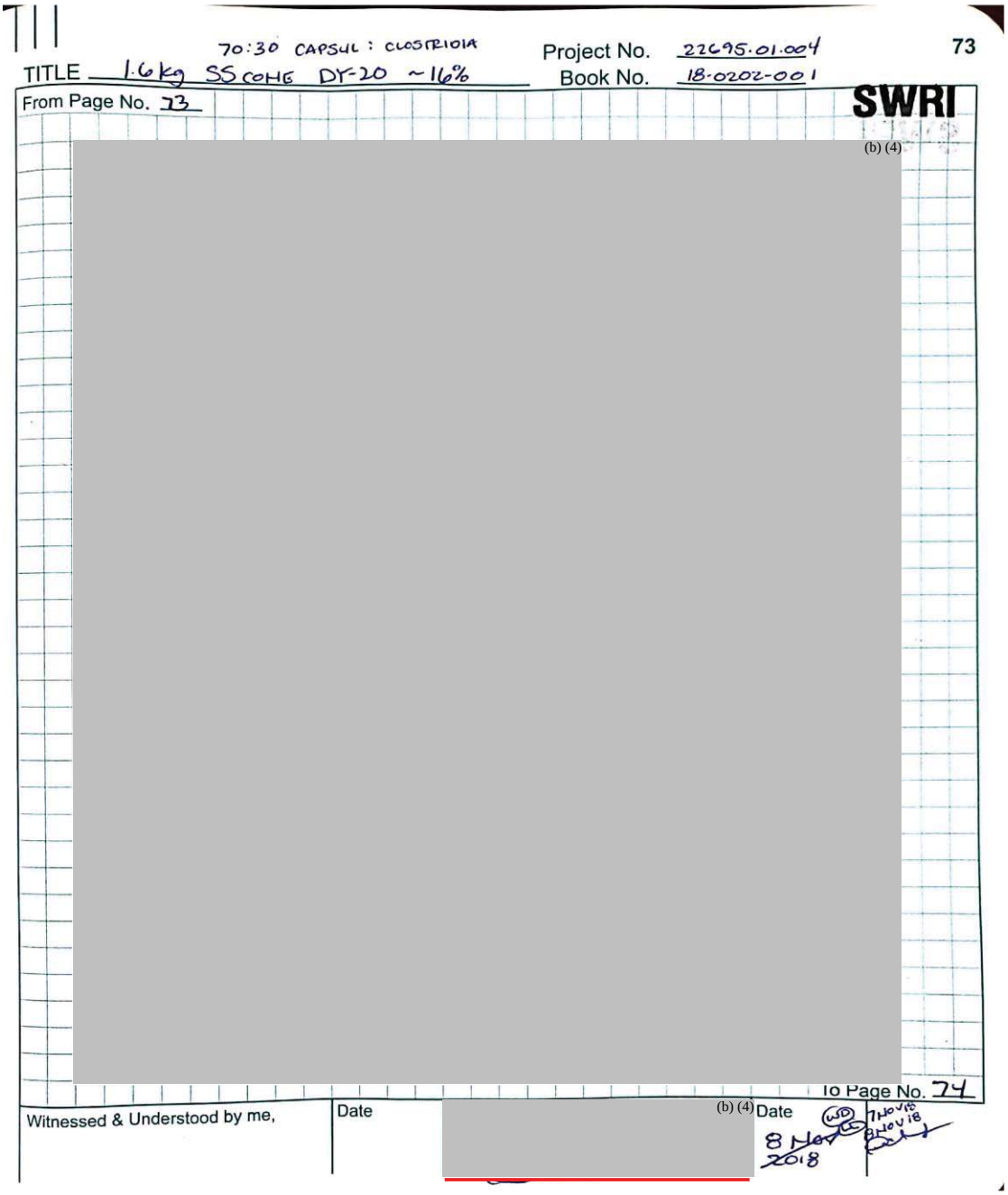
Date

(b) (4)

Date 30 Nov 2018

Scanned by CamScanner

Appendix 3. Lot# 18-0202-001-P73 Master Production Record



TITLE 1.6kg SS COHG DY-20 ~16% 70:30 CAPSUL : CLOSTRIDIA

Project No. 22695.01.004
Book No. 18-0202-001

73

From Page No. 73

SWRI

(b) (4)

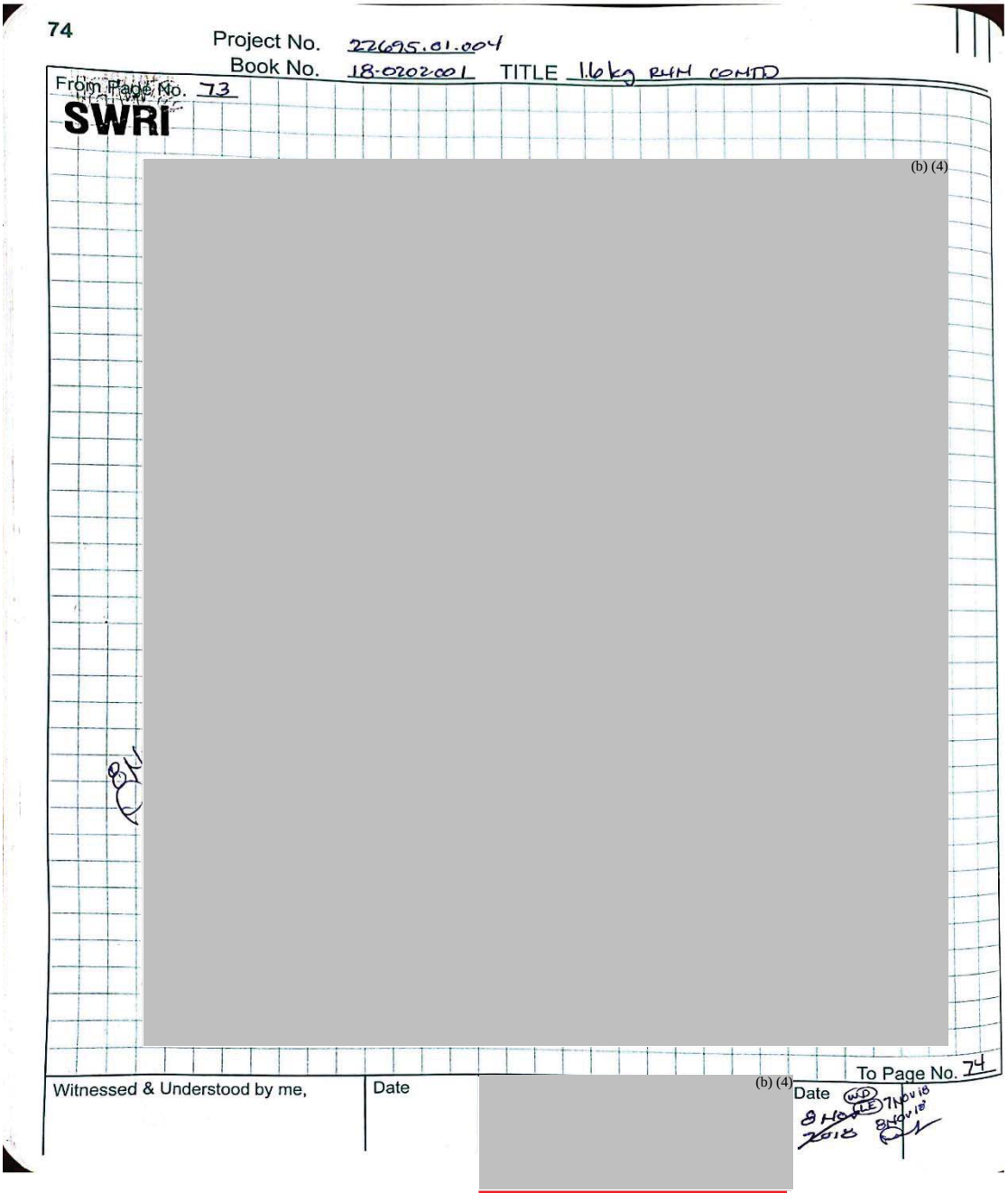
To Page No. 74

Witnessed & Understood by me,

Date

(b) (4)

Date 8 Nov 2018



74

Project No. 22695.01.004
Book No. 18-0202-001 TITLE 1.6kg RHM COMTD

From Page No. 73

SWRI

(b) (4)

To Page No. 74

Witnessed & Understood by me,

Date

(b) (4)

Date 7 NOV 18 8 NOV 18

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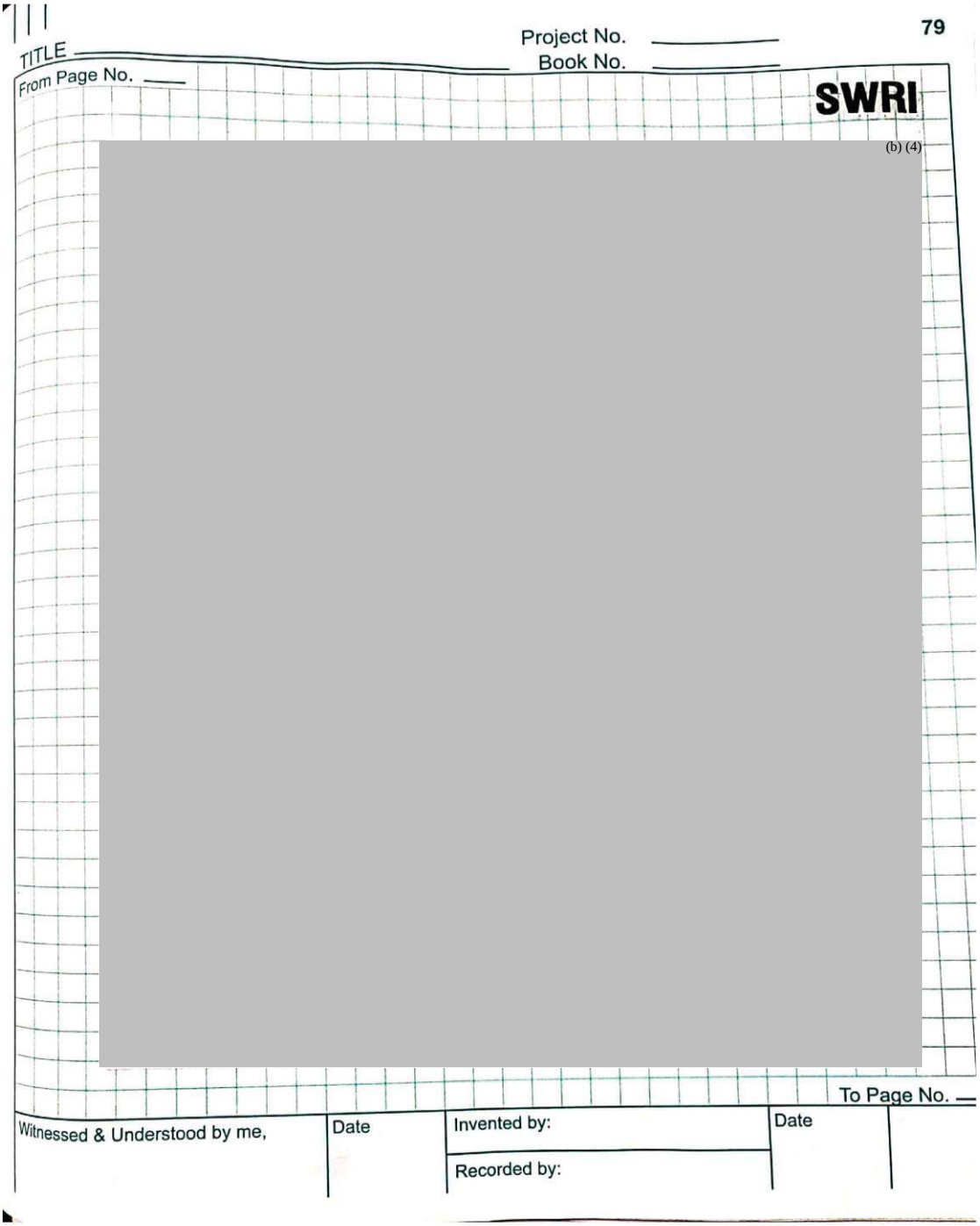
Appendix 4. Lot# 18-0202-001-P79 Master Production Record



TITLE
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Project No.
Book No.
79
SWRI
(b) (4)
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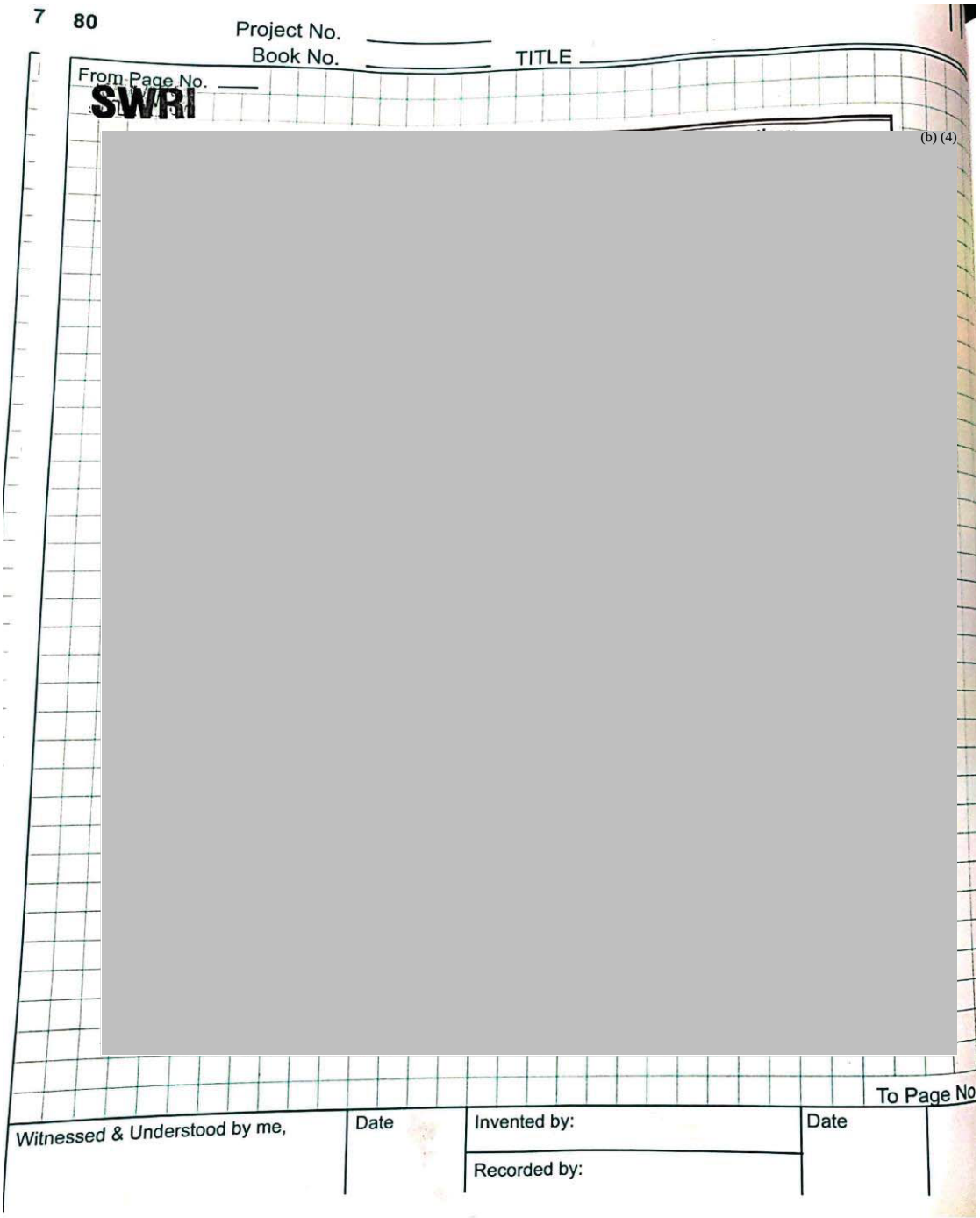
Witnessed & Understood by me,
Date
Invented by:
Recorded by:
Date

Scanned by CamScanner



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Appendix 5. *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder Microbe Enumeration Method V4

ASCUS BIOSCIENCES

Method

Title	DY20-SDP Microbe Enumeration
Version	04
Effective Date	07May2019
Author	Miranda Striluk
Approver (Signature & Date)	Corey Dodge FAA4AE21D1C745C... 5/3/2019 Corey Dodge Director – Process Development

Scope

The purpose of this assay is to determine the number of viable spores of Dairy-20 in Dairy-20 Spray Dried Powder (DY20-SDP) by counting colony forming units (CFU) on solid media.

Safety

Consult the Safety Data Sheet for all reagents prior to handling. Use caution in working with a hot water bath and hot liquids. Wear appropriate personal protective equipment (safety glasses and gloves) at all times.

Materials

BD GasPak™ EZ large incubation container (BD 260672)
BD GasPak™ EZ anaerobe container system sachets (BD 260678
Corning® 15mL Polypropylene Centrifuge Tubes (Corning 430052)
Petri dishes, 100x15 mm, sterile
Test tubes, 13x100 mm, sterile
Test tube cap, 16 mm, polypropylene
1.5 mL polypropylene microcentrifuge tube with snap cap
1000 µL Pipette
200 µL Pipette
1000 µL pipette tips, sterile
200 µL pipette tips, sterile
Glass beads, 3 mm, sterile, new

Equipment

Autoclave
Water bath set to 50°C
Laboratory Vortexer
Class I/II Biosafety Cabinet
pH meter
Magnet Stir Plate

Media & Reagents

NOTE: *Comparable quality ingredients (Laboratory, NF, USP, Reagent, or ACS grade) from different suppliers may be used.*

BD® Bacto™ Tryptic Soy Broth (BD 211822)
Growcells 10X Phosphate Buffered Saline pH 7.4 (PBS), sterile (Growcells MRGF-6235)
Growcells 1X Phosphate Buffered Saline with 0.05% TWEEN pH 7.4, sterile (Growcells MRGF-6275)
Research Products International Corp. GELRITE (Fisher Scientific 50-488-682)

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Page 1 of 6

DY20-SDP Microbe Enumeration

Sigma-Aldrich® Resazurin sodium salt (Sigma-Aldrich R7017)
Spectrum® Alpha Lipoic Acid, USP (Spectrum L1506)
Spectrum® Aminobenzoic Acid, USP (Spectrum AM150)
Spectrum® Biotin, Powder, USP (Spectrum B1103)
Spectrum® L-Cysteine Hydrochloride, Monohydrate (Spectrum CY115)
Spectrum® Ferric Ammonium Citrate, Brown, Powder, FCC (Spectrum F1000)
Spectrum® Folic Acid, Powder, USP (Spectrum FO105)
Spectrum® Niacin, Powder, USP (Spectrum NI100)
Spectrum® Phytonadione, USP (Spectrum PH195)
Spectrum® Pyridoxine Hydrochloride, USP (Spectrum PY103)
Spectrum® Riboflavin, USP (Spectrum RI103)
Spectrum® Thiamine Hydrochloride, FCC (Spectrum T1053)
Spectrum® DL-Pantothenic Acid Calcium Salt (Spectrum P2630) or Calcium Pantothenate (Spectrum CA 159)
Spectrum® Vitamin B12, FCC (Spectrum C1454)
Spectrum® Polysorbate 20, FCC (Spectrum P1177)
Reagent grade 95% Ethanol
1N Hydrochloric Acid
1N Sodium Hydroxide

Method

1. Prepare Tryptic Soy Broth and Ferric Ammonium Citrate Gelrite (TSB+FAC) Plates. This step should be performed at least 24 hours prior to commencement of testing.

(b) (4)

Ingredient	Amount/ liter
Pyridoxine Hydrochloride	(b) (4)
p- Aminobenzoic Acid	
Alpha Lipoic Acid	
Nicotinic acid	
Riboflavin	
Thiamine Hydrochloride	
Calcium Pantothenate	
Biotin, Powder	
Folic Acid, Powder	
Vitamin B12	
diH2O	

(b) (4)

DY20-SDP Microbe Enumeration

(b) (4)

2. Preparation of sterile 1X Phosphate Buffered Saline (PBS), pH 7.4 with 0.05% Polysorbate 20

(b) (4)

3. Prepare the Primary Dilution Mix

(b) (4)

DY20-SDP Microbe Enumeration

(b) (4)

4. DY20-SDP Heat Shock Anaerobic Plating

(b) (4)

DY20-SDP Microbe Enumeration

5. Negative Control Plating

(b) (4)

6. Plate Counting

(b) (4)

DY20-SDP Microbe Enumeration

(b) (4)

Reasons for Revision

(b) (4)

Appendix 6. *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder Microbe Enumeration Method V3

ASCUS BIOSCIENCES

Method

Title	DY20-SDP Microbe Enumeration
Version	03
Effective Date	07Dec2018
Author	[illegible]
Approver (Signature & Date)	Corey Dodge 12/5/2018 8:17:09 AM PST FAA4AE21D1C745C... Corey Dodge Director – Process Development

Scope

The purpose of this assay is to determine the number of viable spores of Dairy-20 in Dairy-20 Spray Dried Powder (DY20-SDP) by counting colony forming units (CFU) on solid media.

Safety

Consult the Safety Data Sheet for all reagents prior to handling. Use caution in working with a hot water bath and hot liquids. Wear appropriate personal protective equipment (safety glasses and gloves) at all times.

Materials

BD GasPak™ EZ large incubation container (BD 260672)
BD GasPak™ EZ anaerobe container system sachets (BD 260678
Corning® 15mL Polypropylene Centrifuge Tubes (Corning 430052)
Petri dishes, 100x15 mm, sterile
Test tubes, 13x100 mm, sterile
Test tube cap, 16 mm, polypropylene
1.5 mL polypropylene microcentrifuge tube with snap cap
1000 µL Pipette
200 µL Pipette
1000 µL pipette tips, sterile
200 µL pipette tips, sterile
Glass beads, 3 mm, sterile, new

Equipment

Autoclave
Water bath set to 50°C
Laboratory Vortexer
Class I/II Biosafety Cabinet
pH meter
Magnet Stir Plate

Media & Reagents

BD® Bacto™ Tryptic Soy Broth (BD 211822)
Growcells 10X Phosphate Buffered Saline pH 7.4 (PBS), sterile (Growcells MRGF-6235)
Growcells 1X Phosphate Buffered Saline with 0.05% TWEEN pH 7.4, sterile (Growcells MRGF-6275)
Research Products International Corp. GELRITE (Fisher Scientific 50-488-682)
Sigma-Aldrich® Resazurin sodium salt (Sigma-Aldrich R7017)
Spectrum® Alpha Lipoic Acid, USP (Spectrum L1506)
Spectrum® Aminobenzoic Acid, USP (Spectrum AM150)
Spectrum® Biotin, Powder, USP (Spectrum B1103)
Spectrum® L-Cysteine Hydrochloride, Monohydrate (Spectrum CY115)

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DY20-SDP Microbe Enumeration

Spectrum® Ferric Ammonium Citrate, Brown, Powder, FCC (Spectrum F1000)
Spectrum® Folic Acid, Powder, USP (Spectrum FO105)
Spectrum® Niacin, Powder, USP (Spectrum NI100)
Spectrum® Phytonadione, USP (Spectrum PH195)
Spectrum® Pyridoxine Hydrochloride, USP (Spectrum PY103)
Spectrum® Riboflavin, USP (Spectrum RI103)
Spectrum® Thiamine Hydrochloride, FCC (Spectrum T1053)
Spectrum® DL-Pantothenic Acid Calcium Salt (Spectrum P2630) or Calcium Pantothenate (Spectrum CA 159)
Spectrum® Vitamin B12, FCC (Spectrum C1454)
Spectrum® Polysorbate 20, FCC (Spectrum P1177)
Reagent grade 95% Ethanol
1N Hydrochloric Acid
1N Sodium Hydroxide

Method

1. Prepare Tryptic Soy Broth and Ferric Ammonium Citrate Gelrite (TSB+FAC) Plates. This step should be performed at least 24 hours prior to commencement of testing.

(b) (4)

Ingredient	Amount
Spectrum® Pyridoxine Hydrochloride, USP	(b) (4)
Spectrum® Alpha Lipoic Acid, USP	
Spectrum® Aminobenzoic Acid, USP	
Spectrum® Niacin, Powder, USP	
Spectrum® Riboflavin, USP	
Spectrum® Thiamine Hydrochloride, FCC	
Spectrum® Biotin, Powder, USP	
Spectrum® Folic Acid, Powder, USP	
Spectrum® DL-Pantothenic Acid Calcium Salt or Calcium Pantothenate	
Spectrum® Vitamin B12, FCC	

(b) (4)

DY20-SDP Microbe Enumeration

(b) (4)

2. Preparation of sterile 1X Phosphate Buffered Saline (PBS), pH 7.4 with 0.05% Polysorbate 20

(b) (4)

3. Prepare the Primary Dilution Mix

(b) (4)

DY20-SDP Microbe Enumeration

(b) (4)

4. DY20-SDP Heat Shock Anaerobic Plating

(b) (4)

DY20-SDP Microbe Enumeration

5. Negative Control Plating

(b) (4)

6. Plate Counting

(b) (4)

DY20-SDP Microbe Enumeration

(b) (4)

Reasons for Revision

(b) (4)

Appendix 7. *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder 40°C Data for Tables & Graphs

									DY20 Plating CFU Counts, CFU/100uL									DY 20								
									1E-04			1E-05			1E-06			CFU/mL			CFU/g					
Date of creation	Date of assay	Timepoint	Batch Number	Lot Number	Analyst Initials	Sample	Mass (g)	Volume 1X PBST (mL)	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	Avg. CFU/g	Std. Dev.	CV
8-Nov-18	10-Dec-18	T=0	1	18-0202-001-P73	MS	Batch 1-1	0.1024	10	(b) (4)																	
						Batch 1-2	0.1009	10																		
						Batch 1-3	0.1020	10																		
7-Dec-18	12-Dec-18	T=0	2	18-0202-041-P22	AT	P22-1	0.1008	10																		
						P22-2	0.1006	10																		
						P22-3	0.1007	10																		
17-Dec-18	20-Dec-18	T=0	3	18-0202-001-P79	SM	P79-1	0.1002	10																		
						P79-2	0.1000	10																		
						P-79-3	0.1015	10																		

										DY20 Plating CFU Counts, CFU/100uL									DY 20								
										1E-04			1E-05			1E-06			CFU/mL			CFU/g					
	Scheduled Pull Date	Date Sample Was Pulled	Testing Condition	Timepoint	Batch Number	Lot Number	Analyst Initials	Sample	Mass (g)	Volume 1X PBST (mL)	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	Avg. CFU/g	Std. Dev.	CV
DUS1806	20-Dec-18	20-Dec-18	40C	1 week	1	18-0202-001-P73	SM	22-1	0.1018	10	(b) (4)																
								22-2	0.1014	10																	
								22-3	0.1003	10																	
	27-Dec-18	27-Dec-18	40C	2 week	1	18-0202-001-P73	SM	19-1	0.1003	10																	
								19-2	0.1009	10																	
								19-3	0.1009	10																	
	3-Jan-19	3-Jan-19	40C	3 week	1	18-0202-001-P73	SM	21-1	0.1006	10																	
								21-2	0.1010	10																	
								21-3	0.1007	10																	
	10-Jan-19	10-Jan-19	40C	4 week	1	18-0202-001-P73	MS	20-1	0.1011	10																	
								20-2	0.1027	10																	
								20-3	0.1007	10																	
	13-Jun-19	11-Jun-19	40C	6 Month	1	18-0202-001-P73	RL	23-1	0.1050	10																	
								23-2	0.1090	10																	
								23-3	0.1080	10																	
DUS1809	20-Dec-18	20-Dec-18	40C	1 week	2	18-0202-041-P22	SM	47-1	0.1004	10																	
								47-2	0.1006	10																	
								47-3	0.1016	10																	
	27-Dec-18	27-Dec-18	40C	2 week	2	18-0202-041-P22	SM	46-1	0.1017	10																	
								46-2	0.1015	10																	
								46-3	0.1001	10																	
	3-Jan-19	3-Jan-19	40C	3 week	2	18-0202-041-P22	SM	44-1	0.1009	10																	
								44-2	0.1001	10																	
								44-3	0.1005	10																	
	10-Jan-19	10-Jan-19	40C	4 week	2	18-0202-041-P22	MS	45-1	0.1024	10																	
								45-2	0.1023	10																	
								45-3	0.1020	10																	
	13-Jun-19	11-Jun-19	40C	6 Month	2	18-0202-041-P22	RL	48-1	0.1010	10																	
								48-2	0.1010	10																	
								48-3	0.1040	10																	
DUS1812	27-Jan-19	27-Dec-18	40C	1 week	3	18-0202-001-P79	SM	69-1	0.1014	10																	
								69-2	0.1013	10																	
								69-3	0.1012	10																	
	3-Jan-19	3-Jan-19	40C	2 week	3	18-0202-001-P79	SM	71-1	0.1017	10																	
								71-2	0.1008	10																	
								71-3	0.1007	10																	
	10-Jan-19	10-Jan-19	40C	3 week	3	18-0202-001-P79	SM/MS	72-1	0.1002	10																	
								72-2	0.1017	10																	
								72-3	0.1010	10																	
	17-Jan-19	16-Jan-19	40C	4 week	3	18-0202-001-P79	MS	70-1	0.1000	10																	
								70-2	0.1006	10																	
								70-3	0.1009	10																	
	20-Jun-19	6/18/19	40C	6 Month	3	18-0202-001-P79	AT	75-1	0.1000	10																	
								75-2	0.1050	10																	
								75-3	0.1070	10																	

Appendix 8. D2019-005: Wrong Vitamin Concentration Used in Galaxis / Altius and *Clostridium beijerinckii* ASCUSDY20 Spray-Dried Powder Assays

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Deviation Number: D2019-005

Deviation Title: Wrong Vitamin Concentration Used for in Galaxis/Alitus and DY20 SDP Assays

Deviation Investigator: Adam Taylor

Description of the Deviation:
In April 2019 (b) (4) informed Ascus of problems in execution of Vitamin Mix section of the Galaxis/Altius Microbe Enumeration methods. The issue was that the solids did not fully dissolve into solution.

Investigation:
The methods used at (b) (4) (Microbe Enumeration of Galaxis 100 V5 and Microbe Enumeration of Altius and Galaxis 5 V8) were compared to methods used at Ascus for the preparation of the 0.1% Vitamin mix. The (b) (4) Argentinian labs followed the methods as written. However, Ascus personnel were deviating from the methods by increasing the solvent/solute ratio by 10X. This allowed the solutes to readily dissolve, but resulted in an incorrect amount of vitamins in the media.

Further investigation indicated that Ascus personnel have been preparing the vitamin solution this way since August 2017 due to unclear wording in the method. In addition, all methods were validated with the lower amount of vitamins in the media.

Impacted results since 2017 include:

- Stability studies involving Galaxis 100, Galaxis 5, Altius, and DY20SDP
- Product release results for DY20SDP.

Impacted methods used since 2017 include:

- Microbe Enumeration for Galaxis 100
- Microbe Enumeration for Altius and Galaxis 5
- DY20 SDP Microbe Enumeration V3

Deviation Number: D2019-005

Impacted commercial cell banks:

- DY20 Master Cell Bank 15Aug2018
- DY20 Working Cell Bank 1
- DY20 Working Cell Bank PCC1
- DY20 Working Cell Bank PCC5
- DY20 Working Cell Bank 3

To determine if the different vitamin preparation impacted the assay results, a comparison study was conducted with 2 analysts, 2 samples, and both preparation methods. See the attachment. The comparison study confirmed that the vitamin preparation method did not impact the assay results. Therefore, all the results generated at Ascus are valid. Methods will not be re-validated and cell banks will not be re-tested.

To ensure that the methods are executed correctly from now on, they will be revised to more clearly state how to prepare the vitamin mixture.

Immediate Corrections:

Action	Completed by	Date Completed	Comments
None			

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Deviation Number: D2019-005

CAPA:

CAPA Log #	Action	Assigned to	Due Date	Comments
CA2019-005	Clarify the section on vitamin mix preparation for the following methods: DY20SDP, Galaxis 5/Altius, and Galaxis 100	Pat Williams	08May2019	
CA2019-006	Send revised methods to (b) (4)	Adam Taylor	09May2019	
CA2019-007	Clarify the section on vitamin mix preparation for the following cell bank protocols: DY20 Working Cell Bank, DY20 Master Cell Bank, DY20 Cell Bank Retesting	Pat Williams	15May2019	

Approvers:

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AF21D1C745C	5/3/2019
Patricia A. Williams – Quality	DocuSigned by: Patricia Williams 5B301285A10843D...	5/3/2019
Howard Green – Regulatory	DocuSigned by: Howard B Green 3FAA38037DF8453...	5/3/2019

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Comparison of Vitamin Concentrations in DY20 SDP Method Enumeration

Method Titles and Versions

Title	DY20-SDP Microbe Enumeration
Version	03

Lab Performing the Comparison: Ascus Biosciences Inc.

Pre-Execution Approval:

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AE21D1C745C...	4/22/2019

Post Execution Approval (includes Summary Report):

Printed Name & Title	Signature	
Corey Dodge – Process Development	DocuSigned by: Corey Dodge FAA4AE21D1C745C...	5/3/2019
Patricia A. Williams – Quality	DocuSigned by: Patricia Williams 5B301285A10643D...	4/30/2019

Personnel Executing the Comparison:
Your signature indicates that you have read and understand this protocol.

Printed Name	Signature	Tasks Performed
Rich La		Analyst 1
Adam Taylor		Analyst 2
Samantha Marroquin		Media preparation

Purpose:
Deviation D2019-005 documents issues with execution of the DY20-SDP Microbe Enumeration method. Specifically, some analysts were using a 1000X less of the vitamin solution than what the method requires. See the deviation for details of the investigation.

This protocol will determine if a 1000X concentration difference in the Vitamin Solution has an impact on the results obtained from the DY20-SDP Microbe Enumeration method. The method

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will be run by 2 analysts, using 3 different lots of DY20 SDP, and the high and low concentration of vitamins. This will provide enough data to determine if the vitamin concentration impacts the results.

The intent is to use the validated method with the high concentration of vitamins going forward; therefore, this is not a method validation protocol. The method will be run as validated, with the exception of changing the vitamin concentration. Raw data will be recorded as listed in the method. The full method is retained in the Ascus Google Drive/Commercial Documents/Analytical Documents.

Directions for preparation of the 2 different vitamin concentrations are attached to this protocol.

The closeness of results from both vitamin concentrations will be assessed to determine if there is an impact on results.

Acceptance Criteria and Summary:
If the CVs between the vitamin solutions are ≤75% then the concentration of vitamins does not impact the results. (For example, if the CV between analyst 1, sample 1, for both vitamin concentrations is ≤75%, then there is no impact.)

A summary of the study and copy of Plate Count Data will be written after execution and approved by the Director of Product Development and Quality.

Analyst 1 Sample 1 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0202-041-P22				

(b) (4)

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Analyst 1 Sample 2 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0202 041-726				

(b) (4)

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Analyst 1 Sample 3 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0702-041-P30				

(b) (4)

[redacted]

Entered into database by (initial and date): AT 23 Apr 2019
Verification of database entries (initial and date): RL 24 Apr 2019

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Analyst 2 Sample 1 Data						
Study Number	Date & Time	Lot Number				
	22 Apr 2019 11:00 AM	18-0202-041 -P22				

(b) (4)

[redacted]

Verification of database entries (initial and date): RL 24 Apr 2019

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Analyst 2 Sample 2 Data						
Study Number	Date & Time	Lot Number				
	22Apr2019 11:00AM	18-0202-041 -P26				

(b) (4)

[redacted]

Entered into database by (initial and date): AH 23Apr 2019
Verification of database entries (initial and date): ZL 24 Apr 2019

Analyst 2 Sample 3 Data						
Study Number	Date & Time	Lot Number				
	22Apr2019 11:00AM	18-0202-041 -P30				

(b) (4)

[redacted]

Verification of database entries (initial and date): RL 24 Apr 2019

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Sample Information

Analyst 1

Sample ID	DY20 SDP Lot Number	Initials and Date
P22 (1,2,3)	18-0202-041-P22	RL 24 Apr 2019
P26(4,5,6,7①)	18-0202-041-P26	RL 24 Apr 2019
P30(7,8,9)	18-0202-041-P30	RL 24 Apr 2019

① RL 24 Apr 2019 Entry Error

Analyst 2

Sample ID	DY20 SDP Lot Number	Initials and Date
P22	18-0202-041-P22	AT 24 Apr 2019
P26	18-0202-041-P26	AT 24 Apr 2019
P30	18-0202-041-P30	AT 24 Apr 2019

Comparison of Results

Analyst	Sample	Low Conc. Result (CFU/g)	High Conc. Result (CFU/g)	CV between samples	Pass/Fail	Initials & Date
RL	P22	[redacted] (b) (4)			Pass	RL 24 Apr 2019
RL	P26				Pass	RL 24 Apr 2019
RL	P30				Pass	RL 24 Apr 2019
AT	P22				Pass	AT 24 Apr 2019
AT	P26				Pass	AT 24 Apr 2019
AT	P30				Pass	AT 24 Apr 2019

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Attachment

1000X Wolf's Vitamin Solution

Ingredient	Catalog Number	Amount/ liter	Amount Added
Pyridoxine Hydrochloride	Spectrum PY103	(b) (4)	
p- Aminobenzoic Acid	Spectrum AM150		
Alpha Lipoic Acid	Spectrum L1506		
Nicotinic acid	Spectrum NI100		
Riboflavin	Spectrum RI103		
Thiamine Hydrochloride	Spectrum T1053		
Calcium Pantothenate	Spectrum CA159		
Biotin, Powder	Spectrum B1103		
Folic Acid, Powder	Spectrum FO105		
Vitamin B12	Spectrum C1454		
diH2O			

(b) (4)

pH (initial): 3.60

pH (adjusted): 6.77

Note Acid/Base Concentration used: 1.9 mL of 1N NaOH

Initials and date: SM 19 Apr 2019

0.1% Wolf's Vitamin Solution

(b) (4)

Initials and date: S.M 19 Apr 2019

Comparison of Vitamin Concentrations in DY20 SDP Method Enumeration – Summary Report

Organism: *Clostridium butyricum*

Tested Lots: 18-0202-041-P22, 18-0202-041-P26, 18-0202-041-P30

Purpose: To determine effects, if any, of using high or low concentrations of vitamins with the DY20 enumeration method.

Acceptance Criteria: If the CVs between vitamin solutions are ≤75% then the concentration of vitamins does not impact the results.

Results

Table 1. Analyst 1 vitamin concentration comparison results.

Analyst 1 Results					
Lot Number	Low Conc CFU/g	High Conc CFU/g	Avg. CFU/g	Std. Dev.	CV
18-0202-041-P22	(b) (4)				
18-0202-041-P26					
18-0202-041-P30					

Table 2. Analyst 2 vitamin concentration comparison results

Analyst 2 Results					
Lot Number	Low Conc CFU/g	High Conc CFU/g	Avg. CFU/g	Std. Dev.	CV
18-0202-041-P22	(b) (4)				
18-0202-041-P26					
18-0202-041-P30					

Discussion

The vitamin concentration effect was tested on DY20-SDP on three separate lots by two analysts. Results between the vitamin concentrations were comparable and indicate that the vitamin concentration does not impact the growth of DY20.

Variability (CV) of the 3 lots remained less than 75% across 6 replicates comparing the different vitamin concentrations. There is no significant effect of vitamin concentration on the growth of DY20.

Deviations from the Protocol: None.

Changes from the protocol: None

Location of raw data: Executed protocol (attached)

ASCUS P. oduct Mix Uniformity Report for Protocol #1064

Approvers:

DocuSigned by:
Martin Mayhew
D1605F1B4C3E49A...

12/9/2019

Martin Mayhew
Vice President . Product Development
& Manufacturing

Date

DocuSigned by:
Patricia A Williams
5B301285A10643D...

12/6/2019

Patricia A. Williams
Quality

Date

DocuSigned by:
Howard B Green
0FAA38037D49453...

12/6/2019

Howard B. Green
Regulatory

Date

Table of Contents

ASCUS Product Mix Uniformity Report for Protocol #1064

1 Objective

This homogeneity study was conducted to demonstrate that a mixture of *Clostridium beijerinckii* ASCUSDY20 and *Pichia kudriavzevii* ASCUSDY21 with diluents can be blended homogenously with premix at scale. The data will be used for regulatory agency submissions.

2 Diet Manufacturing

3 Treatments

Figure 1. Sampling Locations

4 Shipping Addresses

1) Ten samples from each replication were sent to ASCUS Biosciences for analysis:

Adam Taylor
6450 Lusk Blvd
Suite E209
San Diego, Ca 92121
Phone: 707-601-2553
Fed Ex number is 724611141

5 Summary Report of Results from Homogeneity Study

5.1 Purpose

This homogeneity study was conducted to demonstrate that a mixture of *C. beijerinckii* ASCUSDY20 and *P. kudriavzevii* ASCUSDY21 with diluents can be blended homogenously with premix at scale. The data will be used for regulatory agency submissions.

Three separate blends of premix containing *C. beijerinckii* ASCUSDY20 and *P. kudriavzevii* ASCUSDY21 were generated at (b) (4) (b) (4) and tested at Ascus Biosciences using the method "Premix Testing of Galaxis, version 1" (Appendix D).

5.2 Assay Result Summarization

All samples were assayed in triplicate and the coefficient of variation was calculated by determining the average of triplicates for each sample point of a batch then determining the coefficient of variation of those ten samples.

5.3 Results

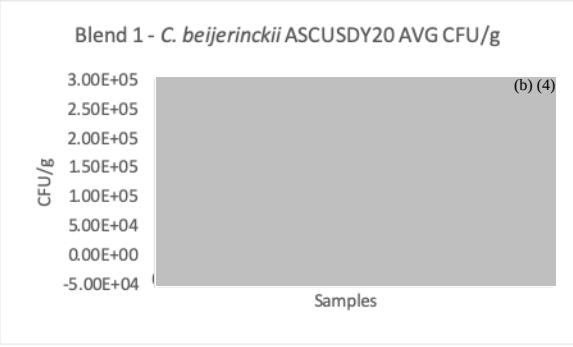
Table1. Results of 3 Blends of Galaxis 5 into Premix

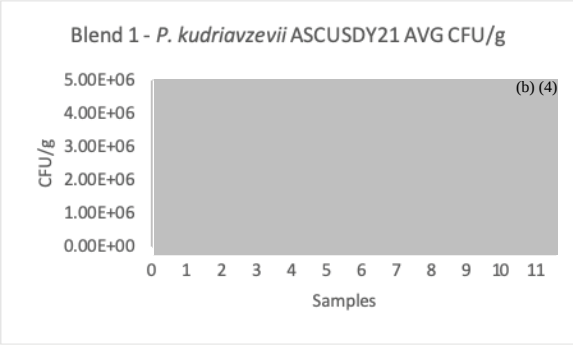
Note: Results are reported in average colony forming unites (CFU)/gram.

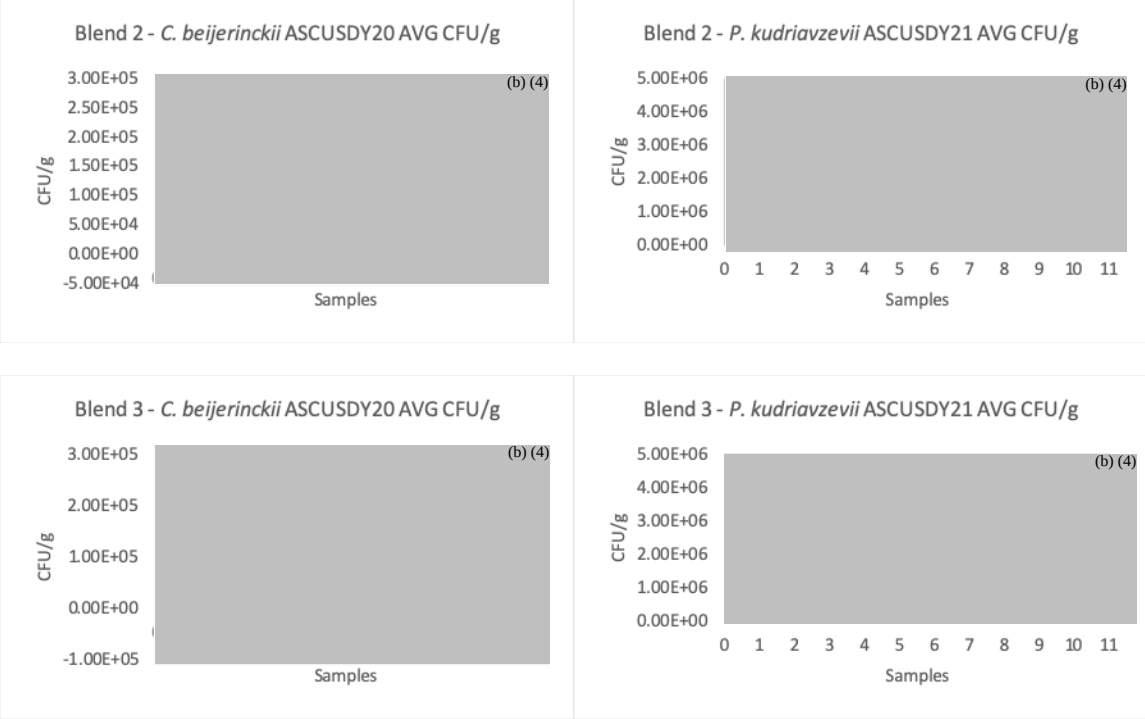
	***C. beijerinckii* ASCUSDY20**			***P. kudriavzevii* ASCUSDY21**		
	Final Result			**Final Result**		
	Avg CFU/g	**Std. Dev.**	**CV**	**Avg CFU/g**	**Std. Dev.**	**CV**
Blend 1	(b) (4)					
Blend 2						
Blend 3						

5.4 Analysis

The CV values for blend 1 are 33.38% and 24.67% respectively for *C. beijerinckii* ASCUSDY20 and *P. kudriavzevii* ASCUSDY21. The CV values for blend 2 are 61.78% and 29.69% respectively for *C. beijerinckii* ASCUSDY20 and *P. kudriavzevii* ASCUSDY21. The CV values for blend 3 are 42.69% and 28.08% respectively for *C. beijerinckii* ASCUSDY20 and *P. kudriavzevii* ASCUSDY21. Graphs of the *C. beijerinckii* ASCUSDY20 and *P. kudriavzevii* ASCUSDY21 for each blend are provided below.







5.5 Deviations and Changes

There were no deviations or changes from the protocol.

5.6 Conclusion

The protocol was executed as written and the results indicate that all 3 blends were homogenous, and the results pass per the acceptance criteria.

5.7 Appendices

Appendix A: Basal Mix

Appendix B: Basal Premix – Lot 20190729009280MM

Appendix C: Batch Sheets

Appendix D: Premix Testing of Galaxis, version 1 (Note: Galaxis is test name assigned to mixture of C. beijerinckii ASCUSDY20 and P. kudriavzevii ASCUSDY21 with calcium carbonate as carrier and hydrated sodium calcium aluminosilicate as anticaking agent)

Appendix E: Premix Testing of Galaxis 5 Method Validation Report (Note: Galaxis is test name assigned to mixture of C. beijerinckii ASCUSDY20 and P. kudriavzevii ASCUSDY21 with calcium carbonate as carrier and hydrated sodium calcium aluminosilicate as anticaking agent)

Appendix F: Excel of Data for Study

6.0 Reasons for Revision

- Addition of graphs and revision of raw data excel tables

Appendix A: Basal Mix

INGREDIENTS, %	Lactation
Premix	
Ground Corn	(b) (4)
Soy Plus	
Limestone	
Magnesium Oxide	
Vitamin E, 20,000 IU/lb	
Sodium Bicarbonate	
Megalac Essentiom	
Zinpro 120	
Zinpro 4 Plex	
Rumensin 90	
Lactation PMX	
Added with the test article	
Salt	
TM Salt	
Total	100

Activities on the day of mixing and sampling for the homogeneity study

1. Basal premix lot 20190729009280MM (Appendix B) with formula number 420920M0309310 was weighed into a tub on platform scale. Weight of basal premix added was recorded on master formula sheet and verified by second person. The mixer was loaded with basal premix and mixer started.

2. Each of the other ingredients (salt, Trace Mineral (TM) salt, and lactation PMX) were weighed into tubs. Weights were recorded on master formula sheet and verified by second person. Salt, TM salt and lactation PMX were added to the mixer.

3. The mixer was started and pre-weighed one kilo bag of Galaxis 5 containing *C. beijerinckii* ASCUSDY20 and *P. kudriavzevii* ASCUSDY21 was added to the mixer. Once the Galaxis bag was emptied, a timer was set for 300 seconds. At the completion of the 300 seconds, mixer was stopped, and sampling began.

4. [redacted] The backup samples were not sent to ASCUS Biosciences and were discarded once initial samples were received at ASCUS Biosciences.

5. The core sampler and riffler were cleaned using compressed air between each sample collected from the mixer. In total, 10 samples from each batch were collected in ten different location (see Figure 1).

6. Once all ten samples were collected from the mixer locations, the remaining feed was collected and destroyed. The mixer was cleaned by sweeping clean then using air from compressor to blow remaining dust and feed from mixer. The mixer was inspected and bottom discharge was closed.

7. Steps 1-6 above were repeated for a total of three batches. Samples for ASCUS Biosciences were placed on ice and shipped overnight to San Diego laboratory. Samples for salt determination (if needed) were taken by [redacted] for holding and the extra Ascus sample was put in box for storage in refrigerator. Batch sheets are presented in Appendix C.

8. Samples arrived in San Diego and were analyzed at ASCUS Biosciences.

Appendix B: Basal Premix – Lot 20190729009280MM

7/29/19 15:33

(b) (4)

BATCH RUN SUMMARY REPORT

System: BATCHING Run ID: 29063

20190729009280MM **Formula:** 420920M030931O ~ Paulk Mixer Uniform **Work Order #:** 29955
Destination: 601 **Oper:**
Start Time: 7/29/19 10:58 **End Time:** 7/29/19 15:39 **Number of Batches:** 1 **Batch Size:** 1000 lb

Item Code	Description	Lot Code	Source Equip	Target Quantity UOM	Actual Quantity UOM	Dev. %	Comments
HANDADD SCALE							
32007	MEGALAC R		WAREH(	(b) (4)			
52275	SODIUM BICARBONATE		WAREH(				
55300	ZINPRO 4 PLEX		WAREH(				
86001	Zinpro 120		WAREH(				
92310	RUMENSIN 90		WAREH(				
	Total for HANDADD SCALE:						
MAJOR SCALE							
11102	GROUND CORN		304				
41201	Soy Plus		315				
52120	LIMESTONE		302				
	Total for MAJOR SCALE:						
MICRO SCALE							
52150	MAGNESIUM OXIDE		009				
73100	VITAMIN E 20,000		006				
	Total for MICRO SCALE:						
	Total for 20190729009280MM:						

Run Time: 04:40:57 **Down Time:** 00:00:00 **Total Time:** 04:40:57

(b) (4)

Page 1 of 1

FILE: 0000029063.001

RECIPE: 420920M03093 REVISION#: 1 DESC: Paulk Mixer LOT: 20190729009280MM B
RUN ID: 29063 SALES ORDER: (none) OPERATOR: F

MATERIAL	DESCRIPTION	BIN	TARGET	ACTUAL	UOM	DEV.	DEV%	OVERRIDE
11102	GROUND CORN	304						
73100	VITAMIN E 20,00	006						
41201	Soy Plus	315						
52120	LIMESTONE	302						
52150	MAGNESIUM OXIDE	009						
52275	SODIUM BICARBON	WAREHO						
32007	MEGALAC R	WAREHO						
55300	ZINPRO 4 PLEX	WAREHO						
86001	Zinpro 120	WAREHO						
92310	RUMENSIN 90	WAREHO						
TOTALS								

(b) (4)

BATCH START TIME 2019-07-29 15:31:06
MIXER DISCHARGE TIME 2019-07-29 15:39:23
DESTINATION: 601 BATCH SIZE: 1000 lb

	TARGET	ACTUAL		TARGET	ACTUAL
WET MIX TIME:	120	0	DRY WIX TIME:	60	180

(b) (4)

7/29/2019 10:59:46AM

Run ID: 29,063
System: BATCHING
Formula: 420920M030931O
Paulk Mixer Uniform
Batches: 1
Batch Size: 1,000

Item	Target Weight	Batch	Actual Weight	Lot
32007 MEGALAC R Active Lot: (None)	(b) (4)	1	✓	
52275 SODIUM BICARBONATE Active Lot: (None)		1	✓	
55300 ZINPRO 4 PLEX Active Lot: (None)		1	✓	
86001 Zinpro 120 Active Lot: (None)		1	✓	
92310 RUMENSIN 90 Active Lot: (None)		1	✓	C93111

Page 1

Appendix C: Batch Sheets

(b) (4)

Master Formula Sheet

Formula Number	420920M030931O	PI	
Formula Name/Label	Batch 1	Account	
Number of Batches		Feed Form (M/P/C)	
Batch Size	200	Packaging (Bag/Bulk)	

Ingredient		Amount	Verified
Scale	Description	(lbs)	Manager
HA	Paulk Mixer Uniform (Lact 6-1-18)	(b) (4)	
HA	Salt		
HA	TM Salt		
HA	Lactation PMX		
HA	Test Ingredient Lot AD 50-14		
	Total	200	

Special Instructions:

PROJECT LEADER APPROVAL

(b) (4)

Signature _____ Date 07-30-19

(b) (4)

(b) (4)

Master Formula Sheet

Formula Number	420920M0309310	PI	
Formula Name/Label	Batch 2	Account	
Number of Batches		Feed Form (M/P/C)	
Batch Size	200	Packaging (Bag/Bulk)	

Ingredient		Amount	Verified
Scale	Description	(lbs)	Manager
HA	Paulk Mixer Uniform (Lact 6-1-18)	(b) (4)	
HA	Salt		
HA	TM Salt		
HA	Lactation PMX		
HA	Test Ingredient Lot AJ-SD-14		
	Total	200	

Special Instructions:

PROJECT LEADER APPROVAL

Signature (b) (4) Date 7-30-15

(b) (4)

(b) (4)

Master Formula Sheet

Formula Number	420920M030931O	PI	
Formula Name/Label	BATCH 3	Account	
Number of Batches		Feed Form (M/P/C)	
Batch Size	200	Packaging (Bag/Bulk)	

Ingredient		Amount	Verified
Scale	Description	(lbs)	Manager
HA	Paulk Mixer Uniform (Lact 6-1-18)	(b) (4)	
HA	Salt		
HA	TM Salt		
HA	Lactation PMX		
HA	Test Ingredient		
	Total	200	

Special Instructions:

PROJECT LEADER APPROVAL

Signature (b) (4) Date 07-30-19

(b) (4)

Appendix D: Premix Testing of Galaxis, version 1

ASCUS BIOSCIENCES

Method

Title	Premix Testing of Galaxis
Version	01
Effective Date	30Jul2019
Author	Adam Taylor
Approver (Signature & Date)	Rich La – Ascus Technical

Scope

The purpose of this assay is to determine the number of viable spores of Dairy-20 and cells of Dairy-21 in Altius and Galaxis premixes containing any or all of the following ingredients:

- Corn products
- Soy products
- Limestone

Safety

Consult the Safety Data Sheet for all reagents prior to handling. Use caution in working with a hot water bath, hot liquids, liquid nitrogen, and extremely cold material. Liquid nitrogen can cause cold burns, frostbite, and permanent eye damage from brief exposure. Avoid skin and eye contact with liquid nitrogen and wear appropriate personal protective equipment (safety glasses and gloves) at all times. Analyst should be trained on liquid nitrogen handling before continuing this method.

Materials

BD GasPak™ EZ large incubation container (BD 260672)
BD GasPak™ EZ anaerobe container system sachets (BD 260678)
Petri dishes, 100x15 mm, sterile
Test tubes, 13x100 mm, sterile
Test tube cap, 16 mm, polypropylene

Premix Testing of Galaxis

1.5 mL polypropylene microcentrifuge tube with snap cap
1000 µL Pipette
200 µL Pipette
1000 µL pipette tips, sterile
200 µL pipette tips, sterile
New glass beads, 3 mm, sterile

Equipment

Water bath set to 50°C
Laboratory Vortexer
Class I/II Biosafety Cabinet
pH meter
Mortar and Pestle

Media & Reagents

NOTE: *Comparable quality ingredients (Laboratory, NF, USP, Reagent, or ACS grade) from different suppliers may be used.*

BD® Bacto™ Tryptic Soy Broth (BD 211822)
BD® Difco® Yeast Peptone Dextrose Broth (BD 242810)
Growcells 1X Phosphate Buffered Saline pH 7.4 (PBS), sterile (Growcells MRGF-6230)
Growcells 1X Phosphate Buffered Saline with 0.05% TWEEN pH 7.4, sterile (Growcells MRGF-6275)
Growcells 10X Phosphate Buffered Saline pH 7.4 (PBS), sterile (Growcells MRGF-6235)
Research Products International Corp. GELRITE (Fisher Scientific 50-488-682)
Sigma-Aldrich® Resazurin sodium salt (Sigma-Aldrich R7017)
Spectrum® Alpha Lipoic Acid, USP (Spectrum L1506)
Spectrum® Aminobenzoic Acid, USP (Spectrum AM150)
Spectrum® Agar, Powder, FCC (Spectrum A1672)
Spectrum® Biotin, Powder, USP (Spectrum B1103)
Spectrum® L-Cysteine Hydrochloride, Monohydrate (Spectrum CY115)

Premix Testing of Galaxis

Spectrum® Ferric Ammonium Citrate, Brown, Powder, FCC (Spectrum F1000)
Spectrum® Folic Acid, Powder, USP (Spectrum FO105)
Spectrum® Niacin, Powder, USP (Spectrum NI100)
Spectrum® Phytonadione, USP (Spectrum PH195)
Spectrum® Pyridoxine Hydrochloride, USP (Spectrum PY103)
Spectrum® Riboflavin, USP (Spectrum RI103)
Spectrum® Thiamine Hydrochloride, FCC (Spectrum T1053)
Spectrum® DL-Pantothenic Acid Calcium Salt (Spectrum P2630) or Calcium Pantothenate (Spectrum CA159)
Spectrum® Vitamin B12, FCC (Spectrum C1454)
Spectrum® Polysorbate 20, FCC (Spectrum P1177)
Reagent grade 95% Ethanol
70% Ethanol
Liquid Nitrogen

Method

1. Prepare Tryptic Soy Broth and Ferric Ammonium Citrate Gelrite (TSB+FAC) Plates. This step should be performed at least 24 hours prior to commencement of testing.

(b) (4)

Premix Testing of Galaxis

Premix Testing of Galaxis

(b) (4)

2. Prepare Yeast Peptone Dextrose (YPD) Agar Plates. This step should be performed at least 24 hours prior to commencement of testing.

(b) (4)

Premix Testing of Galaxis

(b) (4)

3. Prepare Sterile 1X Phosphate Buffered Saline (PBS), pH 7.4 with 0.05% Polysorbate 20

(b) (4)

Premix Testing of Galaxis

4. De-Encapsulate Spray Congealed Dairy-21

(b) (4)

5. Prepare the Primary Dilution Mix

(b) (4)

6. Heat Shock Anaerobic Plating

(b) (4)

Premix Testing of Galaxis

Premix Testing of Galaxis

(b) (4)

7. Aerobic Plating

(b) (4)

Premix Testing of Galaxis

(b) (4)

8. Plate Counting and Calculations

(b) (4)

Premix Testing of Galaxis

(b) (4)

Reasons for Revision

1. Initial version (which addresses low plate counts for Dairy-20 during the method validation).

Appendix E: Premix Testing of Galaxis 5 Method Validation Report

ASCUS BIOSCIENCES

Premix Testing of Galaxis Method Validation Summary Report

Objective:
The objective of this validation protocol was to demonstrate the repeatability, robustness, and specificity of the method "Premix Testing of Galaxis".

Results:
The following parameters were tested in the validation.

Repeatability: Closeness of results obtained on the same sample of blended premix with Galaxis (premix #1) when assayed multiple times by the same person with the same reagents and equipment.

Robustness: Reliability of the method to withstand small variations such as different technicians and reagent preparations on the 3 blended premixes with Galaxis (premix #1, premix #3, premix #4).

Specificity: Accuracy of detection for DY20 and DY21 when mixed with different premixes.

A summary of the CFU results are shown in the table below. All samples fit the criteria for validation with the coefficient of variation of 75% or less.

ASCUS BIOSCIENCES

Analyst 1 Summary								
	DY20				DY21			
Sample Description	Avg. CFU/g	Avg. CFU/g	Std. Dev.	CV	Avg. CFU/g	Avg. CFU/g	Std. Dev.	CV
	1.50E+04				2.39E+06			
	1.90E+04				2.90E+06			
Sample 1A	1.75E+04	1.72E+04	2.04E+03	12%	1.93E+06	2.41E+06	4.87E+05	20%
	2.50E+04				2.00E+06			
	2.32E+04				3.10E+06			
Sample 1B	1.26E+04	2.03E+04	6.72E+03	33%	2.47E+06	2.52E+06	5.51E+05	22%
	2.22E+04				6.75E+06			
	2.30E+04				1.63E+06			
Sample 1C	1.50E+04	2.00E+04	4.40E+03	22%	4.19E+06	4.19E+06	2.56E+06	61%
	1.85E+04				2.80E+06			
	2.69E+04				1.94E+06			
Sample 2	1.54E+04	2.03E+04	5.98E+03	29%	2.68E+06	2.47E+06	4.69E+05	19%
	2.20E+04				1.40E+06			
	1.33E+04				2.29E+06			
Sample 3	3.91E+04	2.48E+04	1.31E+04	53%	1.85E+06	1.84E+06	4.45E+05	24%

ASCUS BIOSCIENCES

Analyst 2 Summary								
	DY20				DY21			
Sample Description	Avg. CFU/g	Avg. CFU/g	Std. Dev.	CV	Avg. CFU/g	Avg. CFU/g	Std. Dev.	CV
Sample 1	(b) (4)							
Sample 2								
Sample 3								

Repeatability:
From Analyst 1, the average CFU/g of samples 1A, 1B, and 1C is 1.92E4 and 3.04E6 with standard deviations of 7.72E3 and 9.97E5 for DY20 and DY21 respectively. The coefficient of variance for these samples was 9% and 33% for DY20 and DY21 respectively. These results indicate that the assay is repeatable.

Robustness:
All samples tested by both analysts had CVs less than 75%, indicating low variation of results when slight variations of the method occur.

Specificity:
DY20 and DY21 were able to be detected by both analysts when mixed into these different types of premixes.

ASCUS BIOSCIENCES

Deviations:
There was a dose change from 1g Galaxis 5 per pound of premix to 5g Galaxis 5 per pound of premix to more accurately reflect dosing on farms. This only impacted the sample preparation and no deviation is required.

Conclusion:
Repeatability, robustness, and specificity were tested for the Premix Testing of Galaxis method, and in all parameters this method validation has passed. The method is validated for the testing of premix (containing corn, soy, and /or limestone materials) and Galaxis at a dose of approximately 5g/pound.

The method will be approved.

Raw data is included in the executed protocol and can be found on the Ascus Biosciences Google Drive.

Approvers:

Rich La Ascus Technical	DocuSigned by: Rich La C4F920E8CAE2489...	7/29/2019
Patricia A. Williams Quality	DocuSigned by: Patricia Williams 5B301285A10643D...	7/29/2019

Appendix F: Excel Data for Study

Blend 1								DY20 Anaerobic Plating, CFU/100uL								
								1E+00			1E-01			1E-02		
Sample Description	Sample	Test Tube + Cap (g)	Sample + Tube & Cap (g)	Actual Mass (g)	Volume PBST (mL)	Heat Shock Start	Heat Shock End	A	B	C	A	B	C	A	B	C
1	PDM-1	6.287	7.290	1.003	10	11:16AM	11:26AM	(b) (4)								
	PDM-2	6.325	7.356	1.031	10	11:16AM	11:26AM									
	PDM-3	6.278	7.339	1.061	10	11:16AM	11:26AM									
2	PDM-1	6.248	7.259	1.011	10	11:16AM	11:26AM									
	PDM-2	6.254	7.261	1.007	10	11:16AM	11:26AM									
	PDM-3	6.386	7.427	1.041	10	11:16AM	11:26AM									
3	PDM-1	6.339	7.354	1.015	10	11:16AM	11:26AM									
	PDM-2	6.213	7.241	1.028	10	11:16AM	11:26AM									
	PDM-3	6.316	7.338	1.022	10	11:16AM	11:26AM									
4	PDM-1	6.242	7.277	1.035	10	11:16AM	11:26AM									
	PDM-2	6.210	7.263	1.053	10	11:16AM	11:26AM									
	PDM-3	6.312	7.354	1.042	10	11:16AM	11:26AM									
5	PDM-1	6.572	7.618	1.046	10	12:19PM	12:29PM									
	PDM-2	6.620	7.628	1.008	10	12:19PM	12:29PM									
	PDM-3	6.534	7.584	1.050	10	12:19PM	12:29PM									
6	PDM-1	6.628	7.669	1.041	10	12:19PM	12:29PM									
	PDM-2	6.594	7.595	1.001	10	12:19PM	12:29PM									
	PDM-3	6.551	7.594	1.043	10	12:19PM	12:29PM									
7	PDM-1	6.628	7.647	1.019	10	12:19PM	12:29PM									
	PDM-2	6.638	7.644	1.006	10	12:19PM	12:29PM									(b) (4)
	PDM-3	6.559	7.626	1.067	10	12:19PM	12:29PM									
8	PDM-1	6.481	7.497	1.016	10	1:14PM	1:24PM									
	PDM-2	6.596	7.601	1.005	10	1:14PM	1:24PM									
	PDM-3	6.518	7.544	1.026	10	1:14PM	1:24PM									
9	PDM-1	6.551	7.548	0.997	10	1:14PM	1:24PM									
	PDM-2	6.499	7.511	1.012	10	1:14PM	1:24PM									
	PDM-3	6.515	7.544	1.029	10	1:14PM	1:24PM									
10	PDM-1	6.710	7.719	1.009	10	1:14PM	1:24PM									
	PDM-2	6.597	7.615	1.018	10	1:14PM	1:24PM									
	PDM-3	6.667	7.667	1.000	10	1:14PM	1:24PM									

Table 1. *C. beijerinckii* ASCUSDY20 - Blend 1 Data

DY20 Analysis												
CFU/mL			CFU/mL			CFU/mL						
A	B	C	A	B	C	A	B	C	CFU/g	Avg. CFU/g	Std. Dev.	CV
(b) (4)												

Table 2. *C. beijerinckii* ASCUSDY20 - Blend 1 Analysis

Blend 1								DY21 Aerobic Plating, CFU/100uL								
								1E-01			1E-02			1E-03		
Sample Description	Sample	Test Tube + Cap (g)	Sample + Tube & Cap (g)	Actual Mass (g)	Volume PBST (mL)	Heat Shock Start	Heat Shock End	A	B	C	A	B	C	A	B	C
1	PDM-4	6.620	7.643	1.023	10	N/A	N/A	(b) (4)								
	PDM-5	6.652	7.671	1.019	10	N/A	N/A									
	PDM-6	6.695	7.736	1.041	10	N/A	N/A									
2	PDM-4	6.577	7.608	1.031	10	N/A	N/A									
	PDM-5	6.549	7.570	1.021	10	N/A	N/A									
	PDM-6	6.529	7.621	1.092	10	N/A	N/A									
3	PDM-4	6.734	7.745	1.011	10	N/A	N/A									
	PDM-5	6.890	7.914	1.024	10	N/A	N/A									
	PDM-6	6.793	7.817	1.024	10	N/A	N/A									
4	PDM-4	6.802	7.809	1.007	10	N/A	N/A									
	PDM-5	6.797	7.824	1.027	10	N/A	N/A									
	PDM-6	6.732	7.780	1.048	10	N/A	N/A									
5	PDM-4	6.715	7.808	1.093	10	N/A	N/A									
	PDM-5	6.706	7.744	1.038	10	N/A	N/A									
	PDM-6	6.735	7.744	1.009	10	N/A	N/A									
6	PDM-4	6.651	7.734	1.083	10	N/A	N/A									
	PDM-5	6.779	7.795	1.016	10	N/A	N/A									
	PDM-6	6.734	7.777	1.043	10	N/A	N/A									
7	PDM-4	6.762	7.792	1.030	10	N/A	N/A									
	PDM-5	6.774	7.833	1.059	10	N/A	N/A									
	PDM-6	6.772	7.854	1.082	10	N/A	N/A									
8	PDM-4	6.491	7.499	1.008	10	N/A	N/A									
	PDM-5	6.611	7.606	0.995	10	N/A	N/A									
	PDM-6	6.618	7.630	1.012	10	N/A	N/A									
9	PDM-4	6.660	7.669	1.009	10	N/A	N/A									
	PDM-5	6.520	7.528	1.008	10	N/A	N/A									
	PDM-6	6.533	7.533	1.000	10	N/A	N/A									
10	PDM-4	6.451	7.452	1.001	10	N/A	N/A									
	PDM-5	6.778	7.786	1.008	10	N/A	N/A									
	PDM-6	6.669	7.676	1.007	10	N/A	N/A									

Table 3. *P. kudriavzevii* ASCUSDY21- Blend 1 Data

DY 21 Analysis												
CFU/mL			CFU/mL			CFU/mL						
A	B	C	A	B	C	A	B	C	CFU/g	Avg. CFU/g	Std. Dev.	CV
(b) (4)												

Table 4. *P. kudriavzevii* ASCUSDY21- Blend 1 Analysis

Blend 2								DY20 Anaerobic Plating, CFU/100uL								
								1E+00			1E-01			1E-02		
Sample Description	Sample	Test Tube + Cap (g)	Sample + Tube & Cap (g)	Actual Mass (g)	Volume PBST (mL)	Heat Shock Start	Heat Shock End	A	B	C	A	B	C	A	B	C
1	PDM-1	6.635	7.689	1.054	10	3:15PM	3:25PM									
	PDM-2	6.561	7.650	1.089	10	3:15PM	3:25PM									
	PDM-3	6.582	7.610	1.028	10	3:15PM	3:25PM									
2	PDM-1	6.632	7.648	1.016	10	3:15PM	3:25PM									
	PDM-2	6.572	7.616	1.044	10	3:15PM	3:25PM									
	PDM-3	6.576	7.607	1.031	10	3:15PM	3:25PM									
3	PDM-1	6.635	7.679	1.044	10	3:15PM	3:25PM									
	PDM-2	6.589	7.592	1.003	10	3:15PM	3:25PM									
	PDM-3	6.575	7.673	1.098	10	3:15PM	3:25PM									
4	PDM-1	6.588	7.616	1.028	10	3:15PM	3:25PM									
	PDM-2	6.559	7.634	1.075	10	3:15PM	3:25PM									
	PDM-3	6.573	7.602	1.029	10	3:15PM	3:25PM									
5	PDM-1	6.577	7.629	1.052	10	3:15PM	3:25PM									
	PDM-2	6.628	7.675	1.047	10	3:15PM	3:25PM									
	PDM-3	6.556	7.559	1.003	10	3:15PM	3:25PM									
6	PDM-1	6.641	7.736	1.095	10	3:15PM	3:25PM									
	PDM-2	6.631	7.729	1.098	10	3:15PM	3:25PM									
	PDM-3	6.563	7.653	1.090	10	3:15PM	3:25PM									
7	PDM-1	6.580	7.662	1.082	10	3:04PM	3:14PM									
	PDM-2	6.584	7.620	1.036	10	3:04PM	3:14PM									
	PDM-3	6.569	7.646	1.077	10	3:04PM	3:14P									
8	PDM-1	6.587	7.596	1.009	10	3:04PM	3:14PM									
	PDM-2	6.592	7.627	1.035	10	3:04PM	3:14PM									
	PDM-3	6.612	7.673	1.061	10	3:04PM	3:14PM									
9	PDM-1	6.613	7.668	1.055	10	3:04PM	3:14PM									
	PDM-2	6.626	7.619	0.993	10	3:04PM	3:14PM									
	PDM-3	6.613	7.632	1.019	10	3:04PM	3:14PM									
10	PDM-1	6.726	7.742	1.016	10	3:04PM	3:14PM									
	PDM-2	6.719	7.756	1.037	10	3:04PM	3:14PM									
	PDM-3	6.627	7.704	1.077	10	3:04PM	3:14PM									

(b) (4)

Table 5. *C. beijerinckii* ASCUSDY20 – Blend 2 Data

DY20 Analysis												
CFU/mL			CFU/mL			CFU/mL						
A	B	C	A	B	C	A	B	C	CFU/g	Avg. CFU/g	Std. Dev.	CV
(b) (4)												

Table 6. *C. beijerinckii* ASCUSDY20 - Blend 2 Analysis

Blend 2								DY21 Aerobic Plating, CFU/100uL								
								1E-01			1E-02			1E-03		
Sample Description	Sample	Test Tube + Cap (g)	Sample + Tube & Cap (g)	Actual Mass (g)	Volume PBST (mL)	Heat Shock Start	Heat Shock End	A	B	C	A	B	C	A	B	C
1	PDM-4	6.731	7.815	1.084	10	N/A	N/A	(b) (4)								
	PDM-5	6.775	7.873	1.098	10	N/A	N/A									
	PDM-6	6.812	7.821	1.009	10	N/A	N/A									
2	PDM-4	6.690	7.707	1.017	10	N/A	N/A									
	PDM-5	-0.122	0.956	1.078	10	N/A	N/A									
	PDM-6	6.898	7.911	1.013	10	N/A	N/A									
3	PDM-4	6.734	7.733	0.999	10	N/A	N/A									
	PDM-5	6.903	7.916	1.013	10	N/A	N/A									
	PDM-6	6.830	7.879	1.049	10	N/A	N/A									
4	PDM-4	6.790	7.785	0.995	10	N/A	N/A									
	PDM-5	6.715	7.768	1.053	10	N/A	N/A									
	PDM-6	6.899	7.937	1.038	10	N/A	N/A									
5	PDM-4	6.718	7.754	1.036	10	N/A	N/A									
	PDM-5	6.974	8.034	1.060	10	N/A	N/A									
	PDM-6	6.779	7.881	1.102	10	N/A	N/A									
6	PDM-4	6.831	7.841	1.010	10	N/A	N/A									
	PDM-5	6.698	7.783	1.085	10	N/A	N/A									
	PDM-6	6.898	7.920	1.022	10	N/A	N/A									
7	PDM-4	6.722	7.724	1.002	10	N/A	N/A									
	PDM-5	6.715	7.728	1.013	10	N/A	N/A									
	PDM-6	6.656	7.652	0.996	10	N/A	N/A									
8	PDM-4	6.639	7.654	1.015	10	N/A	N/A									
	PDM-5	6.797	7.875	1.078	10	N/A	N/A									
	PDM-6	6.775	7.782	1.007	10	N/A	N/A									
9	PDM-4	6.524	7.555	1.031	10	N/A	N/A									
	PDM-5	6.872	7.877	1.005	10	N/A	N/A									
	PDM-6	6.745	7.783	1.038	10	N/A	N/A									
10	PDM-4	6.713	7.712	0.999	10	N/A	N/A									
	PDM-5	6.804	7.885	1.081	10	N/A	N/A									
	PDM-6	6.713	7.773	1.060	10	N/A	N/A									

Table 7. *P. kudriavzevii* ASCUSDY21- Blend 2 Data

DY21 Analysis												
CFU/mL			CFU/mL			CFU/mL						
A	B	C	A	B	C	A	B	C	CFU/g	Avg. CFU/g	Std. Dev.	CV
(b) (4)												

Blend 3								DY20 Anaerobic Plating, CFU/100uL								
								1E+00			1E-01			1E-02		
Sample Description	Sample	Test Tube + Cap (g)	Sample + Tube & Cap (g)	Actual Mass (g)	Volume PBST (mL)	Heat Shock Start	Heat Shock End	A	B	C	A	B	C	A	B	C
1	PDM-1	6.607	7.690	1.083	10	5:06PM	5:16PM	(b) (4)								
	PDM-2	6.630	7.640	1.010	10	5:06PM	5:16PM									
	PDM-3	6.604	7.665	1.061	10	5:06PM	5:16PM									
2	PDM-1	6.600	7.694	1.094	10	5:06PM	5:16PM									
	PDM-2	6.579	7.595	1.016	10	5:06PM	5:16PM									
	PDM-3	6.595	7.627	1.032	10	5:06PM	5:16PM									
3	PDM-1	6.623	7.692	1.069	10	5:06PM	5:16PM									
	PDM-2	6.633	7.685	1.052	10	5:06PM	5:16PM									
	PDM-3	6.630	7.667	1.037	10	5:06PM	5:16PM									
4	PDM-1	6.582	7.622	1.040	10	5:06PM	5:16PM									
	PDM-2	6.573	7.643	1.070	10	5:06PM	5:16PM									
	PDM-3	6.586	7.604	1.018	10	5:06PM	5:16PM									
5	PDM-1	6.020	7.700	1.680	10	3:43PM	3:53PM									
	PDM-2	6.563	7.600	1.037	10	3:43PM	3:53PM									
	PDM-3	6.570	7.612	1.042	10	3:43PM	3:53PM									
6	PDM-1	6.655	7.742	1.087	10	3:43PM	3:53PM									
	PDM-2	6.592	7.680	1.088	10	3:43PM	3:53PM									
	PDM-3	6.565	7.565	1.000	10	3:43PM	3:53PM									
7	PDM-1	6.589	7.661	1.072	10	3:43PM	3:53PM									
	PDM-2	6.614	7.650	1.036	10	3:43PM	3:53PM									
	PDM-3	6.578	7.638	1.060	10	3:43PM	3:53PM									
8	PDM-1	6.518	7.532	1.014	10	4:12PM	4:22PM									
	PDM-2	6.617	7.628	1.011	10	4:12PM	4:22PM									
	PDM-3	6.772	7.772	1.000	10	4:12PM	4:22PM									
9	PDM-1	6.526	7.554	1.028	10	4:12PM	4:22PM									
	PDM-2	6.522	7.523	1.001	10	4:12PM	4:22PM									
	PDM-3	6.627	7.633	1.006	10	4:12PM	4:22PM									
10	PDM-1	6.499	7.501	1.002	10	4:12PM	4:22PM									
	PDM-2	6.644	7.642	0.998	10	4:12PM	4:22PM									
	PDM-3	6.748	7.762	1.014	10	4:12PM	4:22PM									

Table 9. *C. beijerinckii* ASCUSDY20 - Blend 2 Data

DY20 Analysis												
CFU/mL			CFU/mL			CFU/mL						
A	B	C	A	B	C	A	B	C	CFU/g	Avg. CFU/g	Std. Dev.	CV
(b) (4)												

Blend 3								DY21 Aerobic Plating, CFU/100uL								
								1E-01			1E-02			1E-03		
Sample Description	Sample	Test Tube + Cap (g)	Sample + Tube & Cap (g)	Actual Mass (g)	Volume PBST (mL)	Heat Shock Start	Heat Shock End	A	B	C	A	B	C	A	B	C
1	PDM-4	6.709	7.720	1.011	10	N/A	N/A	(b) (4)								
	PDM-5	6.811	7.887	1.076	10	N/A	N/A									
	PDM-6	6.719	7.731	1.012	10	N/A	N/A									
2	PDM-4	6.780	7.821	1.041	10	N/A	N/A									
	PDM-5	6.684	7.770	1.086	10	N/A	N/A									
	PDM-6	6.636	7.638	1.002	10	N/A	N/A									
3	PDM-4	6.770	7.782	1.012	10	N/A	N/A									
	PDM-5	6.600	7.600	1.000	10	N/A	N/A									
	PDM-6	6.675	7.721	1.046	10	N/A	N/A									
4	PDM-4	6.599	7.678	1.079	10	N/A	N/A									
	PDM-5	6.606	7.686	1.080	10	N/A	N/A									
	PDM-6	6.745	7.804	1.059	10	N/A	N/A									
5	PDM-4	6.771	7.790	1.019	10	N/A	N/A									
	PDM-5	6.683	7.732	1.049	10	N/A	N/A									
	PDM-6	6.599	7.634	1.035	10	N/A	N/A									
6	PDM-4	6.807	7.833	1.026	10	N/A	N/A									
	PDM-5	6.747	7.811	1.064	10	N/A	N/A									
	PDM-6	6.734	7.757	1.023	10	N/A	N/A									
7	PDM-4	6.768	7.847	1.079	10	N/A	N/A									
	PDM-5	6.724	7.745	1.021	10	N/A	N/A									
	PDM-6	6.676	7.753	1.077	10	N/A	N/A									
8	PDM-4	6.596	7.600	1.004	10	N/A	N/A									
	PDM-5	6.661	7.677	1.016	10	N/A	N/A									
	PDM-6	6.611	7.620	1.009	10	N/A	N/A									
9	PDM-4	6.801	7.799	0.998	10	N/A	N/A									
	PDM-5	6.754	7.780	1.026	10	N/A	N/A									
	PDM-6	6.555	7.565	1.010	10	N/A	N/A									
10	PDM-4	6.677	7.697	1.020	10	N/A	N/A									
	PDM-5	6.812	7.815	1.003	10	N/A	N/A									
	PDM-6	6.798	7.806	1.008	10	N/A	N/A									

Table 11. *P. kudriavzevii* ASCUSDY21- Blend 3 Data

DY21 Analysis												
CFU/mL			CFU/mL			CFU/mL						
A	B	C	A	B	C	A	B	C	CFU/g	Avg. CFU/g	Std. Dev.	CV
(b) (4)												

Table 12. *P. kudriavzevii* ASCUSDY21- Blend 3 Analysis

Cerrito, Chelsea

From: Kristi Smedley <smedley@cfr-services.com>
Sent: Wednesday, August 05, 2020 12:29 PM
To: Cerrito, Chelsea
Cc: Howard@ascusbiosciences.com
Subject: AGRN ASCUS Clostridium beijerinckii--Figure 2.4
Attachments: Page 16 ASCUS AGRN figure 2.4.pdf

Chelsea,

I have attached the page with the simple figure 2.4

This should complete the file as discussed this morning.

Thank you, again.

Kristi O. Smedley, Ph.D.

Center for Regulatory Services, Inc.
5200 Wolf Run Shoals Rd.
Woodbridge, VA 22192

Ph. 703-590-7337
Cell (b) (4)
Fax 703-580-8637

From: Kristi Smedley [mailto:smedley@cfr-services.com]
Sent: Wednesday, August 05, 2020 10:50 AM
To: Animalfood-premarket (Animalfood-premarket@fda.hhs.gov)
Cc: Howard@ascusbiosciences.com
Subject: RE: Appendices to ASCUS Clostridium beijerinckii AGRN

Appendix 15 C and D.

This is the third of the 3 appendices emails.

Kristi O. Smedley, Ph.D.

Center for Regulatory Services, Inc.
5200 Wolf Run Shoals Rd.
Woodbridge, VA 22192

Ph. 703-590-7337
Cell (b) (4)
Fax 703-580-8637

From: Kristi Smedley [mailto:smedley@cfr-services.com]
Sent: Wednesday, August 05, 2020 10:40 AM
To: Animalfood-premarket (Animalfood-premarket@fda.hhs.gov)
Cc: Howard@ascusbiosciences.com
Subject: Appendices to ASCUS Clostridium beijerinckii AGRN

Thank you for the discussion this morning on the appendices supporting the AGRN for Clostridium beijerinckii. It appears when I downloaded the appendices from the shared website, the download was not complete. I apologize for this inconvenience and I appreciate your permitting us to provide the missing information by email.

This email contains appendix 13, appendix 12, appendix 9, and appendix 3D.

I will send a few emails with the needed information.

Kristi O. Smedley, Ph.D.

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Copy of Figure 2.4 (page 16)

Figure 2.4: ***C. beijerinckii*** **ASCUSDY20 Assembly Graph as Generated by Bandage**

2.1.6 *In-vitro* and *In-silico* Analysis of Antibiotic Susceptibility

Phenotypic testing was conducted on *C. beijerinckii* ASCUSDY20 to determine the minimum inhibitory concentrations (MICs) against a selected group of antimicrobials of relevance to human and veterinary medicine. The full study report is provided in Appendix 004. The results were evaluated against the microbiological cut-off values reported by the European Food Safety Authority for "other gram positive bacteria" (EFSA, 2018), as well as the resistant breakpoints set by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) for "gram positive anaerobes" and the Clinical and Laboratory Standards Institute (CLSI) for "anaerobes" (where available). The MIC values reported for *C. beijerinckii* ASCUSDY20 were equal, or lower than, the cut-off values and break-points established by EFSA, EUCAST and/or CLSI for all antimicrobials except chloramphenicol, gentamycin and tetracycline. Results can be found in Table 2.6.

MIC testing revealed values above one or more breakpoints for three antimicrobial compounds; chloramphenicol, gentamicin, and tetracycline. For chloramphenicol , the MIC of 16 µg/mL exhibited by *C. beijerinckii* ASCUSDY20 is higher than the EFSA microbiological cut-off value (4 µg/mL) and the EUCAST resistant breakpoint value (8 µg/mL) but lower than the CLSI resistant breakpoint value (32 µg/mL). Resistance to aminoglycosides (gentamicin and streptomycin) is recognized to be intrinsic in anaerobic bacteria because the mechanism of uptake requires respiration (Bryan *et al*., 1979). Consistent with this expectation, the MIC of >32 µg/mL for gentamicin exhibited by *C. beijerinckii* ASCUSDY20 is not considered a concern. However, streptomycin MIC for *C. beijerinckii* ASCUSDY20 was equal to EFSA cut-off value of 8 ug/mL and would be considered susceptible to streptomycin. The tetracycline MIC of 4 µg/mL reported for *C. beijerinckii* ASCUSDY20 is higher than the EFSA microbiological cut-off value (2 µg/mL) but lower than the CLSI resistant breakpoint value (16 µg/mL). Additionally, tetracycline resistance was observed to be relatively common among 68 livestock derived *Clostridium* strains analyzed by Dutta *et al.* (1983) with 17/68 (25%) strains displaying MIC values above the EFSA microbiological cut-off value.

ATTACHMENT 1

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier

Appendix 10 (Revised)

Detailed Manufacturing Summary

(b) (4)

Appendix 10 (revised)
Detailed Manufacturing Summary of Spray Dried *Clostridium beijerinckii* ASCUSDY20

Confidential Manufacturing Information

The raw materials used in the manufacture of *Clostridium beijerinckii* ASCUSDY20 are listed inTable 1 below. Specifications for the raw materials are provided in Appendices 009A to 009S.

Table 1: Raw Materials and Processing Aids Used in the manufacture of *Clostridium beijerinckii* ASCUSDY20

Material	Function	Regulatory Status	Grade
Acetic Acid Glacial	Nutrient	GRAS substance for use as a general purpose food additive (21 CFR 582.1005)	FCC
Ammonium Chloride	Nutrient	AAFCO OP ingredient definition (mineral product) 57.265	FCC
Ammonium Hydroxide	Nutrient	GRAS substance for use as a general purpose food additive (21 CFR §582.1139)	FCC
Biotin	Nutrient	GRAS substance for use as a nutrient and/or dietary supplement (21 CFR §582.5159)	FCC
Condensed Fermented Corn Extractives (Solulys 095K Corn Steep Powder)	Nutrient	AAFCO OP ingredient definition (corn product) 48.24	Feed grade
Dextrose Monohydrate	Nutrient	Common ingredient (*e.g.*, 21 CFR §168.111; 21 CFR §184.1857)	FCC
Dipotassium Phosphate	Buffering agent	GRAS substance for use as a sequestrant (21 CFR §582.6285)	FCC
Ferrous Sulfate Heptahydrate	Nutrient	AAFCO OP ingredient definition (mineral product)57.83; GRAS substance for use as a nutrient and/or dietary supplement (21 CFR 582.5315)	Feed grade
Folic Acid	Nutrient	GRAS substance for use as a nutrient and/or dietary supplement (21 CFR 172.345)	FCC
L-Cysteine Hydrochloride	Nutrient	GRAS substance for use as a nutrient and/or dietary supplement (21 CFR 582.5271)	FCC
Magnesium Sulfate Heptahydrate	Nutrient	GRAS substance for use as a nutrient and/or dietarysupplement (21 CFR §582.5443) AAFCO OP ingredient definition (mineral product) 57.88	FCC

Manganese Sulfate Monohydrate	Nutrient	GRAS substance for use as a nutrient and/or dietary supplement (21 CFR §582.5461) and trace mineral (21CFR §582.80)	FCC
Modified Starch; CAPSUL® 06670103	Carrier	GRAS substance for use as a general purpose food additive 21 CFR 172.892	Food grade
Monopotassium Phosphate	Primary seed buffering agent	Permitted for use as a food additive in frozen FCC eggs (21 CFR §160.110) – safety for use in feed assessed by ASCUS (Appendix 009N2)	FCC
Polyoxythylene-polyoxypropylene block copolymer	Anti-foaming agent	Acceptable for use as an anti-foaming agent for the production of enzymes and DFMs in accordance withthe letter issued by the FDA to the Enzyme TechnicalAssociation (ETA, Appendix 009O2)	Food grade
Sodium Chloride	Nutrient	AAFCO OP ingredient definition (mineral product) 57.31	Food grade
Thiamine Hydrochloride	Nutrient	GRAS substance for use as a nutrient and/or dietary supplement (21 CFR §582.5875) AAFCO OP ingredient definition (recognized vitamin ingredients) 90.25	FCC
Yeast Extract (Amberex 1003 AG)	Nutrient	Yeast extract obtained by mechanical rupturing of cellsis accepted for use in feed (AAFCO OP 96.11); use of autolysis in the production of the extract is not expected to introduce any different substances and should yield a product with equivalent composition – history of use in food (*e.g.*, FCC monograph established Appendix 009S2)	Food grade
Yeast Extract (Procelys Springer 0251/ 0-MG-L)	Nutrient	Yeast extract obtained by mechanical rupturing of cellsis accepted for use in feed (AAFCO OP 96.11); use of autolysis in the production of the extract is not expected to introduce any different substances and should yield a product with equivalent composition – history of use in food (e.g., FCC monograph established Appendix 009S2)	Food grade

Abbreviations: OP – Official Publication; FCC – Food Chemicals Codex; USP – United StatesPharmacopoeia

Confidential Detailed Manufacturing Summary of *Clostridium beijerinckii* ASCUSDY20 SDP

1 Overview

Clostridium beijerinckii ASCUSDY20 SDP (Spray Dried Powder) is produced through a seriesof processes: Fermentation, Centrifugation and Spray Drying. A process diagram of the production of *Clostridium beijerinckii* ASCUSDY20 SDP is below (Appendix A). The strain (*Clostridium beijerinckii* ASCUSDY20) is an obligate anaerobic spore-forming *Clostridium beijerinckii* bacterium, that is produced by dextrose fed-batch anaerobic fermentation in such away as to induce sporulation of the strain.

(b) (4) to yield the *Clostridium beijerinckii* ASCUSDY20 SDP notified substance. *Clostridium beijerinckii* ASCUSDY20 SDP is then packaged into moisture barrier mylar bags, heat sealed, and stored at less than 25°C.

2 Master Cell Bank / Working Cell Bank

(b) (4)

3 Fermentation

(b) (4)

(b) (4)

(b) (4)

(b) (4)

(b) (4)

4 Biomass Harvest by Centrifugation

(b) (4)

5 Spray Drying

(b) (4)

(b) (4)

(b) (4)

(b) (4)

Appendix A. Process Diagram of the Production of *Clostridium beijerinckii* ASCUSDY20 SDP

***Clostridium beijerinckii* ASCUSDY20 Manufacturing Process**

22 Apr 2021

(b) (4)

CONFIDENTIAL

ATTACHMENT 2

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

CAPSUL Regulatory Document

(b) (4)

Food Starch Products

Regulatory Status, (b) (4)

Each of the (b) (4) manufactures & supplies their food starch products in compliance with:

For Modified Starches;

- EU food additives regulation[1] and the associated specifications[2] for modified starches,
- JECFA specifications for modified starches[3]

For Native & Physically Treated Starches;

- The Food Chemicals Codex (FCC) specifications for food starch unmodified[4].

These criteria specify either the process chemicals or process treatments that can be applied to edible starch to make it suitable for use in food and its intended application.

Any processing aid used is done so in accordance with the definition specified in Regulation 1333/2008[5]. Each of the (b) (4) has procedures in place to ensure that any processing aid used does not present a health risk or have any technological effects on the final product.

The food products sold by each of the (b) (4) are labelled in accordance with the provisions of food additives that are not sold to the ultimate consumer[6].

Please note, the information given in this statement is in relation to products supplied by any of the (b) (4) and is based upon their interpretation of relevant legislation. Although it is offered in good faith, the advice is not legal advice to you. It is therefore necessary that you satisfy yourself of the use and any labelling obligations, in accordance with relevant legislation, for your products as sold to the ultimate consumer. Each of the (b) (4) cannot accept any liability in this regard. The (b) (4)' (b) (4)

[1] Regulation (EC) No 1333/2008 of the European Parliament and of the Council of 16 December 2008 on food additives, amended by Regulation (EU) No 1129/2011 establishing a Union list of food additives (Annex II) and Regulation (EU) No 1130/2011 establishing a Union list of food additives approved for use in food additives, food enzymes, food flavourings and nutrients (Annex III)

[2] Commission Regulation (EU) No 231/2012 of 9 March 2012 laying down specifications for food additives listed in Annexes II and III to Regulation (EC) No 1333/2008 of the European Parliament and of the Council, as amended

[3] JECFA (Joint Expert Committee on Food Additives) Specifications for modified starch, prepared at the 79th JECFA (2014) and published in FAO JECFA Monograph 16 (2014)

[4] Food Chemicals Codex 12th Edition : Food Starch, Unmodified

[5] Regulation (EC) 1333/2008 on food additives, Article 3,2(b) "Processing aid shall mean any substance that (i) is not consumed as a food by itself; (ii) is intentionally used in the processing of raw materials, foods or their ingredients, to fulfil a certain technological purpose during treatment or processing, (ii) may result in the unintentional but technically unavoidable presence in the final product of residues of the substance or its derivatives provided they do not present any health risk and do not have any technological effect on the final product."

[6] Regulation (EC) 1333/2008 on food additives, Article 22.

(b) (4)

SAFETY DATA SHEET

CAPSUL®

1. Identification

Product identifier used on the label:

PRODUCT NUMBER (NEW):	06670103
PRODUCT NUMBER (OLD):	051-6336
PRODUCT NAME:	CAPSUL®

Other means of identification

Chemical Family: Modified Starch

Recommended use of the chemical and restrictions on use

Recommended use: food starch
Restrictions on uses: Not Available

Name, address, and telephone number of the chemical manufacturer, importer, or other responsible party:
Emergency phone number:

(b) (4)

2. Hazard(s) identification

Classification of the chemical in accordance with paragraph (d) of §1910.1200

GHS Classification: Combustible Dust Category 1
GHS Signal Word: Warning
GHS Hazard Statements: May form combustible dust concentrations in air.

Hazards not otherwise classified: No data available

3. Composition/information on ingredients

Chemical Name:	CAS number and other unique identifiers	% (or range) of ingredient
None classified as hazardous under the OSHA Hazard Communication Standard (29CFR 1910.1200).		

4. First-aid measures

Description of necessary measures, subdivided according to the different routes of exposure, i.e., inhalation, skin and eye contact, and ingestion

Inhalation:	Remove patient from exposure.
Eyes:	Remove particles by irrigating with eye wash solution or clean water, holding the eyelids apart. If symptoms develop, obtain medical attention.
Skin Contact:	Wash skin with soap and water.
Ingestion:	None required.
Most important symptoms/effects, acute and delayed:	Possible physical irritant from dust particles. Potential for dust explosion. Contributes to effluent BOD. Not considered as hazardous.
Indication of immediate medical attention and special treatment needed, if necessary:	No further first aid information is available.

5. Fire-fighting measures

Suitable (and unsuitable) extinguishing media

Suitable extinguishing media:	CO2; Dry Chemical; Foam; Water Fog
Unsuitable extinguishing media:	None known.
Specific hazards arising from the chemical (e.g., nature of any hazardous combustion products):	Minimum ignition temperature of dust cloud- approx. 390 C. Minimum explosive concentration- approx. 62 mg/l. Minimum energy to ignite cloud by electrical spark- approx. 0.045 joules.
Hazardous Combustion Products:	Thermal decomposition could produce carbon monoxide, carbon dioxide, and unidentified organic compounds.
Special protective equipment and precautions for fire-fighters:	No special procedures are required.

6. Accidental release measures

Personal precautions, protective equipment and emergency procedures:	Use personal protective equipment as required.
Methods and materials for containment and cleaning up:	Normal precautions for "nuisance dust" should be observed. Avoid prolonged inhalation of dust. Sweep up or vacuum up and place in suitable container for disposal.

7. Handling and storage

Precautions for safe handling:	Store in a clean,dry, well ventilated warehouse away from odorous materials.
Conditions for safe storage, including any incompatibilities	Ambient.
Special Sensitivity:	No special sensitivity.
:	No
:	Yes
Other Precautions:	Use care to minimize dust generation in normal use conditions. Avoid dispersing the powder in the air. Prevent buildup of powder on surfaces.
Materials to Avoid/Chemical	None known

Incompatibility:

8. Exposure controls/personal protection

OSHA permissible exposure limit (PEL), American Conference of Governmental Industrial Hygienists (ACGIH) Threshold Limit Value (TLV), and any other exposure limit used or recommended by the chemical manufacturer, importer, or employer preparing the safety data sheet, where available:

Chemical Component	OSHA PEL	ACGIH TLV-TWA	AIHA Exposure limits
No data available			

This product can produce a nuisance dust which should be maintained below a time weighted average of 10 mg/m3.

Appropriate engineering controls

Ventilation Requirements: General.

Individual protection measures, such as personal protective equipment.:

Eye Protection: Wear safety glasses. Personal eye protection should conform to EN 166.

Skin Protection: Gloves are recommended due to possible irritation. Gloves should conform to EN 374.

Respiratory Protection: NIOSH approved dust mask.
Dust masks should conform to EN 149.

Other Protective Equipment: Not available

General Hygiene Conditions: Wash before eating, drinking, or using toilet facilities.

Change/Removal of Clothing: Uniforms, coveralls, or a lab coat should be worn.

9. Physical and chemical properties

Appearance (physical state): Powder.
Color: White
Odor: Starch
Odor threshold: Not available
pH: Not available
Melting Point/Freezing Point (°C): Not available
Initial Boiling Point and Boiling Range (°C): Not available
Flash Point (°C): Not applicable
Evaporation Rate: Not applicable
Flammability (solid, gas): No
Upper Flammable/Explosive Limit: Not applicable
Lower Flammable/Explosive Limit: Not applicable
Vapor Pressure: Not applicable
Vapor Density: Not applicable
Relative Density: Not available

Specific Gravity	No data available
Solubility(ies) in Water:	Soluble in water
Partition coefficient: n-octanol/water:	Not applicable
Auto-ignition Temperature (°C):	Not available
Decomposition Temperature:	Not determined.
Viscosity:	Not applicable
Volatiles	None
Volatile Organic Compounds	Not available

10. Stability and reactivity

Reactivity:	Not expected to be reactive
Chemical stability:	Material is stable under normal temperatures and pressures.
Possibility of hazardous reactions:	Hazardous polymerization will not occur.
Conditions to avoid (e.g., static discharge, shock, or vibration):	None known
Incompatible materials:	None known
Hazardous decomposition products:	This product does not undergo spontaneous decomposition. Typical combustion products are carbon monoxide, carbon dioxide, nitrogen and water.

11. Toxicological information

Symptoms related to the physical, chemical and toxicological characteristics:	No data available

Delayed and immediate effects and also chronic effects from short- and long-term exposure:

Acute (Short Term) Effects of Exposure

Effects of Acute Exposure	Not established.

Chronic (Long Term) Effects of Exposure

Effects of Chronic Exposure	This product is considered as being non-toxic. Use of good industrial hygiene practices is recommended.
Target Organs	None known.

Numerical measures of toxicity (such as acute toxicity estimates)

No data available

Has the chemical been classified as a Carcinogen by NTP, IARC or OSHA.

Chemical Name	OSHA Carcinogen	IARC Carcinogen	NTP Carcinogen
There is no evidence that this product poses a carcinogenic risk under normal conditions of handling and use.			

12. Ecological information

Ecotoxicity (aquatic and terrestrial, where available): Low, but has a BOD contribution.

Persistence and degradability: Readily biodegradable.

Bioaccumulative potential: Unknown.

Mobility in soil: Unknown.

Other adverse effects (such as hazardous to the ozone layer): Contributes to effluent BOD.

13. Disposal considerations

Waste Disposal Methods: Disposal should be in accordance with local, state or national legislation.

Empty Container Warnings: Not needed.

Waste Disposal Code(s): No data available

14. Transport information

DOT Classification Not regulated

UN number: No data available

UN proper shipping name: Not Applicable

Transport hazard class(es): Not Applicable

Packing group, if applicable: Not Applicable

Environmental hazards: Not available

Transport in bulk according to Annex II of MARPOL73/78 and the IBC Code: Not available

15. Regulatory information

TSCA Status: This product is manufactured in compliance with all provisions of the Toxic Substances Control Act, 15 U.S.C. 2601 et. seq.

SARA - Section 313 (Superfund Amendments and Reauthorization Act of 1986 - 40CFR 372)

CAS NUMBER CONCENTRATION (% by weight)

Contains no substances at or above the reporting threshold under Section 313.

CALIFORNIA PROPOSITION 65

WARNING: This product contains the following chemicals that are known to the State of California to cause cancer, birth defects or other reproductive harm.
Unless a concentration is specified in Section 2 of the MSDS, the below chemical/s are present in trace amounts.
Component CAS NUMBER
None reportable.

16. Other information, including date of preparation or last revision.

HMIS® Hazard Ratings

HMIS® ratings are based on a 0-4 rating scale, with 0 representing minimal hazards or risks, and 4 representing significant hazards or risks. Although HMIS® ratings are not required on SDSs by OSHA's 29 CFR 1910.1200, we choose to provide them as a service to our customers using HMIS®. These ratings are to be used only with a fully implemented HMIS® program. To deal adequately with the safe handling of this material, all the information contained in this SDS must be considered. NPCA recommends that employers must determine appropriate PPE for the actual conditions under which this product is used in their workplace. For information on PPE codes, consult the HMIS® Implementation Manual. When two ratings are provided for Health, the first represents the material 'as supplied', and the second represents the material 'in use'. * = chronic health hazard HMIS® is a registered trademark of the National Paint and Coatings Association (NPCA).

Health	**Flammability**	**Reactivity**

SDS DATE	17-May-2019
FOR INFORMATION CONTACT:	For product information, contact: Ingredion Incorporated Customer Service: 1-800-713-0208
CHANGES SINCE PREVIOUS ISSUE	Entire Material Safety Data Sheet.

The attached data has been compiled from sources which (b) (4) believe to be dependable and, to our knowledge and belief is accurate. However, (b) (4) cannot make any warranty or representation respecting the accuracy or completeness of the data. We assume no responsibility for any liability or damages relating thereto, or for advising you regarding the protection of your employees, customers, or others. You should make your own tests to determine the applicability of such information to, or the suitability of any products for your specific use. (b) (4) expressly disclaims all warranties, expressed or implied, including but not limited to, warranties of merchantability, accuracy, fitness for use or for a particular purpose, and noninfringement. The United Nations Convention on Contracts for the International Sale of Goods shall not apply to sales of products by (b) (4). The (b) (4) (b) (4).

ATTACHMENT 3

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

FAO/WHO Monograph on Sodium Octenyl Succinate

(b) (4)

STARCH SODIUM OCTENYL SUCCINATE

Explanation

This compound was previously evaluated for an ADI for man by the Joint FAO/WHO Expert Committee on Food Additives in 1969 (Annex I, Ref. 19). No toxicological monograph was prepared.

Introduction

Modification is carried out by treating a slurry of the starch with octenyl succinic anhydride. The finished product has a degree of substitution of 0.02.

BIOLOGICAL DATA

BIOCHEMICAL ASPECTS

In a caloric utilization study, groups each of 10 male albino rats, 20 to 22 days old, were fed either 2.74 g of a basal diet, or the basal diet supplemented with 1.5 or 3.0 g of cornstarch or 1.5 or 3.0 g of the starch sodium octenyl succinate (O.S.), or with 0.75, 1.5, 3.0 or 4.5 g of sucrose for a period of 4 weeks. No adverse effects were noted during the test period. The weight gains of the test group fed starch or substitutes were similar to the sucrose group. The caloric value of the substituted cornstarch (O.S.) was similar to cornstarch (Anon., 1960).

TOXICOLOGICAL STUDIES

Short-term studies

Rat

Groups each of 12 weanling albino rats (equally divided by sex) were maintained on diets containing 64% carbohydrate ingredients consisting of 29% cellulose and the remaining 35% consisting of cornstarch, or starch sodium octenyl succinate (O.S.). Rats fed the substituted starch showed a slightly slower growth rate than control rats fed cornstarch. The decreased growth rate was associated with decreased food consumption. Efficiency of food utilization was not affected by the test compound (Anon., 1950).

In another study, rats (Charles River) maintained on diets containing 6%, 12% or 30% of O.S. (plus cornstarch to 30% of the diet) or 30% cornstarch were bred twice. The F_{1b} generation was maintained on the same test diet as the parents and used for the study. One hundred weanling rats (equally divided by sex) were used for the 6% and 12% groups, and 120 weanling rats (equally divided by sex) were

used for the 30% O.S. group and 30% cornstarch group. Twenty animals from the 30% O.S. and control groups were killed at 30 days post-weaning, and the remainder of the animals killed 90 days post-weaning. Body weights and food intake were measured during the course of the study. Clinical chemistry (sodium, potassium, chloride, glucose, BUN, magnesium, alkaline phosphate, SGOT, SGPT, calcium, phosphates, total protein and albumin), haematology (RBC, WBC, haematocrit, haemoglobin, total protein and differential blood count) and urinalysis (pH, total

protein, glucose, ketone, occult blood, sodium, potassium, creatinine, calcium and magnesium) was carried out on select animals at the termination of the study. All animals that were killed at interval or at the termination of the study were subjected to complete necropsy. Relative and absolute weights of organs (kidneys, liver, spleen, brain, thymus, testes or uterus) were determined, and a complete histological evaluation was made of the principal organs and tissues. There was no significant effect on growth rate. Serum chemistry and haematology were within normal levels and showed no compound-related effects. Urine chemistry showed higher concentrations of urinary calcium and magnesium in the females but not in the males. Relative organ weight data showed a trend for increased liver and kidney weight with increased concentration of the substituted starch. There was an increased caecal weight after 30 days on the 30% O.S. starch in both sexes, but this was only observed in the females after 90 days on the test diet. The only significant histological finding was an incidence of kidney pathology, consisting of corticomedullary mineralization. The effect was more severe in the female than in the male, and occurred in animals fed either the modified or unmodified starch. The occurrence of corticomedullary mineralization was considered to result from a marginal deficiency of dietary magnesium when carbohydrate comprises a major proportion of the diet (Newberne & Buttolph, 1979).

Comments

The available data from short-term feeding studies in the rat, indicate that the only significant lesion observed was corticomedullary mineralization of the kidney. This contrasts with reports of calcification of the kidney in other studies with phosphate modified starches where the lesion was located in the pelvic region of the kidney. The effect was more severe in females than in the males, and occurred in animals fed either modified or unmodified starch. The occurrence of the lesion was associated with increased urinary excretion of magnesium, and the effect may be related to a marginal magnesium deficiency when carbohydrate comprises a major proportion of the diet.

EVALUATION

Estimate of acceptable daily intake for man

Not specified.*

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* The statement "ADI not specified" means that, on the basis of the available data (toxicological, biochemical, and other), the total daily intake of the substance, arising from its use or uses at the levels necessary to achieve the desired effect and from its acceptable background in food, does not, in the opinion of the Committee, represent a hazard to health. For this reason, and for the reasons stated in individual evaluations, the establishment of an acceptable daily intake (ADI) in mg/kg bw is not deemed necessary.

REFERENCES

Anon. (1950) Toxicological studies of certain starch products. Unpublished report of Food Research Laboratories, Inc. (Report No. 58380-1). Submitted to the World Health Organization by the National Starch and Chemical Corporation, Bridgewater, New Jersey, USA

Anon. (1960) Caloric evaluation of RX12XI and cornstarch. Unpublished report of Food Research Laboratories, Inc. (Report

No. 80878b-e). Submitted to the World Health Organization by the National Starch and Chemical Corporation, Bridgewater, New Jersey, USA

Newberne, P. M. & Buttolph, M. L. (1979) 90-day *in utero* feeding study on rats. Unpublished report prepared for National Starch and Chemical Corporation. Submitted to the World Health Organization by the National Starch and Chemical Corporation, Bridgewater, New Jersey, USA

See Also:
Toxicological Abbreviations

ATTACHMENT 4

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

(b) (4) Antifoam Letter

(b) (4)

ISO 9001
Certified Worldwide

April 14, 2021

(b) (4)

SUBJECT: FDA 21 CFR COMPLIANCE – KFO™ 402

To whom it may concern,

This product complies with the United State Food and Drug Administration's Code of Federal Regulations Title 21-Part 173.340, Secondary Direct Food Additives Permitted in Food for Human Consumption when used as a defoaming agent and its ingredients are listed under §173.340(a)(2).

The composition of (b) (4) Foam Control's product **KFO™ 402** is described as **Polyoxythylene-polyoxypropylene block copolymer.**

We hope this information is useful to you. If you should have any further questions, please feel free to contact us.

Sincerely,

(b) (4)

Operation Manager

(b) (4)

ATTACHMENT 5

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

(Revised) Certificates of Analysis for ASCUSDY20 Specification Testing

(b) (4)

(b) (4)

Product Certificate of Analysis

Product Name	*Clostridium beijerinckii* ASCUSDY20 Spray Dried Powder
Batch Number	18-0202-001-P73
Date of Manufacture	07Nov2018
Expiration Date	07Nov2019
Retest Date	N/A
Storage Conditions	2 - 10 °C

Clostridium beijerinckii ASCUSDY20 Spray Dried Powder

Analytical Property	Specification	Result
Viable cells count	(b) (4)	
Coliform		
E. coli		
Salmonella		
Listeria		
Botulinum toxins		

Clostridium beijerinckii ASCUSDY20 Concentrate

Analytical Property	Specification	Result
Spore Count *	(b) (4)	

*Testing done at end of fermentation process of cell concentrate lot 1801.2002.

Approval (Name, Title, Signature, and Date)

This batch was manufactured and tested according to the product registration and regulatory agency requirements.

DocuSigned by:
Kelly Mercier
7BD513E026E94C0...

4/23/2021

Kelly Mercier
Quality Manager

(b) (4)

(b) (4)

Product Certificate of Analysis

Product Name	*Clostridium beijerinckii* ASCUSDY20 Spray Dried Powder
Batch Number	18-0202-001-P79
Date of Manufacture	17Dec2018
Expiration Date	17Dec2019
Retest Date	N/A
Storage Conditions	2 - 10 °C

Clostridium beijerinckii ASCUSDY20 Spray Dried Powder

Analytical Property	Specification	Result
Viable cells count	(b) (4)	
Coliform		
E. coli		
Salmonella		
Listeria		
Botulinum toxins		

Clostridium beijerinckii ASCUSDY20 Concentrate

Analytical Property	Specification	Result
Spore Count *	(b) (4)	

*Testing done at end of fermentation process of cell concentrate lot 1801.2003.

Approval (Name, Title, Signature, and Date)

This batch was manufactured and tested according to the product registration and regulatory agency requirements.

DocuSigned by:
Kelly Mercier
7BD513E026E94C0...

4/23/2021

Kelly Mercier
Quality Manager

(b) (4)

(b) (4)

Product Certificate of Analysis

Product Name	*Clostridium beijerinckii* ASCUSDY20 Spray Dried Powder
Batch Number	18-0202-041-P22
Date of Manufacture	27Nov2018
Expiration Date	27Nov2019
Retest Date	N/A
Storage Conditions	2 - 10 °C

Clostridium beijerinckii ASCUSDY20 Spray Dried Powder

Analytical Property	Specification	Result
Viable cells count	(b) (4)	
Coliform		
E. coli		
Salmonella		
Listeria		

Clostridium beijerinckii ASCUSDY20 Concentrate

Analytical Property	Specification	Result
Spore Count *	(b) (4)	
Botulinum toxins *	(b) (4)	

*Testing done at end of fermentation process of cell concentrate lot AS111218F4.

Approval (Name, Title, Signature, and Date)

This batch was manufactured and tested according to the product registration and regulatory agency requirements.

DocuSigned by:
Kelly Mercier
7BD513E026E94C0...

4/23/2021

Kelly Mercier
Quality Manager

ATTACHMENT 6

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

Heavy Metals Testing for Recent Commercial Batches

(b) (4)

Consolidated COA

ANALYZED BY:

(b) (4)

MANUFACTURER:

(b) (4)

(b) (4)

SAMPLE INFORMATION

Sample No.: 1065122
Product Name: Dairy-20 Spray Dried Powder
Batch #: FOEM12520201029002

Date Received: 12/01/2020
Date Reported: 12/07/2020

TEST SUMMARY

Microbiological Screen: Tested
Overall: In Progress

Heavy Metals - Food: Tested

MICROBIOLOGICAL SCREEN

12/07/2020

Analyte	Findings	Units	Method
Coliforms	<10	cfu/g	AOAC 2018.13
E. coli	<10	cfu/g	AOAC 2018.13
Listeria	Negative	/25g	AOAC 2013.10
Salmonella	Negative	/25g	AOAC 2013.01

HEAVY METALS - FOOD

12/07/2020

Method: ICP-MS

Analyte	LOD / LOQ (ppm)	ppm
Arsenic	0.004/0.004	0.270
Cadmium	0.0008/0.0008	0.016
Mercury	0.001/0.001	None detected
Lead	0.001/0.001	0.020

(-) = Not Tested, **ND** = None Detected, **<LOQ** = Below Limit of Quantitation, **LOD** = Limit of Detection

All LQC samples were performed and met the prescribed acceptance criteria in 16 CCR section 5730, pursuant to 16 CCR section 5726(e)(13)

(b) (4)

Reported by

(b) (4)

Lab Co Director

December 07, 2020

(b) (4)

(b) (4)

Consolidated COA

ANALYZED BY:

(b) (4)

MANUFACTURER:

(b) (4)

(b) (4)

SAMPLE INFORMATION

Sample No.: 1065121
Product Name: Dairy-20 Spray Dried Powder
Batch #: FOEM12520201029003

Date Received: 12/01/2020
Date Reported: 12/07/2020

TEST SUMMARY

Microbiological Screen: Tested
Overall: In Progress
Heavy Metals - Food: Tested

MICROBIOLOGICAL SCREEN

12/07/2020

Analyte	Findings	Units	Method
Coliforms	<10	cfu/g	AOAC 2018.13
E. coli	<10	cfu/g	AOAC 2018.13
Listeria	Negative	/25g	AOAC 2013.10
Salmonella	Negative	/25g	AOAC 2013.01

HEAVY METALS - FOOD

12/07/2020

Method: ICP-MS

Analyte	LOD / LOQ (ppm)	ppm
Arsenic	0.004/0.004	0.359
Cadmium	0.0008/0.0008	0.023
Mercury	0.001/0.001	None detected
Lead	0.001/0.001	0.030

(-) = Not Tested, **ND** = None Detected, **<LOQ** = Below Limit of Quantitation, **LOD** = Limit of Detection

All LQC samples were performed and met the prescribed acceptance criteria in 16 CCR section 5730, pursuant to 16 CCR section 5726(e)(13)

(b) (4)

Scan to verify

Reported by

(b) (4)

Lab Co Director

December 07, 2020

(b) (4)

(b) (4)

Certificate of Analysis

October 01, 2020

(b) (4)

Order No. 516018
Sample No. 1058901

SAMPLE INFORMATION

Description Dairy-20 Spray Dried Powder
Lot Number 5T-05
Received September 29, 2020

ANALYTICAL RESULTS

Analysis Heavy Metals - Food
Method ICP-MS
Analysis Date September 29, 2020 to October 01, 2020

Analyte	LOD / LOQ (ppm)	Findings (ppm)	Method
Arsenic	0.004/0.004	0.22	ICP-MS
Cadmium	0.0008/0.0008	0.006	ICP-MS
Mercury	0.001/0.001	None detected	ICP-MS
Lead	0.001/0.001	0.018	ICP-MS

Reported by

(b) (4)

Lab Co Director

October 01, 2020

(b) (4)

ATTACHMENT 7

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

Cell Culture and Spray Dried Powder Master Production Record

Dairy-20 Cell Culture and Spray Dried Product
Master Production Record
Version 4

1 Fermentation

(b) (4)

Table 1. Primary Seed Basal Media, material quantity per 1L of media

Ingredient	Qty per 1L
Procelys Springer 0251/0-MG-L Yeast Extract	(b) (4)
Monopotassium Phosphate	
Dipotassium Phosphate	
Acetic Acid Glacial	
Ammonia solution	
Dairy-20 TM Mix (See **Error! Reference source not found.**)	
L-Cysteine Hydrochloride	

Table 2. Dairy-20 TM Mix, material quantity per 1L of TM Mix

Ingredient	Qty per 1L
Magnesium Sulfate Heptahydrate	(b) (4)
Manganese Sulfate Monohydrate	
Sodium Chloride	
Iron Sulfate Heptahydrate	

(b) (4)

Table 3. Dairy-20 Vitamin Mix, per 1L of Vitamin Mix

Ingredient	Qty per 1L
Thiamine	(b) (4)

Biotin	(b) (4)

(b) (4)

Table 4. Dairy-20 Primary Seed Media Post-Sterilization Additions

Post-Sterilization Addition	Quantity per L of Primary Seed Complete Media
60% Dextrose Monohydrate	(b) (4)
Dairy-20 Vitamin Mix	(b) (4)

(b) (4)

1.2 Secondary Seed

(b) (4)

Table 5. Dairy-20 Basal Fermentation Media, per L of media

Ingredient	Qty per 1L
Dipotassium Phosphate	(b) (4)
Magnesium Sulfate Heptahydrate	
Solulys 095K Corn Steep Powder	
Amberex 1003 AG Yeast Extract	

	(b) (4)	
L-Cysteine Hydrochloride		
Manganese Sulfate Monohydrate		
Sodium Chloride		
Iron Sulfate Heptahydrate		
Ammonium Chloride		
Folic Acid		
Dystar KFO-402 Antifoam		

(b) (4)

(b) (4)

(b) (4)

(b) (4)

1.3 Main Fermentor

(b) (4)

(b) (4)

2 Harvest

2.1 Centrifugation

(b) (4)

(b) (4)

3 Spray Dried Product

(b) (4)

Table 6. Intended ingredient concentration of Dairy-20 SDP

Component	%w/w Dried Solids
Capsul 06670103 Modified Corn Starch	(b) (4)
Cell Concentrate, dry solids	
Total	

(b) (4)

[redacted]

Master Production Record Approval

Name & Title	Signature & Date
Martin Mayhew VP – Process Development & Manufacturing	DocuSigned by: Martin Mayhew D1605E1B4C3E49A... 8/14/2020
Patricia A. Williams Quality	DocuSigned by: Patricia A Williams 5B301285A10643D... 8/14/2020

ATTACHMENT 8

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

Spore Counting SOP

[redacted] (b) (4)

[redacted] (b) (4)

METHOD

Title	Spore Counting
Version	4
Effective Date	16Apr2021
Author	Kelly Mercier
Approver (Signature & Date)	DocuSigned by: Martin Mayhew ACBDDAD433BF49C... 4/16/2021 Martin Mayhew – VP Process Development & Manufacturing

Scope
The purpose of this method is to determine the number of spores in a sample by counting them in a Petroff-Hausser Haemocytometer.

Safety
Consult the Safety Data Sheet for all reagents prior to handling. Wear appropriate personal protective equipment (lab coat, safety glasses, and gloves) at all times.

Materials
N/A

Equipment
Petroff-Hausser Haemocytometer (Hausser Scientific Cat #3900) with supplied coverslip
Phase Contrast Microscope

Media & Reagents
95% Ethanol
Phosphate-Buffered Saline + 0.05% Tween-20 (PBST)

Component	Amount per 1.0L
10X PBS (Growcells #MRGF-6235)	[redacted] (b) (4)
Tween-20 (Sigma #P1379)	[redacted] (b) (4)
Q.S. to 1.0L with diH2O and sterile filter through 0.22µm filter	

Method
[redacted] (b) (4)

[redacted]

[redacted]

(b) (4)

(b) (4)

(b) (4)

(b) (4)

Reason(s) for Revision

- (b) (4)

ATTACHMENT 9

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

Microbe Enumeration Method Addendum (correcting Table 3 / Figure 4)

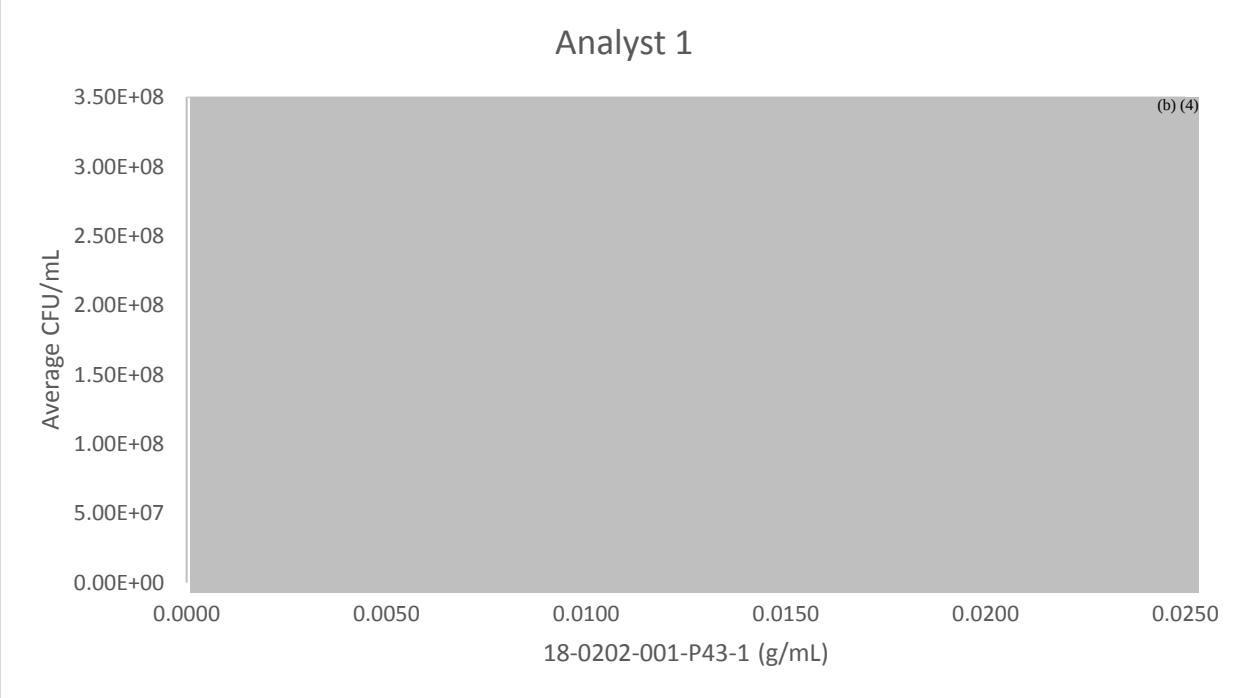
Addendum to DY20-SDP Microbe Enumeration, V1 Method Validation Report

In the original method validation report, some values were incorrectly reported or plotted in Table 3 and Figure 3. Furthermore, the incorrect values of Table 3 conflicted with results displayed in Figure 4. The correct version of Figure 3 and Table 3 are presented below. The corrected results do not change the conclusion that the method is repeatable, robust, and linear and therefore a valid method for enumeration of *Clostridium beijerinckii* ASCUSDY20.

Corrected Table 3

	18-0202-001-P40-3				18-0202-001-P43-1			
Analyst	Average (g/mL)	Average (CFU/mL)	STD Dev.	CV	Average (g/mL)	Average (CFU/mL)	STD Dev.	CV
1	(b) (4)							
2								

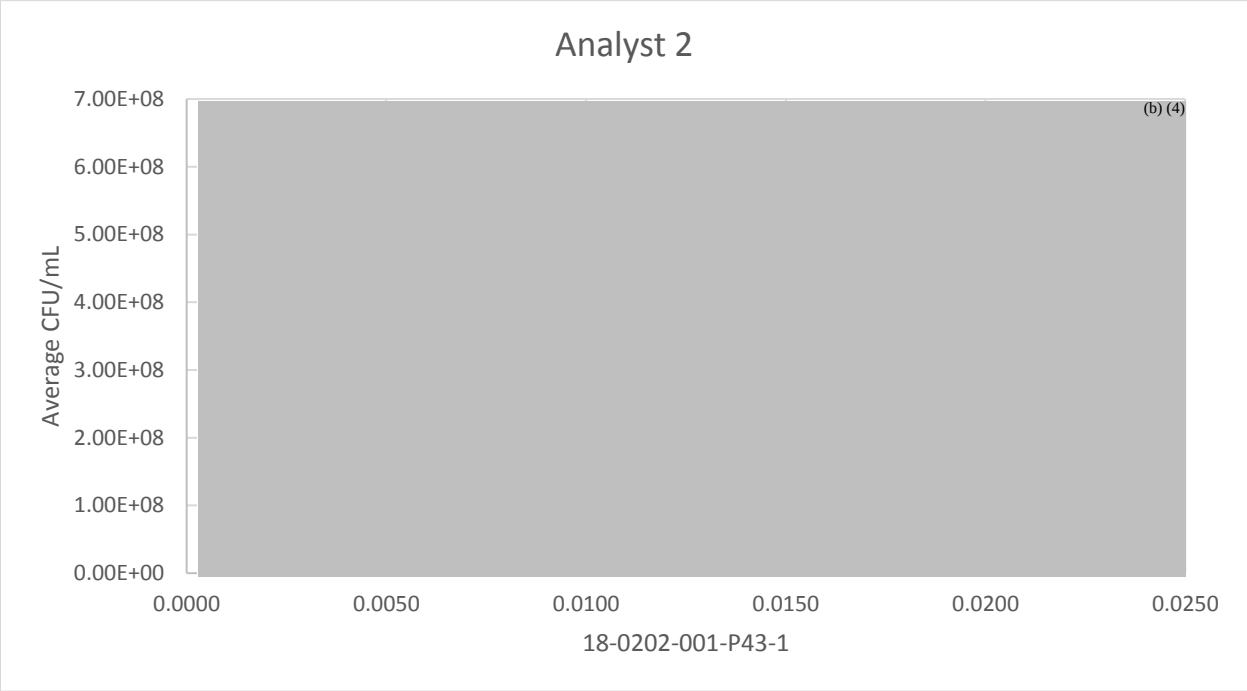
Corrected Figure 3



(b) (4)

(b) (4)

Unchanged Figure 4, which previously conflicted with Table 3



Name & Title	Signature & Date
Martin Mayhew VP – Process Development & Manufacturing	DocuSigned by: Martin Mayhew ACBDDAD433BF491... 4/22/2021
Howard Green Regulatory	DocuSigned by: Howard B Green 432FC873A25645F... 4/22/2021
Kelly Mercier Quality	DocuSigned by: Kelly Mercier 7BD513E026E94C0... 4/22/2021

ATTACHMENT 10

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

[redacted] Letter: Botulinum Testing Method

[redacted]

(b) (4)

April 14, 2021

(b) (4)

To Whom It May Concern:

(b) (4) is a Tier 1 Select Agent facility regulated by the Centers for Disease Control and Prevention (CDC) and is approved to work with botulinal toxins and neurotoxin-producing strains of *Clostridium botulinum*. The lab is audited by the CDC routinely to ensure compliance to internal procedures and federal regulations.

Sample analysis follows procedures in the Food and Drug Administration (FDA) Bacteriological Analytical Manual https://www.fda.gov/food/laboratory-methods-food/bam-chapter-17-clostridium-botulinum. The lab performs routine botulinal toxin screens on uninoculated client samples via the mouse bioassay. This assays for total biologically active botulinal toxin and does not differentiate by toxin type. Trypsin is added to a portion of the supernatant to activate toxin from nonproteolytic strains, if present. If the assay is negative, the result is reported to the client and no further testing is performed. If the assay is presumptive, additional testing can be performed to confirm the presence of botulinal toxin and the toxin type(s).

Regards,

(b) (4)
Director of Operations
Corporate

(b) (4)

(b) (4)

ATTACHMENT 11

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

Results of Metabolic Reconstruction

ASCUSDY20 PATRIC Specialty Gene

Evidence	Property	Source	Genome Name	PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	Source ID	Source Organism	Gene	Product	Function	Classification	PubMed	Subject Coverage	Query Coverage	Identity	E-value
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4986					eidB	16S rRNA (euanine(527)-N(7))-methvltransferase (EC 2.1.1.170)	16S rRNA (euaninel527)-N(7)l-methvltransferase (EC 2.1.1.170)	aene conferrine resistance via absence	17238915				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.1547					CatA1S/A16 familv	Chloramphenicol O-acetvltransferase (EC 2.3.1.28) => CatA1S/A16 familv	Chloramohenicol O-acetvltransferase (EC 2.3.1.28) => CatA1S/A16 familv	antibiotic inactivation enzvme	1489203:2039197				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.5242						weak similarity to aminoglycoside N(3)-acetyltransferase	weak similarity to aminoglycoside N(3)-acetyltransferase	antibiotic inactivation enzvme					
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4973					gyrB	DNA gyrase subunit B (EC 5.99.1.3)	DNA gyrase subunit B (EC 5.99.1.3)	antibiotic target in susceptible species	21693461;22279180;9293187				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.1078					folA, Dfr	Dihydrofolate reductase (EC 1.5.1.3)	Dihydrofolate reductase (EC 1.5.1.3)	antibiotic target in susceptible species	20169085;25288078				
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.4259			Q2QKM3	Lactobacillus casei		PTS system, mannose-specific IIC component	the pts mannose-fructose-sorbose (man) family.	4.A.6.1.6	16385119	91	92	80	1.00E-112
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.2449			A6LW11	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052)		D-xylose ABC transporter, ATP-binding protein XylG	the atp-binding cassette (abc) superfamily.	3.A.1.2.26		100	100	100	1.00E-297
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.626					kasA	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	antibiotic target in susceptible species	10428945				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4819					EF-G	Translation elongation factor G	Translation elongation factor G	antibiotic target in susceptible species	17980694				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.5378					GdpD	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	protein altering cell wall charge conferring antibiotic resistance	21899450				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.3875					FabK	Enoyl-[acyl-carrier-protein] reductase [FMN, NADH] (EC 1.3.1.9), FabK => refractory to triclosan	Enoyl-[acyl-carrier-protein] reductase [FMN, NADH] (EC 1.3.1.9), FabK => refractory to triclosan	antibiotic target replacement protein	10910344				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.1156						Streptogramin O-acetyltransferase, putative	Streptogramin O-acetyltransferase, putative	antibiotic inactivation enzvme					
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.4622			O32332	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052)		PTS system, glucitol/sorbitol-specific IIC component	the pts glucitol (gut) family.	4.A.4.1.2	9572925	100	100	100	1.00E-101
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.1010					TetB(P)	Tetracvcline resistance. ribosomal protection tvoe => TetB(P)	Tetracvcline resistance. ribosomal protection tvoe => TetB(P)	antibiotic taraet protection protein	8170402:11717269				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.3721					PgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	protein altering cell wall charge conferring antibiotic resistance	22238576				
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.2616						PTS system, gluconate-specific IID component	the pts mannose-fructose-sorbose (man) family.	4.A.6.1.8	12663927				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4530			Q82ZC6	Enterococcus faecalis	MurA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	antibiotic target in susceptible species	8994972	94	96	83	1.00E-130
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.2450			A6LW10	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052)		D-xylose ABC transporter, substrate-binding protein XylF	the atp-binding cassette (abc) superfamily.	3.A.1.2.26		100	100	100	1.00E-204
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.2066					Alr	Alanine racemase (EC 5.1.1.1)	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species	19748470;24303782				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.3741					dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	antibiotic target in susceptible species	16321944				
BLAT	Drug Target	DrugBank	Bacteria DY20 comolete	fig|2.9855.pee.2419			P00322	Clostridium beijerinckii		Flavodoxin	Riboflavin Monophosphate	Drug target		100	100	98	3.00E-75
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.4621			O32333	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052)		PTS system, glucitol/sorbitol-specific IIB component (EC 2.7.1.198) / PTS system, glucitol/sorbitol-specific IIC component 2	the pts glucitol (gut) family.	4.A.4.1.2	9572925	100	100	100	1.00E-190
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4930					Iso-tRNA	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	antibiotic target in susceptible species	7929087				
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.2448			A6LW12	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052)		D-xylose ABC transporter, permease protein XylH	the atp-binding cassette (abc) superfamily.	3.A.1.2.26		100	100	100	1.00E-215
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4972					gyrA	DNA gyrase subunit A (EC 5.99.1.3)	DNA gyrase subunit A (EC 5.99.1.3)	antibiotic target in susceptible species	9293187				
BLAT	Antibiotic Resistance	CARD	Bacteria DY20 comolete	fig|2.9855.pee.1547			AAA73865.1	Clostridium butvricum	catB	Chloramphenicol O-acetvltransferase (EC 2.3.1.28) => CatA1S/A16 familv		antibiotic inactivation enzvme.chloramohenicol resistance aene		100	100	97	1.00E-128
BLAT	Antibiotic Resistance	CARD	Bacteria DY20 comolete	fig|2.9855.pee.1010			AAA20117.1	Clostridium perfrineens	tetB(P)	Tetracvcline resistance. ribosomal protection tvoe => TetB(P)	Tetracvcline resistance. ribosomal protection tvoe => TetB(P)	antibiotic taraet protection protein.tetracvcline resistance aene		100	100	85	0
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.2617			Q82ZC5	Enterococcus faecalis		PTS system, gluconate-specific IIC component	the pts mannose-fructose-sorbose (man) family.	4.A.6.1.8	12663927	91	92	81	1.00E-114
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.3872					kasA	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	antibiotic target in susceptible species	10428945				
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.1009			Q46305	Clostridium perfringens		Tetracvcline resistance, MFS efflux pump => TetA(P)	the major facilitator superfamily (mfs).	2.A.1.21.6	16788202;8170402	100	100	84	1.00E-201
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.219			A6M1J4	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052)		hypothetical protein	the duf4190 (duf4190) family.	9.B.117.1.3		100	100	95	9.00E-46
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4553					rho	Transcription termination factor Rho	Transcription termination factor Rho	antibiotic target in susceptible species	8466900				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4818					EF-Tu	Translation elongation factor Tu	Translation elongation factor Tu	antibiotic target in susceptible species					
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.2582					BcrC	Undecaprenyl-diphosphatase BcrC (EC 3.6.1.27), conveys bacitracin resistance	Undecaprenyl-diphosphatase BcrC (EC 3.6.1.27), conveys bacitracin resistance	antibiotic target protection protein	12486040;15778224;15946938				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4823					rpoB	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	antibiotic target in susceptible species	3050121;15047531;16723576				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4822					rpoC	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	antibiotic target in susceptible species	16723576				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.2731					fabV	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9), FabV => refractory to triclosan	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9), FabV => refractory to triclosan	antibiotic target replacement protein	19933806;18032386				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.2510					Alr	Alanine racemase (EC 5.1.1.1)	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species	19748470;24303782				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.496					Alr	Alanine racemase (EC 5.1.1.1)	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species	19748470;24303782				
BLAT	Antibiotic Resistance	CARD	Bacteria DY20 comolete	fig|2.9855.pee.1009			AAA20116.1	Clostridium perfrineens	tetA(P)	Tetracvcline resistance. MFS efflux oumo => TetA(P)		efflux oumo conferrine antibiotic resistance		100	100	84	1.00E-201
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.2001					EF-G	Translation elongation factor G	Translation elongation factor G	antibiotic target in susceptible species	17980694				
BLAT	Antibiotic Resistance	NDARO	Bacteria DY20 comolete	fig|2.9855.pee.1010			WP_012478245.1	Clostridium perfringens		Tetracvcline resistance, ribosomal protection tvpe => TetB(P)	tetracvcline resistance ribosomal protection protein TetB(P)			100	100	85	0
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4478					FabK-like	Putative FabK-like enoyl-[acyl-carrier-protein] reductase	Putative FabK-like enoyl-[acyl-carrier-protein] reductase	protein involved in antibiotic sequestration	27577999				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.5120					folA, Dfr	Dihydrofolate reductase (EC 1.5.1.3)	Dihydrofolate reductase (EC 1.5.1.3)	antibiotic target in susceptible species	20169085;25288078				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.5024					MurA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	antibiotic target in susceptible species	8994972				
BLAT	Antibiotic Resistance	NDARO	Bacteria DY20 comolete	fig|2.9855.pee.1547			WP_063843219.1	Clostridium butyricum		Chloramphenicol O-acetvltransferase (EC 2.3.1.28) => CatA1S/A16 familv	MULTISPECIES: class A beta-lactamase TEM-156			100	100	97	1.00E-128
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4375					Ddl	D-alanine--D-alanine ligase (EC 6.3.2.4)	D-alanine--D-alanine ligase (EC 6.3.2.4)	antibiotic target in susceptible species	24303782;24033232				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4817					S10p	SSU ribosomal protein S10p (S20e)	SSU ribosomal protein S10p (S20e)	antibiotic target in susceptible species	26124155				
BLAT	Transporter	TCDB	Bacteria DY20 comolete	fig|2.9855.pee.4619			O32334	Clostridium beijerinckii		PTS system, glucitol/sorbitol-specific IIA component (EC 2.7.1.198)	the pts glucitol (gut) family.	4.A.4.1.2	9572925	100	100	100	4.00E-63
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4821					S12p	SSU ribosomal protein S12p (S23e)	SSU ribosomal protein S12p (S23e)	antibiotic target in susceptible species	7934937				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4760					folP	Dihydropteroate synthase (EC 2.5.1.15)	Dihydropteroate synthase (EC 2.5.1.15)	antibiotic target in susceptible species	15673783				
BLAT	Antibiotic Resistance	NDARO	Bacteria DY20 comolete	fig|2.9855.pee.1009			WP_006440994.1	Firmicutes		Tetracvcline resistance. MFS efflux oumo => TetA(P)	MULTISPECIES: tetracvcline efflux MFS transporter TetA(P)			100	100	86	1.00E-208
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.1009					TetA(P)	Tetracvcline resistance. MFS efflux oumo => TetA(P)	Tetracvcline resistance. MFS efflux oumo => TetA(P)	efflux oumo conferrine antibiotic resistance	8170402:11717269				
K-mer Search	Antibiotic Resistance	PATRIC	Bacteria DY20 comolete	fig|2.9855.pee.4831					EF-Tu	Translation elongation factor Tu	Translation elongation factor Tu	antibiotic target in susceptible species	364475;9678602				

PATRIC Genes with Functional Assignments

Genome	Genome ID	Accession	PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	Feature ID	Annotation	Feature Type	Start	End	Length	Strand	FIGfam ID	PATRIC genus-specific families (PLfams)	PATRIC cross-genus families (PGfams)	Protein ID	AA Length	Gene Symbol	Product	GO
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.913			PATRIC.2.9855.2.9855.con.0001.CDS.1000143.1000964.fwd	PATRIC	CDS	1000143	1000964	822	+			PGF_04438420		273		Cobalt ECF transporter, ATPase component of energizing module CbiO	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.914			PATRIC.2.9855.2.9855.con.0001.CDS.1001145.1001897.fwd	PATRIC	CDS	1001145	1001897	753	+			PGF_00054359		250		Cobalt ECF transporter, substrate-binding protein CbiM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.915			PATRIC.2.9855.2.9855.con.0001.CDS.1001897.1002214.fwd	PATRIC	CDS	1001897	1002214	318	+			PGF_00034775		105		Cobalt ECF transporter, additional substrate-binding protein CbiN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.916			PATRIC.2.9855.2.9855.con.0001.CDS.1002694.1003809.fwd	PATRIC	CDS	1002694	1003809	1116	+			PGF_08036141		371		Inner membrane protein YbiR, putative anion permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.917			PATRIC.2.9855.2.9855.con.0001.CDS.1004735.1005832.fwd	PATRIC	CDS	1004735	1005832	1098	+			PGF_00006821		365		GGDEF domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.918			PATRIC.2.9855.2.9855.con.0001.CDS.1006201.1007169.fwd	PATRIC	CDS	1006201	1007169	969	+			PGF_10365903		322		Transcriptional regulator, LuxR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.919			PATRIC.2.9855.2.9855.con.0001.CDS.1007592.1008062.fwd	PATRIC	CDS	1007592	1008062	471	+			PGF_01282248		156		Histone acetyltransferase HPA2 and related acetyltransferases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.920			PATRIC.2.9855.2.9855.con.0001.CDS.1008438.1009193.rev	PATRIC	CDS	1008438	1009193	756	-			PGF_00004438		251		Vitamin B12 ABC transporter, ATP-binding protein BtuD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.93			PATRIC.2.9855.2.9855.con.0001.CDS.100849.102072.fwd	PATRIC	CDS	100849	102072	1224	+			PGF_00005919		407		Probable flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.921			PATRIC.2.9855.2.9855.con.0001.CDS.1009216.1010238.rev	PATRIC	CDS	1009216	1010238	1023	-			PGF_00066706		340		Vitamin B12 ABC transporter, permease protein BtuC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.922			PATRIC.2.9855.2.9855.con.0001.CDS.1010231.1011145.rev	PATRIC	CDS	1010231	1011145	915	-			PGF_03799122		304		Vitamin B12 ABC transporter, substrate-binding protein BtuF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.923			PATRIC.2.9855.2.9855.con.0001.CDS.1012966.1014012.fwd	PATRIC	CDS	1012966	1014012	1047	+			PGF_06690407		348		FAD:protein FMN transferase (EC 2.7.1.180)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.924			PATRIC.2.9855.2.9855.con.0001.CDS.1014086.1015327.fwd	PATRIC	CDS	1014086	1015327	1242	+			PGF_03817355		413		putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.925			PATRIC.2.9855.2.9855.con.0001.CDS.1015615.1017060.rev	PATRIC	CDS	1015615	1017060	1446	-			PGF_01785064		481		Beta-lactamase class C-like and penicillin binding proteins (PBPs) superfamily / DUF3471 domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.926			PATRIC.2.9855.2.9855.con.0001.CDS.1017087.1017635.rev	PATRIC	CDS	1017087	1017635	549	-			PGF_10423881		182		Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.929			PATRIC.2.9855.2.9855.con.0001.CDS.1018862.1019521.fwd	PATRIC	CDS	1018862	1019521	660	+			PGF_00067788		219		[NiFe] hydrogenase nickel incorporation-associated protein HypB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.930			PATRIC.2.9855.2.9855.con.0001.CDS.1019845.1020834.fwd	PATRIC	CDS	1019845	1020834	990	+			PGF_00645051		329		Substrate-specific component NikM of nickel ECF transporter / Additional substrate-specific component NikN of nickel ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.931			PATRIC.2.9855.2.9855.con.0001.CDS.1021002.1021796.fwd	PATRIC	CDS	1021002	1021796	795	+			PGF_00060519		264		Transmembrane component NikQ of energizing module of nickel ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.932			PATRIC.2.9855.2.9855.con.0001.CDS.1021801.1022529.fwd	PATRIC	CDS	1021801	1022529	729	+			PGF_01013659		242		ATPase component NikO of energizing module of nickel ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.933			PATRIC.2.9855.2.9855.con.0001.CDS.1023229.1024329.fwd	PATRIC	CDS	1023229	1024329	1101	+			PGF_01284136		366		ABC transporter, permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.94			PATRIC.2.9855.2.9855.con.0001.CDS.102371.103624.fwd	PATRIC	CDS	102371	103624	1254	+			PGF_00064398		417		Similar to DNA photolyase, but of unknown function	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.934			PATRIC.2.9855.2.9855.con.0001.CDS.1024335.1025558.fwd	PATRIC	CDS	1024335	1025558	1224	+			PGF_01285253		407		ABC transporter, permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.935			PATRIC.2.9855.2.9855.con.0001.CDS.1025555.1026232.fwd	PATRIC	CDS	1025555	1026232	678	+			PGF_10347576		225		ABC-type antimicrobial peptide transport system, ATPase component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.941			PATRIC.2.9855.2.9855.con.0001.CDS.1028898.1029443.fwd	PATRIC	CDS	1028898	1029443	546	+			PGF_01653535		181		RNA polymerase sigma factor SigZ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.943			PATRIC.2.9855.2.9855.con.0001.CDS.1030781.1031773.rev	PATRIC	CDS	1030781	1031773	993	-			PGF_00931013		330		Choloylglycine hydrolase (EC 3.5.1.24)	GO:0045302|choloylglycine hydrolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.944			PATRIC.2.9855.2.9855.con.0001.CDS.1032298.1034763.fwd	PATRIC	CDS	1032298	1034763	2466	+			PGF_00038696		821		Protein tyrosine phosphatase II superfamily protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.17			PATRIC.2.9855.2.9855.con.0001.CDS.10323.11459.rev	PATRIC	CDS	10323	11459	1137	-			PGF_04282519		378		N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	GO:0008448|N-acetylglucosamine-6-phosphate deacetylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.946			PATRIC.2.9855.2.9855.con.0001.CDS.1036236.1036667.fwd	PATRIC	CDS	1036236	1036667	432	+			PGF_06718396		143		L-fucose mutarotase (EC 5.1.3.29)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.947			PATRIC.2.9855.2.9855.con.0001.CDS.1036711.1038225.fwd	PATRIC	CDS	1036711	1038225	1515	+			PGF_07639199		504		Xylulose kinase (EC 2.7.1.17)	GO:0004856|xylulokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.95			PATRIC.2.9855.2.9855.con.0001.CDS.103737.106271.fwd	PATRIC	CDS	103737	106271	2535	+			PGF_00005919		844		Probable flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.948			PATRIC.2.9855.2.9855.con.0001.CDS.1038228.1039259.fwd	PATRIC	CDS	1038228	1039259	1032	+			PGF_00007078		343		Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)	GO:0008868|galactitol-1-phosphate 5-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.949			PATRIC.2.9855.2.9855.con.0001.CDS.1039386.1040396.fwd	PATRIC	CDS	1039386	1040396	1011	+			PGF_00038615		336		Aldehyde reductase(EC:1.1.1.21)	GO:0004032|alditol:NADP+ 1-oxidoreductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.952			PATRIC.2.9855.2.9855.con.0001.CDS.1043157.1044137.fwd	PATRIC	CDS	1043157	1044137	981	+			PGF_10234027		326		ABC transporter, permease protein (cluster 2, ribose/xylose/arabinose/galactose)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.955			PATRIC.2.9855.2.9855.con.0001.CDS.1047639.1048493.fwd	PATRIC	CDS	1047639	1048493	855	+			PGF_00055986		284		Tagatose 1,6-bisphosphate aldolase (EC 4.1.2.40)	GO:0009025|tagatose-bisphosphate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.956			PATRIC.2.9855.2.9855.con.0001.CDS.1048545.1049471.fwd	PATRIC	CDS	1048545	1049471	927	+			PGF_10567595		308		Tagatose-6-phosphate kinase (EC 2.7.1.144)	GO:0009024|tagatose-6-phosphate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.957			PATRIC.2.9855.2.9855.con.0001.CDS.1049707.1050585.fwd	PATRIC	CDS	1049707	1050585	879	+			PGF_00016470		292		LacX protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.963			PATRIC.2.9855.2.9855.con.0001.CDS.1056547.1058988.fwd	PATRIC	CDS	1056547	1058988	2442	+			PGF_00068225		813		alpha-xylosidase (EC 3.2.1.177)	GO:0061634|alpha-D-xyloside xylohydrolase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.964			PATRIC.2.9855.2.9855.con.0001.CDS.1059327.1061324.fwd	PATRIC	CDS	1059327	1061324	1998	+			PGF_02910829		665		Membrane assosiated methyl-accepting chemotaxis protein with HAMP domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.969			PATRIC.2.9855.2.9855.con.0001.CDS.1064082.1065065.fwd	PATRIC	CDS	1064082	1065065	984	+			PGF_09188652		327		Molybdopterin molybdenumtransferase (EC 2.10.1.1)	GO:0061599|molybdopterin molybdotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.970			PATRIC.2.9855.2.9855.con.0001.CDS.1065132.1065611.fwd	PATRIC	CDS	1065132	1065611	480	+			PGF_00419913		159		Cyclic pyranopterin monophosphate synthase (EC 4.6.1.17)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.971			PATRIC.2.9855.2.9855.con.0001.CDS.1065636.1066604.fwd	PATRIC	CDS	1065636	1066604	969	+			PGF_10244701		322		GTP 3',8-cyclase (EC 4.1.99.22)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.972			PATRIC.2.9855.2.9855.con.0001.CDS.1066608.1067543.fwd	PATRIC	CDS	1066608	1067543	936	+			PGF_00022507		311		Molybdopterin adenylyltransferase (EC 2.7.7.75)	GO:0061598|molybdopterin adenylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.973			PATRIC.2.9855.2.9855.con.0001.CDS.1068116.1068802.fwd	PATRIC	CDS	1068116	1068802	687	+			PGF_03981123		228		D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	GO:0009002|serine-type D-Ala-D-Ala carboxypeptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.974			PATRIC.2.9855.2.9855.con.0001.CDS.1068823.1069512.fwd	PATRIC	CDS	1068823	1069512	690	+			PGF_07420062		229		Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.96			PATRIC.2.9855.2.9855.con.0001.CDS.106891.108177.fwd	PATRIC	CDS	106891	108177	1287	+			PGF_00420963		428		D-glycerate transporter (predicted)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.975			PATRIC.2.9855.2.9855.con.0001.CDS.1069502.1070605.fwd	PATRIC	CDS	1069502	1070605	1104	+			PGF_02620852		367		Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.977			PATRIC.2.9855.2.9855.con.0001.CDS.1071008.1071652.fwd	PATRIC	CDS	1071008	1071652	645	+			PGF_02776217		214		Inner membrane protein translocase and chaperone YidC, OxaA protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.978			PATRIC.2.9855.2.9855.con.0001.CDS.1072189.1072881.fwd	PATRIC	CDS	1072189	1072881	693	+			PGF_04305571		230		Glycosyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.981			PATRIC.2.9855.2.9855.con.0001.CDS.1074735.1075586.fwd	PATRIC	CDS	1074735	1075586	852	+			PGF_00900085		283		UDP-glucose 4-epimerase (EC 5.1.3.2)	GO:0003978|UDP-glucose 4-epimerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.982			PATRIC.2.9855.2.9855.con.0001.CDS.1075971.1076426.rev	PATRIC	CDS	1075971	1076426	456	-			PGF_03518291		151		Transcriptional regulator LrpC, AsnC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.983			PATRIC.2.9855.2.9855.con.0001.CDS.1076577.1077422.fwd	PATRIC	CDS	1076577	1077422	846	+			PGF_00402268		281		oxidoreductase of aldo/keto reductase family, subgroup 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.984			PATRIC.2.9855.2.9855.con.0001.CDS.1077710.1079533.fwd	PATRIC	CDS	1077710	1079533	1824	+			PGF_00023412		607		MutS-related protein, family 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.985			PATRIC.2.9855.2.9855.con.0001.CDS.1079808.1080632.rev	PATRIC	CDS	1079808	1080632	825	-			PGF_07201805		274		Permease of the drug/metabolite transporter (DMT) superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.986			PATRIC.2.9855.2.9855.con.0001.CDS.1080852.1082186.fwd	PATRIC	CDS	1080852	1082186	1335	+			PGF_09985786		444		Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	GO:0004069|L-aspartate:2-oxoglutarate aminotransferase activity;GO:0004069|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.987			PATRIC.2.9855.2.9855.con.0001.CDS.1082362.1083744.fwd	PATRIC	CDS	1082362	1083744	1383	+			PGF_02278882		460		Iron-sulfur flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.97			PATRIC.2.9855.2.9855.con.0001.CDS.108253.109395.fwd	PATRIC	CDS	108253	109395	1143	+			PGF_06728837		380		Glycerate kinase (EC 2.7.1.31)	GO:0008887|glycerate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.991			PATRIC.2.9855.2.9855.con.0001.CDS.1085825.1086514.fwd	PATRIC	CDS	1085825	1086514	690	+			PGF_01042714		229		ABC transporter amino acid-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.992			PATRIC.2.9855.2.9855.con.0001.CDS.1086528.1086668.fwd	PATRIC	CDS	1086528	1086668	141	+			PGF_01042714		46		ABC transporter amino acid-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.993			PATRIC.2.9855.2.9855.con.0001.CDS.1086991.1088235.rev	PATRIC	CDS	1086991	1088235	1245	-			PGF_00667120		414		Putative transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.994			PATRIC.2.9855.2.9855.con.0001.CDS.1088536.1089135.fwd	PATRIC	CDS	1088536	1089135	600	+			PGF_07182652		199		Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.995			PATRIC.2.9855.2.9855.con.0001.CDS.1089445.1089912.fwd	PATRIC	CDS	1089445	1089912	468	+			PGF_01321203		155		Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.996			PATRIC.2.9855.2.9855.con.0001.CDS.1089939.1090514.fwd	PATRIC	CDS	1089939	1090514	576	+			PGF_02568001		191		Putative protein-S-isoprenylcysteine methyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.999			PATRIC.2.9855.2.9855.con.0001.CDS.1091454.1092020.rev	PATRIC	CDS	1091454	1092020	567	-			PGF_07182652		188		Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1000			PATRIC.2.9855.2.9855.con.0001.CDS.1092137.1092382.fwd	PATRIC	CDS	1092137	1092382	246	+			PGF_08546938		81		Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1001			PATRIC.2.9855.2.9855.con.0001.CDS.1092455.1092895.fwd	PATRIC	CDS	1092455	1092895	441	+			PGF_08546938		146		Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1003			PATRIC.2.9855.2.9855.con.0001.CDS.1093235.1093813.fwd	PATRIC	CDS	1093235	1093813	579	+			PGF_07182652		192		Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1004			PATRIC.2.9855.2.9855.con.0001.CDS.1094214.1095020.fwd	PATRIC	CDS	1094214	1095020	807	+			PGF_00425232		268		4Fe-4S dicluster domain / Nitroreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1005			PATRIC.2.9855.2.9855.con.0001.CDS.1095176.1096024.rev	PATRIC	CDS	1095176	1096024	849	-			PGF_03977347		282		2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase, beta subunit (EC 1.2.7.-)	GO:0043873|pyruvate-flavodoxin oxidoreductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1006			PATRIC.2.9855.2.9855.con.0001.CDS.1096028.1097695.rev	PATRIC	CDS	1096028	1097695	1668	-			PGF_00410279		555		2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase, gamma subunit (EC 1.2.7.-) / 2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.-)	GO:0043873|pyruvate-flavodoxin oxidoreductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1009			PATRIC.2.9855.2.9855.con.0001.CDS.1098913.1100175.fwd	PATRIC	CDS	1098913	1100175	1263	+			PGF_03094765		420		Tetracycline resistance, MFS efflux pump => TetA(P)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1010			PATRIC.2.9855.2.9855.con.0001.CDS.1100159.1102117.fwd	PATRIC	CDS	1100159	1102117	1959	+			PGF_03010833		652		Tetracycline resistance, ribosomal protection type => TetB(P)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.98			PATRIC.2.9855.2.9855.con.0001.CDS.110094.111125.fwd	PATRIC	CDS	110094	111125	1032	+			PGF_07225933		343		Sugar diacid utilization regulator SdaR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1011			PATRIC.2.9855.2.9855.con.0001.CDS.1102429.1102953.fwd	PATRIC	CDS	1102429	1102953	525	+			PGF_01304795		174		Uncharacterized membrane spanning protein, contains VanZ-like domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1026			PATRIC.2.9855.2.9855.con.0001.CDS.1112211.1113029.fwd	PATRIC	CDS	1112211	1113029	819	+			PGF_00057506		272		Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1027			PATRIC.2.9855.2.9855.con.0001.CDS.1113101.1113568.fwd	PATRIC	CDS	1113101	1113568	468	+			PGF_02635429		155		tRNA (adenine(37)-N6)-methyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.99			PATRIC.2.9855.2.9855.con.0001.CDS.111446.113227.fwd	PATRIC	CDS	111446	113227	1782	+			PGF_02030844		593		ATP-dependent DNA helicase RecQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1030			PATRIC.2.9855.2.9855.con.0001.CDS.1115983.1116420.fwd	PATRIC	CDS	1115983	1116420	438	+			PGF_10423881		145		Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1031			PATRIC.2.9855.2.9855.con.0001.CDS.1116505.1117866.fwd	PATRIC	CDS	1116505	1117866	1362	+			PGF_08913741		453		Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1032			PATRIC.2.9855.2.9855.con.0001.CDS.1118095.1119276.fwd	PATRIC	CDS	1118095	1119276	1182	+			PGF_04493258		393		Cobalt-zinc-cadmium resistance protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1034			PATRIC.2.9855.2.9855.con.0001.CDS.1121331.1121753.rev	PATRIC	CDS	1121331	1121753	423	-			PGF_00057506		140		Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1035			PATRIC.2.9855.2.9855.con.0001.CDS.1121983.1122747.fwd	PATRIC	CDS	1121983	1122747	765	+			PGF_10532194		254		Oxidoreductase, short-chain dehydrogenase/reductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1037			PATRIC.2.9855.2.9855.con.0001.CDS.1124213.1125103.rev	PATRIC	CDS	1124213	1125103	891	-			PGF_07987589		296		Transcriptional regulator, LysR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1038			PATRIC.2.9855.2.9855.con.0001.CDS.1125342.1126520.fwd	PATRIC	CDS	1125342	1126520	1179	+			PGF_10164212		392		Acetyl-CoA acetyltransferase (EC 2.3.1.9)	GO:0003985|acetyl-CoA C-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1039			PATRIC.2.9855.2.9855.con.0001.CDS.1126707.1127738.fwd	PATRIC	CDS	1126707	1127738	1032	+			PGF_06566462		343		Epoxyqueuosine reductase (EC 1.17.99.6) QueG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1042			PATRIC.2.9855.2.9855.con.0001.CDS.1129100.1129948.fwd	PATRIC	CDS	1129100	1129948	849	+			PGF_00069536		282		carboxylesterase NA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1043			PATRIC.2.9855.2.9855.con.0001.CDS.1130458.1132452.fwd	PATRIC	CDS	1130458	1132452	1995	+			PGF_07849456		664		Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.100			PATRIC.2.9855.2.9855.con.0001.CDS.113407.116157.fwd	PATRIC	CDS	113407	116157	2751	+			PGF_00036972		916		Probable calcium-transporting ATPase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1047			PATRIC.2.9855.2.9855.con.0001.CDS.1135625.1136206.fwd	PATRIC	CDS	1135625	1136206	582	+			PGF_03963719		193		RNA polymerase sigma factor SigW	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1049	PATRIC.2.9855.2.9855.con.0001.CDS.1137141.1137503.rev	PATRIC	CDS	1137141	1137503	363	-	PGF_03320197	120	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1050	PATRIC.2.9855.2.9855.con.0001.CDS.1137699.1138262.fwd	PATRIC	CDS	1137699	1138262	564	+	PGF_02278882	187	Iron-sulfur flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1051	PATRIC.2.9855.2.9855.con.0001.CDS.1138387.1138908.rev	PATRIC	CDS	1138387	1138908	522	-	PGF_07182652	173	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1052	PATRIC.2.9855.2.9855.con.0001.CDS.1139024.1139785.fwd	PATRIC	CDS	1139024	1139785	762	+	PGF_06839522	253	NAD-dependent, hopanoid-associated epimerase/dehydratase family acting on nucleotide-sugars	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1053	PATRIC.2.9855.2.9855.con.0001.CDS.1139782.1140051.fwd	PATRIC	CDS	1139782	1140051	270	+	PGF_06839522	89	NAD-dependent, hopanoid-associated epimerase/dehydratase family acting on nucleotide-sugars	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1054	PATRIC.2.9855.2.9855.con.0001.CDS.1140597.1141277.fwd	PATRIC	CDS	1140597	1141277	681	+	PGF_06335969	226	Transcriptional regulator, Xre family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1055	PATRIC.2.9855.2.9855.con.0001.CDS.1141298.1142167.fwd	PATRIC	CDS	1141298	1142167	870	+	PGF_06629251	289	Methionine aminopeptidase (EC 3.4.11.18)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1058	PATRIC.2.9855.2.9855.con.0001.CDS.1142625.1143077.rev	PATRIC	CDS	1142625	1143077	453	-	PGF_03055333	150	PhnB protein; putative DNA binding 3-demethylubiquinone-9 3-methyltransferase domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1059	PATRIC.2.9855.2.9855.con.0001.CDS.1143205.1144143.fwd	PATRIC	CDS	1143205	1144143	939	+	PGF_08548202	312	Transcriptional regulator, YafY family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1060	PATRIC.2.9855.2.9855.con.0001.CDS.1144409.1144936.fwd	PATRIC	CDS	1144409	1144936	528	+	PGF_00012116	175	Histone acetyltransferase HPA2 and related acetyltransferases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1064	PATRIC.2.9855.2.9855.con.0001.CDS.1147114.1147653.fwd	PATRIC	CDS	1147114	1147653	540	+	PGF_10519603	179	Acetyltransferase, GNAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1065	PATRIC.2.9855.2.9855.con.0001.CDS.1147734.1148315.fwd	PATRIC	CDS	1147734	1148315	582	+	PGF_07182652	193	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1066	PATRIC.2.9855.2.9855.con.0001.CDS.1148426.1149268.rev	PATRIC	CDS	1148426	1149268	843	-	PGF_00425232	280	4Fe-4S dicluster domain / Nitroreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1067	PATRIC.2.9855.2.9855.con.0001.CDS.1149680.1150483.fwd	PATRIC	CDS	1149680	1150483	804	+	PGF_00008106	267	Glutamate racemase (EC 5.1.1.3)	GO:0008881|glutamate racemase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1068	PATRIC.2.9855.2.9855.con.0001.CDS.1150601.1150993.rev	PATRIC	CDS	1150601	1150993	393	-	PGF_00057506	130	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1069	PATRIC.2.9855.2.9855.con.0001.CDS.1151231.1151803.fwd	PATRIC	CDS	1151231	1151803	573	+	PGF_00809978	190	Flavoredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1070	PATRIC.2.9855.2.9855.con.0001.CDS.1152241.1153089.fwd	PATRIC	CDS	1152241	1153089	849	+	PGF_00028483	282	Acetylxylan esterase related enzyme	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1071	PATRIC.2.9855.2.9855.con.0001.CDS.1153153.1153674.fwd	PATRIC	CDS	1153153	1153674	522	+	PGF_00059741	173	Transcriptional regulator, PadR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1073	PATRIC.2.9855.2.9855.con.0001.CDS.1154455.1155021.rev	PATRIC	CDS	1154455	1155021	567	-	PGF_07182652	188	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1074	PATRIC.2.9855.2.9855.con.0001.CDS.1155182.1156135.fwd	PATRIC	CDS	1155182	1156135	954	+	PGF_01281758	317	similar to Ketopantoate reductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1076	PATRIC.2.9855.2.9855.con.0001.CDS.1156382.1156906.rev	PATRIC	CDS	1156382	1156906	525	-	PGF_07182652	174	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1077	PATRIC.2.9855.2.9855.con.0001.CDS.1157026.1157772.fwd	PATRIC	CDS	1157026	1157772	747	+	PGF_08546938	248	Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1078	PATRIC.2.9855.2.9855.con.0001.CDS.1157916.1158455.fwd	PATRIC	CDS	1157916	1158455	540	+	PGF_09348764	179	Dihydrofolate reductase (EC 1.5.1.3)	GO:0004146|dihydrofolate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1079	PATRIC.2.9855.2.9855.con.0001.CDS.1159100.1160626.fwd	PATRIC	CDS	1159100	1160626	1527	+	PGF_00710545	508	Lysyl-tRNA synthetase (class II) (EC 6.1.1.6)	GO:0004824|lysine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1081	PATRIC.2.9855.2.9855.con.0001.CDS.1161806.1162366.rev	PATRIC	CDS	1161806	1162366	561	-	PGF_10153092	186	Nitroreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1082	PATRIC.2.9855.2.9855.con.0001.CDS.1162661.1163554.fwd	PATRIC	CDS	1162661	1163554	894	+	PGF_07987589	297	Transcriptional regulator, LysR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.101	PATRIC.2.9855.2.9855.con.0001.CDS.116451.117071.fwd	PATRIC	CDS	116451	117071	621	+	PGF_00048204	206	Response regulators consisting of a CheY-like receiver domain and an HD-GYP domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1086	PATRIC.2.9855.2.9855.con.0001.CDS.1165597.1166370.fwd	PATRIC	CDS	1165597	1166370	774	+	PGF_08546938	257	Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1087	PATRIC.2.9855.2.9855.con.0001.CDS.1166564.1166725.rev	PATRIC	CDS	1166564	1166725	162	-	PGF_10563189	53	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1088	PATRIC.2.9855.2.9855.con.0001.CDS.1166872.1167072.fwd	PATRIC	CDS	1166872	1167072	201	+	PGF_01671660	66	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1090	PATRIC.2.9855.2.9855.con.0001.CDS.1167354.1168442.fwd	PATRIC	CDS	1167354	1168442	1089	+	PGF_01281695	362	Choline-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1092	PATRIC.2.9855.2.9855.con.0001.CDS.1169372.1169932.rev	PATRIC	CDS	1169372	1169932	561	-	PGF_00015588	186	Iron-sulfur flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1094	PATRIC.2.9855.2.9855.con.0001.CDS.1170278.1171234.rev	PATRIC	CDS	1170278	1171234	957	-	PGF_01671660	318	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.102	PATRIC.2.9855.2.9855.con.0001.CDS.117206.117799.fwd	PATRIC	CDS	117206	117799	594	+	PGF_12875542	197	Two-component transcriptional response regulator, LuxR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1096	PATRIC.2.9855.2.9855.con.0001.CDS.1172394.1172747.fwd	PATRIC	CDS	1172394	1172747	354	+	PGF_03320197	117	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1098	PATRIC.2.9855.2.9855.con.0001.CDS.1173497.1174066.fwd	PATRIC	CDS	1173497	1174066	570	+	PGF_07182652	189	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1101	PATRIC.2.9855.2.9855.con.0001.CDS.1175458.1175880.fwd	PATRIC	CDS	1175458	1175880	423	+	PGF_00010009	140	Glyoxalase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.18	PATRIC.2.9855.2.9855.con.0001.CDS.11767.12492.fwd	PATRIC	CDS	11767	12492	726	+	PGF_07256906	241	Predicted transcriptional regulator of N-Acetylglucosamine utilization, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1107	PATRIC.2.9855.2.9855.con.0001.CDS.1178190.1178870.fwd	PATRIC	CDS	1178190	1178870	681	+	PGF_07420062	226	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1108	PATRIC.2.9855.2.9855.con.0001.CDS.1178863.1180125.fwd	PATRIC	CDS	1178863	1180125	1263	+	PGF_02620852	420	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2	PATRIC.2.9855.2.9855.con.0001.CDS.118.255.fwd	PATRIC	CDS	118	255	138	+	PGF_00417840	45	Chorismate synthase (EC 4.2.3.5)	GO:0004107|chorismate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1109	PATRIC.2.9855.2.9855.con.0001.CDS.1180396.1180845.fwd	PATRIC	CDS	1180396	1180845	450	+	PGF_00005916	149	Flavodoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1110	PATRIC.2.9855.2.9855.con.0001.CDS.1181067.1182158.fwd	PATRIC	CDS	1181067	1182158	1092	+	PGF_05606505	363	Cell surface protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1111	PATRIC.2.9855.2.9855.con.0001.CDS.1182358.1182876.fwd	PATRIC	CDS	1182358	1182876	519	+	PGF_01316440	172	Histone acetyltransferase HPA2 and related acetyltransferases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.104	PATRIC.2.9855.2.9855.con.0001.CDS.118309.119001.rev	PATRIC	CDS	118309	119001	693	-	PGF_01737397	230	FIG00031715: Predicted metal-dependent phosphoesterases (PHP family)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1114	PATRIC.2.9855.2.9855.con.0001.CDS.1185995.1187455.fwd	PATRIC	CDS	1185995	1187455	1461	+	PGF_00043814	486	Putative ribonucleoprotein related-protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1115	PATRIC.2.9855.2.9855.con.0001.CDS.1187624.1188847.fwd	PATRIC	CDS	1187624	1188847	1224	+	PGF_01771963	407	RNA-2',3'-PO4:RNA-5'-OH ligase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1117	PATRIC.2.9855.2.9855.con.0001.CDS.1189405.1190184.fwd	PATRIC	CDS	1189405	1190184	780	+	PGF_00065446	259	Uncharacterized protein YcgL	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1121	PATRIC.2.9855.2.9855.con.0001.CDS.1193261.1194553.fwd	PATRIC	CDS	1193261	1194553	1293	+	PGF_00400326	430	BchE/P-methylase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1122	PATRIC.2.9855.2.9855.con.0001.CDS.1194800.1195663.fwd	PATRIC	CDS	1194800	1195663	864	+	PGF_03055832	287	DUF89 protein CxxC subfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1125	PATRIC.2.9855.2.9855.con.0001.CDS.1197199.1198107.fwd	PATRIC	CDS	1197199	1198107	909	+	PGF_01462159	302	Uncharacterized di-4Fe-4S ferredoxin domain-containing protein, Cbei_3544 type	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1126	PATRIC.2.9855.2.9855.con.0001.CDS.1198272.1199576.fwd	PATRIC	CDS	1198272	1199576	1305	+	PGF_04792526	434	O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) @ O-succinylhomoserine sulfhydrylase (EC 2.5.1.48)	GO:0003961|O-acetylhomoserine aminocarboxypropyltransferase activity;GO:0003962|cystathionine gamma-synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1127	PATRIC.2.9855.2.9855.con.0001.CDS.1199967.1200617.fwd	PATRIC	CDS	1199967	1200617	651	+	PGF_00925719	216	ABC transporter, permease protein (cluster 13, osmolytes)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1128	PATRIC.2.9855.2.9855.con.0001.CDS.1200736.1201638.fwd	PATRIC	CDS	1200736	1201638	903	+	PGF_06513264	300	ABC transporter, substrate-binding protein (cluster 13, osmolytes)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1129	PATRIC.2.9855.2.9855.con.0001.CDS.1201661.1202404.fwd	PATRIC	CDS	1201661	1202404	744	+	PGF_06784466	247	ABC transporter, ATP-binding protein (cluster 13, osmolytes)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1130	PATRIC.2.9855.2.9855.con.0001.CDS.1202591.1203202.fwd	PATRIC	CDS	1202591	1203202	612	+	PGF_00925719	203	ABC transporter, permease protein (cluster 13, osmolytes)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1131	PATRIC.2.9855.2.9855.con.0001.CDS.1203513.1204079.fwd	PATRIC	CDS	1203513	1204079	567	+	PGF_01653535	188	RNA polymerase sigma factor SigZ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1133	PATRIC.2.9855.2.9855.con.0001.CDS.1205290.1205568.fwd	PATRIC	CDS	1205290	1205568	279	+	PGF_08030842	92	Transcriptional regulator, ArsR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1134	PATRIC.2.9855.2.9855.con.0001.CDS.1205555.1206187.fwd	PATRIC	CDS	1205555	1206187	633	+	PGF_00409683	210	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1135	PATRIC.2.9855.2.9855.con.0001.CDS.1206656.1207417.rev	PATRIC	CDS	1206656	1207417	762	-	PGF_00059193	253	Transcriptional regulator, DeoR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1136	PATRIC.2.9855.2.9855.con.0001.CDS.1207759.1208094.rev	PATRIC	CDS	1207759	1208094	336	-	PGF_03320197	111	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1137	PATRIC.2.9855.2.9855.con.0001.CDS.1208240.1209256.fwd	PATRIC	CDS	1208240	1209256	1017	+	PGF_00024770	338	NADH:flavin oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1138	PATRIC.2.9855.2.9855.con.0001.CDS.1209457.1209633.rev	PATRIC	CDS	1209457	1209633	177	-	PGF_01282222	58	4Fe-4S ferredoxin, iron-sulfur binding	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1139	PATRIC.2.9855.2.9855.con.0001.CDS.1209658.1210029.rev	PATRIC	CDS	1209658	1210029	372	-	PGF_00045876	123	Pyridoxamine 5'-phosphate oxidase-related, FMN-binding	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.107	PATRIC.2.9855.2.9855.con.0001.CDS.120990.121697.fwd	PATRIC	CDS	120990	121697	708	+	PGF_06916656	235	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1140	PATRIC.2.9855.2.9855.con.0001.CDS.1210234.1210737.fwd	PATRIC	CDS	1210234	1210737	504	+	PGF_00049228	167	Rrf2 family transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1141	PATRIC.2.9855.2.9855.con.0001.CDS.1211116.1211403.rev	PATRIC	CDS	1211116	1211403	288	-	PGF_00054286	95	Stress responsive alpha-beta barrel domain protein Dabb	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1142	PATRIC.2.9855.2.9855.con.0001.CDS.1211595.1212392.rev	PATRIC	CDS	1211595	1212392	798	-	PGF_10532194	265	Oxidoreductase, short-chain dehydrogenase/reductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1143	PATRIC.2.9855.2.9855.con.0001.CDS.1212917.1213741.fwd	PATRIC	CDS	1212917	1213741	825	+	PGF_00425232	274	4Fe-4S dicluster domain / Nitroreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1144	PATRIC.2.9855.2.9855.con.0001.CDS.1214178.1214318.fwd	PATRIC	CDS	1214178	1214318	141	+	PGF_00049228	46	Rrf2 family transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1145	PATRIC.2.9855.2.9855.con.0001.CDS.1214704.1216779.fwd	PATRIC	CDS	1214704	1216779	2076	+	PGF_07849456	691	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1147	PATRIC.2.9855.2.9855.con.0001.CDS.1216974.1218323.fwd	PATRIC	CDS	1216974	1218323	1350	+	PGF_01546616	449	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1148	PATRIC.2.9855.2.9855.con.0001.CDS.1218385.1219677.fwd	PATRIC	CDS	1218385	1219677	1293	+	PGF_00055147	430	Anaerobic C4-dicarboxylate transporter DcuC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1150	PATRIC.2.9855.2.9855.con.0001.CDS.1220580.1221446.fwd	PATRIC	CDS	1220580	1221446	867	+	PGF_02146256	288	Sialic acid utilization regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.108	PATRIC.2.9855.2.9855.con.0001.CDS.122162.123028.fwd	PATRIC	CDS	122162	123028	867	+	PGF_02899915	288	Hydrolase, HAD superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1151	PATRIC.2.9855.2.9855.con.0001.CDS.1221773.1223917.fwd	PATRIC	CDS	1221773	1223917	2145	+	PGF_00012478	714	Hydantoinase/oxoprolinase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1152	PATRIC.2.9855.2.9855.con.0001.CDS.1223959.1224957.fwd	PATRIC	CDS	1223959	1224957	999	+	PGF_02975857	332	Galactose mutarotase related enzyme	

Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1154	PATRIC.2.9855.2.9855.con.0001.CDS.1225423.1226316.fwd	PATRIC	CDS	1225423	1226316	894	+	PGF_00054802	297	Sugar kinase and transcription regulator (EC 2.7.1.-)	regulator activity;GO:0008443|cobinamide kinase activity;GO:0008443|phytol kinase activity;GO:0008443|phosphatidylinositol phosphate kinase activity;GO:0008443|cyclin-dependent protein serine/threonine kinase regulator activity;GO:0008443|phenol kinase activity;GO:0008443|cyclin-dependent protein kinase activating kinase regulator activity;GO:0008443|inositol tetrakisphosphate 2-kinase activity;GO:0008443|heptose 7-phosphate kinase activity;GO:0008443|aminoglycoside phosphotransferase activity;GO:0008443|phosphatidylinositol 3-kinase activity;GO:0008443|eukaryotic elongation factor-2 kinase regulator activity;GO:0008443|eukaryotic elongation factor-2 kinase activator activity;GO:0008443|LPPG:FO 2-phospho-L-lactate transferase activity;GO:0008443|cytidine kinase activity;GO:0008443|glycerate 2-kinase activity;GO:0008443|(S)-lactate 2-kinase activity;GO:0008443|phosphoserine:homoserine phosphotransferase activity;GO:0008443|L-seryl-tRNA(Sec) kinase activity;GO:0008443|phosphocholine transferase activity;GO:0008443|polynucleotide 5'-hydroxyl-kinase activity;GO:0008443|ATP-dependent polynucleotide kinase activity;GO:0008443|GTP-dependent polynucleotide kinase activity;GO:0008443|farnesol kinase activity;GO:0008443|CTP:2-trans,-6-trans-farnesol kinase activity;GO:0008443|geraniol kinase activity;GO:0008443|geranylgeraniol kinase activity;GO:0008443|CTP:geranylgeraniol kinase activity;GO:0008443|prenol kinase activity;GO:0008443|1-phosphatidylinositol-5-kinase activity;GO:0008443|1-phosphatidylinositol-3-phosphate 4-kinase activity;GO:0008443|phosphatidylinositol-3,4-bisphosphate 5-kinase activity;GO:0008443|phosphatidylinositol bisphosphate kinase activity;GO:0008443|inositol-3,4,6-trisphosphate 1-kinase activity;GO:0008443|inositol 5-diphosphate pentakisphosphate 5-kinase activity;GO:0008443|inositol diphosphate tetrakisphosphate kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1155	PATRIC.2.9855.2.9855.con.0001.CDS.1226874.1229546.fwd	PATRIC	CDS	1226874	1229546	2673	+	PGF_05438553	890	Phosphoenolpyruvate synthase (EC 2.7.9.2)	GO:0008986|pyruvate, water dikinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1156	PATRIC.2.9855.2.9855.con.0001.CDS.1229698.1230339.fwd	PATRIC	CDS	1229698	1230339	642	+	PGF_00067887	213	Streptogramin O-acetyltransferase, putative	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.109	PATRIC.2.9855.2.9855.con.0001.CDS.123195.124898.rev	PATRIC	CDS	123195	124898	1704	-	PGF_06837078	567	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1158	PATRIC.2.9855.2.9855.con.0001.CDS.1232129.1232473.fwd	PATRIC	CDS	1232129	1232473	345	+	PGF_08030842	114	Transcriptional regulator, ArsR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1159	PATRIC.2.9855.2.9855.con.0001.CDS.1232650.1233414.fwd	PATRIC	CDS	1232650	1233414	765	+	PGF_00402268	254	oxidoreductase of aldo/keto reductase family, subgroup 1	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1160	PATRIC.2.9855.2.9855.con.0001.CDS.1233750.1234160.fwd	PATRIC	CDS	1233750	1234160	411	+	PGF_00030655	136	Peptide deformylase (EC 3.5.1.88)	GO:0042586|peptide deformylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1164	PATRIC.2.9855.2.9855.con.0001.CDS.1235310.1236182.fwd	PATRIC	CDS	1235310	1236182	873	+	PGF_00046948	290	Radical SAM domain protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1165	PATRIC.2.9855.2.9855.con.0001.CDS.1236278.1237222.rev	PATRIC	CDS	1236278	1237222	945	-	PGF_00012987	314	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	GO:0004617|phosphoglycerate dehydrogenase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1166	PATRIC.2.9855.2.9855.con.0001.CDS.1237311.1238426.rev	PATRIC	CDS	1237311	1238426	1116	-	PGF_00033873	371	Phosphonoacetate hydrolase-related protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1167	PATRIC.2.9855.2.9855.con.0001.CDS.1238556.1239452.fwd	PATRIC	CDS	1238556	1239452	897	+	PGF_07987589	298	Transcriptional regulator, LysR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1173	PATRIC.2.9855.2.9855.con.0001.CDS.1243772.1245085.rev	PATRIC	CDS	1243772	1245085	1314	-	PGF_03587816	437	FAD-linked oxidoreductase family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1174	PATRIC.2.9855.2.9855.con.0001.CDS.1245504.1246226.fwd	PATRIC	CDS	1245504	1246226	723	+	PGF_10420457	240	MBL-fold metallo-hydrolase superfamily	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1175	PATRIC.2.9855.2.9855.con.0001.CDS.1246399.1246647.fwd	PATRIC	CDS	1246399	1246647	249	+	PGF_10329977	82	Phenazine biosynthesis protein PhzF like	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1176	PATRIC.2.9855.2.9855.con.0001.CDS.1246655.1248193.rev	PATRIC	CDS	1246655	1248193	1539	-	PGF_01285655	512	putative resolvase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1181	PATRIC.2.9855.2.9855.con.0001.CDS.1249434.1250159.fwd	PATRIC	CDS	1249434	1250159	726	+	PGF_03962887	241	Phage antirepressor protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.19	PATRIC.2.9855.2.9855.con.0001.CDS.12514.13242.fwd	PATRIC	CDS	12514	13242	729	+	PGF_00007920	242	Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	GO:0004342|glucosamine-6-phosphate deaminase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.110	PATRIC.2.9855.2.9855.con.0001.CDS.125512.126567.rev	PATRIC	CDS	125512	126567	1056	-	PGF_07410757	351	Aldose 1-epimerase (EC 5.1.3.3)	GO:0004034|aldose 1-epimerase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1207	PATRIC.2.9855.2.9855.con.0001.CDS.1260477.1260908.fwd	PATRIC	CDS	1260477	1260908	432	+	PGF_02142873	143	Single-stranded DNA-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1218	PATRIC.2.9855.2.9855.con.0001.CDS.1265265.1266203.fwd	PATRIC	CDS	1265265	1266203	939	+	PGF_07220970	312	Phage terminase, small subunit	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1219	PATRIC.2.9855.2.9855.con.0001.CDS.1266169.1267560.fwd	PATRIC	CDS	1266169	1267560	1392	+	PGF_07990983	463	Phage terminase, large subunit	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.111	PATRIC.2.9855.2.9855.con.0001.CDS.126905.128107.fwd	PATRIC	CDS	126905	128107	1203	+	PGF_00062533	400	Two-component response regulator yesN	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1228	PATRIC.2.9855.2.9855.con.0001.CDS.1274871.1275764.fwd	PATRIC	CDS	1274871	1275764	894	+	PGF_00032700	297	Phage tail fiber protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5	PATRIC.2.9855.2.9855.con.0001.CDS.1275.2414.fwd	PATRIC	CDS	1275	2414	1140	+	PGF_02877184	379	Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51)	GO:0004106|chorismate mutase activity;GO:0004664|prephenate dehydratase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.112	PATRIC.2.9855.2.9855.con.0001.CDS.128109.129056.fwd	PATRIC	CDS	128109	129056	948	+	PGF_03017683	315	Two-component system sensor histidine kinase/response regulator hybrid	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1240	PATRIC.2.9855.2.9855.con.0001.CDS.1287780.1288598.rev	PATRIC	CDS	1287780	1288598	819	-	PGF_00413397	272	tcdA-E operon negative regulator	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.113	PATRIC.2.9855.2.9855.con.0001.CDS.129180.130181.fwd	PATRIC	CDS	129180	130181	1002	+	PGF_00830263	333	Galactofuranose ABC transporter, substrate-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1254	PATRIC.2.9855.2.9855.con.0001.CDS.1297065.1297979.fwd	PATRIC	CDS	1297065	1297979	915	+	PGF_01956796	304	Recombinational DNA repair protein RecT (prophage associated)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1255	PATRIC.2.9855.2.9855.con.0001.CDS.1297979.1298686.fwd	PATRIC	CDS	1297979	1298686	708	+	PGF_00020531	235	Metallo-beta-lactamase superfamily domain protein in prophage	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1261	PATRIC.2.9855.2.9855.con.0001.CDS.1301481.1302185.fwd	PATRIC	CDS	1301481	1302185	705	+	PGF_10329977	234	Phenazine biosynthesis protein PhzF like	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1262	PATRIC.2.9855.2.9855.con.0001.CDS.1302414.1303631.fwd	PATRIC	CDS	1302414	1303631	1218	+	PGF_12809587	405	Transcriptional regulator, MerR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.114	PATRIC.2.9855.2.9855.con.0001.CDS.130285.131802.fwd	PATRIC	CDS	130285	131802	1518	+	PGF_08113587	505	Galactofuranose ABC transporter, ATP-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1263	PATRIC.2.9855.2.9855.con.0001.CDS.1303767.1305026.fwd	PATRIC	CDS	1303767	1305026	1260	+	PGF_09996723	419	Uncharacterized MFS-type transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1265	PATRIC.2.9855.2.9855.con.0001.CDS.1305538.1306137.fwd	PATRIC	CDS	1305538	1306137	600	+	PGF_10251053	199	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1266	PATRIC.2.9855.2.9855.con.0001.CDS.1306202.1307002.fwd	PATRIC	CDS	1306202	1307002	801	+	PGF_00051577	266	Short-chain alcohol dehydrogenase family enzyme	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1269	PATRIC.2.9855.2.9855.con.0001.CDS.1308077.1308940.fwd	PATRIC	CDS	1308077	1308940	864	+	PGF_00417736	287	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1270	PATRIC.2.9855.2.9855.con.0001.CDS.1309457.1309783.fwd	PATRIC	CDS	1309457	1309783	327	+	PGF_00005956	108	Flavoredoxin	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1271	PATRIC.2.9855.2.9855.con.0001.CDS.1309826.1310005.fwd	PATRIC	CDS	1309826	1310005	180	+	PGF_00005956	59	Flavoredoxin	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1273	PATRIC.2.9855.2.9855.con.0001.CDS.1310906.1311727.fwd	PATRIC	CDS	1310906	1311727	822	+	PGF_07849456	273	Methyl-accepting chemotaxis protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1274	PATRIC.2.9855.2.9855.con.0001.CDS.1311972.1312292.rev	PATRIC	CDS	1311972	1312292	321	-	PGF_03320197	106	Transcriptional regulator, HxlR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1275	PATRIC.2.9855.2.9855.con.0001.CDS.1312441.1312992.fwd	PATRIC	CDS	1312441	1312992	552	+	PGF_02278882	183	Iron-sulfur flavoprotein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1276	PATRIC.2.9855.2.9855.con.0001.CDS.1313149.1313385.fwd	PATRIC	CDS	1313149	1313385	237	+	PGF_06335969	78	Transcriptional regulator, Xre family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1277	PATRIC.2.9855.2.9855.con.0001.CDS.1313386.1313841.fwd	PATRIC	CDS	1313386	1313841	456	+	PGF_00030655	151	Peptide deformylase (EC 3.5.1.88)	GO:0042586|peptide deformylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1278	PATRIC.2.9855.2.9855.con.0001.CDS.1314296.1314925.fwd	PATRIC	CDS	1314296	1314925	630	+	PGF_06788576	209	SAM-dependent methyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1279	PATRIC.2.9855.2.9855.con.0001.CDS.1314950.1315399.fwd	PATRIC	CDS	1314950	1315399	450	+	PGF_10423881	149	Transcriptional regulator, MarR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1281	PATRIC.2.9855.2.9855.con.0001.CDS.1316239.1316445.fwd	PATRIC	CDS	1316239	1316445	207	+	PGF_06335969	68	Transcriptional regulator, Xre family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1285	PATRIC.2.9855.2.9855.con.0001.CDS.1317931.1318893.fwd	PATRIC	CDS	1317931	1318893	963	+	PGF_05804203	320	similar to Ketopantoate reductase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.115	PATRIC.2.9855.2.9855.con.0001.CDS.131804.132844.fwd	PATRIC	CDS	131804	132844	1041	+	PGF_04872915	346	Galactofuranose ABC transporter, permease protein 1	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1286	PATRIC.2.9855.2.9855.con.0001.CDS.1319222.1320001.fwd	PATRIC	CDS	1319222	1320001	780	+	PGF_03589817	259	Peptidoglycan N-acetylglucosamine deacetylase (EC 3.5.1.-)	GO:0008418|protein-N-terminal asparagine amidohydrolase activity;GO:0008418|UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity;GO:0008418|iprodione amidohydrolase activity;GO:0008418|(3,5-dichlorophenylurea)acetate amidohydrolase activity;GO:0008418|4'-(2-hydroxyisopropyl)phenylurea amidohydrolase activity;GO:0008418|didemethylisoproturon amidohydrolase activity;GO:0008418|N-isopropylacetanilide amidohydrolase activity;GO:0008418|N-cyclohexylformamide amidohydrolase activity;GO:0008418|isonicotinic acid hydrazide hydrolase activity;GO:0008418|cis-aconitamide amidase activity;GO:0008418|gamma-N-formylaminovinylacetate hydrolase activity;GO:0008418|N2-acetyl-L-lysine deacetylase activity;GO:0008418|O-succinylbenzoate synthase activity;GO:0008418|indoleacetamide hydrolase activity;GO:0008418|N-acetylcitrulline deacetylase activity;GO:0008418|N-acetylgalactosamine-6-phosphate deacetylase activity;GO:0008418|diacetylchitobiose deacetylase activity;GO:0008418|chitooligosaccharide deacetylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1287	PATRIC.2.9855.2.9855.con.0001.CDS.1320265.1320837.fwd	PATRIC	CDS	1320265	1320837	573	+	PGF_01442978	190	CDP-alcohol phosphatidyltransferase family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1288	PATRIC.2.9855.2.9855.con.0001.CDS.1320867.1322135.fwd	PATRIC	CDS	1320867	1322135	1269	+	PGF_01325990	422	Putative oxidoreductase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1290	PATRIC.2.9855.2.9855.con.0001.CDS.1323109.1323576.fwd	PATRIC	CDS	1323109	1323576	468	+	PGF_08946513	155	Flavodoxin	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1291	PATRIC.2.9855.2.9855.con.0001.CDS.1323797.1324543.fwd	PATRIC	CDS	1323797	1324543	747	+	PGF_00057506	248	Transcriptional regulator, MerR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1292	PATRIC.2.9855.2.9855.con.0001.CDS.1324850.1325707.rev	PATRIC	CDS	1324850	1325707	858	-	PGF_07987589	285	Transcriptional regulator, LysR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1296	PATRIC.2.9855.2.9855.con.0001.CDS.1328266.1328838.fwd	PATRIC	CDS	1328266	1328838	573	+	PGF_01313471	190	Tellurite methyltransferase (EC 2.1.1.265)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.116	PATRIC.2.9855.2.9855.con.0001.CDS.132841.133848.fwd	PATRIC	CDS	132841	133848	1008	+	PGF_10285065	335	Galactofuranose ABC transporter, permease protein 2	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1297	PATRIC.2.9855.2.9855.con.0001.CDS.1329056.1329874.fwd	PATRIC	CDS	1329056	1329874	819	+	PGF_02679108	272	CAAX amino terminal protease family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1299	PATRIC.2.9855.2.9855.con.0001.CDS.1330721.1331467.fwd	PATRIC	CDS	1330721	1331467	747	+	PGF_12698184	248	ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1300	PATRIC.2.9855.2.9855.con.0001.CDS.1331524.1332354.fwd	PATRIC	CDS	1331524	1332354	831	+	PGF_03781997	276	Iron-sulfur cluster-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1301	PATRIC.2.9855.2.9855.con.0001.CDS.1332928.1333560.fwd	PATRIC	CDS	1332928	1333560	633	+	PGF_06114369	210	Xenobiotic acyltransferase XAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1303	PATRIC.2.9855.2.9855.con.0001.CDS.1334925.1335797.fwd	PATRIC	CDS	1334925	1335797	873	+	PGF_01671660	290	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1307	PATRIC.2.9855.2.9855.con.0001.CDS.1337630.1338088.fwd	PATRIC	CDS	1337630	1338088	459	+	PGF_01285270	152	MutT-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1308	PATRIC.2.9855.2.9855.con.0001.CDS.1338835.1340175.fwd	PATRIC	CDS	1338835	1340175	1341	+	PGF_01282545	446	no hits	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1309	PATRIC.2.9855.2.9855.con.0001.CDS.1340549.1340869.fwd	PATRIC	CDS	1340549	1340869	321	+	PGF_00412640	106	small multidrug resistance family (SMR) protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.117	PATRIC.2.9855.2.9855.con.0001.CDS.134115.135884.fwd	PATRIC	CDS	134115	135884	1770	+	PGF_12762435	589	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1312	PATRIC.2.9855.2.9855.con.0001.CDS.1342151.1342951.rev	PATRIC	CDS	1342151	1342951	801	-	PGF_03781997	266	Iron-sulfur cluster-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1313	PATRIC.2.9855.2.9855.con.0001.CDS.1343104.1343814.rev	PATRIC	CDS	1343104	1343814	711	-	PGF_10462688	236	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1316	PATRIC.2.9855.2.9855.con.0001.CDS.1346490.1347497.fwd	PATRIC	CDS	1346490	1347497	1008	+	PGF_00417443	335	3-dehydro-L-gulonate 2-dehydrogenase (EC 1.1.1.130)	GO:0047559|3-dehydro-L-gulonate 2-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1318	PATRIC.2.9855.2.9855.con.0001.CDS.1348282.1349175.rev	PATRIC	CDS	1348282	1349175	894	-	PGF_01671660	297	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1319	PATRIC.2.9855.2.9855.con.0001.CDS.1349445.1350692.fwd	PATRIC	CDS	1349445	1350692	1248	+	PGF_06962500	415	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1320	PATRIC.2.9855.2.9855.con.0001.CDS.1350773.1351387.fwd	PATRIC	CDS	1350773	1351387	615	+	PGF_00660064	204	Galactoside O-acetyltransferase (EC 2.3.1.18)	GO:0008870|galactoside O-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1321	PATRIC.2.9855.2.9855.con.0001.CDS.1351444.1351833.fwd	PATRIC	CDS	1351444	1351833	390	+	PGF_00035192	129	Possible glyoxylase family protein (Lactoylglutathione lyase) (EC 4.4.1.5)	GO:0004462|lactoylglutathione lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1322	PATRIC.2.9855.2.9855.con.0001.CDS.1352487.1353326.fwd	PATRIC	CDS	1352487	1353326	840	+	PGF_03066404	279	Uncharacterized transcriptional regulator YbfI, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1323	PATRIC.2.9855.2.9855.con.0001.CDS.1353319.1354260.fwd	PATRIC	CDS	1353319	1354260	942	+	PGF_07201805	313	Permease of the drug/metabolite transporter (DMT) superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1324	PATRIC.2.9855.2.9855.con.0001.CDS.1354429.1354851.fwd	PATRIC	CDS	1354429	1354851	423	+	PGF_08837849	140	Cytidine deaminase (EC 3.5.4.5)	GO:0004126|cytidine deaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1325	PATRIC.2.9855.2.9855.con.0001.CDS.1355357.1356187.fwd	PATRIC	CDS	1355357	1356187	831	+	PGF_10425579	276	ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1326	PATRIC.2.9855.2.9855.con.0001.CDS.1356202.1356918.fwd	PATRIC	CDS	1356202	1356918	717	+	PGF_01284110	238	ABC transporter, permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1330	PATRIC.2.9855.2.9855.con.0001.CDS.1358982.1359347.fwd	PATRIC	CDS	1358982	1359347	366	+	PGF_03320197	121	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1331	PATRIC.2.9855.2.9855.con.0001.CDS.1359430.1359933.fwd	PATRIC	CDS	1359430	1359933	504	+	PGF_04232510	167	Phospholipid-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1332	PATRIC.2.9855.2.9855.con.0001.CDS.1360013.1360510.fwd	PATRIC	CDS	1360013	1360510	498	+	PGF_10519603	165	Acetyltransferase, GNAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1333	PATRIC.2.9855.2.9855.con.0001.CDS.1360611.1361003.fwd	PATRIC	CDS	1360611	1361003	393	+	PGF_03751069	130	Hemerythrin domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.118	PATRIC.2.9855.2.9855.con.0001.CDS.136081.137550.rev	PATRIC	CDS	136081	137550	1470	-	PGF_00016028	489	L-arabinose isomerase (EC 5.3.1.4)	GO:0008733|L-arabinose isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1335	PATRIC.2.9855.2.9855.con.0001.CDS.1361736.1362353.rev	PATRIC	CDS	1361736	1362353	618	-	PGF_03741671	205	Phosphoglycerate mutase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1336	PATRIC.2.9855.2.9855.con.0001.CDS.1362486.1363367.fwd	PATRIC	CDS	1362486	1363367	882	+	PGF_07987589	293	Transcriptional regulator, LysR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.20	PATRIC.2.9855.2.9855.con.0001.CDS.13630.14349.fwd	PATRIC	CDS	13630	14349	720	+	PGF_07256906	239	Predicted transcriptional regulator of N-Acetylglucosamine utilization, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1337	PATRIC.2.9855.2.9855.con.0001.CDS.1363704.1364756.fwd	PATRIC	CDS	1363704	1364756	1053	+	PGF_05728830	350	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1339	PATRIC.2.9855.2.9855.con.0001.CDS.1365258.1365515.fwd	PATRIC	CDS	1365258	1365515	258	+	PGF_00058243	85	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1340	PATRIC.2.9855.2.9855.con.0001.CDS.1365969.1366574.fwd	PATRIC	CDS	1365969	1366574	606	+	PGF_00018138	201	M. jannaschii predicted coding region MJ0455	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1343	PATRIC.2.9855.2.9855.con.0001.CDS.1367384.1367947.fwd	PATRIC	CDS	1367384	1367947	564	+	PGF_06672158	187	Nitroreductase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1345	PATRIC.2.9855.2.9855.con.0001.CDS.1368522.1369265.fwd	PATRIC	CDS	1368522	1369265	744	+	PGF_00061981	247	Truncated-SA protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1347	PATRIC.2.9855.2.9855.con.0001.CDS.1369990.1370409.fwd	PATRIC	CDS	1369990	1370409	420	+	PGF_01281258	139	Histone acetyltransferase HPA2 and related acetyltransferases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1348	PATRIC.2.9855.2.9855.con.0001.CDS.1370579.1371175.fwd	PATRIC	CDS	1370579	1371175	597	+	PGF_03950680	198	Transporter, LysE family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1349	PATRIC.2.9855.2.9855.con.0001.CDS.1371181.1371957.fwd	PATRIC	CDS	1371181	1371957	777	+	PGF_00062480	258	AraC-type DNA-binding domain-containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1351	PATRIC.2.9855.2.9855.con.0001.CDS.1373206.1374108.rev	PATRIC	CDS	1373206	1374108	903	-	PGF_10440473	300	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1352	PATRIC.2.9855.2.9855.con.0001.CDS.1374393.1375286.fwd	PATRIC	CDS	1374393	1375286	894	+	PGF_07201805	297	Permease of the drug/metabolite transporter (DMT) superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1356	PATRIC.2.9855.2.9855.con.0001.CDS.1378186.1380150.fwd	PATRIC	CDS	1378186	1380150	1965	+	PGF_00417736	654	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1357	PATRIC.2.9855.2.9855.con.0001.CDS.1380398.1380970.rev	PATRIC	CDS	1380398	1380970	573	-	PGF_00046564	190	RNA polymerase sigma factor RpoE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.119	PATRIC.2.9855.2.9855.con.0001.CDS.138113.139186.fwd	PATRIC	CDS	138113	139186	1074	+	PGF_00016941	357	Arabinose metabolism transcriptional repressor AraR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1358	PATRIC.2.9855.2.9855.con.0001.CDS.1381547.1382758.rev	PATRIC	CDS	1381547	1382758	1212	-	PGF_01285261	403	FOG: PAS/PAC domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1359	PATRIC.2.9855.2.9855.con.0001.CDS.1382751.1385501.rev	PATRIC	CDS	1382751	1385501	2751	-	PGF_10416542	916	Sensory box histidine kinase/response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1360	PATRIC.2.9855.2.9855.con.0001.CDS.1386075.1386629.fwd	PATRIC	CDS	1386075	1386629	555	+	PGF_02075044	184	RNA:NAD 2'-phosphotransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1365	PATRIC.2.9855.2.9855.con.0001.CDS.1389015.1390136.fwd	PATRIC	CDS	1389015	1390136	1122	+	PGF_00032922	373	Phage-like element PBSX protein xkdK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1366	PATRIC.2.9855.2.9855.con.0001.CDS.1390149.1390580.fwd	PATRIC	CDS	1390149	1390580	432	+	PGF_00032927	143	Phage-like element PBSX protein xkdM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1368	PATRIC.2.9855.2.9855.con.0001.CDS.1391564.1393984.fwd	PATRIC	CDS	1391564	1393984	2421	+	PGF_00056044	806	Tail tape meausure protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.120	PATRIC.2.9855.2.9855.con.0001.CDS.139322.140008.fwd	PATRIC	CDS	139322	140008	687	+	PGF_05225955	228	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	GO:0008742|L-ribulose-phosphate 4-epimerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1369	PATRIC.2.9855.2.9855.con.0001.CDS.1393998.1394477.fwd	PATRIC	CDS	1393998	1394477	480	+	PGF_00032937	159	Phage-like element PBSX protein xkdP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1370	PATRIC.2.9855.2.9855.con.0001.CDS.1394474.1395478.fwd	PATRIC	CDS	1394474	1395478	1005	+	PGF_00032942	334	Phage-like element PBSX protein xkdQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1372	PATRIC.2.9855.2.9855.con.0001.CDS.1395794.1396234.fwd	PATRIC	CDS	1395794	1396234	441	+	PGF_00032944	146	Phage-like element PBSX protein xkdS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1373	PATRIC.2.9855.2.9855.con.0001.CDS.1396227.1397333.fwd	PATRIC	CDS	1396227	1397333	1107	+	PGF_01011503	368	Phage-like element PBSX protein xkdT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1374	PATRIC.2.9855.2.9855.con.0001.CDS.1397326.1398030.fwd	PATRIC	CDS	1397326	1398030	705	+	PGF_01281720	234	Phage-like element PBSX protein xkdU	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1377	PATRIC.2.9855.2.9855.con.0001.CDS.1399099.1399452.fwd	PATRIC	CDS	1399099	1399452	354	+	PGF_04243916	117	Phage tail fiber protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.121	PATRIC.2.9855.2.9855.con.0001.CDS.140247.140894.fwd	PATRIC	CDS	140247	140894	648	+	PGF_00057399	215	Transaldolase (EC 2.2.1.2)	GO:0004801|sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1383	PATRIC.2.9855.2.9855.con.0001.CDS.1403069.1403731.fwd	PATRIC	CDS	1403069	1403731	663	+	PGF_03510298	220	Surface protein PspC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1384	PATRIC.2.9855.2.9855.con.0001.CDS.1404063.1404557.fwd	PATRIC	CDS	1404063	1404557	495	+	PGF_00674334	164	FIG042921: similarity to aminoacyl-tRNA editing enzymes YbaK, ProX	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1386	PATRIC.2.9855.2.9855.con.0001.CDS.1405047.1408157.fwd	PATRIC	CDS	1405047	1408157	3111	+	PGF_02620852	1036	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1387	PATRIC.2.9855.2.9855.con.0001.CDS.1408518.1409549.fwd	PATRIC	CDS	1408518	1409549	1032	+	PGF_00416771	343	Cation transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1388	PATRIC.2.9855.2.9855.con.0001.CDS.1409719.1409967.fwd	PATRIC	CDS	1409719	1409967	249	+	PGF_02595637	82	Transcriptional regulator, AbrB family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1390	PATRIC.2.9855.2.9855.con.0001.CDS.1411151.1412080.rev	PATRIC	CDS	1411151	1412080	930	-	PGF_08406542	309	Phage endolysin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1391	PATRIC.2.9855.2.9855.con.0001.CDS.1412265.1413122.rev	PATRIC	CDS	1412265	1413122	858	-	PGF_00058793	285	Transcriptional regulator of rhamnose utilization, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.122	PATRIC.2.9855.2.9855.con.0001.CDS.141315.143306.fwd	PATRIC	CDS	141315	143306	1992	+	PGF_01136362	663	Transketolase (EC 2.2.1.1)	GO:0004802|transketolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1392	PATRIC.2.9855.2.9855.con.0001.CDS.1413314.1414117.fwd	PATRIC	CDS	1413314	1414117	804	+	PGF_00061907	267	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase (EC 1.1.1.127) @ 2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)	GO:0047001|2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase activity;GO:0008678|2-deoxy-D-gluconate 3-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1393	PATRIC.2.9855.2.9855.con.0001.CDS.1414133.1414771.fwd	PATRIC	CDS	1414133	1414771	639	+	PGF_00403733	212	predicted 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)	GO:0008697|4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1395	PATRIC.2.9855.2.9855.con.0001.CDS.1415774.1416892.fwd	PATRIC	CDS	1415774	1416892	1119	+	PGF_01126005	372	Rod shape-determining protein RodA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1396	PATRIC.2.9855.2.9855.con.0001.CDS.1417217.1418458.rev	PATRIC	CDS	1417217	1418458	1242	-	PGF_00905234	413	Manganese transport protein MntH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1397	PATRIC.2.9855.2.9855.con.0001.CDS.1418455.1419711.rev	PATRIC	CDS	1418455	1419711	1257	-	PGF_04560429	418	Mg/Co/Ni transporter MgtE, CBS domain-containing	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1398	PATRIC.2.9855.2.9855.con.0001.CDS.1420351.1420857.fwd	PATRIC	CDS	1420351	1420857	507	+	PGF_00417736	168	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1399	PATRIC.2.9855.2.9855.con.0001.CDS.1421109.1421801.rev	PATRIC	CDS	1421109	1421801	693	-	PGF_00425969	230	Pyrimidine 5'-nucleotidase YjjG (EC 3.1.3.5)	GO:0008253|5'-nucleotidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1400	PATRIC.2.9855.2.9855.con.0001.CDS.1421931.1422620.fwd	PATRIC	CDS	1421931	1422620	690	+	PGF_03122406	229	Predicted N-ribosylNicotinamide CRP-like regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1401	PATRIC.2.9855.2.9855.con.0001.CDS.1423007.1423663.fwd	PATRIC	CDS	1423007	1423663	657	+	PGF_07420062	218	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1402	PATRIC.2.9855.2.9855.con.0001.CDS.1423669.1425129.fwd	PATRIC	CDS	1423669	1425129	1461	+	PGF_00051038	486	Sensory transduction histidine kinase (with HAMP domain)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1404	PATRIC.2.9855.2.9855.con.0001.CDS.1426529.1428241.rev	PATRIC	CDS	1426529	1428241	1713	-	PGF_06837078	570	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1405	PATRIC.2.9855.2.9855.con.0001.CDS.1428859.1429200.rev	PATRIC	CDS	1428859	1429200	342	-	PGF_03320197	113	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1406	PATRIC.2.9855.2.9855.con.0001.CDS.1429555.1430190.fwd	PATRIC	CDS	1429555	1430190	636	+	PGF_00023289	211	Multimeric flavodoxin WrbA family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1407	PATRIC.2.9855.2.9855.con.0001.CDS.1430327.1431127.rev	PATRIC	CDS	1430327	1431127	801	-	PGF_03139283	266	Chitinase (EC 3.2.1.14)	GO:0004568|chitinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1408	PATRIC.2.9855.2.9855.con.0001.CDS.1431648.1433372.fwd	PATRIC	CDS	1431648	1433372	1725	+	PGF_00058726	574	Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1409	PATRIC.2.9855.2.9855.con.0001.CDS.1433662.1435206.fwd	PATRIC	CDS	1433662	1435206	1545	+	PGF_00026247	514	Acyl-CoA:acetate CoA-transferase, alpha subunit (EC 2.8.3.8) / Acyl-CoA:acetate CoA-transferase, beta subunit (EC 2.8.3.8) @ Acyl-CoA:acetate CoA transferase (EC 2.8.3.8)	GO:0008775|acetate CoA-transferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1410	PATRIC.2.9855.2.9855.con.0001.CDS.1435281.1436675.fwd	PATRIC	CDS	1435281	1436675	1395	+	PGF_05940986	464	D-beta-hydroxybutyrate permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1411	PATRIC.2.9855.2.9855.con.0001.CDS.1436740.1437156.fwd	PATRIC	CDS	1436740	1437156	417	+	PGF_03241496	138	MaoC-like dehydratase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1412	PATRIC.2.9855.2.9855.con.0001.CDS.1437417.1437800.rev	PATRIC	CDS	1437417	1437800	384	-	PGF_00055284	127	Superoxide reductase (EC 1.15.1.2)	GO:0050605|superoxide reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1413	PATRIC.2.9855.2.9855.con.0001.CDS.1438166.1439224.rev	PATRIC	CDS	1438166	1439224	1059	-	PGF_05728830	352	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.123	PATRIC.2.9855.2.9855.con.0001.CDS.143914.145521.fwd	PATRIC	CDS	143914	145521	1608	+	PGF_00048964	535	Ribulokinase (EC 2.7.1.16)	GO:0008741|ribulokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1414	PATRIC.2.9855.2.9855.con.0001.CDS.1439520.1440641.rev	PATRIC	CDS	1439520	1440641	1122	-	PGF_09679949	373	DNA alkylation repair enzyme	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1415	PATRIC.2.9855.2.9855.con.0001.CDS.1440800.1441714.rev	PATRIC	CDS	1440800	1441714	915	-	PGF_08548202	304	Transcriptional regulator, YafY family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1416	PATRIC.2.9855.2.9855.con.0001.CDS.1441824.1442249.fwd	PATRIC	CDS	1441824	1442249	426	+	PGF_06621789	141	PTS system, mannose-specific IIA component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1417	PATRIC.2.9855.2.9855.con.0001.CDS.1442396.1443148.rev	PATRIC	CDS	1442396	1443148	753	-	PGF_05728830	250	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1419	PATRIC.2.9855.2.9855.con.0001.CDS.1443866.1444381.fwd	PATRIC	CDS	1443866	1444381	516	+	PGF_00896280	171	RNA polymerase ECF-type sigma factor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1421	PATRIC.2.9855.2.9855.con.0001.CDS.1444811.1445338.fwd	PATRIC	CDS	1444811	1445338	528	+	PGF_10470801	175	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1422	PATRIC.2.9855.2.9855.con.0001.CDS.1445331.1445636.fwd	PATRIC	CDS	1445331	1445636	306	+	PGF_01281275	101	Predicted membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1423	PATRIC.2.9855.2.9855.con.0001.CDS.1446014.1447681.rev	PATRIC	CDS	1446014	1447681	1668	-	PGF_10333181	555	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1424	PATRIC.2.9855.2.9855.con.0001.CDS.1447834.1448481.fwd	PATRIC	CDS	1447834	1448481	648	+	PGF_12919466	215	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1426	PATRIC.2.9855.2.9855.con.0001.CDS.1449940.1450749.fwd	PATRIC	CDS	1449940	1450749	810	+	PGF_10519324	269	ABC transporter, permease protein (cluster 10, nitrate/sulfonate/bicarbonate)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1427	PATRIC.2.9855.2.9855.con.0001.CDS.1450848.1451888.fwd	PATRIC	CDS	1450848	1451888	1041	+	PGF_08616437	346	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1428	PATRIC.2.9855.2.9855.con.0001.CDS.1451904.1452731.fwd	PATRIC	CDS	1451904	1452731	828	+	PGF_03097747	275	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1431	PATRIC.2.9855.2.9855.con.0001.CDS.1455501.1456724.fwd	PATRIC	CDS	1455501	1456724	1224	+	PGF_01625234	407	Thioredoxin reductase (EC 1.8.1.9)	GO:0004791|thioredoxin-disulfide reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1432	PATRIC.2.9855.2.9855.con.0001.CDS.1457064.1458401.fwd	PATRIC	CDS	1457064	1458401	1338	+	PGF_02818638	445	Hemolysins and related proteins containing CBS domains	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1433	PATRIC.2.9855.2.9855.con.0001.CDS.1458794.1459429.fwd	PATRIC	CDS	1458794	1459429	636	+	PGF_00599208	211	Integral membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1434	PATRIC.2.9855.2.9855.con.0001.CDS.1459739.1460443.fwd	PATRIC	CDS	1459739	1460443	705	+	PGF_12869856	234	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1435	PATRIC.2.9855.2.9855.con.0001.CDS.1460443.1461195.fwd	PATRIC	CDS	1460443	1461195	753	+	PGF_12817339	250	bacteriocin ABC transporter, permease protein subunit, putative	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1436	PATRIC.2.9855.2.9855.con.0001.CDS.1461200.1461976.fwd	PATRIC	CDS	1461200	1461976	777	+	PGF_01284480	258	putative MutG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1437	PATRIC.2.9855.2.9855.con.0001.CDS.1462044.1462706.fwd	PATRIC	CDS	1462044	1462706	663	+	PGF_02472217	220	Response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1438	PATRIC.2.9855.2.9855.con.0001.CDS.1462694.1464070.fwd	PATRIC	CDS	1462694	1464070	1377	+	PGF_02620852	458	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.21	PATRIC.2.9855.2.9855.con.0001.CDS.14633.15055.fwd	PATRIC	CDS	14633	15055	423	+	PGF_02921606	140	PTS system, mannose/fructose/sorbose family, IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1439	PATRIC.2.9855.2.9855.con.0001.CDS.1464525.1466537.fwd	PATRIC	CDS	1464525	1466537	2013	+	PGF_07849456	670	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.126	PATRIC.2.9855.2.9855.con.0001.CDS.146662.147801.fwd	PATRIC	CDS	146662	147801	1140	+	PGF_03742549	379	L-arabinose ABC transporter, substrate-binding protein AraF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1441	PATRIC.2.9855.2.9855.con.0001.CDS.1467447.1468010.rev	PATRIC	CDS	1467447	1468010	564	-	PGF_07182652	187	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1442	PATRIC.2.9855.2.9855.con.0001.CDS.1468209.1469465.fwd	PATRIC	CDS	1468209	1469465	1257	+	PGF_01520109	418	Multidrug-efflux transporter, major facilitator superfamily (MFS)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1443	PATRIC.2.9855.2.9855.con.0001.CDS.1469437.1469595.fwd	PATRIC	CDS	1469437	1469595	159	+	PGF_00064767	52	Uncharacterized isochorismatase family protein YwoC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1444	PATRIC.2.9855.2.9855.con.0001.CDS.1469691.1470746.rev	PATRIC	CDS	1469691	1470746	1056	-	PGF_00024594	351	NADH oxidase (EC 1.-.-.-)	GO:0008748|N-ethylmaleimide reductase activity;GO:0008748|reduced coenzyme F420 dehydrogenase activity;GO:0008748|sulfur oxygenase reductase activity;GO:0008748|malolactic enzyme activity;GO:0008748|NADPH:sulfur oxidoreductase activity;GO:0008748|epoxyqueuosine reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1445	PATRIC.2.9855.2.9855.con.0001.CDS.1470876.1471241.fwd	PATRIC	CDS	1470876	1471241	366	+	PGF_03320197	121	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1446	PATRIC.2.9855.2.9855.con.0001.CDS.1471307.1473013.rev	PATRIC	CDS	1471307	1473013	1707	-	PGF_01284183	568	Signaling protein with a acyltransferase and GGDEF domains	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1449	PATRIC.2.9855.2.9855.con.0001.CDS.1475106.1476089.rev	PATRIC	CDS	1475106	1476089	984	-	PGF_05219980	327	Oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1450	PATRIC.2.9855.2.9855.con.0001.CDS.1476499.1476903.fwd	PATRIC	CDS	1476499	1476903	405	+	PGF_00057506	134	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1451	PATRIC.2.9855.2.9855.con.0001.CDS.1477075.1478793.fwd	PATRIC	CDS	1477075	1478793	1719	+	PGF_08577967	572	Efflux ABC transporter, permease/ATP-binding protein YfiB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.127	PATRIC.2.9855.2.9855.con.0001.CDS.147872.149407.fwd	PATRIC	CDS	147872	149407	1536	+	PGF_10409748	511	L-arabinose ABC transporter, ATP-binding protein AraG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1452	PATRIC.2.9855.2.9855.con.0001.CDS.1478800.1480650.fwd	PATRIC	CDS	1478800	1480650	1851	+	PGF_03752797	616	Efflux ABC transporter, permease/ATP-binding protein YfiC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1453	PATRIC.2.9855.2.9855.con.0001.CDS.1480673.1481371.fwd	PATRIC	CDS	1480673	1481371	699	+	PGF_10420457	232	MBL-fold metallo-hydrolase superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1454	PATRIC.2.9855.2.9855.con.0001.CDS.1481541.1482284.fwd	PATRIC	CDS	1481541	1482284	744	+	PGF_00123216	247	Uncharacterized protein YoxB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1455	PATRIC.2.9855.2.9855.con.0001.CDS.1482483.1483043.fwd	PATRIC	CDS	1482483	1483043	561	+	PGF_08585032	186	Ribosomal RNA adenine dimethylase domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1456	PATRIC.2.9855.2.9855.con.0001.CDS.1483299.1484021.rev	PATRIC	CDS	1483299	1484021	723	-	PGF_01281724	240	Predicted membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1457	PATRIC.2.9855.2.9855.con.0001.CDS.1484249.1486036.fwd	PATRIC	CDS	1484249	1486036	1788	+	PGF_02709485	595	EAL domain/GGDEF domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1458	PATRIC.2.9855.2.9855.con.0001.CDS.1486126.1487457.rev	PATRIC	CDS	1486126	1487457	1332	-	PGF_00410817	443	putative sialidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1459	PATRIC.2.9855.2.9855.con.0001.CDS.1487836.1488267.fwd	PATRIC	CDS	1487836	1488267	432	+	PGF_10423881	143	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1460	PATRIC.2.9855.2.9855.con.0001.CDS.1488548.1490281.fwd	PATRIC	CDS	1488548	1490281	1734	+	PGF_10540665	577	Heterodimeric efflux ABC transporter, permease/ATP-binding subunit 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1461	PATRIC.2.9855.2.9855.con.0001.CDS.1490274.1492205.fwd	PATRIC	CDS	1490274	1492205	1932	+	PGF_08128839	643	Heterodimeric efflux ABC transporter, permease/ATP-binding subunit 2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1462	PATRIC.2.9855.2.9855.con.0001.CDS.1492442.1493494.fwd	PATRIC	CDS	1492442	1493494	1053	+	PGF_05728830	350	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1464	PATRIC.2.9855.2.9855.con.0001.CDS.1493840.1494163.fwd	PATRIC	CDS	1493840	1494163	324	+	PGF_02275874	107	Uncharacterized protein MJ1492	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.128	PATRIC.2.9855.2.9855.con.0001.CDS.149420.150616.fwd	PATRIC	CDS	149420	150616	1197	+	PGF_10500186	398	L-arabinose ABC transporter, permease protein AraH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1465	PATRIC.2.9855.2.9855.con.0001.CDS.1494215.1494778.fwd	PATRIC	CDS	1494215	1494778	564	+	PGF_10487056	187	ABC transporter, substrate-binding protein (cluster 2, ribose/xylose/arabinose/galactose)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1466	PATRIC.2.9855.2.9855.con.0001.CDS.1495113.1495574.fwd	PATRIC	CDS	1495113	1495574	462	+	PGF_01281484	153	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1467	PATRIC.2.9855.2.9855.con.0001.CDS.1495576.1495899.fwd	PATRIC	CDS	1495576	1495899	324	+	PGF_01282288	107	Thioredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1468	PATRIC.2.9855.2.9855.con.0001.CDS.1496145.1496576.fwd	PATRIC	CDS	1496145	1496576	432	+	PGF_05859228	143	Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase (EC 3.1.7.2)	GO:0008893|guanosine-3',5'-bis(diphosphate) 3'-diphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1469	PATRIC.2.9855.2.9855.con.0001.CDS.1496776.1497246.fwd	PATRIC	CDS	1496776	1497246	471	+	PGF_01314750	156	Histone acetyltransferase HPA2 and related acetyltransferases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1470	PATRIC.2.9855.2.9855.con.0001.CDS.1497561.1498355.fwd	PATRIC	CDS	1497561	1498355	795	+	PGF_00037043	264	Probable endo-1,4-beta-xylanase	[illegible] activity;GO:0000179|protein C-terminal carboxyl O-methyltransferase activity;GO:0000179|tRNA (guanine-N2-)-methyltransferase activity;GO:0000179|C-methyltransferase activity;GO:0000179|N-methyltransferase activity;GO:0000179|O-methyltransferase activity;GO:0000179|S-methyltransferase activity;GO:0000179|RNA methyltransferase activity;GO:0000179|mRNA methyltransferase activity;GO:0000179|tRNA methyltransferase activity;GO:0000179|protein methyltransferase activity;GO:0000179|2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity;GO:0000179|rRNA methyltransferase activity;GO:0000179|rRNA (uridine-2'-O-)-methyltransferase activity;GO:0000179|rRNA (adenine-N6-)-methyltransferase activity;GO:0000179|DNA-methyltransferase activity;GO:0000179|tRNA (guanine-N1-)-methyltransferase activity;GO:0000179|rRNA (cytosine-C5-)-methyltransferase activity;GO:0000179|selenocysteine methyltransferase activity;GO:0000179|arginine N-methyltransferase activity;GO:0000179|protein-arginine N-methyltransferase activity;GO:0000179|lysine N-methyltransferase activity;GO:0000179|protein-lysine N-methyltransferase activity;GO:0000179|tRNA (uracil) methyltransferase activity;GO:0000179|tRNA (guanine) methyltransferase activity;GO:0000179|tRNA (adenine) methyltransferase activity;GO:0000179|tRNA (cytosine) methyltransferase activity;GO:0000179|tRNA (cytosine-5-)-methyltransferase activity;GO:0000179|tRNA (adenine-N1-)-methyltransferase activity;GO:0000179|rRNA (adenine) methyltransferase activity;GO:0000179|rRNA (cytosine) methyltransferase activity;GO:0000179|rRNA (guanine) methyltransferase activity;GO:0000179|rRNA (uridine) methyltransferase activity;GO:0000179|protein C-terminal leucine carboxyl O-methyltransferase activity;GO:0000179|1-phenanthrol methyltransferase activity;GO:0000179|protein-arginine NS-methyltransferase activity;GO:0000179|methylarsonite methyltransferase activity;GO:0000179|dimethylarsinite methyltransferase activity;GO:0000179|4,5-
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1479	PATRIC.2.9855.2.9855.con.0001.CDS.1503585.1504727.fwd	PATRIC	CDS	1503585	1504727	1143	+	PGF_00018000	380	Lysine-N-methylase (EC 2.1.1.-)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.22	PATRIC.2.9855.2.9855.con.0001.CDS.15052.15522.fwd	PATRIC	CDS	15052	15522	471	+	PGF_08661804	156	PTS system, mannose-specific IIB component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1480	PATRIC.2.9855.2.9855.con.0001.CDS.1505381.1505800.fwd	PATRIC	CDS	1505381	1505800	420	+	PGF_01282232	139	Asparagine-rich protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1481	PATRIC.2.9855.2.9855.con.0001.CDS.1506056.1506877.fwd	PATRIC	CDS	1506056	1506877	822	+	PGF_00024615	273	NADH pyrophosphatase (EC 3.6.1.22), decaps 5'-NAD modified RNA	GO:0000210|NAD+ diphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1483	PATRIC.2.9855.2.9855.con.0001.CDS.1508744.1509634.fwd	PATRIC	CDS	1508744	1509634	891	+	PGF_04493258	296	Cobalt-zinc-cadmium resistance protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1484	PATRIC.2.9855.2.9855.con.0001.CDS.1510232.1511779.fwd	PATRIC	CDS	1510232	1511779	1548	+	PGF_07834560	515	Coenzyme A transferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.129	PATRIC.2.9855.2.9855.con.0001.CDS.151093.151926.fwd	PATRIC	CDS	151093	151926	834	+	PGF_00845945	277	DegV family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1485	PATRIC.2.9855.2.9855.con.0001.CDS.1511810.1512445.fwd	PATRIC	CDS	1511810	1512445	636	+	PGF_01468574	211	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1487	PATRIC.2.9855.2.9855.con.0001.CDS.1512925.1514331.fwd	PATRIC	CDS	1512925	1514331	1407	+	PGF_00778630	468	Uncharacterized amino acid permease, GabP family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1488	PATRIC.2.9855.2.9855.con.0001.CDS.1514612.1514821.fwd	PATRIC	CDS	1514612	1514821	210	+	PGF_00053039	69	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1489	PATRIC.2.9855.2.9855.con.0001.CDS.1515379.1516209.fwd	PATRIC	CDS	1515379	1516209	831	+	PGF_03514578	276	Beta-glucoside bgl operon antiterminator, BglG family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1490	PATRIC.2.9855.2.9855.con.0001.CDS.1516543.1517955.fwd	PATRIC	CDS	1516543	1517955	1413	+	PGF_04512237	470	PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component / PTS system, beta-glucoside-specific IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1491	PATRIC.2.9855.2.9855.con.0001.CDS.1517930.1518448.fwd	PATRIC	CDS	1517930	1518448	519	+	PGF_04512237	172	PTS system, beta-glucoside-specific IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1492	PATRIC.2.9855.2.9855.con.0001.CDS.1518543.1519943.fwd	PATRIC	CDS	1518543	1519943	1401	+	PGF_00405750	466	putative BglB fragment	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1493	PATRIC.2.9855.2.9855.con.0001.CDS.1520015.1521460.fwd	PATRIC	CDS	1520015	1521460	1446	+	PGF_08148954	481	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1497	PATRIC.2.9855.2.9855.con.0001.CDS.1523050.1524084.fwd	PATRIC	CDS	1523050	1524084	1035	+	PGF_05179218	344	Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (EC 3.2.1.17)	GO:0003796|lysozyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1501	PATRIC.2.9855.2.9855.con.0001.CDS.1527035.1527241.fwd	PATRIC	CDS	1527035	1527241	207	+	PGF_00053039	68	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1502	PATRIC.2.9855.2.9855.con.0001.CDS.1527606.1528343.fwd	PATRIC	CDS	1527606	1528343	738	+	PGF_00417736	245	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1503	PATRIC.2.9855.2.9855.con.0001.CDS.1528455.1529273.rev	PATRIC	CDS	1528455	1529273	819	-	PGF_04848882	272	Uncharacterized membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1504	PATRIC.2.9855.2.9855.con.0001.CDS.1529862.1531472.rev	PATRIC	CDS	1529862	1531472	1611	-	PGF_03342342	536	Uncharacterized membrane protein, YraQ family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1505	PATRIC.2.9855.2.9855.con.0001.CDS.1531983.1532663.fwd	PATRIC	CDS	1531983	1532663	681	+	PGF_00425969	226	Pyrimidine 5'-nucleotidase YjjG (EC 3.1.3.5)	GO:0008253|5'-nucleotidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1506	PATRIC.2.9855.2.9855.con.0001.CDS.1532919.1533920.fwd	PATRIC	CDS	1532919	1533920	1002	+	PGF_12905405	333	Oxidoreductase, Gfo/Idh/MocA family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.131	PATRIC.2.9855.2.9855.con.0001.CDS.153441.154733.fwd	PATRIC	CDS	153441	154733	1293	+	PGF_08161714	430	N-acetyl-D-glucosamine ABC transporter, substrate-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1511	PATRIC.2.9855.2.9855.con.0001.CDS.1537268.1537915.rev	PATRIC	CDS	1537268	1537915	648	-	PGF_00059157	215	Transcriptional regulator, Crp/Fnr family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1512	PATRIC.2.9855.2.9855.con.0001.CDS.1537983.1538873.fwd	PATRIC	CDS	1537983	1538873	891	+	PGF_03087500	296	Uncharacterized UPF0750 membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1514	PATRIC.2.9855.2.9855.con.0001.CDS.1539486.1539695.fwd	PATRIC	CDS	1539486	1539695	210	+	PGF_00053039	69	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1515	PATRIC.2.9855.2.9855.con.0001.CDS.1540013.1540723.fwd	PATRIC	CDS	1540013	1540723	711	+	PGF_04038070	236	Alkaline phosphatase like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1516	PATRIC.2.9855.2.9855.con.0001.CDS.1540880.1541572.fwd	PATRIC	CDS	1540880	1541572	693	+	PGF_10522720	230	Metal-dependent hydrolase	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1519	PATRIC.2.9855.2.9855.con.0001.CDS.1543383.1543958.rev	PATRIC	CDS	1543383	1543958	576	-	PGF_01282224	191	5-carboxymethyl uridine and 5-carboxymethyl 2-thiouridine methyltransferase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1520	PATRIC.2.9855.2.9855.con.0001.CDS.1544292.1545848.fwd	PATRIC	CDS	1544292	1545848	1557	+	PGF_00053873	518	Spore cortex-lytic enzyme pre-pro-form		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1521	PATRIC.2.9855.2.9855.con.0001.CDS.1545906.1547303.rev	PATRIC	CDS	1545906	1547303	1398	-	PGF_00066854	465	Aspartate ammonia-lyase (EC 4.3.1.1)	GO:0008797|aspartate ammonia-lyase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1522	PATRIC.2.9855.2.9855.con.0001.CDS.1547459.1548697.fwd	PATRIC	CDS	1547459	1548697	1239	+	PGF_00286985	412	[FeFe]-hydrogenase maturation protein HydF		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.132	PATRIC.2.9855.2.9855.con.0001.CDS.154807.155382.fwd	PATRIC	CDS	154807	155382	576	+	PGF_05110907	191	N-acetyl-D-glucosamine ABC transporter, permease protein 1		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1525	PATRIC.2.9855.2.9855.con.0001.CDS.1550565.1551170.fwd	PATRIC	CDS	1550565	1551170	606	+	PGF_01286621	201	Transcriptional regulators of sugar metabolism		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1526	PATRIC.2.9855.2.9855.con.0001.CDS.1551438.1551674.fwd	PATRIC	CDS	1551438	1551674	237	+	PGF_00416536	78	Carboxyl esterase, a/b hydrolase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1527	PATRIC.2.9855.2.9855.con.0001.CDS.1551723.1552325.fwd	PATRIC	CDS	1551723	1552325	603	+	PGF_00416536	200	Carboxyl esterase, a/b hydrolase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1528	PATRIC.2.9855.2.9855.con.0001.CDS.1552657.1553304.rev	PATRIC	CDS	1552657	1553304	648	-	PGF_02278882	215	Iron-sulfur flavoprotein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1529	PATRIC.2.9855.2.9855.con.0001.CDS.1553544.1553801.fwd	PATRIC	CDS	1553544	1553801	258	+	PGF_03320197	85	Transcriptional regulator, HxlR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.23	PATRIC.2.9855.2.9855.con.0001.CDS.15538.16302.fwd	PATRIC	CDS	15538	16302	765	+	PGF_01653368	254	PTS system, mannose-specific IIC component		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1530	PATRIC.2.9855.2.9855.con.0001.CDS.1553965.1554351.fwd	PATRIC	CDS	1553965	1554351	387	+	PGF_01302878	128	Glyoxylase family protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1531	PATRIC.2.9855.2.9855.con.0001.CDS.1554561.1555184.rev	PATRIC	CDS	1554561	1555184	624	-	PGF_06788576	207	SAM-dependent methyltransferase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.133	PATRIC.2.9855.2.9855.con.0001.CDS.155467.155727.fwd	PATRIC	CDS	155467	155727	261	+	PGF_05110907	86	N-acetyl-D-glucosamine ABC transporter, permease protein 1		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1532	PATRIC.2.9855.2.9855.con.0001.CDS.1555715.1556041.rev	PATRIC	CDS	1555715	1556041	327	-	PGF_03320197	108	Transcriptional regulator, HxlR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1534	PATRIC.2.9855.2.9855.con.0001.CDS.1556856.1557464.fwd	PATRIC	CDS	1556856	1557464	609	+	PGF_00723627	202	Intracellular protease		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.134	PATRIC.2.9855.2.9855.con.0001.CDS.155744.156583.fwd	PATRIC	CDS	155744	156583	840	+	PGF_10552060	279	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1538	PATRIC.2.9855.2.9855.con.0001.CDS.1558322.1558678.fwd	PATRIC	CDS	1558322	1558678	357	+	PGF_02690675	118	RidA/YER057c/UK114 superfamily protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1543	PATRIC.2.9855.2.9855.con.0001.CDS.1560823.1561779.rev	PATRIC	CDS	1560823	1561779	957	-	PGF_07987589	318	Transcriptional regulator, LysR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1544	PATRIC.2.9855.2.9855.con.0001.CDS.1561861.1563408.fwd	PATRIC	CDS	1561861	1563408	1548	+	PGF_00066854	515	Aspartate ammonia-lyase (EC 4.3.1.1)	GO:0008797|aspartate ammonia-lyase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1545	PATRIC.2.9855.2.9855.con.0001.CDS.1564224.1565489.fwd	PATRIC	CDS	1564224	1565489	1266	+	PGF_00008168	421	Glutamate-aspartate carrier protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.135	PATRIC.2.9855.2.9855.con.0001.CDS.156634.158844.fwd	PATRIC	CDS	156634	158844	2211	+	PGF_03854585	736	alpha-galactosidase (EC 3.2.1.22)	GO:0004557|alpha-galactosidase activity;GO:0004557|raffinose alpha-galactosidase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1547	PATRIC.2.9855.2.9855.con.0001.CDS.1567173.1567832.fwd	PATRIC	CDS	1567173	1567832	660	+	PGF_01056563	219	Chloramphenicol O-acetyltransferase (EC 2.3.1.28) => CatA15/A16 family	GO:0008811|chloramphenicol O-acetyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1549	PATRIC.2.9855.2.9855.con.0001.CDS.1569083.1569646.fwd	PATRIC	CDS	1569083	1569646	564	+	PGF_10153092	187	Nitroreductase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1553	PATRIC.2.9855.2.9855.con.0001.CDS.1572144.1572557.rev	PATRIC	CDS	1572144	1572557	414	-	PGF_09978608	137	Transposase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1554	PATRIC.2.9855.2.9855.con.0001.CDS.1572542.1572931.rev	PATRIC	CDS	1572542	1572931	390	-	PGF_09978608	129	Transposase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1560	PATRIC.2.9855.2.9855.con.0001.CDS.1577320.1578216.fwd	PATRIC	CDS	1577320	1578216	897	+	PGF_00012030	298	Histone acetyltransferase HPA2 and related acetyltransferases		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1562	PATRIC.2.9855.2.9855.con.0001.CDS.1578914.1579477.fwd	PATRIC	CDS	1578914	1579477	564	+	PGF_00005956	187	Flavoredoxin		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1563	PATRIC.2.9855.2.9855.con.0001.CDS.1579787.1580929.fwd	PATRIC	CDS	1579787	1580929	1143	+	PGF_05606505	380	Cell surface protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1564	PATRIC.2.9855.2.9855.con.0001.CDS.1581879.1583786.fwd	PATRIC	CDS	1581879	1583786	1908	+	PGF_01175575	635	Threonyl-tRNA synthetase (EC 6.1.1.3)	GO:0004829|threonine-tRNA ligase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1566	PATRIC.2.9855.2.9855.con.0001.CDS.1585118.1589458.fwd	PATRIC	CDS	1585118	1589458	4341	+	PGF_02154745	1446	DNA polymerase III polC-type (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.136	PATRIC.2.9855.2.9855.con.0001.CDS.159054.161150.fwd	PATRIC	CDS	159054	161150	2097	+	PGF_03854585	698	alpha-galactosidase (EC 3.2.1.22)	GO:0004557|alpha-galactosidase activity;GO:0004557|raffinose alpha-galactosidase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1578	PATRIC.2.9855.2.9855.con.0001.CDS.1599277.1600047.fwd	PATRIC	CDS	1599277	1600047	771	+	PGF_05792788	256	Phage recombination protein Bet		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1579	PATRIC.2.9855.2.9855.con.0001.CDS.1600125.1601111.fwd	PATRIC	CDS	1600125	1601111	987	+	PGF_12690820	328	Phage replication initiation		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1580	PATRIC.2.9855.2.9855.con.0001.CDS.1601074.1601787.fwd	PATRIC	CDS	1601074	1601787	714	+	PGF_00421821	237	DNA replication helicase loader DnaC/DnaI		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1581	PATRIC.2.9855.2.9855.con.0001.CDS.1601928.1602170.fwd	PATRIC	CDS	1601928	1602170	243	+	PGF_02595637	80	Transcriptional regulator, AbrB family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1582	PATRIC.2.9855.2.9855.con.0001.CDS.1602196.1602948.fwd	PATRIC	CDS	1602196	1602948	753	+	PGF_12859583	250	Antirepressor [Bacteriophage A118]		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1584	PATRIC.2.9855.2.9855.con.0001.CDS.1603343.1604548.fwd	PATRIC	CDS	1603343	1604548	1206	+	PGF_00009042	401	Glycosyl transferase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1594	PATRIC.2.9855.2.9855.con.0001.CDS.1611735.1613702.fwd	PATRIC	CDS	1611735	1613702	1968	+	PGF_00020781	655	Methionyl-tRNA synthetase-related protein 2		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1595	PATRIC.2.9855.2.9855.con.0001.CDS.1614298.1615107.fwd	PATRIC	CDS	1614298	1615107	810	+	PGF_00057506	269	Transcriptional regulator, MerR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1597	PATRIC.2.9855.2.9855.con.0001.CDS.1616835.1617293.rev	PATRIC	CDS	1616835	1617293	459	-	PGF_00057506	152	Transcriptional regulator, MerR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1598	PATRIC.2.9855.2.9855.con.0001.CDS.1617525.1618436.fwd	PATRIC	CDS	1617525	1618436	912	+	PGF_00423124	303	Dienelactone hydrolase domain protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1599	PATRIC.2.9855.2.9855.con.0001.CDS.1618707.1619600.rev	PATRIC	CDS	1618707	1619600	894	-	PGF_07987589	297	Transcriptional regulator, LysR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.138	PATRIC.2.9855.2.9855.con.0001.CDS.161889.163307.fwd	PATRIC	CDS	161889	163307	1419	+	PGF_03752280	472	[FeFe]-hydrogenase maturation protein HydG		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1600	PATRIC.2.9855.2.9855.con.0001.CDS.1619735.1620454.fwd	PATRIC	CDS	1619735	1620454	720	+	PGF_10426350	239	Short-chain dehydrogenase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1602	PATRIC.2.9855.2.9855.con.0001.CDS.1620960.1621571.rev	PATRIC	CDS	1620960	1621571	612	-	PGF_03950680	203	Transporter, LysE family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1603	PATRIC.2.9855.2.9855.con.0001.CDS.1621703.1622440.fwd	PATRIC	CDS	1621703	1622440	738	+	PGF_07987589	245	Transcriptional regulator, LysR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1604	PATRIC.2.9855.2.9855.con.0001.CDS.1622447.1622590.fwd	PATRIC	CDS	1622447	1622590	144	+	PGF_07987589	47	Transcriptional regulator, LysR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1605	PATRIC.2.9855.2.9855.con.0001.CDS.1622869.1623558.fwd	PATRIC	CDS	1622869	1623558	690	+	PGF_04122372	229	Uncharacterized protein YgeA of aspartate/glutamate/hydantoin racemase family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1607	PATRIC.2.9855.2.9855.con.0001.CDS.1625550.1626074.fwd	PATRIC	CDS	1625550	1626074	525	+	PGF_07182652	174	Transcriptional regulator, AcrR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.24	PATRIC.2.9855.2.9855.con.0001.CDS.16317.17141.fwd	PATRIC	CDS	16317	17141	825	+	PGF_00644224	274	PTS system, mannose-specific IID component		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1623	PATRIC.2.9855.2.9855.con.0001.CDS.1633446.1634129.fwd	PATRIC	CDS	1633446	1634129	684	+	PGF_01281686	227	Accessory gene regulator protein B (EC 3.4.-.-)	GO:0008234|cysteine-type peptidase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1626	PATRIC.2.9855.2.9855.con.0001.CDS.1635020.1636852.fwd	PATRIC	CDS	1635020	1636852	1833	+	PGF_02620852	610	Two-component system sensor histidine kinase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.139	PATRIC.2.9855.2.9855.con.0001.CDS.163582.165294.fwd	PATRIC	CDS	163582	165294	1713	+	PGF_06837078	570	Methyl-accepting chemotaxis sensor/transducer protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1627	PATRIC.2.9855.2.9855.con.0001.CDS.1636988.1637596.fwd	PATRIC	CDS	1636988	1637596	609	+	PGF_03741671	202	Phosphoglycerate mutase family protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1629	PATRIC.2.9855.2.9855.con.0001.CDS.1637981.1638412.fwd	PATRIC	CDS	1637981	1638412	432	+	PGF_01896482	143	Rrf2 family transcriptional regulator, group III		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1632	PATRIC.2.9855.2.9855.con.0001.CDS.1640645.1640845.rev	PATRIC	CDS	1640645	1640845	201	-	PGF_03281009	66	Uncharacterized protein Bsu3320.5		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1633	PATRIC.2.9855.2.9855.con.0001.CDS.1642001.1642876.fwd	PATRIC	CDS	1642001	1642876	876	+	PGF_10535474	291	Transcriptional regulator, AraC family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1634	PATRIC.2.9855.2.9855.con.0001.CDS.1642935.1644326.fwd	PATRIC	CDS	1642935	1644326	1392	+	PGF_08913741	463	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1636	PATRIC.2.9855.2.9855.con.0001.CDS.1646700.1647272.rev	PATRIC	CDS	1646700	1647272	573	-	PGF_00046564	190	RNA polymerase sigma factor RpoE		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1638	PATRIC.2.9855.2.9855.con.0001.CDS.1647736.1648497.fwd	PATRIC	CDS	1647736	1648497	762	+	PGF_02630413	253	Hydrolase, alpha/beta fold family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.140	PATRIC.2.9855.2.9855.con.0001.CDS.165378.165818.rev	PATRIC	CDS	165378	165818	441	-	PGF_01283109	146	Site-specific tyrosine recombinase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1647	PATRIC.2.9855.2.9855.con.0001.CDS.1660947.1663610.fwd	PATRIC	CDS	1660947	1663610	2664	+	PGF_01444054	887	ATP-dependent RNA helicase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.141	PATRIC.2.9855.2.9855.con.0001.CDS.166369.166689.fwd	PATRIC	CDS	166369	166689	321	+	PGF_10538082	106	Sensory box/GGDEF family protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1648	PATRIC.2.9855.2.9855.con.0001.CDS.1663762.1665837.fwd	PATRIC	CDS	1663762	1665837	2076	+	PGF_10471233	691	ATP-dependent DNA helicase UvrD/PcrA (EC 3.6.4.12)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1649	PATRIC.2.9855.2.9855.con.0001.CDS.1665956.1667062.fwd	PATRIC	CDS	1665956	1667062	1107	+	PGF_00028342	368	Outer membrane protein expression inhibitor		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1651	PATRIC.2.9855.2.9855.con.0001.CDS.1668196.1668846.fwd	PATRIC	CDS	1668196	1668846	651	+	PGF_01304750	216	Flagellar protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.142	PATRIC.2.9855.2.9855.con.0001.CDS.166877.167800.fwd	PATRIC	CDS	166877	167800	924	+	PGF_10538082	307	Sensory box/GGDEF family protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1652	PATRIC.2.9855.2.9855.con.0001.CDS.1668941.1669246.fwd	PATRIC	CDS	1668941	1669246	306	+	PGF_03787622	101	DNA polymerase IV (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1654	PATRIC.2.9855.2.9855.con.0001.CDS.1669850.1670038.rev	PATRIC	CDS	1669850	1670038	189	-	PGF_00045396	62	Transposase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1656	PATRIC.2.9855.2.9855.con.0001.CDS.1671792.1672370.rev	PATRIC	CDS	1671792	1672370	579	-	PGF_07182652	192	Transcriptional regulator, AcrR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1657	PATRIC.2.9855.2.9855.con.0001.CDS.1672659.1672832.fwd	PATRIC	CDS	1672659	1672832	174	+	PGF_10471233	57	ATP-dependent DNA helicase UvrD/PcrA (EC 3.6.4.12)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1658	PATRIC.2.9855.2.9855.con.0001.CDS.1672987.1674030.rev	PATRIC	CDS	1672987	1674030	1044	-	PGF_05728830	347	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1660	PATRIC.2.9855.2.9855.con.0001.CDS.1674803.1675429.fwd	PATRIC	CDS	1674803	1675429	627	+	PGF_00056480	208	ThiJ/Pfpl family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1661	PATRIC.2.9855.2.9855.con.0001.CDS.1675585.1676007.rev	PATRIC	CDS	1675585	1676007	423	-	PGF_02920407	140	Membrane protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1662	PATRIC.2.9855.2.9855.con.0001.CDS.1676101.1676409.rev	PATRIC	CDS	1676101	1676409	309	-	PGF_01282251	102	Mannose-6-phosphate isomerase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1663	PATRIC.2.9855.2.9855.con.0001.CDS.1676634.1676969.fwd	PATRIC	CDS	1676634	1676969	336	+	PGF_03320197	111	Transcriptional regulator, HxlR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1664	PATRIC.2.9855.2.9855.con.0001.CDS.1677111.1677620.fwd	PATRIC	CDS	1677111	1677620	510	+	PGF_10519603	169	Acetyltransferase, GNAT family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1665	PATRIC.2.9855.2.9855.con.0001.CDS.1677870.1678928.fwd	PATRIC	CDS	1677870	1678928	1059	+	PGF_05728830	352	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.143	PATRIC.2.9855.2.9855.con.0001.CDS.167829.169535.fwd	PATRIC	CDS	167829	169535	1707	+	PGF_06837078	568	Methyl-accepting chemotaxis sensor/transducer protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1667	PATRIC.2.9855.2.9855.con.0001.CDS.1679532.1680185.rev	PATRIC	CDS	1679532	1680185	654	-	PGF_02278882	217	Iron-sulfur flavoprotein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1668	PATRIC.2.9855.2.9855.con.0001.CDS.1680311.1680637.fwd	PATRIC	CDS	1680311	1680637	327	+	PGF_03320197	108	Transcriptional regulator, HxlR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1671	PATRIC.2.9855.2.9855.con.0001.CDS.1681540.1682010.fwd	PATRIC	CDS	1681540	1682010	471	+	PGF_00417736	156	Choline binding protein A		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1673	PATRIC.2.9855.2.9855.con.0001.CDS.1682997.1683542.rev	PATRIC	CDS	1682997	1683542	546	-	PGF_02278882	181	Iron-sulfur flavoprotein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1674	PATRIC.2.9855.2.9855.con.0001.CDS.1683660.1684001.fwd	PATRIC	CDS	1683660	1684001	342	+	PGF_03320197	113	Transcriptional regulator, HxlR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1675	PATRIC.2.9855.2.9855.con.0001.CDS.1684301.1685320.fwd	PATRIC	CDS	1684301	1685320	1020	+	PGF_10300269	339	Oxidoreductase, aldo/keto reductase family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1676	PATRIC.2.9855.2.9855.con.0001.CDS.1685401.1686288.rev	PATRIC	CDS	1685401	1686288	888	-	PGF_00017886	295	Transcriptional activator CysL, LysR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1677	PATRIC.2.9855.2.9855.con.0001.CDS.1686431.1687462.fwd	PATRIC	CDS	1686431	1687462	1032	+	PGF_08102025	343	Putative membrane protein YeiH		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1680	PATRIC.2.9855.2.9855.con.0001.CDS.1688646.1689800.rev	PATRIC	CDS	1688646	1689800	1155	-	PGF_09978608	384	Transposase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1683	PATRIC.2.9855.2.9855.con.0001.CDS.1692985.1693725.rev	PATRIC	CDS	1692985	1693725	741	-	PGF_00036238	246	Predicted regulator for deoxynucleoside utilization, GntR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1684	PATRIC.2.9855.2.9855.con.0001.CDS.1694110.1694895.fwd	PATRIC	CDS	1694110	1694895	786	+	PGF_00066257	261	Uridine phosphorylase (EC 2.4.2.3)	GO:0004850|uridine phosphorylase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1685	PATRIC.2.9855.2.9855.con.0001.CDS.1694929.1695330.fwd	PATRIC	CDS	1694929	1695330	402	+	PGF_08837849	133	Cytidine deaminase (EC 3.5.4.5)	GO:0004126|cytidine deaminase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1686	PATRIC.2.9855.2.9855.con.0001.CDS.1695407.1696597.fwd	PATRIC	CDS	1695407	1696597	1191	+	PGF_00033904	396	Phosphopentomutase (EC 5.4.2.7)	GO:0008973|phosphopentomutase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1687	PATRIC.2.9855.2.9855.con.0001.CDS.1696622.1697305.fwd	PATRIC	CDS	1696622	1697305	684	+	PGF_04172176	227	putative membrane protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1688	PATRIC.2.9855.2.9855.con.0001.CDS.1697331.1698044.fwd	PATRIC	CDS	1697331	1698044	714	+	PGF_00038987	237	Purine nucleoside phosphorylase (EC 2.4.2.1)	GO:0004731|purine-nucleoside phosphorylase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1689	PATRIC.2.9855.2.9855.con.0001.CDS.1698068.1699120.fwd	PATRIC	CDS	1698068	1699120	1053	+	PGF_10314822	350	ABC transporter, substrate-binding protein (cluster 11, riboflavin/purine nucleoside/unknown)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1690	PATRIC.2.9855.2.9855.con.0001.CDS.1699231.1700781.rev	PATRIC	CDS	1699231	1700781	1551	+	PGF_01899917	516	ABC transporter, ATP-binding protein (cluster 11, riboflavin/purine nucleoside/unknown) / ABC transporter, ATP-binding protein (cluster 11, riboflavin/purine nucleoside/unknown)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1691	PATRIC.2.9855.2.9855.con.0001.CDS.1700756.1701883.fwd	PATRIC	CDS	1700756	1701883	1128	+	PGF_04065085	375	ABC transporter, permease protein 1 (cluster 11, riboflavin/purine nucleoside/unknown)		

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.144	PATRIC.2.9855.2.9855.con.0001.CDS.170158.171228.fwd	PATRIC	CDS	170158	171228	1071	+	PGF_05728830	356	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1692	PATRIC.2.9855.2.9855.con.0001.CDS.1701873.1702325.fwd	PATRIC	CDS	1701873	1702325	453	+	PGF_04055837	150	ABC transporter, permease protein 2 (cluster 11, riboflavin/purine nucleoside/unknown)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1693	PATRIC.2.9855.2.9855.con.0001.CDS.1702423.1702758.fwd	PATRIC	CDS	1702423	1702758	336	+	PGF_04055837	111	ABC transporter, permease protein 2 (cluster 11, riboflavin/purine nucleoside/unknown)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1694	PATRIC.2.9855.2.9855.con.0001.CDS.1702969.1703619.fwd	PATRIC	CDS	1702969	1703619	651	+	PGF_05026985	216	Deoxyribose-phosphate aldolase (EC 4.1.2.4)	GO:0004139|deoxyribose-phosphate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1695	PATRIC.2.9855.2.9855.con.0001.CDS.1704899.1706608.fwd	PATRIC	CDS	1704899	1706608	1710	+	PGF_06837078	569	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1696	PATRIC.2.9855.2.9855.con.0001.CDS.1706782.1708038.fwd	PATRIC	CDS	1706782	1708038	1257	+	PGF_01291726	418	Uncharacterized amino acid permease, GabP family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1701	PATRIC.2.9855.2.9855.con.0001.CDS.1711504.1712409.rev	PATRIC	CDS	1711504	1712409	906	-	PGF_00409305	301	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1703	PATRIC.2.9855.2.9855.con.0001.CDS.1713146.1713358.fwd	PATRIC	CDS	1713146	1713358	213	+	PGF_00053039	70	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.145	PATRIC.2.9855.2.9855.con.0001.CDS.171317.172816.fwd	PATRIC	CDS	171317	172816	1500	+	PGF_00007128	499	Galactose/methyl galactoside ABC transporter, ATP-binding protein MglA (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1705	PATRIC.2.9855.2.9855.con.0001.CDS.1713911.1715167.rev	PATRIC	CDS	1713911	1715167	1257	-	PGF_12866845	418	Regulator of polyketide synthase expression	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1706	PATRIC.2.9855.2.9855.con.0001.CDS.1715397.1716350.fwd	PATRIC	CDS	1715397	1716350	954	+	PGF_00065180	317	Uncharacterized protein MJ1083	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1707	PATRIC.2.9855.2.9855.con.0001.CDS.1716811.1719945.fwd	PATRIC	CDS	1716811	1719945	3135	+	PGF_00409452	1044	Transmembrane transport protein MmpL family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1708	PATRIC.2.9855.2.9855.con.0001.CDS.1720074.1720616.rev	PATRIC	CDS	1720074	1720616	543	-	PGF_07182652	180	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.25	PATRIC.2.9855.2.9855.con.0001.CDS.17205.18173.fwd	PATRIC	CDS	17205	18173	969	+	PGF_00043266	322	Putative phosphosugar isomerase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1710	PATRIC.2.9855.2.9855.con.0001.CDS.1721639.1722604.fwd	PATRIC	CDS	1721639	1722604	966	+	PGF_03696321	321	tRNA-dihydrouridine synthase BT3326	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1711	PATRIC.2.9855.2.9855.con.0001.CDS.1723001.1723375.fwd	PATRIC	CDS	1723001	1723375	375	+	PGF_04154299	124	Beta-lactamase repressor BlaI	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1712	PATRIC.2.9855.2.9855.con.0001.CDS.1723379.1725223.fwd	PATRIC	CDS	1723379	1725223	1845	+	PGF_00715121	614	Regulatory sensor-transducer, BlaR1/MecR1 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1713	PATRIC.2.9855.2.9855.con.0001.CDS.1725482.1726015.fwd	PATRIC	CDS	1725482	1726015	534	+	PGF_00896280	177	RNA polymerase ECF-type sigma factor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1715	PATRIC.2.9855.2.9855.con.0001.CDS.1727827.1731468.fwd	PATRIC	CDS	1727827	1731468	3642	+	PGF_00426722	1213	5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	GO:0008705|methionine synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.146	PATRIC.2.9855.2.9855.con.0001.CDS.173022.174248.fwd	PATRIC	CDS	173022	174248	1227	+	PGF_00007133	408	Galactose/methyl galactoside ABC transporter, permease protein MglC (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1716	PATRIC.2.9855.2.9855.con.0001.CDS.1731685.1732677.rev	PATRIC	CDS	1731685	1732677	993	-	PGF_10387123	330	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1718	PATRIC.2.9855.2.9855.con.0001.CDS.1733285.1733887.fwd	PATRIC	CDS	1733285	1733887	603	+	PGF_03100174	200	Substrate-specific component BL0695 of predicted ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1719	PATRIC.2.9855.2.9855.con.0001.CDS.1733890.1734585.fwd	PATRIC	CDS	1733890	1734585	696	+	PGF_06853101	231	Transmembrane component BL0694 of energizing module of predicted ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1720	PATRIC.2.9855.2.9855.con.0001.CDS.1734582.1735964.fwd	PATRIC	CDS	1734582	1735964	1383	+	PGF_03285992	460	Duplicated ATPase component BL0693 of energizing module of predicted ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1721	PATRIC.2.9855.2.9855.con.0001.CDS.1736358.1737329.rev	PATRIC	CDS	1736358	1737329	972	-	PGF_10348987	323	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1722	PATRIC.2.9855.2.9855.con.0001.CDS.1737624.1739420.fwd	PATRIC	CDS	1737624	1739420	1797	+	PGF_10540665	598	Heterodimeric efflux ABC transporter, permease/ATP-binding subunit 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1723	PATRIC.2.9855.2.9855.con.0001.CDS.1739414.1741165.fwd	PATRIC	CDS	1739414	1741165	1752	+	PGF_08128839	583	Heterodimeric efflux ABC transporter, permease/ATP-binding subunit 2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1724	PATRIC.2.9855.2.9855.con.0001.CDS.1741279.1742664.fwd	PATRIC	CDS	1741279	1742664	1386	+	PGF_08913741	461	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1726	PATRIC.2.9855.2.9855.con.0001.CDS.1743753.1745048.fwd	PATRIC	CDS	1743753	1745048	1296	+	PGF_03004613	431	Histidyl-tRNA synthetase (EC 6.1.1.21)	GO:0004821|histidine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1727	PATRIC.2.9855.2.9855.con.0001.CDS.1745468.1745623.fwd	PATRIC	CDS	1745468	1745623	156	+	PGF_00067473	51	Zinc-ribbon domain Caur_1000.N	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.147	PATRIC.2.9855.2.9855.con.0001.CDS.174585.176201.fwd	PATRIC	CDS	174585	176201	1617	+	PGF_00062533	538	Two-component response regulator yesN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1728	PATRIC.2.9855.2.9855.con.0001.CDS.1746462.1747940.fwd	PATRIC	CDS	1746462	1747940	1479	+	PGF_03013281	492	Bis-ABC ATPase CAC0528	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1729	PATRIC.2.9855.2.9855.con.0001.CDS.1748005.1748373.rev	PATRIC	CDS	1748005	1748373	369	-	PGF_00015463	122	Iron-dependent repressor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1732	PATRIC.2.9855.2.9855.con.0001.CDS.1749920.1750441.fwd	PATRIC	CDS	1749920	1750441	522	+	PGF_06938364	173	Isochorismatase (EC 3.3.2.1)	GO:0008908|isochorismatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1734	PATRIC.2.9855.2.9855.con.0001.CDS.1751578.1752132.rev	PATRIC	CDS	1751578	1752132	555	-	PGF_10153092	184	Nitroreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1735	PATRIC.2.9855.2.9855.con.0001.CDS.1752291.1752644.fwd	PATRIC	CDS	1752291	1752644	354	+	PGF_03320197	117	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1736	PATRIC.2.9855.2.9855.con.0001.CDS.1752755.1753270.fwd	PATRIC	CDS	1752755	1753270	516	+	PGF_00015735	171	Isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2)	GO:0004452|isopentenyl-diphosphate delta-isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1737	PATRIC.2.9855.2.9855.con.0001.CDS.1753879.1754088.fwd	PATRIC	CDS	1753879	1754088	210	+	PGF_00053039	69	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1738	PATRIC.2.9855.2.9855.con.0001.CDS.1754362.1757436.fwd	PATRIC	CDS	1754362	1757436	3075	+	PGF_12718402	1024	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1739	PATRIC.2.9855.2.9855.con.0001.CDS.1757483.1759747.fwd	PATRIC	CDS	1757483	1759747	2265	+	PGF_10416542	754	Sensory box histidine kinase/response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1740	PATRIC.2.9855.2.9855.con.0001.CDS.1760110.1760691.fwd	PATRIC	CDS	1760110	1760691	582	+	PGF_10379370	193	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1741	PATRIC.2.9855.2.9855.con.0001.CDS.1760796.1761914.fwd	PATRIC	CDS	1760796	1761914	1119	+	PGF_01282282	372	Sensory box/GGDEF domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1742	PATRIC.2.9855.2.9855.con.0001.CDS.1761904.1763658.fwd	PATRIC	CDS	1761904	1763658	1755	+	PGF_08632970	584	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.148	PATRIC.2.9855.2.9855.con.0001.CDS.176213.178021.fwd	PATRIC	CDS	176213	178021	1809	+	PGF_00062719	602	Two-component sensor kinase YesM (EC 2.7.3.-)	GO:0000155|phosphorelay sensor kinase activity;GO:0000155|histone arginine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1743	PATRIC.2.9855.2.9855.con.0001.CDS.1763760.1765769.fwd	PATRIC	CDS	1763760	1765769	2010	+	PGF_10416542	669	Sensory box histidine kinase/response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1744	PATRIC.2.9855.2.9855.con.0001.CDS.1766124.1767191.rev	PATRIC	CDS	1766124	1767191	1068	-	PGF_05728830	355	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1745	PATRIC.2.9855.2.9855.con.0001.CDS.1767476.1768522.rev	PATRIC	CDS	1767476	1768522	1047	-	PGF_05728830	348	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1746	PATRIC.2.9855.2.9855.con.0001.CDS.1769039.1769440.rev	PATRIC	CDS	1769039	1769440	402	-	PGF_01284176	133	Rubrerythrin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1749	PATRIC.2.9855.2.9855.con.0001.CDS.1772066.1772569.fwd	PATRIC	CDS	1772066	1772569	504	+	PGF_01333742	167	Histone acetyltransferase HPA2 and related acetyltransferases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1750	PATRIC.2.9855.2.9855.con.0001.CDS.1772877.1774742.rev	PATRIC	CDS	1772877	1774742	1866	-	PGF_00036994	621	Probable cation-transporting P-type ATPase C (EC 3.6.3.-) (Metal-transporting ATPase Mta72)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1752	PATRIC.2.9855.2.9855.con.0001.CDS.1775814.1776545.fwd	PATRIC	CDS	1775814	1776545	732	+	PGF_01769544	243	Putative transmembrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1754	PATRIC.2.9855.2.9855.con.0001.CDS.1777939.1779384.fwd	PATRIC	CDS	1777939	1779384	1446	+	PGF_01280394	481	Probable oxidoreductase, with Rieske iron-sulfur protein 2Fe-2S subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1755	PATRIC.2.9855.2.9855.con.0001.CDS.1779552.1779998.fwd	PATRIC	CDS	1779552	1779998	447	+	PGF_10423881	148	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1756	PATRIC.2.9855.2.9855.con.0001.CDS.1780252.1780953.fwd	PATRIC	CDS	1780252	1780953	702	+	PGF_08462977	233	Pirin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1757	PATRIC.2.9855.2.9855.con.0001.CDS.1781035.1781655.fwd	PATRIC	CDS	1781035	1781655	621	+	PGF_00028947	206	Oxygen-insensitive NAD(P)H nitroreductase (EC 1.-.-.-) / Dihydropteridine reductase (EC 1.5.1.34)	GO:0008748|N-ethylmaleimide reductase activity;GO:0008748|reduced coenzyme F420 dehydrogenase activity;GO:0008748|sulfur oxygenase reductase activity;GO:0008748|malolactic enzyme activity;GO:0008748|NADPH:sulfur oxidoreductase activity;GO:0008748|epoxyqueuosine reductase activity;GO:0004155|6,7-dihydropteridine reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1758	PATRIC.2.9855.2.9855.con.0001.CDS.1781804.1781983.fwd	PATRIC	CDS	1781804	1781983	180	+	PGF_01265835	59	Iron-sulfur cluster assembly scaffold protein NifU	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1759	PATRIC.2.9855.2.9855.con.0001.CDS.1782252.1783469.fwd	PATRIC	CDS	1782252	1783469	1218	+	PGF_03760919	405	Putative metal-dependent phosphohydrolase with tandem HD motifs	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1761	PATRIC.2.9855.2.9855.con.0001.CDS.1784174.1785727.fwd	PATRIC	CDS	1784174	1785727	1554	+	PGF_03244749	517	Bis-ABC ATPase SPy1206	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1762	PATRIC.2.9855.2.9855.con.0001.CDS.1786131.1788410.rev	PATRIC	CDS	1786131	1788410	2280	-	PGF_00058983	759	Transcriptional regulator, AraC family / Glycoside hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1763	PATRIC.2.9855.2.9855.con.0001.CDS.1788385.1788657.rev	PATRIC	CDS	1788385	1788657	273	-	PGF_00058983	90	Transcriptional regulator, AraC family / Glycoside hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1764	PATRIC.2.9855.2.9855.con.0001.CDS.1788975.1789910.fwd	PATRIC	CDS	1788975	1789910	936	+	PGF_02278882	311	Iron-sulfur flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.150	PATRIC.2.9855.2.9855.con.0001.CDS.179052.180137.fwd	PATRIC	CDS	179052	180137	1086	+	PGF_05728830	361	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1765	PATRIC.2.9855.2.9855.con.0001.CDS.1790580.1792301.fwd	PATRIC	CDS	1790580	1792301	1722	+	PGF_06837078	573	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1769	PATRIC.2.9855.2.9855.con.0001.CDS.1793892.1794509.fwd	PATRIC	CDS	1793892	1794509	618	+	PGF_01281725	205	Predicted membrane protein; CF-20 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1773	PATRIC.2.9855.2.9855.con.0001.CDS.1796171.1796815.fwd	PATRIC	CDS	1796171	1796815	645	+	PGF_00186174	214	Endo-1,4-beta-xylanase (EC 3.2.1.8)	GO:0031176|endo-1,4-beta-xylanase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1775	PATRIC.2.9855.2.9855.con.0001.CDS.1798077.1798964.fwd	PATRIC	CDS	1798077	1798964	888	+	PGF_00006392	295	Fructose-bisphosphate aldolase class I (EC 4.1.2.13)	GO:0004332|fructose-bisphosphate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1776	PATRIC.2.9855.2.9855.con.0001.CDS.1799336.1800019.fwd	PATRIC	CDS	1799336	1800019	684	+	PGF_07723617	227	Putative membrane protease YugP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1777	PATRIC.2.9855.2.9855.con.0001.CDS.1800111.1801994.fwd	PATRIC	CDS	1800111	1801994	1884	+	PGF_06275407	627	Cell division-associated, ATP-dependent zinc metalloprotease FtsH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1778	PATRIC.2.9855.2.9855.con.0001.CDS.1802307.1802984.fwd	PATRIC	CDS	1802307	1802984	678	+	PGF_00417736	225	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1779	PATRIC.2.9855.2.9855.con.0001.CDS.1803171.1803635.rev	PATRIC	CDS	1803171	1803635	465	-	PGF_04681578	154	Alkyl hydroperoxide reductase subunit C-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1780	PATRIC.2.9855.2.9855.con.0001.CDS.1803901.1804356.fwd	PATRIC	CDS	1803901	1804356	456	+	PGF_00047955	151	Response regulator of the LytR/AlgR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1781	PATRIC.2.9855.2.9855.con.0001.CDS.1804356.1805057.fwd	PATRIC	CDS	1804356	1805057	702	+	PGF_00019716	233	Membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.151	PATRIC.2.9855.2.9855.con.0001.CDS.180512.181573.fwd	PATRIC	CDS	180512	181573	1062	+	PGF_05728830	353	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1782	PATRIC.2.9855.2.9855.con.0001.CDS.1805448.1805924.fwd	PATRIC	CDS	1805448	1805924	477	+	PGF_02715281	158	Uncharacterized membrane protein YoaS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1783	PATRIC.2.9855.2.9855.con.0001.CDS.1805981.1806190.fwd	PATRIC	CDS	1805981	1806190	210	+	PGF_04743045	69	Uncharacterized transcriptional regulator YozG, Cro/CI family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1785	PATRIC.2.9855.2.9855.con.0001.CDS.1806527.1807873.fwd	PATRIC	CDS	1806527	1807873	1347	+	PGF_00400326	448	BchE/P-methylase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1789	PATRIC.2.9855.2.9855.con.0001.CDS.1810766.1812058.fwd	PATRIC	CDS	1810766	1812058	1293	+	PGF_01280313	430	ABC transporter, RND-adapter-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1790	PATRIC.2.9855.2.9855.con.0001.CDS.1812070.1815144.fwd	PATRIC	CDS	1812070	1815144	3075	+	PGF_05237064	1024	RND efflux system, inner membrane transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1792	PATRIC.2.9855.2.9855.con.0001.CDS.1816157.1817530.rev	PATRIC	CDS	1816157	1817530	1374	-	PGF_09996723	457	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.152	PATRIC.2.9855.2.9855.con.0001.CDS.181630.182673.fwd	PATRIC	CDS	181630	182673	1044	+	PGF_05728830	347	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1793	PATRIC.2.9855.2.9855.con.0001.CDS.1817527.1818054.rev	PATRIC	CDS	1817527	1818054	528	-	PGF_01662006	175	Transcriptional regulator, PadR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1796	PATRIC.2.9855.2.9855.con.0001.CDS.1819795.1821384.rev	PATRIC	CDS	1819795	1821384	1590	-	PGF_01317438	529	Ferredoxin--sulfite reductase, bacillial type (EC 1.8.7.1)	GO:0050311|sulfite reductase (ferredoxin) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1799	PATRIC.2.9855.2.9855.con.0001.CDS.1822414.1823361.fwd	PATRIC	CDS	1822414	1823361	948	+	PGF_07849456	315	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1801	PATRIC.2.9855.2.9855.con.0001.CDS.1824129.1826057.rev	PATRIC	CDS	1824129	1826057	1929	-	PGF_00052554	642	Similar to carbon monoxide dehydrogenase CooS subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1802	PATRIC.2.9855.2.9855.con.0001.CDS.1826486.1827676.fwd	PATRIC	CDS	1826486	1827676	1191	+	PGF_08033215	396	Nitric oxide reductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.153	PATRIC.2.9855.2.9855.con.0001.CDS.182782.183354.fwd	PATRIC	CDS	182782	183354	573	+	PGF_00416525	190	Carbonic anhydrase, beta class (EC 4.2.1.1)	GO:0004089|carbonate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1803	PATRIC.2.9855.2.9855.con.0001.CDS.1827873.1829105.rev	PATRIC	CDS	1827873	1829105	1233	-	PGF_00776673	410	Anaerobic nitric oxide reductase flavorubredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1804	PATRIC.2.9855.2.9855.con.0001.CDS.1829376.1830089.fwd	PATRIC	CDS	1829376	1830089	714	+	PGF_00059157	237	Transcriptional regulator, Crp/Fnr family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1805	PATRIC.2.9855.2.9855.con.0001.CDS.1830281.1830697.fwd	PATRIC	CDS	1830281	1830697	417	+	PGF_08946513	138	Flavodoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1806	PATRIC.2.9855.2.9855.con.0001.CDS.1830813.1832459.rev	PATRIC	CDS	1830813	1832459	1647	-	PGF_00736089	548	Hydroxylamine reductase (EC 1.7.99.1)	GO:0050418|hydroxylamine reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1807	PATRIC.2.9855.2.9855.con.0001.CDS.1832906.1833781.fwd	PATRIC	CDS	1832906	1833781	876	+	PGF_00669741	291	[Ni/Fe] hydrogenase, group 1, small subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1808	PATRIC.2.9855.2.9855.con.0001.CDS.1833852.1835243.fwd	PATRIC	CDS	1833852	1835243	1392	+	PGF_03368369	463	[Ni/Fe] hydrogenase, group 1, large subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1809	PATRIC.2.9855.2.9855.con.0001.CDS.1835565.1836038.fwd	PATRIC	CDS	1835565	1836038	474	+	PGF_01283042	157	Hydrogenase maturation protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1811	PATRIC.2.9855.2.9855.con.0001.CDS.1836515.1838815.fwd	PATRIC	CDS	1836515	1838815	2301	+	PGF_03098349	766	Acylphosphate phosphohydrolase (EC 3.6.1.7) / [NiFe] hydrogenase metallocenter assembly protein HypF	GO:0003998|acylphosphatase activity

Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1812	PATRIC.2.9855.2.9855.con.0001.CDS.1838975.1839202.fwd	PATRIC	CDS	1838975	1839202	228	+	PGF_00067769	75	[NiFe] hydrogenase metallocenter assembly protein HypC	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1813	PATRIC.2.9855.2.9855.con.0001.CDS.1839199.1840278.fwd	PATRIC	CDS	1839199	1840278	1080	+	PGF_00067771	359	[NiFe] hydrogenase metallocenter assembly protein HypD	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.154	PATRIC.2.9855.2.9855.con.0001.CDS.184001.184747.rev	PATRIC	CDS	184001	184747	747	-	PGF_03114708	248	Domain often clustered or fused with uracil-DNA glycosylase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1814	PATRIC.2.9855.2.9855.con.0001.CDS.1840279.1841280.fwd	PATRIC	CDS	1840279	1841280	1002	+	PGF_00067772	333	[NiFe] hydrogenase metallocenter assembly protein HypE	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1815	PATRIC.2.9855.2.9855.con.0001.CDS.1841447.1842580.fwd	PATRIC	CDS	1841447	1842580	1134	+	PGF_00039689	377	Putative ROK-family transcriptional regulator	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1816	PATRIC.2.9855.2.9855.con.0001.CDS.1842600.1843382.fwd	PATRIC	CDS	1842600	1843382	783	+	PGF_05621995	260	Prolipoprotein diacylglyceryl transferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1817	PATRIC.2.9855.2.9855.con.0001.CDS.1843791.1844447.fwd	PATRIC	CDS	1843791	1844447	657	+	PGF_00015600	218	Iron-sulfur-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1819	PATRIC.2.9855.2.9855.con.0001.CDS.1845559.1846425.fwd	PATRIC	CDS	1845559	1846425	867	+	PGF_00044298	288	Putative sulfite reductase, GSU1351 type	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1820	PATRIC.2.9855.2.9855.con.0001.CDS.1846765.1848465.fwd	PATRIC	CDS	1846765	1848465	1701	+	PGF_01932237	566	CoA-disulfide reductase (EC 1.8.1.14) / Polysulfide binding and transferase domain	GO:0050451|CoA-disulfide reductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.155	PATRIC.2.9855.2.9855.con.0001.CDS.184750.186174.rev	PATRIC	CDS	184750	186174	1425	-	PGF_00404432	474	Biotin synthase related domain containing protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.26	PATRIC.2.9855.2.9855.con.0001.CDS.18491.21238.fwd	PATRIC	CDS	18491	21238	2748	+	PGF_00026324	915	NtrC family Transcriptional regulator, ATPase domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1824	PATRIC.2.9855.2.9855.con.0001.CDS.1851351.1851707.fwd	PATRIC	CDS	1851351	1851707	357	+	PGF_02719231	118	NADH-ubiquinone oxidoreductase chain A (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1825	PATRIC.2.9855.2.9855.con.0001.CDS.1851698.1852207.fwd	PATRIC	CDS	1851698	1852207	510	+	PGF_04380075	169	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1826	PATRIC.2.9855.2.9855.con.0001.CDS.1852200.1852637.fwd	PATRIC	CDS	1852200	1852637	438	+	PGF_04571944	145	NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1827	PATRIC.2.9855.2.9855.con.0001.CDS.1852656.1853768.fwd	PATRIC	CDS	1852656	1853768	1113	+	PGF_00024687	370	NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1828	PATRIC.2.9855.2.9855.con.0001.CDS.1853782.1854816.fwd	PATRIC	CDS	1853782	1854816	1035	+	PGF_01514111	344	NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1829	PATRIC.2.9855.2.9855.con.0001.CDS.1854989.1855378.fwd	PATRIC	CDS	1854989	1855378	390	+	PGF_01761390	129	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1830	PATRIC.2.9855.2.9855.con.0001.CDS.1855468.1855959.fwd	PATRIC	CDS	1855468	1855959	492	+	PGF_10348836	163	NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1831	PATRIC.2.9855.2.9855.con.0001.CDS.1855960.1856268.fwd	PATRIC	CDS	1855960	1856268	309	+	PGF_08749001	102	NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1832	PATRIC.2.9855.2.9855.con.0001.CDS.1856277.1858130.fwd	PATRIC	CDS	1856277	1858130	1854	+	PGF_04757308	617	NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1833	PATRIC.2.9855.2.9855.con.0001.CDS.1858131.1859654.fwd	PATRIC	CDS	1858131	1859654	1524	+	PGF_00024742	507	NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1834	PATRIC.2.9855.2.9855.con.0001.CDS.1859657.1861075.fwd	PATRIC	CDS	1859657	1861075	1419	+	PGF_00024746	472	NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)	GO:0008137|NADH dehydrogenase (ubiquinone) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1835	PATRIC.2.9855.2.9855.con.0001.CDS.1861447.1862130.fwd	PATRIC	CDS	1861447	1862130	684	+	PGF_07420062	227	Two-component transcriptional response regulator, OmpR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1836	PATRIC.2.9855.2.9855.con.0001.CDS.1862127.1863500.fwd	PATRIC	CDS	1862127	1863500	1374	+	PGF_02620852	457	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1840	PATRIC.2.9855.2.9855.con.0001.CDS.1865130.1866035.rev	PATRIC	CDS	1865130	1866035	906	-	PGF_02905791	301	Multicopper oxidase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1841	PATRIC.2.9855.2.9855.con.0001.CDS.1866376.1866585.fwd	PATRIC	CDS	1866376	1866585	210	+	PGF_05313742	69	Uncharacterized membrane protein YuzA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1842	PATRIC.2.9855.2.9855.con.0001.CDS.1866811.1867380.fwd	PATRIC	CDS	1866811	1867380	570	+	PGF_00599179	189	putative membrane protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.156	PATRIC.2.9855.2.9855.con.0001.CDS.186690.187703.rev	PATRIC	CDS	186690	187703	1014	-	PGF_03047945	337	Galactose operon repressor, GalR-LacI family of transcriptional regulators	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1843	PATRIC.2.9855.2.9855.con.0001.CDS.1867436.1867810.rev	PATRIC	CDS	1867436	1867810	375	-	PGF_02565090	124	Thiol:disulfide oxidoreductase related to ResA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1844	PATRIC.2.9855.2.9855.con.0001.CDS.1868104.1869816.fwd	PATRIC	CDS	1868104	1869816	1713	+	PGF_02910829	570	Membrane assosiated methyl-accepting chemotaxis protein with HAMP domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1846	PATRIC.2.9855.2.9855.con.0001.CDS.1870310.1871203.rev	PATRIC	CDS	1870310	1871203	894	-	PGF_03701810	297	Cell-division-associated, ABC-transporter-like signaling protein FtsX	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1847	PATRIC.2.9855.2.9855.con.0001.CDS.1871193.1871879.rev	PATRIC	CDS	1871193	1871879	687	-	PGF_06857975	228	Cell-division-associated, ABC-transporter-like signaling protein FtsE	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1848	PATRIC.2.9855.2.9855.con.0001.CDS.1872111.1873214.fwd	PATRIC	CDS	1872111	1873214	1104	+	PGF_10521947	367	Murein hydrolase activator EnvC	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1850	PATRIC.2.9855.2.9855.con.0001.CDS.1873467.1874300.fwd	PATRIC	CDS	1873467	1874300	834	+	PGF_05621995	277	Prolipoprotein diacylglyceryl transferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1851	PATRIC.2.9855.2.9855.con.0001.CDS.1874620.1875447.fwd	PATRIC	CDS	1874620	1875447	828	+	PGF_08136687	275	Heptaprenyl diphosphate synthase component II (EC 2.5.1.30)	GO:0036422|heptaprenyl diphosphate synthase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1854	PATRIC.2.9855.2.9855.con.0001.CDS.1876627.1878018.fwd	PATRIC	CDS	1876627	1878018	1392	+	PGF_00025868	463	Nitrogen assimilation regulatory protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.157	PATRIC.2.9855.2.9855.con.0001.CDS.187716.189215.rev	PATRIC	CDS	187716	189215	1500	-	PGF_00007119	499	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	GO:0017103|UTP:galactose-1-phosphate uridylyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1855	PATRIC.2.9855.2.9855.con.0001.CDS.1878145.1879044.fwd	PATRIC	CDS	1878145	1879044	900	+	PGF_00876943	299	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1856	PATRIC.2.9855.2.9855.con.0001.CDS.1879060.1879686.fwd	PATRIC	CDS	1879060	1879686	627	+	PGF_01312499	208	CAAX amino terminal protease family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1857	PATRIC.2.9855.2.9855.con.0001.CDS.1879803.1880507.fwd	PATRIC	CDS	1879803	1880507	705	+	PGF_01187824	234	Demethylmenaquinone methyltransferase (EC 2.1.1.163)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1858	PATRIC.2.9855.2.9855.con.0001.CDS.1880743.1881216.fwd	PATRIC	CDS	1880743	1881216	474	+	PGF_08338115	157	Transposase, IS200 family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1859	PATRIC.2.9855.2.9855.con.0001.CDS.1881575.1882021.fwd	PATRIC	CDS	1881575	1882021	447	+	PGF_00010704	148	HTH DNA-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1860	PATRIC.2.9855.2.9855.con.0001.CDS.1882110.1882466.rev	PATRIC	CDS	1882110	1882466	357	-	PGF_00602094	118	MTH1175-like domain family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1861	PATRIC.2.9855.2.9855.con.0001.CDS.1882768.1883445.fwd	PATRIC	CDS	1882768	1883445	678	+	PGF_08142031	225	Cytochrome c-type biogenesis protein CcdA (DsbD analog)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1862	PATRIC.2.9855.2.9855.con.0001.CDS.1883455.1884057.fwd	PATRIC	CDS	1883455	1884057	603	+	PGF_02565090	200	Thiol:disulfide oxidoreductase related to ResA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1863	PATRIC.2.9855.2.9855.con.0001.CDS.1884203.1884520.fwd	PATRIC	CDS	1884203	1884520	318	+	PGF_10345259	105	Thioredoxin	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1864	PATRIC.2.9855.2.9855.con.0001.CDS.1884714.1885610.rev	PATRIC	CDS	1884714	1885610	897	-	PGF_04493258	298	Cobalt-zinc-cadmium resistance protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1868	PATRIC.2.9855.2.9855.con.0001.CDS.1886671.1887258.fwd	PATRIC	CDS	1886671	1887258	588	+	PGF_03142037	195	Uncharacterized protein YrkC	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1869	PATRIC.2.9855.2.9855.con.0001.CDS.1887464.1889572.fwd	PATRIC	CDS	1887464	1889572	2109	+	PGF_07849456	702	Methyl-accepting chemotaxis protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1872	PATRIC.2.9855.2.9855.con.0001.CDS.1890141.1890857.fwd	PATRIC	CDS	1890141	1890857	717	+	PGF_07420062	238	Two-component transcriptional response regulator, OmpR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1873	PATRIC.2.9855.2.9855.con.0001.CDS.1890854.1892269.fwd	PATRIC	CDS	1890854	1892269	1416	+	PGF_02620852	471	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.158	PATRIC.2.9855.2.9855.con.0001.CDS.189399.190391.rev	PATRIC	CDS	189399	190391	993	-	PGF_01033123	330	UDP-glucose 4-epimerase (EC 5.1.3.2)	GO:0003978|UDP-glucose 4-epimerase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1877	PATRIC.2.9855.2.9855.con.0001.CDS.1894075.1896330.fwd	PATRIC	CDS	1894075	1896330	2256	+	PGF_00066367	751	UvrD/Rep helicase family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1879	PATRIC.2.9855.2.9855.con.0001.CDS.1898738.1901224.fwd	PATRIC	CDS	1898738	1901224	2487	+	PGF_01740148	828	CoA-disulfide reductase (EC 1.8.1.14) / Disulfide bond regulator	GO:0050451|CoA-disulfide reductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1882	PATRIC.2.9855.2.9855.con.0001.CDS.1902217.1902945.rev	PATRIC	CDS	1902217	1902945	729	-	PGF_01315833	242	UPF0702 transmembrane protein YdfS	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1883	PATRIC.2.9855.2.9855.con.0001.CDS.1903359.1904150.rev	PATRIC	CDS	1903359	1904150	792	-	PGF_10387439	263	Oxidoreductase, short-chain dehydrogenase/reductase family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.159	PATRIC.2.9855.2.9855.con.0001.CDS.190499.191668.rev	PATRIC	CDS	190499	191668	1170	-	PGF_00007085	389	Galactokinase (EC 2.7.1.6)	GO:0004335|galactokinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1885	PATRIC.2.9855.2.9855.con.0001.CDS.1905016.1906596.rev	PATRIC	CDS	1905016	1906596	1581	-	PGF_07370370	526	Voltage-gated H(+)/2Cl(-) exchange transporter ClcA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1886	PATRIC.2.9855.2.9855.con.0001.CDS.1906844.1907119.rev	PATRIC	CDS	1906844	1907119	276	-	PGF_00402549	91	Beta-lysine acetyltransferase (EC 2.3.1.-)	GO:0004147|dihydrolipoamide branched chain acyltransferase activity;GO:0004147|sterol O-acyltransferase activity;GO:0004147|N-acetyltransferase activity;GO:0004147|O-acyltransferase activity;GO:0004147|palmitoleoyl [acyl-carrier-protein]-dependent acyltransferase activity;GO:0004147|carnitine O-acyltransferase activity;GO:0004147|acetyltransferase activity;GO:0004147|C-acyltransferase activity;GO:0004147|palmitoyltransferase activity;GO:0004147|N-acyltransferase activity;GO:0004147|acylglycerol O-acyltransferase activity;GO:0004147|serine O-acyltransferase activity;GO:0004147|O-acetyltransferase activity;GO:0004147|O-octanoyltransferase activity;GO:0004147|octanoyltransferase activity;GO:0004147|O-palmitoyltransferase activity;GO:0004147|S-acyltransferase activity;GO:0004147|S-acetyltransferase activity;GO:0004147|S-malonyltransferase activity;GO:0004147|malonyltransferase activity;GO:0004147|C-palmitoyltransferase activity;GO:0004147|succinyltransferase activity;GO:0004147|N-succinyltransferase activity;GO:0004147|O-succinyltransferase activity;GO:0004147|S-succinyltransferase activity;GO:0004147|sinapoyltransferase activity;GO:0004147|O-sinapoyltransferase activity;GO:0004147|peptidyl-lysine N6-myristoyltransferase activity;GO:0004147|peptidyl-lysine N6-palmitoyltransferase activity;GO:0004147|benzoyl acetate-CoA thiolase activity;GO:0004147|3-hydroxybutyryl-CoA thiolase activity;GO:0004147|3-ketopimelyl-CoA thiolase activity;GO:0004147|N-palmitoyltransferase activity;GO:0004147|myristoyltransferase activity;GO:0004147|acyl-CoA N-acyltransferase activity;GO:0004147|protein-cysteine S-myristoyltransferase activity;GO:0004147|protein-cysteine S-acyltransferase activity;GO:0004147|dihydrolipoamide S-acyltransferase activity;GO:0004147|glucosaminyl-phosphotidylinositol O-acyltransferase activity;GO:0004147|ergosterol O-acyltransferase activity;GO:0004147|lanosterol O-
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1888	PATRIC.2.9855.2.9855.con.0001.CDS.1907349.1908209.rev	PATRIC	CDS	1907349	1908209	861	-	PGF_01176589	286	4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)	GO:0008839|4-hydroxy-tetrahydrodipicolinate reductase
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1889	PATRIC.2.9855.2.9855.con.0001.CDS.1908772.1909389.fwd	PATRIC	CDS	1908772	1909389	618	+	PGF_00006821	205	GGDEF domain protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1890	PATRIC.2.9855.2.9855.con.0001.CDS.1909636.1910850.fwd	PATRIC	CDS	1909636	1910850	1215	+	PGF_06945838	404	Na+/H+ antiporter NhaA type	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1892	PATRIC.2.9855.2.9855.con.0001.CDS.1911444.1912142.fwd	PATRIC	CDS	1911444	1912142	699	+	PGF_06916656	232	Transcriptional regulator, GntR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1894	PATRIC.2.9855.2.9855.con.0001.CDS.1912753.1912944.fwd	PATRIC	CDS	1912753	1912944	192	+	PGF_02049468	63	Cold shock protein of CSP family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1895	PATRIC.2.9855.2.9855.con.0001.CDS.1913070.1914644.fwd	PATRIC	CDS	1913070	1914644	1575	+	PGF_00421098	524	DEAD-box ATP-dependent RNA helicase DeaD (= CshA) (EC 3.6.4.13)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1896	PATRIC.2.9855.2.9855.con.0001.CDS.1914993.1915199.fwd	PATRIC	CDS	1914993	1915199	207	+	PGF_07182652	68	Transcriptional regulator, AcrR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1897	PATRIC.2.9855.2.9855.con.0001.CDS.1915228.1916214.fwd	PATRIC	CDS	1915228	1916214	987	+	PGF_00012184	328	HlyD family secretion protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1898	PATRIC.2.9855.2.9855.con.0001.CDS.1916230.1916883.fwd	PATRIC	CDS	1916230	1916883	654	+	PGF_06780452	217	Multidrug resistance protein [function not yet clear]	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1899	PATRIC.2.9855.2.9855.con.0001.CDS.1916892.1918436.fwd	PATRIC	CDS	1916892	1918436	1545	+	PGF_00799877	514	Uncharacterized MFS-type transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1900	PATRIC.2.9855.2.9855.con.0001.CDS.1918854.1920308.fwd	PATRIC	CDS	1918854	1920308	1455	+	PGF_02620852	484	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1901	PATRIC.2.9855.2.9855.con.0001.CDS.1920483.1921181.fwd	PATRIC	CDS	1920483	1921181	699	+	PGF_10382251	232	Two-component response regulator yycF	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1902	PATRIC.2.9855.2.9855.con.0001.CDS.1921868.1923130.fwd	PATRIC	CDS	1921868	1923130	1263	+	PGF_01280313	420	ABC transporter, RND-adapter-like protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1903	PATRIC.2.9855.2.9855.con.0001.CDS.1923143.1926235.fwd	PATRIC	CDS	1923143	1926235	3093	+	PGF_05237064	1030	RND efflux system, inner membrane transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1905	PATRIC.2.9855.2.9855.con.0001.CDS.1928170.1929468.fwd	PATRIC	CDS	1928170	1929468	1299	+	PGF_00418127	432	Citrate/H+ symporter of CitMHS family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1906	PATRIC.2.9855.2.9855.con.0001.CDS.1929854.1931209.fwd	PATRIC	CDS	1929854	1931209	1356	+	PGF_00038254	451	Protein of unknown function DUF1446	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1907	PATRIC.2.9855.2.9855.con.0001.CDS.1931214.1931513.fwd	PATRIC	CDS	1931214	1931513	300	+	PGF_00053286	99	Small uncharacterized protein Bpro_4170						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1908	PATRIC.2.9855.2.9855.con.0001.CDS.1931558.1932214.fwd	PATRIC	CDS	1931558	1932214	657	+	PGF_00959691	218	Butyrate--acetoacetate CoA-transferase subunit A (EC 2.8.3.9)	GO:0047371|butyrate-acetoacetate CoA-transferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1909	PATRIC.2.9855.2.9855.con.0001.CDS.1932214.1932870.fwd	PATRIC	CDS	1932214	1932870	657	+	PGF_08079989	218	Butyrate--acetoacetate CoA-transferase subunit B (EC 2.8.3.9)	GO:0047371|butyrate-acetoacetate CoA-transferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1910	PATRIC.2.9855.2.9855.con.0001.CDS.1933533.1935527.fwd	PATRIC	CDS	1933533	1935527	1995	+	PGF_07849456	664	Methyl-accepting chemotaxis protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1911	PATRIC.2.9855.2.9855.con.0001.CDS.1935759.1937354.rev	PATRIC	CDS	1935759	1937354	1596	-	PGF_01281253	531	FOG: PKD repeat						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1912	PATRIC.2.9855.2.9855.con.0001.CDS.1937902.1938573.fwd	PATRIC	CDS	1937902	1938573	672	+	PGF_10446847	223	putative phosphatidylinositol-4-phosphate 5-kinase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.163	PATRIC.2.9855.2.9855.con.0001.CDS.193858.194421.fwd	PATRIC	CDS	193858	194421	564	+	PGF_00010581	187	HDIG domain protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1913	PATRIC.2.9855.2.9855.con.0001.CDS.1938741.1939793.rev	PATRIC	CDS	1938741	1939793	1053	-	PGF_05728830	350	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1914	PATRIC.2.9855.2.9855.con.0001.CDS.1940047.1942065.rev	PATRIC	CDS	1940047	1942065	2019	-	PGF_10361261	672	Na+/H+ antiporter						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1915	PATRIC.2.9855.2.9855.con.0001.CDS.1942678.1944681.fwd	PATRIC	CDS	1942678	1944681	2004	+	PGF_07849456	667	Methyl-accepting chemotaxis protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1916	PATRIC.2.9855.2.9855.con.0001.CDS.1945144.1945569.fwd	PATRIC	CDS	1945144	1945569	426	+	PGF_01323780	141	Acetyltransferase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.164	PATRIC.2.9855.2.9855.con.0001.CDS.194816.195418.fwd	PATRIC	CDS	194816	195418	603	+	PGF_00404539	200	HAD superfamily hydrolase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1919	PATRIC.2.9855.2.9855.con.0001.CDS.1950182.1950517.rev	PATRIC	CDS	1950182	1950517	336	-	PGF_03495000	111	Mobile element protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1920	PATRIC.2.9855.2.9855.con.0001.CDS.1951907.1953079.rev	PATRIC	CDS	1951907	1953079	1173	-	PGF_08632970	390	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1921	PATRIC.2.9855.2.9855.con.0001.CDS.1953588.1954034.fwd	PATRIC	CDS	1953588	1954034	447	+	PGF_00056558	148	Thioesterase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1922	PATRIC.2.9855.2.9855.con.0001.CDS.1954618.1956501.fwd	PATRIC	CDS	1954618	1956501	1884	+	PGF_12878485	627	Two-component system sensor histidine kinase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.165	PATRIC.2.9855.2.9855.con.0001.CDS.195619.195963.fwd	PATRIC	CDS	195619	195963	345	+	PGF_00065695	114	Uncharacterized protein YwsA						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1923	PATRIC.2.9855.2.9855.con.0001.CDS.1956513.1958045.fwd	PATRIC	CDS	1956513	1958045	1533	+	PGF_00062533	510	Two-component response regulator yesN						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1924	PATRIC.2.9855.2.9855.con.0001.CDS.1958234.1959487.fwd	PATRIC	CDS	1958234	1959487	1254	+	PGF_00035106	417	Possible alpha-xyloside ABC transporter, substrate-binding component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1926	PATRIC.2.9855.2.9855.con.0001.CDS.1960007.1960915.fwd	PATRIC	CDS	1960007	1960915	909	+	PGF_12954995	302	Possible alpha-xyloside ABC transporter, permease component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1927	PATRIC.2.9855.2.9855.con.0001.CDS.1960915.1961760.fwd	PATRIC	CDS	1960915	1961760	846	+	PGF_00035105	281	Possible alpha-xyloside ABC transporter, permease component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1928	PATRIC.2.9855.2.9855.con.0001.CDS.1961800.1963827.fwd	PATRIC	CDS	1961800	1963827	2028	+	PGF_00068225	675	alpha-xylosidase (EC 3.2.1.177)	GO:0061634|alpha-D-xyloside xylohydrolase					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.166	PATRIC.2.9855.2.9855.con.0001.CDS.196186.196878.fwd	PATRIC	CDS	196186	196878	693	+	PGF_01303242	230	HD domain protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1929	PATRIC.2.9855.2.9855.con.0001.CDS.1964030.1964893.fwd	PATRIC	CDS	1964030	1964893	864	+	PGF_01042714	287	ABC transporter amino acid-binding protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1930	PATRIC.2.9855.2.9855.con.0001.CDS.1965196.1966575.fwd	PATRIC	CDS	1965196	1966575	1380	+	PGF_03106082	459	Amino-acid permease AapA						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1931	PATRIC.2.9855.2.9855.con.0001.CDS.1967609.1968394.fwd	PATRIC	CDS	1967609	1968394	786	+	PGF_05318435	261	Electron transfer flavoprotein, beta subunit						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1932	PATRIC.2.9855.2.9855.con.0001.CDS.1968414.1969352.fwd	PATRIC	CDS	1968414	1969352	939	+	PGF_07072294	312	Electron transfer flavoprotein, alpha subunit						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1933	PATRIC.2.9855.2.9855.con.0001.CDS.1969653.1971188.fwd	PATRIC	CDS	1969653	1971188	1536	+	PGF_10504454	511	Uncharacterized substrate:H+ symporter, LctP family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1934	PATRIC.2.9855.2.9855.con.0001.CDS.1971393.1972820.fwd	PATRIC	CDS	1971393	1972820	1428	+	PGF_00411187	475	(S)-2-hydroxy-acid oxidase chain D						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.167	PATRIC.2.9855.2.9855.con.0001.CDS.197165.197980.fwd	PATRIC	CDS	197165	197980	816	+	PGF_00049323	271	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic class 1A	GO:0004014|adenosylmethionine decarboxylase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1935	PATRIC.2.9855.2.9855.con.0001.CDS.1972907.1974046.fwd	PATRIC	CDS	1972907	1974046	1140	+	PGF_00424109	379	Electron bifurcating butyryl-CoA dehydrogenase (NAD+, ferredoxin)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1938	PATRIC.2.9855.2.9855.con.0001.CDS.1976129.1977238.fwd	PATRIC	CDS	1976129	1977238	1110	+	PGF_00004164	369	Fe-S oxidoreductase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1940	PATRIC.2.9855.2.9855.con.0001.CDS.1978878.1979747.fwd	PATRIC	CDS	1978878	1979747	870	+	PGF_01284161	289	Predicted membrane protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1941	PATRIC.2.9855.2.9855.con.0001.CDS.1979887.1980450.rev	PATRIC	CDS	1979887	1980450	564	-	PGF_07182652	187	Transcriptional regulator, AcrR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.168	PATRIC.2.9855.2.9855.con.0001.CDS.197998.199455.fwd	PATRIC	CDS	197998	199455	1458	+	PGF_00962420	485	Arginine decarboxylase (EC 4.1.1.19)	GO:0008792|arginine decarboxylase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1942	PATRIC.2.9855.2.9855.con.0001.CDS.1980612.1981709.fwd	PATRIC	CDS	1980612	1981709	1098	+	PGF_10509026	365	RND efflux system, membrane fusion protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1943	PATRIC.2.9855.2.9855.con.0001.CDS.1981709.1984759.fwd	PATRIC	CDS	1981709	1984759	3051	+	PGF_05237064	1016	RND efflux system, inner membrane transporter						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1945	PATRIC.2.9855.2.9855.con.0001.CDS.1987544.1988479.fwd	PATRIC	CDS	1987544	1988479	936	+	PGF_00037043	311	Probable endo-1,4-beta-xylanase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1946	PATRIC.2.9855.2.9855.con.0001.CDS.1988698.1989324.fwd	PATRIC	CDS	1988698	1989324	627	+	PGF_06916656	208	Transcriptional regulator, GntR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1947	PATRIC.2.9855.2.9855.con.0001.CDS.1989687.1990814.fwd	PATRIC	CDS	1989687	1990814	1128	+	PGF_06784466	375	ABC transporter, ATP-binding protein (cluster 13, osmolytes) ABC transporter, permease protein (cluster 13, osmolytes) / ABC transporter, substrate-binding protein (cluster 13, osmolytes)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1948	PATRIC.2.9855.2.9855.con.0001.CDS.1990816.1992390.fwd	PATRIC	CDS	1990816	1992390	1575	+	PGF_10512147	524							
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1950	PATRIC.2.9855.2.9855.con.0001.CDS.1993050.1994720.fwd	PATRIC	CDS	1993050	1994720	1671	+	PGF_00406529	556	2-oxoglutarate decarboxylase (EC 4.1.1.71)	GO:0008683|2-oxoglutarate decarboxylase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.169	PATRIC.2.9855.2.9855.con.0001.CDS.199456.200310.fwd	PATRIC	CDS	199456	200310	855	+	PGF_12908096	284	Spermidine synthase (EC 2.5.1.16)	GO:0004766|spermidine synthase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1951	PATRIC.2.9855.2.9855.con.0001.CDS.1995068.1996015.fwd	PATRIC	CDS	1995068	1996015	948	+	PGF_07987589	315	Transcriptional regulator, LysR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1953	PATRIC.2.9855.2.9855.con.0001.CDS.1996532.1997113.rev	PATRIC	CDS	1996532	1997113	582	-	PGF_07182652	193	Transcriptional regulator, AcrR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1954	PATRIC.2.9855.2.9855.con.0001.CDS.1997303.1998649.fwd	PATRIC	CDS	1997303	1998649	1347	+	PGF_01282235	448	Chromosome partition protein smc						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1955	PATRIC.2.9855.2.9855.con.0001.CDS.1998741.1999949.fwd	PATRIC	CDS	1998741	1999949	1209	+	PGF_02945982	402	CzcABC family efflux RND transporter, membrane fusion protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1956	PATRIC.2.9855.2.9855.con.0001.CDS.1999963.2003043.fwd	PATRIC	CDS	1999963	2003043	3081	+	PGF_00029572	1026	Acriflavin resistance protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1957	PATRIC.2.9855.2.9855.con.0001.CDS.2003168.2004310.rev	PATRIC	CDS	2003168	2004310	1143	-	PGF_01003946	380	Epoxide hydrolase (EC 3.3.2.9)	GO:0033961|cis-stilbene-oxide hydrolase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.170	PATRIC.2.9855.2.9855.con.0001.CDS.200454.201656.fwd	PATRIC	CDS	200454	201656	1203	+	PGF_00416623	400	Carboxynorspermidine synthase (EC 1.5.1.43)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1958	PATRIC.2.9855.2.9855.con.0001.CDS.2004616.2005467.fwd	PATRIC	CDS	2004616	2005467	852	+	PGF_00058791	283	Transcriptional regulator of rhamnose utilization, AraC family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1959	PATRIC.2.9855.2.9855.con.0001.CDS.2006046.2008376.fwd	PATRIC	CDS	2006046	2008376	2331	+	PGF_10538082	776	Sensory box/GGDEF family protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1962	PATRIC.2.9855.2.9855.con.0001.CDS.2010042.2010791.fwd	PATRIC	CDS	2010042	2010791	750	+	PGF_02282777	249	Trans-aconitate 2-methyltransferase (EC 2.1.1.144)	GO:0030798|trans-aconitate 2-methyltransferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1963	PATRIC.2.9855.2.9855.con.0001.CDS.2010971.2011579.fwd	PATRIC	CDS	2010971	2011579	609	+	PGF_10419038	202	Uridine kinase, type 2 (EC 2.7.1.48)	GO:0004849|uridine kinase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1965	PATRIC.2.9855.2.9855.con.0001.CDS.2012301.2012858.rev	PATRIC	CDS	2012301	2012858	558	-	PGF_07182652	185	Transcriptional regulator, AcrR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1966	PATRIC.2.9855.2.9855.con.0001.CDS.2013499.2014692.fwd	PATRIC	CDS	2013499	2014692	1194	+	PGF_01520109	397	Multidrug-efflux transporter, major facilitator superfamily (MFS)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1967	PATRIC.2.9855.2.9855.con.0001.CDS.2014733.2015329.fwd	PATRIC	CDS	2014733	2015329	597	+	PGF_00064767	198	Uncharacterized isochorismatase family protein YwoC						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1970	PATRIC.2.9855.2.9855.con.0001.CDS.2017047.2018765.fwd	PATRIC	CDS	2017047	2018765	1719	+	PGF_07849456	572	Methyl-accepting chemotaxis protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.171	PATRIC.2.9855.2.9855.con.0001.CDS.202066.203205.fwd	PATRIC	CDS	202066	203205	1140	+	PGF_00416622	379	Carboxynorspermidine decarboxylase (EC 4.1.1.96)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1973	PATRIC.2.9855.2.9855.con.0001.CDS.2022316.2022462.rev	PATRIC	CDS	2022316	2022462	147	-	PGF_07182652	48	Transcriptional regulator, AcrR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1974	PATRIC.2.9855.2.9855.con.0001.CDS.2022695.2024218.rev	PATRIC	CDS	2022695	2024218	1524	-	PGF_00048270	507	Rhamnogalacturonide transporter RhiT						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1975	PATRIC.2.9855.2.9855.con.0001.CDS.2024221.2025522.rev	PATRIC	CDS	2024221	2025522	1302	-	PGF_00034641	433	Polygalacturonase (EC 3.2.1.15)	GO:0004650|polygalacturonase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1977	PATRIC.2.9855.2.9855.con.0001.CDS.2026775.2027656.fwd	PATRIC	CDS	2026775	2027656	882	+	PGF_01671660	293	Transcriptional regulator, AraC family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1979	PATRIC.2.9855.2.9855.con.0001.CDS.2029137.2029901.rev	PATRIC	CDS	2029137	2029901	765	-	PGF_00028606	254	Oxidoreductase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1980	PATRIC.2.9855.2.9855.con.0001.CDS.2030027.2032021.rev	PATRIC	CDS	2030027	2032021	1995	-	PGF_07849456	664	Methyl-accepting chemotaxis protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1981	PATRIC.2.9855.2.9855.con.0001.CDS.2032044.2032517.rev	PATRIC	CDS	2032044	2032517	474	-	PGF_10423881	157	Transcriptional regulator, MarR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1983	PATRIC.2.9855.2.9855.con.0001.CDS.2032836.2034038.fwd	PATRIC	CDS	2032836	2034038	1203	+	PGF_01283036	400	Gll2959 protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1984	PATRIC.2.9855.2.9855.con.0001.CDS.2034226.2034990.rev	PATRIC	CDS	2034226	2034990	765	-	PGF_08546938	254	Ferredoxin						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1985	PATRIC.2.9855.2.9855.con.0001.CDS.2035196.2035747.fwd	PATRIC	CDS	2035196	2035747	552	+	PGF_07182652	183	Transcriptional regulator, AcrR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1986	PATRIC.2.9855.2.9855.con.0001.CDS.2036206.2037045.fwd	PATRIC	CDS	2036206	2037045	840	+	PGF_03514578	279	Beta-glucoside bgl operon antiterminator, BglG family PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component / PTS system, beta-glucoside-specific IIA component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1987	PATRIC.2.9855.2.9855.con.0001.CDS.2037338.2039230.fwd	PATRIC	CDS	2037338	2039230	1893	+	PGF_04512237	630							
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1988	PATRIC.2.9855.2.9855.con.0001.CDS.2039526.2040941.fwd	PATRIC	CDS	2039526	2040941	1416	+	PGF_08148954	471	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1989	PATRIC.2.9855.2.9855.con.0001.CDS.2041233.2042177.rev	PATRIC	CDS	2041233	2042177	945	-	PGF_03139283	314	Chitinase (EC 3.2.1.14)	GO:0004568|chitinase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1990	PATRIC.2.9855.2.9855.con.0001.CDS.2042252.2044024.rev	PATRIC	CDS	2042252	2044024	1773	-	PGF_03139283	590	Chitinase (EC 3.2.1.14)	GO:0004568|chitinase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1991	PATRIC.2.9855.2.9855.con.0001.CDS.2044507.2045259.fwd	PATRIC	CDS	2044507	2045259	753	+	PGF_06241294	250	SigI-like RNA polymerase sigma factor						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1992	PATRIC.2.9855.2.9855.con.0001.CDS.2045546.2046778.fwd	PATRIC	CDS	2045546	2046778	1233	+	PGF_10368386	410	Beta-glucanase precursor (EC 3.2.1.73)	GO:0042972|licheninase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1994	PATRIC.2.9855.2.9855.con.0001.CDS.2047224.2049056.fwd	PATRIC	CDS	2047224	2049056	1833	+	PGF_03139283	610	Chitinase (EC 3.2.1.14)	GO:0004568|chitinase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1995	PATRIC.2.9855.2.9855.con.0001.CDS.2049245.2051014.rev	PATRIC	CDS	2049245	2051014	1770	-	PGF_00410730	589	putative secreted sugar hydrolase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1998	PATRIC.2.9855.2.9855.con.0001.CDS.2053394.2054041.fwd	PATRIC	CDS	2053394	2054041	648	+	PGF_05357708	215	DNA-3-methyladenine glycosylase (EC 3.2.2.20)	GO:0008725|DNA-3-methyladenine glycosylase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2001	PATRIC.2.9855.2.9855.con.0001.CDS.2056173.2057123.fwd	PATRIC	CDS	2056173	2057123	951	+	PGF_00060409	316	Translation elongation factor G						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2003	PATRIC.2.9855.2.9855.con.0001.CDS.2057755.2058648.fwd	PATRIC	CDS	2057755	2058648	894	+	PGF_01671660	297	Transcriptional regulator, AraC family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2005	PATRIC.2.9855.2.9855.con.0001.CDS.2059252.2060064.fwd	PATRIC	CDS	2059252	2060064	813	+	PGF_12690820	270	Phage replication initiation						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.175	PATRIC.2.9855.2.9855.con.0001.CDS.206827.207264.fwd	PATRIC	CDS	206827	207264	438	+	PGF_10561718	145	DnaJ-class molecular chaperone CbpA						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2016	PATRIC.2.9855.2.9855.con.0001.CDS.2070840.2071715.fwd	PATRIC	CDS	2070840	2071715	876	+		291	DNA-cytosine methyltransferase (EC 2.1.1.37)	GO:0003886|DNA (cytosine-5-)-methyltransferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2017	PATRIC.2.9855.2.9855.con.0001.CDS.2071720.2073240.fwd	PATRIC	CDS	2071720	2073240	1521	+	PGF_01889325	506	DNA-cytosine methyltransferase (EC 2.1.1.37)	GO:0003886|DNA (cytosine-5-)-methyltransferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2019	PATRIC.2.9855.2.9855.con.0001.CDS.2074718.2076889.fwd	PATRIC	CDS	2074718	2076889	2172	+		723	Type II restriction-modification system restriction subunit						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2023	PATRIC.2.9855.2.9855.con.0001.CDS.2079971.2082412.fwd	PATRIC	CDS	2079971	2082412	2442	+	PGF_03810679	813	SOS-response repressor and protease LexA (EC 3.4.21.88)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2024	PATRIC.2.9855.2.9855.con.0001.CDS.2082489.2084633.fwd	PATRIC	CDS	2082489	2084633	2145	+	PGF_00426704	714	5-methylcytosine-specific restriction related enzyme						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.178	PATRIC.2.9855.2.9855.con.0001.CDS.208589.209437.fwd	PATRIC	CDS	208589	209437	849	+	PGF_02966929	282	Protein serine/threonine phosphatase PrpC, regulation of stationary phase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2026	PATRIC.2.9855.2.9855.con.0001.CDS.2087220.2087876.fwd	PATRIC	CDS	2087220	2087876	657	+	PGF_05606505	218	Cell surface protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2028	PATRIC.2.9855.2.9855.con.0001.CDS.2088863.2089345.fwd	PATRIC	CDS	2088863	2089345	483	+	PGF_05383972	160	G:T/U mismatch-specific uracil/thymine DNA-glycosylase (EC 3.2.2.27)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2030	PATRIC.2.9855.2.9855.con.0001.CDS.2091429.2093198.rev	PATRIC	CDS	2091429	2093198	1770	-	PGF_08128839	589	Heterodimeric efflux ABC transporter, permease/ATP-binding subunit 2						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2031	PATRIC.2.9855.2.9855.con.0001.CDS.2093200.2094933.rev	PATRIC	CDS	2093200	2094933	1734	-	PGF_10540665	577	Heterodimeric efflux ABC transporter, permease/ATP-binding subunit 1						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2037	PATRIC.2.9855.2.9855.con.0001.CDS.2097695.2097904.rev	PATRIC	CDS	2097695	2097904	210	-	PGF_02049468	69	Cold shock protein of CSP family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2038	PATRIC.2.9855.2.9855.con.0001.CDS.2098388.2100109.fwd	PATRIC	CDS	2098388	2100109	1722	+	PGF_07849456	573	Methyl-accepting chemotaxis protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2039	PATRIC.2.9855.2.9855.con.0001.CDS.2100453.2102024.fwd	PATRIC	CDS	2100453	2102024	1572	+	PGF_02620852	523	Two-component system sensor histidine kinase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2042	PATRIC.2.9855.2.9855.con.0001.CDS.2104061.2105464.fwd	PATRIC	CDS	2104061	2105464	1404	+	PGF_00018194	467	MATE efflux family protein DinF						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2043	PATRIC.2.9855.2.9855.con.0001.CDS.2105507.2106376.fwd	PATRIC	CDS	2105507	2106376	870	+	PGF_03318195	289	Cof-like hydrolase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2044	PATRIC.2.9855.2.9855.con.0001.CDS.2106603.2108048.fwd	PATRIC	CDS	2106603	2108048	1446	+	PGF_00017863	481	ATP-dependent RNA helicase YxiN						

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2046	PATRIC.2.9855.2.9855.con.0001.CDS.2108712.2109455.rev	PATRIC	CDS	2108712	2109455	744	-	PGF_02144826	247	FMN reductase [NAD(P)H] (EC 1.5.1.39)	GO:0052873|FMN reductase (NADPH) activity;GO:0052873|FMN reductase (NADH) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2047	PATRIC.2.9855.2.9855.con.0001.CDS.2109486.2110235.rev	PATRIC	CDS	2109486	2110235	750	-	PGF_00037198	249	AiiA-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2048	PATRIC.2.9855.2.9855.con.0001.CDS.2110554.2111228.fwd	PATRIC	CDS	2110554	2111228	675	+	PGF_00055054	224	Sulfite reductase, assimilatory-type (EC 1.8.-.-)	GO:0032441|pheophorbide a oxygenase activity;GO:0032441|sulfite reductase (coenzyme F420) activity;GO:0032441|aflatoxin reductase (coenzyme F420) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2049	PATRIC.2.9855.2.9855.con.0001.CDS.2111334.2111738.rev	PATRIC	CDS	2111334	2111738	405	-	PGF_00023476	134	Mutator MutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	GO:0004787|thiamine-pyrophosphatase activity;GO:0004787|8-oxo-7,8-dihydroguanosine triphosphate pyrophosphatase activity;GO:0004787|UDP-2,3-diacylglucosamine hydrolase activity;GO:0004787|bis(5'-nucleosyl)-tetraphosphatase activity;GO:0004787|dATP pyrophosphohydrolase activity;GO:0004787|pyrophosphatase activity;GO:0004787|dihydroneopterin monophosphate phosphatase activity;GO:0004787|dihydroneopterin triphosphate pyrophosphohydrolase activity;GO:0004787|dITP diphosphatase activity;GO:0004787|dTTP diphosphatase activity;GO:0004787|XTP diphosphatase activity;GO:0004787|ATP-dependent 5'-3' DNA helicase activity;GO:0004787|phosphocholine hydrolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2050	PATRIC.2.9855.2.9855.con.0001.CDS.2112031.2113125.fwd	PATRIC	CDS	2112031	2113125	1095	+	PGF_05606505	364	Cell surface protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2052	PATRIC.2.9855.2.9855.con.0001.CDS.2114358.2116097.rev	PATRIC	CDS	2114358	2116097	1740	-	PGF_01255210	579	Bis-ABC ATPase Cphy_0937	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2053	PATRIC.2.9855.2.9855.con.0001.CDS.2116571.2117554.rev	PATRIC	CDS	2116571	2117554	984	-	PGF_01283472	327	methyl-accepting chemotaxis protein (tlpB), putative	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2055	PATRIC.2.9855.2.9855.con.0001.CDS.2119492.2120673.fwd	PATRIC	CDS	2119492	2120673	1182	+	PGF_10343884	393	Branched-chain amino acid ABC transporter, substrate-binding protein LivJ (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2056	PATRIC.2.9855.2.9855.con.0001.CDS.2120777.2121661.fwd	PATRIC	CDS	2120777	2121661	885	+	PGF_06868199	294	Branched-chain amino acid ABC transporter, permease protein LivH (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2057	PATRIC.2.9855.2.9855.con.0001.CDS.2121671.2122717.fwd	PATRIC	CDS	2121671	2122717	1047	+	PGF_03231750	348	Branched-chain amino acid ABC transporter, permease protein LivM (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2058	PATRIC.2.9855.2.9855.con.0001.CDS.2122719.2123489.fwd	PATRIC	CDS	2122719	2123489	771	+	PGF_01726878	256	Branched-chain amino acid ABC transporter, ATP-binding protein LivG (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2059	PATRIC.2.9855.2.9855.con.0001.CDS.2123491.2124195.fwd	PATRIC	CDS	2123491	2124195	705	+	PGF_00700305	234	Branched-chain amino acid ABC transporter, ATP-binding protein LivF (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2060	PATRIC.2.9855.2.9855.con.0001.CDS.2124283.2124906.fwd	PATRIC	CDS	2124283	2124906	624	+	PGF_01667671	207	Cytidylate kinase (EC 2.7.4.25)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2061	PATRIC.2.9855.2.9855.con.0001.CDS.2124920.2125375.fwd	PATRIC	CDS	2124920	2125375	456	+	PGF_01424767	151	Transcriptional regulator, AsnC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.27	PATRIC.2.9855.2.9855.con.0001.CDS.21255.21884.fwd	PATRIC	CDS	21255	21884	630	+	PGF_01284116	209	Beta-phosphoglucomutase (EC 5.4.2.6) (EC 2.7.1.41)	GO:0008801|beta-phosphoglucomutase activity;GO:0047937|glucose-1-phosphate phosphodismutase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2062	PATRIC.2.9855.2.9855.con.0001.CDS.2125630.2126478.fwd	PATRIC	CDS	2125630	2126478	849	+	PGF_00420792	282	D-alanine aminotransferase (EC 2.6.1.21)	GO:0047810|D-alanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2064	PATRIC.2.9855.2.9855.con.0001.CDS.2127628.2128416.fwd	PATRIC	CDS	2127628	2128416	789	+	PGF_02935470	262	UPF0317 protein YcsI	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2065	PATRIC.2.9855.2.9855.con.0001.CDS.2128453.2129220.fwd	PATRIC	CDS	2128453	2129220	768	+	PGF_04710902	255	Lactam utilization protein LamB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2066	PATRIC.2.9855.2.9855.con.0001.CDS.2129240.2130370.fwd	PATRIC	CDS	2129240	2130370	1131	+	PGF_08932911	376	Alanine racemase (EC 5.1.1.1)	GO:0008784|alanine racemase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2067	PATRIC.2.9855.2.9855.con.0001.CDS.2130438.2131148.fwd	PATRIC	CDS	2130438	2131148	711	+	PGF_10380727	236	Allophanate hydrolase 2 subunit 1 (EC 3.5.1.54)	GO:0004039|allophanate hydrolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2068	PATRIC.2.9855.2.9855.con.0001.CDS.2131148.2132149.fwd	PATRIC	CDS	2131148	2132149	1002	+	PGF_01072023	333	Allophanate hydrolase 2 subunit 2 (EC 3.5.1.54)	GO:0004039|allophanate hydrolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2069	PATRIC.2.9855.2.9855.con.0001.CDS.2132164.2132625.fwd	PATRIC	CDS	2132164	2132625	462	+	PGF_00404065	153	Biotin carboxyl carrier protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2070	PATRIC.2.9855.2.9855.con.0001.CDS.2132648.2133991.fwd	PATRIC	CDS	2132648	2133991	1344	+	PGF_09867549	447	Biotin carboxylase (EC 6.3.4.14)	GO:0004075|biotin carboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2071	PATRIC.2.9855.2.9855.con.0001.CDS.2134394.2135485.rev	PATRIC	CDS	2134394	2135485	1092	-	PGF_03456354	363	Glycerol dehydrogenase (EC 1.1.1.6)	GO:0008888|glycerol dehydrogenase [NAD+] activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2073	PATRIC.2.9855.2.9855.con.0001.CDS.2135942.2139337.fwd	PATRIC	CDS	2135942	2139337	3396	+	PGF_00799603	1131	Molybdate metabolism regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2076	PATRIC.2.9855.2.9855.con.0001.CDS.2140220.2143726.fwd	PATRIC	CDS	2140220	2143726	3507	+	PGF_00799603	1168	Molybdate metabolism regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2078	PATRIC.2.9855.2.9855.con.0001.CDS.2144565.2145680.fwd	PATRIC	CDS	2144565	2145680	1116	+	PGF_00065508	371	Uncharacterized protein YehL	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2080	PATRIC.2.9855.2.9855.con.0001.CDS.2148240.2149370.fwd	PATRIC	CDS	2148240	2149370	1131	+	PGF_00067307	376	YehP, CoxE-like von Willebrand factor type A (vWA) domain-containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2083	PATRIC.2.9855.2.9855.con.0001.CDS.2151927.2152415.rev	PATRIC	CDS	2151927	2152415	489	-	PGF_10420503	162	Acetyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2084	PATRIC.2.9855.2.9855.con.0001.CDS.2152670.2153386.fwd	PATRIC	CDS	2152670	2153386	717	+	PGF_00057399	238	Transaldolase (EC 2.2.1.2)	GO:0004801|sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2085	PATRIC.2.9855.2.9855.con.0001.CDS.2153409.2153858.fwd	PATRIC	CDS	2153409	2153858	450	+	PGF_00929663	149	PTS system, IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2086	PATRIC.2.9855.2.9855.con.0001.CDS.2153904.2154188.fwd	PATRIC	CDS	2153904	2154188	285	+	PGF_00029530	94	PTS system, IIB component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2087	PATRIC.2.9855.2.9855.con.0001.CDS.2154200.2155558.fwd	PATRIC	CDS	2154200	2155558	1359	+	PGF_05423656	452	PTS system, IIC component, UlaA-type	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2088	PATRIC.2.9855.2.9855.con.0001.CDS.2155788.2157932.fwd	PATRIC	CDS	2155788	2157932	2145	+	PGF_08377644	714	Putative transcriptional antiterminator, BglG family / PTS system, IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2089	PATRIC.2.9855.2.9855.con.0001.CDS.2158877.2160346.fwd	PATRIC	CDS	2158877	2160346	1470	+	PGF_07629184	489	Cytosol aminopeptidase PepA (EC 3.4.11.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2090	PATRIC.2.9855.2.9855.con.0001.CDS.2160571.2162604.fwd	PATRIC	CDS	2160571	2162604	2034	+	PGF_10361261	677	Na+/H+ antiporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2091	PATRIC.2.9855.2.9855.con.0001.CDS.2162716.2163363.rev	PATRIC	CDS	2162716	2163363	648	-	PGF_02278882	215	Iron-sulfur flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2092	PATRIC.2.9855.2.9855.con.0001.CDS.2163495.2163836.fwd	PATRIC	CDS	2163495	2163836	342	+	PGF_03320197	113	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2094	PATRIC.2.9855.2.9855.con.0001.CDS.2166102.2167541.fwd	PATRIC	CDS	2166102	2167541	1440	+	PGF_02620852	479	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2095	PATRIC.2.9855.2.9855.con.0001.CDS.2167667.2169610.fwd	PATRIC	CDS	2167667	2169610	1944	+	PGF_06890698	647	NADH oxidase (EC 1.-.-.-)	GO:0008748|N-ethylmaleimide reductase activity;GO:0008748|reduced coenzyme F420 dehydrogenase activity;GO:0008748|sulfur oxygenase reductase activity;GO:0008748|malolactic enzyme activity;GO:0008748|NADPH:sulfur oxidoreductase activity;GO:0008748|epoxyqueuosine reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2096	PATRIC.2.9855.2.9855.con.0001.CDS.2169742.2171373.fwd	PATRIC	CDS	2169742	2171373	1632	+	PGF_03428203	543	Acetolactate synthase large subunit homolog	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2097	PATRIC.2.9855.2.9855.con.0001.CDS.2171378.2171746.fwd	PATRIC	CDS	2171378	2171746	369	+	PGF_05406020	122	4-carboxymuconolactone decarboxylase (EC 4.1.1.44)	GO:0047575|4-carboxymuconolactone decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2098	PATRIC.2.9855.2.9855.con.0001.CDS.2172301.2173602.fwd	PATRIC	CDS	2172301	2173602	1302	+	PGF_00011848	433	Histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2099	PATRIC.2.9855.2.9855.con.0001.CDS.2173595.2174770.fwd	PATRIC	CDS	2173595	2174770	1176	+	PGF_01281693	391	C-di-GMP phosphodiesterase A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2100	PATRIC.2.9855.2.9855.con.0001.CDS.2174772.2175797.fwd	PATRIC	CDS	2174772	2175797	1026	+	PGF_12890335	341	Response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2101	PATRIC.2.9855.2.9855.con.0001.CDS.2175810.2177081.fwd	PATRIC	CDS	2175810	2177081	1272	+	PGF_01284177	423	Sensor protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.184	PATRIC.2.9855.2.9855.con.0001.CDS.217731.218339.fwd	PATRIC	CDS	217731	218339	609	+	PGF_01320598	202	Putative exported protein precursor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2102	PATRIC.2.9855.2.9855.con.0001.CDS.2177393.2179630.fwd	PATRIC	CDS	2177393	2179630	2238	+	PGF_12833297	745	ATP-dependent DNA helicase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2103	PATRIC.2.9855.2.9855.con.0001.CDS.2180096.2181127.fwd	PATRIC	CDS	2180096	2181127	1032	+	PGF_06335969	343	Transcriptional regulator, Xre family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2105	PATRIC.2.9855.2.9855.con.0001.CDS.2182079.2182486.fwd	PATRIC	CDS	2182079	2182486	408	+	PGF_00057506	135	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2106	PATRIC.2.9855.2.9855.con.0001.CDS.2182612.2183415.fwd	PATRIC	CDS	2182612	2183415	804	+	PGF_08546938	267	Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.185	PATRIC.2.9855.2.9855.con.0001.CDS.218332.219756.fwd	PATRIC	CDS	218332	219756	1425	+	PGF_12927129	474	Protein previously called VgrG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2109	PATRIC.2.9855.2.9855.con.0001.CDS.2184717.2185172.fwd	PATRIC	CDS	2184717	2185172	456	+	PGF_07383330	151	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2112	PATRIC.2.9855.2.9855.con.0001.CDS.2187092.2188537.fwd	PATRIC	CDS	2187092	2188537	1446	+	PGF_04033086	481	Lipase precursor (EC 3.1.1.3)	GO:0004806|triglyceride lipase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2114	PATRIC.2.9855.2.9855.con.0001.CDS.2189276.2190436.rev	PATRIC	CDS	2189276	2190436	1161	-	PGF_00018000	386	Lysine-N-methylase (EC 2.1.1.-)	GO:0008276|protein methyltransferase activity;GO:0000179|protein C-terminal carboxyl O-methyltransferase activity;GO:0000179|tRNA (guanine-N2-)-methyltransferase activity;GO:0000179|C-methyltransferase activity;GO:0000179|N-methyltransferase activity;GO:0000179|O-methyltransferase activity;GO:0000179|S-methyltransferase activity;GO:0000179|RNA methyltransferase activity;GO:0000179|mRNA methyltransferase activity;GO:0000179|tRNA methyltransferase activity;GO:0000179|protein methyltransferase activity;GO:0000179|2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity;GO:0000179|rRNA methyltransferase activity;GO:0000179|rRNA (uridine-2'-O-)-methyltransferase activity;GO:0000179|rRNA (adenine-N6-)-methyltransferase activity;GO:0000179|DNA-methyltransferase activity;GO:0000179|tRNA (guanine-N1-)-methyltransferase activity;GO:0000179|rRNA (cytosine-C5-)-methyltransferase activity;GO:0000179|selenocysteine methyltransferase activity;GO:0000179|arginine N-methyltransferase activity;GO:0000179|protein-arginine N-methyltransferase activity;GO:0000179|lysine N-methyltransferase activity;GO:0000179|protein-lysine N-methyltransferase activity;GO:0000179|tRNA (uracil) methyltransferase activity;GO:0000179|tRNA (guanine) methyltransferase activity;GO:0000179|tRNA (adenine) methyltransferase activity;GO:0000179|tRNA (cytosine) methyltransferase activity;GO:0000179|tRNA (cytosine-5-)-methyltransferase activity;GO:0000179|tRNA (adenine-N1-)-methyltransferase activity;GO:0000179|rRNA (adenine) methyltransferase activity;GO:0000179|rRNA (cytosine) methyltransferase activity;GO:0000179|rRNA (guanine) methyltransferase activity;GO:0000179|rRNA (uridine) methyltransferase activity;GO:0000179|protein C-terminal leucine carboxyl O-methyltransferase activity;GO:0000179|1-phenanthrol methyltransferase activity;GO:0000179|protein-arginine N5-methyltransferase activity;GO:0000179|methylarsonite methyltransferase activity;GO:0000179|dimethylarsinite methyltransferase activity;GO:0000179|4,5-

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2116	PATRIC.2.9855.2.9855.con.0001.CDS.2191011.2192918.fwd	PATRIC	CDS	2191011	2192918	1908	+	PGF_03059389	635	Transcriptional antiterminator of lichenan operon, BglG family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2117	PATRIC.2.9855.2.9855.con.0001.CDS.2192911.2193972.fwd	PATRIC	CDS	2192911	2193972	1062	+	PGF_00026261	353	Nondeblocking aminopeptidase YpdE (X-X-[^PR]- specific)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2118	PATRIC.2.9855.2.9855.con.0001.CDS.2193965.2194288.fwd	PATRIC	CDS	2193965	2194288	324	+	PGF_00029614	107	PTS system, IIA component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2119	PATRIC.2.9855.2.9855.con.0001.CDS.2194290.2194628.fwd	PATRIC	CDS	2194290	2194628	339	+	PGF_00029598	112	PTS system, IIB component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2120	PATRIC.2.9855.2.9855.con.0001.CDS.2194641.2195954.fwd	PATRIC	CDS	2194641	2195954	1314	+	PGF_08056389	437	PTS system, IIC component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2121	PATRIC.2.9855.2.9855.con.0001.CDS.2196081.2197169.fwd	PATRIC	CDS	2196081	2197169	1089	+	PGF_03750541	362	Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2122	PATRIC.2.9855.2.9855.con.0001.CDS.2197170.2198351.fwd	PATRIC	CDS	2197170	2198351	1182	+	PGF_00420012	393	Cystathionine beta-lyase MalY (EC 4.4.1.8) @ Maltose regulon modulator	GO:0004121|cystathionine beta-lyase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2124	PATRIC.2.9855.2.9855.con.0001.CDS.2199713.2202886.fwd	PATRIC	CDS	2199713	2202886	3174	+	PGF_04640310	1057	RND efflux system, inner membrane transporter						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2125	PATRIC.2.9855.2.9855.con.0001.CDS.2202876.2204132.fwd	PATRIC	CDS	2202876	2204132	1257	+	PGF_12869202	418	ABC transporter, RND-adapter-like protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2126	PATRIC.2.9855.2.9855.con.0001.CDS.2204605.2205771.fwd	PATRIC	CDS	2204605	2205771	1167	+	PGF_01256137	388	Choline binding protein PcpA						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2127	PATRIC.2.9855.2.9855.con.0001.CDS.2206200.2206703.fwd	PATRIC	CDS	2206200	2206703	504	+	PGF_00896280	167	RNA polymerase ECF-type sigma factor						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.28	PATRIC.2.9855.2.9855.con.0001.CDS.22069.22836.rev	PATRIC	CDS	22069	22836	768	-	PGF_00060285	255	Transcriptional repressor of the myo-inositol catabolic operon DeoR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2129	PATRIC.2.9855.2.9855.con.0001.CDS.2208111.2208605.fwd	PATRIC	CDS	2208111	2208605	495	+	PGF_00407798	164	putative kinase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2134	PATRIC.2.9855.2.9855.con.0001.CDS.2209739.2209864.fwd	PATRIC	CDS	2209739	2209864	126	+	PGF_01737958	41	2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	GO:0018784|(S)-2-haloacid dehalogenase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2137	PATRIC.2.9855.2.9855.con.0001.CDS.2210548.2211480.fwd	PATRIC	CDS	2210548	2211480	933	+	PGF_00012289	310	Homocysteine S-methyltransferase domain protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2141	PATRIC.2.9855.2.9855.con.0001.CDS.2212824.2213339.fwd	PATRIC	CDS	2212824	2213339	516	+	PGF_10519603	171	Acetyltransferase, GNAT family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2143	PATRIC.2.9855.2.9855.con.0001.CDS.2214191.2215009.fwd	PATRIC	CDS	2214191	2215009	819	+	PGF_00057506	272	Transcriptional regulator, MerR family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2144	PATRIC.2.9855.2.9855.con.0001.CDS.2215891.2216526.fwd	PATRIC	CDS	2215891	2216526	636	+	PGF_00010499	211	HD domain protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2145	PATRIC.2.9855.2.9855.con.0001.CDS.2216499.2217194.fwd	PATRIC	CDS	2216499	2217194	696	+	PGF_02630413	231	Hydrolase, alpha/beta fold family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2148	PATRIC.2.9855.2.9855.con.0001.CDS.2221949.2222857.fwd	PATRIC	CDS	2221949	2222857	909	+	PGF_01625234	302	Thioredoxin reductase (EC 1.8.1.9)	GO:0004791|thioredoxin-disulfide reductase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2149	PATRIC.2.9855.2.9855.con.0001.CDS.2222903.2223388.fwd	PATRIC	CDS	2222903	2223388	486	+	PGF_00413533	161	Thiol peroxidase, Tpx-type (EC 1.11.1.15)	GO:0051920|peroxiredoxin activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2150	PATRIC.2.9855.2.9855.con.0001.CDS.2223593.2224192.rev	PATRIC	CDS	2223593	2224192	600	-	PGF_01920882	199	putative membrane protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2151	PATRIC.2.9855.2.9855.con.0001.CDS.2224887.2225903.fwd	PATRIC	CDS	2224887	2225903	1017	+	PGF_08462977	338	Pirin						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2152	PATRIC.2.9855.2.9855.con.0001.CDS.2226030.2226647.rev	PATRIC	CDS	2226030	2226647	618	-	PGF_01284139	205	Membrane protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2153	PATRIC.2.9855.2.9855.con.0001.CDS.2226943.2228151.fwd	PATRIC	CDS	2226943	2228151	1209	+	PGF_00038846	402	Aldo/keto reductase, 4Fe-4S-containing, TM1183 family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2154	PATRIC.2.9855.2.9855.con.0001.CDS.2228877.2231144.fwd	PATRIC	CDS	2228877	2231144	2268	+	PGF_10311643	755	putative secreted protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.190	PATRIC.2.9855.2.9855.con.0001.CDS.222932.224476.fwd	PATRIC	CDS	222932	224476	1545	+	PGF_00417736	514	Choline binding protein A						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2155	PATRIC.2.9855.2.9855.con.0001.CDS.2231571.2231747.fwd	PATRIC	CDS	2231571	2231747	177	+	PGF_04034430	58	SSU ribosomal protein S21p						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2160	PATRIC.2.9855.2.9855.con.0001.CDS.2236850.2237770.fwd	PATRIC	CDS	2236850	2237770	921	+	PGF_00884706	306	Efflux ABC transporter, ATP-binding protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2161	PATRIC.2.9855.2.9855.con.0001.CDS.2237767.2238492.fwd	PATRIC	CDS	2237767	2238492	726	+	PGF_00006351	241	Efflux ABC transporter, permease protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2162	PATRIC.2.9855.2.9855.con.0001.CDS.2238901.2239947.rev	PATRIC	CDS	2238901	2239947	1047	-	PGF_08142081	348	Linoleoyl-CoA desaturase (EC 1.14.19.3)	GO:0016213|linoleoyl-CoA desaturase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2163	PATRIC.2.9855.2.9855.con.0001.CDS.2240263.2240571.fwd	PATRIC	CDS	2240263	2240571	309	+	PGF_00029615	102	PTS system, IIB component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2164	PATRIC.2.9855.2.9855.con.0001.CDS.2240600.2241850.fwd	PATRIC	CDS	2240600	2241850	1251	+	PGF_00029521	416	PTS system, IIC component						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2165	PATRIC.2.9855.2.9855.con.0001.CDS.2241931.2243241.fwd	PATRIC	CDS	2241931	2243241	1311	+	PGF_02163575	436	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2166	PATRIC.2.9855.2.9855.con.0001.CDS.2243261.2243566.fwd	PATRIC	CDS	2243261	2243566	306	+	PGF_01629422	101	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2167	PATRIC.2.9855.2.9855.con.0001.CDS.2243678.2244772.fwd	PATRIC	CDS	2243678	2244772	1095	+	PGF_12764946	364	N-acetylmuramoyl-L-alanine amidase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2168	PATRIC.2.9855.2.9855.con.0001.CDS.2244797.2246203.fwd	PATRIC	CDS	2244797	2246203	1407	+	PGF_01281239	468	Basic protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2169	PATRIC.2.9855.2.9855.con.0001.CDS.2246613.2247698.fwd	PATRIC	CDS	2246613	2247698	1086	+	PGF_00028476	361	Outer surface protein of unknown function, cellobiose operon						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2170	PATRIC.2.9855.2.9855.con.0001.CDS.2247922.2248707.fwd	PATRIC	CDS	2247922	2248707	786	+	PGF_09626318	261	SSU rRNA pseudouridine(516) synthase (EC 5.4.99.19)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2172	PATRIC.2.9855.2.9855.con.0001.CDS.2249355.2250146.rev	PATRIC	CDS	2249355	2250146	792	-	PGF_10353298	263	Transcriptional regulator, AraC family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2173	PATRIC.2.9855.2.9855.con.0001.CDS.2250402.2251796.fwd	PATRIC	CDS	2250402	2251796	1395	+	PGF_08913741	464	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2174	PATRIC.2.9855.2.9855.con.0001.CDS.2252106.2253740.fwd	PATRIC	CDS	2252106	2253740	1635	+	PGF_01259166	544	TPR domain protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2175	PATRIC.2.9855.2.9855.con.0001.CDS.2254099.2254704.fwd	PATRIC	CDS	2254099	2254704	606	+	PGF_00959691	201	Butyrate--acetoacetate CoA-transferase subunit A (EC 2.8.3.9)	GO:0047371|butyrate-acetoacetate CoA-transferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2176	PATRIC.2.9855.2.9855.con.0001.CDS.2254682.2254816.fwd	PATRIC	CDS	2254682	2254816	135	+	PGF_00959691	44	Butyrate--acetoacetate CoA-transferase subunit A (EC 2.8.3.9)	GO:0047371|butyrate-acetoacetate CoA-transferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2177	PATRIC.2.9855.2.9855.con.0001.CDS.2254825.2255349.fwd	PATRIC	CDS	2254825	2255349	525	+	PGF_08079989	174	Butyrate--acetoacetate CoA-transferase subunit B (EC 2.8.3.9)	GO:0047371|butyrate-acetoacetate CoA-transferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2178	PATRIC.2.9855.2.9855.con.0001.CDS.2255303.2255482.fwd	PATRIC	CDS	2255303	2255482	180	+	PGF_08079989	59	Butyrate--acetoacetate CoA-transferase subunit B (EC 2.8.3.9)	GO:0047371|butyrate-acetoacetate CoA-transferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2179	PATRIC.2.9855.2.9855.con.0001.CDS.2255811.2257379.fwd	PATRIC	CDS	2255811	2257379	1569	+	PGF_02147779	522	Oligopeptide ABC transporter, substrate-binding protein OppA (TC 3.A.1.5.1)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2180	PATRIC.2.9855.2.9855.con.0001.CDS.2257463.2258416.fwd	PATRIC	CDS	2257463	2258416	954	+	PGF_00977978	317	Oligopeptide ABC transporter, permease protein OppB (TC 3.A.1.5.1)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.193	PATRIC.2.9855.2.9855.con.0001.CDS.225841.227520.fwd	PATRIC	CDS	225841	227520	1680	+	PGF_00417736	559	Choline binding protein A						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2181	PATRIC.2.9855.2.9855.con.0001.CDS.2258422.2259273.fwd	PATRIC	CDS	2258422	2259273	852	+	PGF_10569020	283	Oligopeptide ABC transporter, permease protein OppC (TC 3.A.1.5.1)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2182	PATRIC.2.9855.2.9855.con.0001.CDS.2259278.2260249.fwd	PATRIC	CDS	2259278	2260249	972	+	PGF_09990804	323	Oligopeptide ABC transporter, ATP-binding protein OppD (TC 3.A.1.5.1)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2183	PATRIC.2.9855.2.9855.con.0001.CDS.2260314.2261288.fwd	PATRIC	CDS	2260314	2261288	975	+	PGF_07131324	324	Oligopeptide ABC transporter, ATP-binding protein OppF (TC 3.A.1.5.1)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2184	PATRIC.2.9855.2.9855.con.0001.CDS.2261490.2263733.rev	PATRIC	CDS	2261490	2263733	2244	-	PGF_00007774	747	ABC transporter, fused permease protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2185	PATRIC.2.9855.2.9855.con.0001.CDS.2263733.2264431.rev	PATRIC	CDS	2263733	2264431	699	-	PGF_10425579	232	ABC transporter, ATP-binding protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2186	PATRIC.2.9855.2.9855.con.0001.CDS.2264952.2265668.fwd	PATRIC	CDS	2264952	2265668	717	+	PGF_01280820	238	Uncharacterized protein TP_0572						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2188	PATRIC.2.9855.2.9855.con.0001.CDS.2266979.2267284.rev	PATRIC	CDS	2266979	2267284	306	-	PGF_00025215	101	Acetolactate synthase small subunit (EC 2.2.1.6)	GO:0003984|acetolactate synthase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2189	PATRIC.2.9855.2.9855.con.0001.CDS.2267277.2268959.rev	PATRIC	CDS	2267277	2268959	1683	-	PGF_00025090	560	Acetolactate synthase large subunit (EC 2.2.1.6)	GO:0003984|acetolactate synthase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2191	PATRIC.2.9855.2.9855.con.0001.CDS.2269856.2271796.fwd	PATRIC	CDS	2269856	2271796	1941	+	PGF_03029859	646	Bis-ABC ATPase Uup						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2193	PATRIC.2.9855.2.9855.con.0001.CDS.2272072.2275329.fwd	PATRIC	CDS	2272072	2275329	3258	+	PGF_10467762	1085	DNA/RNA helicases, SNF2 family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2194	PATRIC.2.9855.2.9855.con.0001.CDS.2275363.2276070.fwd	PATRIC	CDS	2275363	2276070	708	+	PGF_00021389	235	Mg(2+)-transport-ATPase-associated protein MgtC						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2195	PATRIC.2.9855.2.9855.con.0001.CDS.2276441.2277430.fwd	PATRIC	CDS	2276441	2277430	990	+	PGF_07479808	329	Ketopantoate reductase PanG (EC 1.1.1.169)	GO:0008677|2-dehydropantoate 2-reductase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2196	PATRIC.2.9855.2.9855.con.0001.CDS.2277430.2278257.fwd	PATRIC	CDS	2277430	2278257	828	+	PGF_00419915	275	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	GO:0003864|3-methyl-2-oxobutanoate hydroxymethyltransferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2198	PATRIC.2.9855.2.9855.con.0001.CDS.2278607.2279449.fwd	PATRIC	CDS	2278607	2279449	843	+	PGF_00523822	280	Pantoate--beta-alanine ligase (EC 6.3.2.1)	GO:0004592|pantoate-beta-alanine ligase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2199	PATRIC.2.9855.2.9855.con.0001.CDS.2279818.2280192.fwd	PATRIC	CDS	2279818	2280192	375	+	PGF_00985834	124	Aspartate 1-decarboxylase (EC 4.1.1.11)	GO:0004068|aspartate 1-decarboxylase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.195	PATRIC.2.9855.2.9855.con.0001.CDS.228047.228757.fwd	PATRIC	CDS	228047	228757	711	+	PGF_00020332	236	Metal-dependent hydrolase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2203	PATRIC.2.9855.2.9855.con.0001.CDS.2282608.2284140.fwd	PATRIC	CDS	2282608	2284140	1533	+	PGF_00418533	510	Glycosyl transferase, group 2 family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2206	PATRIC.2.9855.2.9855.con.0001.CDS.2286572.2287486.fwd	PATRIC	CDS	2286572	2287486	915	+	PGF_08108653	304	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	GO:0008879|glucose-1-phosphate thymidylyltransferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2207	PATRIC.2.9855.2.9855.con.0001.CDS.2287489.2288064.fwd	PATRIC	CDS	2287489	2288064	576	+	PGF_07115887	191	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	GO:0008830|dTDP-4-dehydrorhamnose 3,5-epimerase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2209	PATRIC.2.9855.2.9855.con.0001.CDS.2289655.2290794.fwd	PATRIC	CDS	2289655	2290794	1140	+	PGF_10025016	379	Cysteine desulfurase (EC 2.8.1.7)	GO:0031071|cysteine desulfurase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2210	PATRIC.2.9855.2.9855.con.0001.CDS.2290861.2292597.fwd	PATRIC	CDS	2290861	2292597	1737	+	PGF_09700850	578	Amine oxidase, flavin-containing						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2211	PATRIC.2.9855.2.9855.con.0001.CDS.2292693.2293787.rev	PATRIC	CDS	2292693	2293787	1095	-	PGF_03753601	364	Aminotransferase, DegT/Dnrj/EryC1/StrS family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2213	PATRIC.2.9855.2.9855.con.0001.CDS.2294418.2294825.rev	PATRIC	CDS	2294418	2294825	408	-	PGF_00070476	135	dTDP-6-deoxy-3,4-keto-hexulose isomerase (EC 5.3.2.3)						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2214	PATRIC.2.9855.2.9855.con.0001.CDS.2294872.2295669.rev	PATRIC	CDS	2294872	2295669	798	-	PGF_00028432	265	Acetyltransferases						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2216	PATRIC.2.9855.2.9855.con.0001.CDS.2296765.2298363.rev	PATRIC	CDS	2296765	2298363	1599	-	PGF_10460846	532	Glycosyltransferase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2217	PATRIC.2.9855.2.9855.con.0001.CDS.2298625.2299698.rev	PATRIC	CDS	2298625	2299698	1074	-	PGF_00009518	357	Glycosyl transferase, group 2 family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2220	PATRIC.2.9855.2.9855.con.0001.CDS.2306117.2306818.fwd	PATRIC	CDS	2306117	2306818	702	+	PGF_07475842	233	Transposase, IS4 family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.29	PATRIC.2.9855.2.9855.con.0001.CDS.23074.24228.fwd	PATRIC	CDS	23074	24228	1155	+	PGF_00004208	384	Fe-containing alcohol dehydrogenase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2221	PATRIC.2.9855.2.9855.con.0001.CDS.2307863.2309668.fwd	PATRIC	CDS	2307863	2309668	1806	+	PGF_00071680	601	glutamine synthetase family protein						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2222	PATRIC.2.9855.2.9855.con.0001.CDS.2310751.2310975.fwd	PATRIC	CDS	2310751	2310975	225	+	PGF_01267521	74	Probable transposase TnpA						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2223	PATRIC.2.9855.2.9855.con.0001.CDS.2311126.2312538.rev	PATRIC	CDS	2311126	2312538	1413	-	PGF_00009518	470	Glycosyl transferase, group 2 family						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2224	PATRIC.2.9855.2.9855.con.0001.CDS.2312689.2313747.rev	PATRIC	CDS	2312689	2313747	1059	-	PGF_04305571	352	Glycosyltransferase						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2229	PATRIC.2.9855.2.9855.con.0001.CDS.2317614.2319113.fwd	PATRIC	CDS	2317614	2319113	1500	+	PGF_01259144	499	Surface antigen						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.200	PATRIC.2.9855.2.9855.con.0001.CDS.231924.232541.fwd	PATRIC	CDS	231924	232541	618	+	PGF_01284168	205	Putative exported protein precursor						
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2230	PATRIC.2.9855.2.9855.con.0001.CDS.2319443.2320324.fwd	PATRIC	CDS	2319443	2320324	882	+	PGF_00571237	293	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	GO:0008831|dTDP-4-dehydrorhamnose reductase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2231	PATRIC.2.9855.2.9855.con.0001.CDS.2320343.2321392.fwd	PATRIC	CDS	2320343	2321392	1050	+	PGF_03056683	349	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	GO:0008460|dTDP-glucose 4,6-dehydratase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2232	PATRIC.2.9855.2.9855.con.0001.CDS.2321585.2322358.fwd	PATRIC	CDS	2321585	2322358	774	+	PGF_04587056	257	Glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33)	GO:0047343|glucose-1-phosphate cytidylyltransferase activity					
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2233	PATRIC.2.9855.2.9855.con.0001.CDS.2322349.2323440.fwd	PATRIC	CDS	2322349	2323440	1092	+	PGF_00414981	363	CDP-glucose 4,6-dehydratase (EC 4.2.1.45)	GO:0047733|CDP-glucose 4,6-dehydratase activity					

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2238	PATRIC.2.9855.2.9855.con.0001.CDS.2325943.2327295.fwd	PATRIC	CDS	2325943	2327295	1353	+	PGF_00414932	450	CDP-4-dehydro-6-deoxy-D-glucose 3-dehydratase (EC 4.2.1.-)	GO:0008659|(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase activity;GO:0008659|6-hydroxycyclohex-1-ene-1-carboxyl-CoA hydratase activity;GO:0008659|trans-4-(1'-hydroxynaphth-2'-yl)-2-oxobut-3-enoate hydratase-aldolase activity;GO:0008659|E-phenylitaconyl-CoA hydratase activity;GO:0008659|trans-4-[2-(3-hydroxy)-thionaphthenyl]-2-oxo-3-butenoate hydratase activity;GO:0008659|cyclohex-1-ene-1-carboxyl-CoA hydratase activity;GO:0008659|3-hydroxyacyl-CoA dehydratase activity;GO:0008659|trans-o-hydroxybenzylidenepyruvate hydratase-aldolase activity;GO:0008659|3-methyl-5-hydroxy-6-(3-carboxy-3-oxopropenyl)-1H-2-pyridon hydratase-aldolase activity;GO:0008659|2-hydroxyisobutyrate dehydratase activity;GO:0008659|2-oxo-hept-3-ene-1,7-dioate hydratase activity;GO:0008659|1,2-bis(4-hydroxyphenyl)-2-proponol dehydratase activity;GO:0008659|limonene 8-hydratase activity;GO:0008659|4-methyloct-2-enoyl-CoA hydratase activity;GO:0008659|2-hydroxydec-2,4-diene-1,10-dioate hydratase activity;GO:0008659|menth-2-enone hydratase activity;GO:0008659|naphthyl-2-methylene-succinyl-CoA lyase activity;GO:0008659|2-hydroxyhexa-2,4-dienoate hydratase activity;GO:0008659|2,4,4-trimethylpent-2-enoyl-CoA hydratase activity;GO:0008659|endosulfan diol hydrolyase (cyclizing) activity;GO:0008659|5-chloro-2-oxopent-4-enoate hydratase activity;GO:0008659|2-methylhex-2-enoyl-CoA hydratase activity;GO:0008659|perillyl-CoA hydratase activity;GO:0008659|2-keto-3-deoxygalactonate aldolase activity;GO:0008659|2-keto-3-deoxygluconate aldolase activity;GO:0008659|3-hydroxypropionyl-CoA dehydratase activity;GO:0008659|L-erythro-3-methylmalyl-CoA dehydratase activity;GO:0008659|3-dehydroshikimate dehydratase activity;GO:0008659|acetylenecarboxylate hydratase activity, producing 3-hydroxypropenoate;GO:0008659|L-serine hydro-lyase (adding indole, L-tryptophan-forming) activity;GO:0008659|ADP-dependent NAD(P)H-hydrate dehydratase activity;GO:0008659|6-carboxy-5,6,7,8-tetrahydropterin synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2239	PATRIC.2.9855.2.9855.con.0001.CDS.2327297.2328595.fwd	PATRIC	CDS	2327297	2328595	1299	+	PGF_00039571	432	Putative O-antigen synthesis protein, WbyH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2243	PATRIC.2.9855.2.9855.con.0001.CDS.2331489.2332277.rev	PATRIC	CDS	2331489	2332277	789	-	PGF_00010468	262	Hydrolase (HAD superfamily) in cluster with DUF1447	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2244	PATRIC.2.9855.2.9855.con.0001.CDS.2332531.2334069.fwd	PATRIC	CDS	2332531	2334069	1539	+	PGF_00028985	512	P-loop ATPase domain / LexA domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2245	PATRIC.2.9855.2.9855.con.0001.CDS.2334266.2334901.fwd	PATRIC	CDS	2334266	2334901	636	+	PGF_00067215	211	Probable iron export ATP-binding protein FetA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2246	PATRIC.2.9855.2.9855.con.0001.CDS.2334894.2335673.fwd	PATRIC	CDS	2334894	2335673	780	+	PGF_05689837	259	Probable iron export permease protein FetB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2248	PATRIC.2.9855.2.9855.con.0001.CDS.2335942.2337402.fwd	PATRIC	CDS	2335942	2337402	1461	+	PGF_00008506	486	Glyceraldehyde-3-phosphate dehydrogenase (NADP(+)) (EC 1.2.1.9)	GO:0008886|glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2250	PATRIC.2.9855.2.9855.con.0001.CDS.2338182.2339183.fwd	PATRIC	CDS	2338182	2339183	1002	+	PGF_00408779	333	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2251	PATRIC.2.9855.2.9855.con.0001.CDS.2339368.2342157.fwd	PATRIC	CDS	2339368	2342157	2790	+	PGF_05340948	929	DNA mismatch repair protein MutS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.204	PATRIC.2.9855.2.9855.con.0001.CDS.234139.235233.fwd	PATRIC	CDS	234139	235233	1095	+	PGF_01284133	364	IcmE protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2252	PATRIC.2.9855.2.9855.con.0001.CDS.2342426.2343283.fwd	PATRIC	CDS	2342426	2343283	858	+	PGF_06861824	285	Uncharacterized protein YybG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2253	PATRIC.2.9855.2.9855.con.0001.CDS.2343449.2344099.fwd	PATRIC	CDS	2343449	2344099	651	+	PGF_00016919	216	Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)	GO:0008914|leucyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2254	PATRIC.2.9855.2.9855.con.0001.CDS.2344260.2345423.fwd	PATRIC	CDS	2344260	2345423	1164	+	PGF_00021125	387	SAM-dependent methyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2256	PATRIC.2.9855.2.9855.con.0001.CDS.2346011.2348005.fwd	PATRIC	CDS	2346011	2348005	1995	+	PGF_05507938	664	DNA mismatch repair protein MutL	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2257	PATRIC.2.9855.2.9855.con.0001.CDS.2348066.2348995.fwd	PATRIC	CDS	2348066	2348995	930	+	PGF_04807486	309	tRNA dimethylallyltransferase (EC 2.5.1.75)	GO:0052381|tRNA dimethylallyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2258	PATRIC.2.9855.2.9855.con.0001.CDS.2349040.2349285.fwd	PATRIC	CDS	2349040	2349285	246	+	PGF_00046622	81	RNA-binding protein Hfq	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2259	PATRIC.2.9855.2.9855.con.0001.CDS.2349350.2350642.fwd	PATRIC	CDS	2349350	2350642	1293	+	PGF_00049731	430	Aluminum resistance protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2260	PATRIC.2.9855.2.9855.con.0001.CDS.2350790.2351395.rev	PATRIC	CDS	2350790	2351395	606	-	PGF_03810679	201	SOS-response repressor and protease LexA (EC 3.4.21.88)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2261	PATRIC.2.9855.2.9855.con.0001.CDS.2351636.2352139.fwd	PATRIC	CDS	2351636	2352139	504	+	PGF_05117700	167	Free methionine-(R)-sulfoxide reductase, contains GAF domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2262	PATRIC.2.9855.2.9855.con.0001.CDS.2352287.2352721.fwd	PATRIC	CDS	2352287	2352721	435	+	PGF_00038052	144	Protein containing Zn-finger domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2264	PATRIC.2.9855.2.9855.con.0001.CDS.2353668.2354657.rev	PATRIC	CDS	2353668	2354657	990	-	PGF_04835795	329	Site-specific tyrosine recombinase XerC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2265	PATRIC.2.9855.2.9855.con.0001.CDS.2355458.2355946.fwd	PATRIC	CDS	2355458	2355946	489	+	PGF_00707140	162	Cys-tRNA(Pro) deacylase YbaK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2266	PATRIC.2.9855.2.9855.con.0001.CDS.2356666.2358033.rev	PATRIC	CDS	2356666	2358033	1368	-	PGF_08562657	455	tRNA-i(6)A37 methylthiotransferase (EC 2.8.4.3)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2268	PATRIC.2.9855.2.9855.con.0001.CDS.2358154.2359023.rev	PATRIC	CDS	2358154	2359023	870	-	PGF_00027718	289	Acetyltransferase Iojap substitute?	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2274	PATRIC.2.9855.2.9855.con.0001.CDS.2361781.2362296.fwd	PATRIC	CDS	2361781	2362296	516	+	PGF_06077968	171	Bacterial non-heme ferritin (EC 1.16.3.2)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2275	PATRIC.2.9855.2.9855.con.0001.CDS.2362409.2363728.rev	PATRIC	CDS	2362409	2363728	1320	-	PGF_00022709	439	ATPase with chaperone activity, ATP-binding domain, diverged	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2276	PATRIC.2.9855.2.9855.con.0001.CDS.2364029.2365321.fwd	PATRIC	CDS	2364029	2365321	1293	+	PGF_00854027	430	Guanine/hypoxanthine permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2277	PATRIC.2.9855.2.9855.con.0001.CDS.2365479.2366087.rev	PATRIC	CDS	2365479	2366087	609	-	PGF_07808527	202	ADP-ribose pyrophosphatase (EC 3.6.1.13)	GO:0047631|ADP-ribose diphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2278	PATRIC.2.9855.2.9855.con.0001.CDS.2366314.2368221.rev	PATRIC	CDS	2366314	2368221	1908	-	PGF_01268623	635	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.7.4) / Ribosomal protein S1 RNA-binding domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2279	PATRIC.2.9855.2.9855.con.0001.CDS.2368235.2368888.rev	PATRIC	CDS	2368235	2368888	654	-	PGF_02455692	217	Cytidylate kinase (EC 2.7.4.25)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2280	PATRIC.2.9855.2.9855.con.0001.CDS.2368981.2370198.rev	PATRIC	CDS	2368981	2370198	1218	-	PGF_00933312	405	Uncharacterized flavin-containing protein YtfP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2281	PATRIC.2.9855.2.9855.con.0001.CDS.2370284.2370787.rev	PATRIC	CDS	2370284	2370787	504	-	PGF_00024855	167	NADPH-dependent 7-cyano-7-deazaguanine reductase (EC 1.7.1.13)	GO:0033739|preQ1 synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2282	PATRIC.2.9855.2.9855.con.0001.CDS.2370818.2371471.rev	PATRIC	CDS	2370818	2371471	654	-	PGF_00625415	217	7-cyano-7-deazaguanine synthase (EC 6.3.4.20)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2283	PATRIC.2.9855.2.9855.con.0001.CDS.2371543.2372136.rev	PATRIC	CDS	2371543	2372136	594	-	PGF_02820109	197	GTP cyclohydrolase I (EC 3.5.4.16) type 1	GO:0003934|GTP cyclohydrolase I activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2284	PATRIC.2.9855.2.9855.con.0001.CDS.2372226.2372894.rev	PATRIC	CDS	2372226	2372894	669	-	PGF_02386833	222	7-carboxy-7-deazaguanine synthase (EC 4.3.99.3)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2285	PATRIC.2.9855.2.9855.con.0001.CDS.2372907.2373335.rev	PATRIC	CDS	2372907	2373335	429	-	PGF_02139563	142	6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2287	PATRIC.2.9855.2.9855.con.0001.CDS.2374766.2375287.rev	PATRIC	CDS	2374766	2375287	522	-	PGF_00409403	173	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2289	PATRIC.2.9855.2.9855.con.0001.CDS.2375705.2377513.rev	PATRIC	CDS	2375705	2377513	1809	-	PGF_12711410	602	FeoB-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2290	PATRIC.2.9855.2.9855.con.0001.CDS.2377567.2377791.rev	PATRIC	CDS	2377567	2377791	225	-	PGF_00652987	74	FeoA-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2293	PATRIC.2.9855.2.9855.con.0001.CDS.2379255.2380169.rev	PATRIC	CDS	2379255	2380169	915	-	PGF_06721510	304	Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2294	PATRIC.2.9855.2.9855.con.0001.CDS.2380970.2381377.fwd	PATRIC	CDS	2380970	2381377	408	+	PGF_01313310	135	Putative sugar translocase in surface polysaccharides biosynthesis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2295	PATRIC.2.9855.2.9855.con.0001.CDS.2381522.2383258.fwd	PATRIC	CDS	2381522	2383258	1737	+	PGF_00949411	578	ATP-dependent zinc metalloproteinase similar to FtsH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2296	PATRIC.2.9855.2.9855.con.0001.CDS.2383544.2384146.fwd	PATRIC	CDS	2383544	2384146	603	+	PGF_01257133	200	Rhomboid family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2297	PATRIC.2.9855.2.9855.con.0001.CDS.2384315.2384917.fwd	PATRIC	CDS	2384315	2384917	603	+	PGF_01284139	200	Membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2298	PATRIC.2.9855.2.9855.con.0001.CDS.2385015.2387480.rev	PATRIC	CDS	2385015	2387480	2466	-	PGF_10538082	821	Sensory box/GGDEF family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2300	PATRIC.2.9855.2.9855.con.0001.CDS.2388507.2389082.rev	PATRIC	CDS	2388507	2389082	576	-	PGF_01281273	191	Peptidoglycan-binding domain-containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2301	PATRIC.2.9855.2.9855.con.0001.CDS.2389412.2390197.rev	PATRIC	CDS	2389412	2390197	786	-	PGF_00010468	261	Hydrolase (HAD superfamily) in cluster with DUF1447	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2302	PATRIC.2.9855.2.9855.con.0001.CDS.2390357.2391205.rev	PATRIC	CDS	2390357	2391205	849	-	PGF_00044298	282	Putative sulfite reductase, GSU1351 type	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2303	PATRIC.2.9855.2.9855.con.0001.CDS.2391719.2393812.fwd	PATRIC	CDS	2391719	2393812	2094	+	PGF_08854233	697	Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1)	GO:0004748|ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2304	PATRIC.2.9855.2.9855.con.0001.CDS.2394147.2395679.fwd	PATRIC	CDS	2394147	2395679	1533	+	PGF_00052121	510	Sigma-L-dependent transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2306	PATRIC.2.9855.2.9855.con.0001.CDS.2397266.2397670.rev	PATRIC	CDS	2397266	2397670	405	-	PGF_01282546	134	no significant homology Putative N-terminal signal sequence was found by PSORT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2307	PATRIC.2.9855.2.9855.con.0001.CDS.2398114.2398746.fwd	PATRIC	CDS	2398114	2398746	633	+	PGF_00418181	210	CoA-acylating propionaldehyde dehydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2308	PATRIC.2.9855.2.9855.con.0001.CDS.2399152.2399514.rev	PATRIC	CDS	2399152	2399514	363	-	PGF_00007706	120	Gll2265 protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2309	PATRIC.2.9855.2.9855.con.0001.CDS.2399945.2400307.rev	PATRIC	CDS	2399945	2400307	363	-	PGF_00417570	120	Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2310	PATRIC.2.9855.2.9855.con.0001.CDS.2400359.2403214.rev	PATRIC	CDS	2400359	2403214	2856	-	PGF_01281252	951	FOG: CheY-like receiver	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2311	PATRIC.2.9855.2.9855.con.0001.CDS.2403230.2404300.rev	PATRIC	CDS	2403230	2404300	1071	-	PGF_01137083	356	HD-GYP hydrolase domain containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2312	PATRIC.2.9855.2.9855.con.0001.CDS.2404745.2405617.rev	PATRIC	CDS	2404745	2405617	873	-	PGF_05873585	290	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2313	PATRIC.2.9855.2.9855.con.0001.CDS.2405641.2406390.rev	PATRIC	CDS	2405641	2406390	750	-	PGF_10106935	249	ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2314	PATRIC.2.9855.2.9855.con.0001.CDS.2406402.2407079.rev	PATRIC	CDS	2406402	2407079	678	-	PGF_07804709	225	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2315	PATRIC.2.9855.2.9855.con.0001.CDS.2407060.2407725.rev	PATRIC	CDS	2407060	2407725	666	-	PGF_07804709	221	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2316	PATRIC.2.9855.2.9855.con.0001.CDS.2408286.2408708.rev	PATRIC	CDS	2408286	2408708	423	-	PGF_00417313	140	Cell wall-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2317	PATRIC.2.9855.2.9855.con.0001.CDS.2409008.2410480.rev	PATRIC	CDS	2409008	2410480	1473	-	PGF_00064184	490	UPF0061 protein YdiU	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2319	PATRIC.2.9855.2.9855.con.0001.CDS.2411454.2412506.rev	PATRIC	CDS	2411454	2412506	1053	-	PGF_05728830	350	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2321	PATRIC.2.9855.2.9855.con.0001.CDS.2412899.2414341.rev	PATRIC	CDS	2412899	2414341	1443	-	PGF_02620852	480	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2323	PATRIC.2.9855.2.9855.con.0001.CDS.2414861.2415907.rev	PATRIC	CDS	2414861	2415907	1047	-	PGF_00008608	348	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	GO:0004367|glycerol-3-phosphate dehydrogenase [NAD+] activity;GO:0004367|glycerol-3-phosphate dehydrogenase [NADP+] activity;GO:0004367|glycerol-3-phosphate dehydrogenase [NAD(P)+] activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2324	PATRIC.2.9855.2.9855.con.0001.CDS.2416043.2416858.rev	PATRIC	CDS	2416043	2416858	816	-	PGF_00667256	271	Hypothetical NagD-like phosphatase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2325	PATRIC.2.9855.2.9855.con.0001.CDS.2417048.2418427.rev	PATRIC	CDS	2417048	2418427	1380	-	PGF_00008548	459	Glycerol-1-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.261)	GO:0050492|glycerol-1-phosphate dehydrogenase [NAD(P)+] activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2326	PATRIC.2.9855.2.9855.con.0001.CDS.2418633.2419907.rev	PATRIC	CDS	2418633	2419907	1275	-	PGF_00029677	424	PTS system, galactitol-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2327	PATRIC.2.9855.2.9855.con.0001.CDS.2420129.2420413.rev	PATRIC	CDS	2420129	2420413	285	-	PGF_00029672	94	PTS system, galactitol-specific IIB component (EC 2.7.1.200)	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2328	PATRIC.2.9855.2.9855.con.0001.CDS.2420465.2420941.rev	PATRIC	CDS	2420465	2420941	477	-	PGF_04724541	158	PTS system, galactitol-specific IIA component (EC 2.7.1.200)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2329	PATRIC.2.9855.2.9855.con.0001.CDS.2421365.2424352.rev	PATRIC	CDS	2421365	2424352	2988	-	PGF_00026324	995	NtrC family Transcriptional regulator, ATPase domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.30	PATRIC.2.9855.2.9855.con.0001.CDS.24234.25091.fwd	PATRIC	CDS	24234	25091	858	+	PGF_00426548	285	5-keto-2-deoxy-D-gluconate-6 phosphate aldolase (EC 4.1.2.29)	GO:0047441|5-dehydro-2-deoxyphosphogluconate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2330	PATRIC.2.9855.2.9855.con.0001.CDS.2424604.2425212.rev	PATRIC	CDS	2424604	2425212	609	-	PGF_00420612	202	Cytoplasmic copper homeostasis protein CutC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2331	PATRIC.2.9855.2.9855.con.0001.CDS.2425509.2426783.fwd	PATRIC	CDS	2425509	2426783	1275	+	PGF_00057866	424	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2332	PATRIC.2.9855.2.9855.con.0001.CDS.2426915.2427982.rev	PATRIC	CDS	2426915	2427982	1068	-	PGF_05728830	355	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2333	PATRIC.2.9855.2.9855.con.0001.CDS.2428240.2428410.rev	PATRIC	CDS	2428240	2428410	171	-	PGF_00821117	56	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	GO:0008825|cyclopropane-fatty-acyl-phospholipid synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2334	PATRIC.2.9855.2.9855.con.0001.CDS.2428580.2429341.rev	PATRIC	CDS	2428580	2429341	762	-	PGF_08546938	253	Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.6	PATRIC.2.9855.2.9855.con.0001.CDS.2429.3241.fwd	PATRIC	CDS	2429	3241	813	+	PGF_08181546	270	Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)	GO:0004764|shikimate 3-dehydrogenase (NADP+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2335	PATRIC.2.9855.2.9855.con.0001.CDS.2429483.2431936.rev	PATRIC	CDS	2429483	2431936	2454	-	PGF_10538082	817	Sensory box/GGDEF family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2336	PATRIC.2.9855.2.9855.con.0001.CDS.2432357.2432899.rev	PATRIC	CDS	2432357	2432899	543	-	PGF_02930287	180	Reverse rubrerythrin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2338	PATRIC.2.9855.2.9855.con.0001.CDS.2433989.2434273.rev	PATRIC	CDS	2433989	2434273	285	-	PGF_01668176	94	Uncharacterized protein YjdJ, possible GNAT acetyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2339	PATRIC.2.9855.2.9855.con.0001.CDS.2434563.2436374.rev	PATRIC	CDS	2434563	2436374	1812	-	PGF_00038707	603	Protein with domain similar to SecA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2340	PATRIC.2.9855.2.9855.con.0001.CDS.2436568.2437365.rev	PATRIC	CDS	2436568	2437365	798	-	PGF_09258168	265	Ribonuclease HI (EC 3.1.26.4)	GO:0004523|RNA-DNA hybrid ribonuclease activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2341	PATRIC.2.9855.2.9855.con.0001.CDS.2437662.2439053.rev	PATRIC	CDS	2437662	2439053	1392	-	PGF_12685003	463	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2343	PATRIC.2.9855.2.9855.con.0001.CDS.2439756.2441009.rev	PATRIC	CDS	2439756	2441009	1254	-	PGF_00408221	417	putative lipoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2345	PATRIC.2.9855.2.9855.con.0001.CDS.2442323.2443783.rev	PATRIC	CDS	2442323	2443783	1461	-	PGF_03495584	486	Glucan-binding domain / Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (EC 3.2.1.17)	GO:0003796|lysozyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2347	PATRIC.2.9855.2.9855.con.0001.CDS.2444778.2445167.fwd	PATRIC	CDS	2444778	2445167	390	+	PGF_00423319	129	Dihydrolipoamide acyltransferases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2348	PATRIC.2.9855.2.9855.con.0001.CDS.2445234.2445839.rev	PATRIC	CDS	2445234	2445839	606	-	PGF_01282243	201	Fatty acid degradation regulator YsiA, TetR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2350	PATRIC.2.9855.2.9855.con.0001.CDS.2447643.2450732.rev	PATRIC	CDS	2447643	2450732	3090	-	PGF_05237064	1029	RND efflux system, inner membrane transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2351	PATRIC.2.9855.2.9855.con.0001.CDS.2450745.2452040.rev	PATRIC	CDS	2450745	2452040	1296	-	PGF_01280313	431	ABC transporter, RND-adapter-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2352	PATRIC.2.9855.2.9855.con.0001.CDS.2452100.2452714.rev	PATRIC	CDS	2452100	2452714	615	-	PGF_10472747	204	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2353	PATRIC.2.9855.2.9855.con.0001.CDS.2453173.2453850.fwd	PATRIC	CDS	2453173	2453850	678	+	PGF_07420062	225	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2354	PATRIC.2.9855.2.9855.con.0001.CDS.2453843.2454877.fwd	PATRIC	CDS	2453843	2454877	1035	+	PGF_02620852	344	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2357	PATRIC.2.9855.2.9855.con.0001.CDS.2456301.2456495.rev	PATRIC	CDS	2456301	2456495	195	-	PGF_00053039	64	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2358	PATRIC.2.9855.2.9855.con.0001.CDS.2456709.2456915.fwd	PATRIC	CDS	2456709	2456915	207	+	PGF_01284184	68	Small acid-soluble spore protein, beta-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2359	PATRIC.2.9855.2.9855.con.0001.CDS.2457122.2458180.rev	PATRIC	CDS	2457122	2458180	1059	-	PGF_00417736	352	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2360	PATRIC.2.9855.2.9855.con.0001.CDS.2458530.2460710.fwd	PATRIC	CDS	2458530	2460710	2181	+	PGF_05732875	726	Limit dextrin alpha-1,6-maltotetraose-hydrolase (EC 3.2.1.196)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2361	PATRIC.2.9855.2.9855.con.0001.CDS.2460846.2462837.fwd	PATRIC	CDS	2460846	2462837	1992	+	PGF_00006377	663	Fructose-1,6-bisphosphatase, Bacillus type (EC 3.1.3.11)	GO:0042132|fructose 1,6-bisphosphate 1-phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2362	PATRIC.2.9855.2.9855.con.0001.CDS.2462892.2463641.rev	PATRIC	CDS	2462892	2463641	750	-	PGF_00010778	249	Transcriptional repressor GlcR, DeoR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2363	PATRIC.2.9855.2.9855.con.0001.CDS.2463889.2464728.fwd	PATRIC	CDS	2463889	2464728	840	+	PGF_01282246	279	HAD superfamily hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2364	PATRIC.2.9855.2.9855.con.0001.CDS.2464837.2465775.rev	PATRIC	CDS	2464837	2465775	939	-	PGF_01258559	312	Metal chaperone, involved in Zn homeostasis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2366	PATRIC.2.9855.2.9855.con.0001.CDS.2466901.2468004.rev	PATRIC	CDS	2466901	2468004	1104	-	PGF_01258559	367	Metal chaperone, involved in Zn homeostasis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2368	PATRIC.2.9855.2.9855.con.0001.CDS.2469310.2469759.rev	PATRIC	CDS	2469310	2469759	450	-	PGF_06594013	149	Peptide-methionine (R)-S-oxide reductase MsrB (EC 1.8.4.12)	GO:0033743|peptide-methionine (R)-S-oxide reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2369	PATRIC.2.9855.2.9855.con.0001.CDS.2469917.2472862.rev	PATRIC	CDS	2469917	2472862	2946	-	PGF_01267342	981	Phytochrome-like protein; Cph2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2370	PATRIC.2.9855.2.9855.con.0001.CDS.2473302.2474324.rev	PATRIC	CDS	2473302	2474324	1023	-	PGF_00071934	340	2-keto-3-deoxygluconate permease (KDG permease)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2371	PATRIC.2.9855.2.9855.con.0001.CDS.2474803.2475639.rev	PATRIC	CDS	2474803	2475639	837	-	PGF_00423470	278	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)	GO:0008697|4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2372	PATRIC.2.9855.2.9855.con.0001.CDS.2475911.2476909.rev	PATRIC	CDS	2475911	2476909	999	-	PGF_00011616	332	Hexuronate utilization operon transcriptional repressor ExuR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.213	PATRIC.2.9855.2.9855.con.0001.CDS.247652.248362.fwd	PATRIC	CDS	247652	248362	711	+	PGF_00424338	236	Endonuclease V (EC 3.1.21.7)	GO:0043737|deoxyribonuclease V activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2374	PATRIC.2.9855.2.9855.con.0001.CDS.2477626.2478156.fwd	PATRIC	CDS	2477626	2478156	531	+	PGF_10359618	176	Heptaprenyl diphosphate synthase component I (EC 2.5.1.30)	GO:0036422|heptaprenyl diphosphate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2375	PATRIC.2.9855.2.9855.con.0001.CDS.2478324.2479175.rev	PATRIC	CDS	2478324	2479175	852	-	PGF_10332317	283	Electron transport complex protein RnfB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2376	PATRIC.2.9855.2.9855.con.0001.CDS.2479194.2479769.rev	PATRIC	CDS	2479194	2479769	576	-	PGF_00424131	191	Electron transport complex protein RnfA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2377	PATRIC.2.9855.2.9855.con.0001.CDS.2479769.2480392.rev	PATRIC	CDS	2479769	2480392	624	-	PGF_00424141	207	Electron transport complex protein RnfE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2378	PATRIC.2.9855.2.9855.con.0001.CDS.2480394.2480960.rev	PATRIC	CDS	2480394	2480960	567	-	PGF_01484108	188	Electron transport complex protein RnfG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2379	PATRIC.2.9855.2.9855.con.0001.CDS.2480965.2482002.rev	PATRIC	CDS	2480965	2482002	1038	-	PGF_01678333	345	Electron transport complex protein RnfD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2380	PATRIC.2.9855.2.9855.con.0001.CDS.2482019.2483332.rev	PATRIC	CDS	2482019	2483332	1314	-	PGF_04400591	437	Electron transport complex protein RnfC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2381	PATRIC.2.9855.2.9855.con.0001.CDS.2483512.2483922.rev	PATRIC	CDS	2483512	2483922	411	-	PGF_12835560	136	Sigma factor RpoE regulatory protein RseC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2382	PATRIC.2.9855.2.9855.con.0001.CDS.2484548.2484826.fwd	PATRIC	CDS	2484548	2484826	279	+	PGF_01668176	92	Uncharacterized protein YjdJ, possible GNAT acetyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2383	PATRIC.2.9855.2.9855.con.0001.CDS.2484957.2485952.rev	PATRIC	CDS	2484957	2485952	996	-	PGF_02346669	331	Ornithine carbamoyltransferase (EC 2.1.3.3)	GO:0004585|ornithine carbamoyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2384	PATRIC.2.9855.2.9855.con.0001.CDS.2486655.2487677.rev	PATRIC	CDS	2486655	2487677	1023	-	PGF_01281703	340	FmtB protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2385	PATRIC.2.9855.2.9855.con.0001.CDS.2487975.2489135.fwd	PATRIC	CDS	2487975	2489135	1161	+	PGF_00242238	386	YibE/F family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2386	PATRIC.2.9855.2.9855.con.0001.CDS.2489140.2489916.fwd	PATRIC	CDS	2489140	2489916	777	+	PGF_00242238	258	YibE/F family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2390	PATRIC.2.9855.2.9855.con.0001.CDS.2492470.2493417.rev	PATRIC	CDS	2492470	2493417	948	-	PGF_00008906	315	Glycoprotein gp2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2391	PATRIC.2.9855.2.9855.con.0001.CDS.2493807.2494835.fwd	PATRIC	CDS	2493807	2494835	1029	+	PGF_00070354	342	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54)	GO:0003849|3-deoxy-7-phosphoheptulonate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2392	PATRIC.2.9855.2.9855.con.0001.CDS.2495022.2495309.rev	PATRIC	CDS	2495022	2495309	288	-	PGF_07086362	95	YlxP-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2393	PATRIC.2.9855.2.9855.con.0001.CDS.2495336.2496238.rev	PATRIC	CDS	2495336	2496238	903	-	PGF_00416436	300	3'->5' exoribonuclease Bsu YhaM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2394	PATRIC.2.9855.2.9855.con.0001.CDS.2496691.2498568.fwd	PATRIC	CDS	2496691	2498568	1878	+	PGF_02620852	625	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2395	PATRIC.2.9855.2.9855.con.0001.CDS.2498644.2499639.rev	PATRIC	CDS	2498644	2499639	996	-	PGF_01281694	331	Cell wall-associated hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.215	PATRIC.2.9855.2.9855.con.0001.CDS.249916.250269.fwd	PATRIC	CDS	249916	250269	354	+	PGF_01286585	117	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2397	PATRIC.2.9855.2.9855.con.0001.CDS.2500640.2501731.rev	PATRIC	CDS	2500640	2501731	1092	-	PGF_00048782	363	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	GO:0004749|ribose phosphate diphosphokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2398	PATRIC.2.9855.2.9855.con.0001.CDS.2502058.2502753.rev	PATRIC	CDS	2502058	2502753	696	-	PGF_10347576	231	ABC-type antimicrobial peptide transport system, ATPase component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2399	PATRIC.2.9855.2.9855.con.0001.CDS.2503007.2504764.rev	PATRIC	CDS	2503007	2504764	1758	-	PGF_00039143	585	Putative ATP-dependent RNA helicase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2401	PATRIC.2.9855.2.9855.con.0001.CDS.2505885.2507105.rev	PATRIC	CDS	2505885	2507105	1221	-	PGF_07416013	406	Tripeptide aminopeptidase (EC 3.4.11.4)	GO:0045148|tripeptide aminopeptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2402	PATRIC.2.9855.2.9855.con.0001.CDS.2507782.2508354.rev	PATRIC	CDS	2507782	2508354	573	-	PGF_00066942	190	Xanthine phosphoribosyltransferase (EC 2.4.2.22)	GO:0000310|xanthine phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2403	PATRIC.2.9855.2.9855.con.0001.CDS.2508356.2509708.rev	PATRIC	CDS	2508356	2509708	1353	-	PGF_00659863	450	Uracil-xanthine permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.31	PATRIC.2.9855.2.9855.con.0001.CDS.25092.26111.fwd	PATRIC	CDS	25092	26111	1020	+	PGF_00426572	339	5-keto-2-deoxygluconokinase (EC 2.7.1.92)	GO:0047590|5-dehydro-2-deoxygluconokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2404	PATRIC.2.9855.2.9855.con.0001.CDS.2510103.2511836.rev	PATRIC	CDS	2510103	2511836	1734	-	PGF_00051221	577	Serine phosphatase RsbU, regulator of sigma subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.216	PATRIC.2.9855.2.9855.con.0001.CDS.251143.251946.fwd	PATRIC	CDS	251143	251946	804	+	PGF_00012307	267	Homolog of eukaryotic DNA ligase III	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2405	PATRIC.2.9855.2.9855.con.0001.CDS.2511868.2514837.rev	PATRIC	CDS	2511868	2514837	2970	-	PGF_08632970	989	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2406	PATRIC.2.9855.2.9855.con.0001.CDS.2514897.2516366.rev	PATRIC	CDS	2514897	2516366	1470	-	PGF_07282910	489	Glycerol-3-phosphate ABC transporter, substrate-binding protein UgpB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2408	PATRIC.2.9855.2.9855.con.0001.CDS.2517508.2518671.rev	PATRIC	CDS	2517508	2518671	1164	-	PGF_02454452	387	NADH-dependent butanol dehydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2409	PATRIC.2.9855.2.9855.con.0001.CDS.2519184.2519753.rev	PATRIC	CDS	2519184	2519753	570	-	PGF_00417736	189	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2410	PATRIC.2.9855.2.9855.con.0001.CDS.2519986.2522043.rev	PATRIC	CDS	2519986	2522043	2058	-	PGF_05195470	685	Polyphosphate kinase (EC 2.7.4.1)	GO:0008976|polyphosphate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2411	PATRIC.2.9855.2.9855.con.0001.CDS.2522247.2523755.fwd	PATRIC	CDS	2522247	2523755	1509	+	PGF_05471309	502	Exopolyphosphatase (EC 3.6.1.11)	GO:0004309|exopolyphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2412	PATRIC.2.9855.2.9855.con.0001.CDS.2523857.2525038.fwd	PATRIC	CDS	2523857	2525038	1182	+	PGF_06866315	393	Uncharacterized UPF0118 membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2413	PATRIC.2.9855.2.9855.con.0001.CDS.2525137.2526348.rev	PATRIC	CDS	2525137	2526348	1212	-	PGF_00063916	403	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	GO:0004831|tyrosine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2414	PATRIC.2.9855.2.9855.con.0001.CDS.2526827.2527852.rev	PATRIC	CDS	2526827	2527852	1026	-	PGF_01984096	341	S-layer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2415	PATRIC.2.9855.2.9855.con.0001.CDS.2528082.2529044.rev	PATRIC	CDS	2528082	2529044	963	-	PGF_00064400	320	UV DNA damage endonuclease (EC 3.-.-.-) (UV-endonuclease) (UVED)	GO:0003923|GPI-anchor transamidase activity;GO:0003923|coenzyme F390-A hydrolase activity;GO:0003923|coenzyme F390-G hydrolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2416	PATRIC.2.9855.2.9855.con.0001.CDS.2529375.2530718.rev	PATRIC	CDS	2529375	2530718	1344	-	PGF_01292241	447	Putative sugar transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2417	PATRIC.2.9855.2.9855.con.0001.CDS.2531338.2531877.rev	PATRIC	CDS	2531338	2531877	540	-	PGF_00023448	179	MutT/Nudix family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2419	PATRIC.2.9855.2.9855.con.0001.CDS.2533076.2533492.rev	PATRIC	CDS	2533076	2533492	417	-	PGF_08946513	138	Flavodoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2420	PATRIC.2.9855.2.9855.con.0001.CDS.2533636.2534496.rev	PATRIC	CDS	2533636	2534496	861	-	PGF_07201805	286	Permease of the drug/metabolite transporter (DMT) superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.218	PATRIC.2.9855.2.9855.con.0001.CDS.253405.254622.rev	PATRIC	CDS	253405	254622	1218	-	PGF_01281276	405	Predicted membrane protein; CF-20 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2423	PATRIC.2.9855.2.9855.con.0001.CDS.2536697.2537737.rev	PATRIC	CDS	2536697	2537737	1041	-	PGF_00023916	346	N-acetylmuramoyl-L-alanine amidase/putative S-layer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2424	PATRIC.2.9855.2.9855.con.0001.CDS.2537965.2542278.rev	PATRIC	CDS	2537965	2542278	4314	-	PGF_01333294	1437	Activator of (R)-2-hydroxyglutaryl-CoA dehydratase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2425	PATRIC.2.9855.2.9855.con.0001.CDS.2542495.2542851.fwd	PATRIC	CDS	2542495	2542851	357	+	PGF_00055642	118	TPR repeats containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2426	PATRIC.2.9855.2.9855.con.0001.CDS.2542853.2543572.rev	PATRIC	CDS	2542853	2543572	720	-	PGF_00060343	239	Transglutaminase-like enzyme, putative cysteine protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2427	PATRIC.2.9855.2.9855.con.0001.CDS.2543711.2544352.rev	PATRIC	CDS	2543711	2544352	642	-	PGF_09027360	213	Regulatory protein RecX	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2428	PATRIC.2.9855.2.9855.con.0001.CDS.2544388.2545629.rev	PATRIC	CDS	2544388	2545629	1242	-	PGF_01169778	413	Zn-dependent protease of MPP family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2430	PATRIC.2.9855.2.9855.con.0001.CDS.2546327.2546998.fwd	PATRIC	CDS	2546327	2546998	672	+	PGF_07420062	223	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2431	PATRIC.2.9855.2.9855.con.0001.CDS.2546999.2548519.fwd	PATRIC	CDS	2546999	2548519	1521	+	PGF_02620852	506	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2432	PATRIC.2.9855.2.9855.con.0001.CDS.2548531.2549274.rev	PATRIC	CDS	2548531	2549274	744	-	PGF_10532194	247	Oxidoreductase, short-chain dehydrogenase/reductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2433	PATRIC.2.9855.2.9855.con.0001.CDS.2549510.2550445.rev	PATRIC	CDS	2549510	2550445	936	-	PGF_10552644	311	Microsomal dipeptidase (EC 3.4.13.19)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2435	PATRIC.2.9855.2.9855.con.0001.CDS.2552299.2553309.rev	PATRIC	CDS	2552299	2553309	1011	-	PGF_00016046	336	L-asparaginase (EC 3.5.1.1)	GO:0004067|asparaginase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2436	PATRIC.2.9855.2.9855.con.0001.CDS.2553567.2554295.rev	PATRIC	CDS	2553567	2554295	729	-	PGF_10106935	242	ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2437	PATRIC.2.9855.2.9855.con.0001.CDS.2554279.2554941.rev	PATRIC	CDS	2554279	2554941	663	-	PGF_07804709	220	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2438	PATRIC.2.9855.2.9855.con.0001.CDS.2554957.2555739.rev	PATRIC	CDS	2554957	2555739	783	-	PGF_05873585	260	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2439	PATRIC.2.9855.2.9855.con.0001.CDS.2556218.2557003.rev	PATRIC	CDS	2556218	2557003	786	-	PGF_05873585	261	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2440	PATRIC.2.9855.2.9855.con.0001.CDS.2557171.2557839.rev	PATRIC	CDS	2557171	2557839	669	-	PGF_06916656	222	Transcriptional regulator, GntR family	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2441	PATRIC.2.9855.2.9855.con.0001.CDS.2558495.2559967.rev	PATRIC	CDS	2558495	2559967	1473	-	PGF_00403859	490	predicted xylose isomerase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2443	PATRIC.2.9855.2.9855.con.0001.CDS.2561199.2563190.rev	PATRIC	CDS	2561199	2563190	1992	-	PGF_01136362	663	Transketolase (EC 2.2.1.1)	GO:0004802|transketolase activity GO:0004801|sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2444	PATRIC.2.9855.2.9855.con.0001.CDS.2563841.2564488.rev	PATRIC	CDS	2563841	2564488	648	-	PGF_00057399	215	Transaldolase (EC 2.2.1.2)	glyceronetransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2445	PATRIC.2.9855.2.9855.con.0001.CDS.2564836.2565984.rev	PATRIC	CDS	2564836	2565984	1149	-	PGF_00794581	382	Xylose-responsive transcription regulator, ROK family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2446	PATRIC.2.9855.2.9855.con.0001.CDS.2566186.2567688.rev	PATRIC	CDS	2566186	2567688	1503	-	PGF_07639199	500	Xylulose kinase (EC 2.7.1.17)	GO:0004856|xylulokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2447	PATRIC.2.9855.2.9855.con.0001.CDS.2568149.2569474.rev	PATRIC	CDS	2568149	2569474	1326	-	PGF_00067063	441	Xylose isomerase (EC 5.3.1.5)	GO:0009045|xylose isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.222	PATRIC.2.9855.2.9855.con.0001.CDS.256945.257967.fwd	PATRIC	CDS	256945	257967	1023	+	PGF_00053903	340	Spore photoproduct lyase (EC 4.1.99.14)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2448	PATRIC.2.9855.2.9855.con.0001.CDS.2570011.2571180.rev	PATRIC	CDS	2570011	2571180	1170	-	PGF_06255546	389	D-xylose ABC transporter, permease protein XylH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2449	PATRIC.2.9855.2.9855.con.0001.CDS.2571182.2572759.rev	PATRIC	CDS	2571182	2572759	1578	-	PGF_10029881	525	D-xylose ABC transporter, ATP-binding protein XylG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2450	PATRIC.2.9855.2.9855.con.0001.CDS.2572824.2573903.rev	PATRIC	CDS	2572824	2573903	1080	-	PGF_01138219	359	D-xylose ABC transporter, substrate-binding protein XylF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2451	PATRIC.2.9855.2.9855.con.0001.CDS.2574197.2575537.rev	PATRIC	CDS	2574197	2575537	1341	-	PGF_00062533	446	Two-component response regulator yesN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2452	PATRIC.2.9855.2.9855.con.0001.CDS.2575515.2577011.rev	PATRIC	CDS	2575515	2577011	1497	-	PGF_00748211	498	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2453	PATRIC.2.9855.2.9855.con.0001.CDS.2577001.2577981.rev	PATRIC	CDS	2577001	2577981	981	-	PGF_01280823	326	Xylose ABC transporter, substrate-binding component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2454	PATRIC.2.9855.2.9855.con.0001.CDS.2578461.2578676.rev	PATRIC	CDS	2578461	2578676	216	-	PGF_00050264	71	Amidases related to nicotinamidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2455	PATRIC.2.9855.2.9855.con.0001.CDS.2578683.2579006.rev	PATRIC	CDS	2578683	2579006	324	-	PGF_00050264	107	Amidases related to nicotinamidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2456	PATRIC.2.9855.2.9855.con.0001.CDS.2579132.2579545.fwd	PATRIC	CDS	2579132	2579545	414	+	PGF_00010730	137	HTH-type transcriptional regulator LrpA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2458	PATRIC.2.9855.2.9855.con.0001.CDS.2580157.2580519.rev	PATRIC	CDS	2580157	2580519	363	-	PGF_00057506	120	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2459	PATRIC.2.9855.2.9855.con.0001.CDS.2580599.2580964.fwd	PATRIC	CDS	2580599	2580964	366	+	PGF_05406020	121	4-carboxymuconolactone decarboxylase (EC 4.1.1.44)	GO:0047575|4-carboxymuconolactone decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2462	PATRIC.2.9855.2.9855.con.0001.CDS.2582083.2582259.rev	PATRIC	CDS	2582083	2582259	177	-	PGF_01285288	58	Acetyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2463	PATRIC.2.9855.2.9855.con.0001.CDS.2582330.2583187.rev	PATRIC	CDS	2582330	2583187	858	-	PGF_12698184	285	ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2464	PATRIC.2.9855.2.9855.con.0001.CDS.2583223.2583657.rev	PATRIC	CDS	2583223	2583657	435	-	PGF_00885140	144	Acetyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2465	PATRIC.2.9855.2.9855.con.0001.CDS.2583699.2584307.rev	PATRIC	CDS	2583699	2584307	609	-	PGF_05657253	202	Ribose-5-phosphate isomerase A (EC 5.3.1.6)	GO:0004751|ribose-5-phosphate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2466	PATRIC.2.9855.2.9855.con.0001.CDS.2585602.2586204.rev	PATRIC	CDS	2585602	2586204	603	-	PGF_02489591	200	Uncharacterized Nudix hydrolase NudL	GO:0004557|alpha-galactosidase activity;GO:0004557|raffinose alpha-galactosidase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.224	PATRIC.2.9855.2.9855.con.0001.CDS.258662.259984.rev	PATRIC	CDS	258662	259984	1323	-	PGF_00047490	440	alpha-galactosidase (EC 3.2.1.22)	activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2467	PATRIC.2.9855.2.9855.con.0001.CDS.2586644.2587435.rev	PATRIC	CDS	2586644	2587435	792	-	PGF_00667256	263	Hypothetical NagD-like phosphatase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2468	PATRIC.2.9855.2.9855.con.0001.CDS.2587440.2588612.rev	PATRIC	CDS	2587440	2588612	1173	-	PGF_00008548	390	Glycerol-1-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.261)	GO:0050492|glycerol-1-phosphate dehydrogenase [NAD(P)+] activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2469	PATRIC.2.9855.2.9855.con.0001.CDS.2588724.2590676.rev	PATRIC	CDS	2588724	2590676	1953	-	PGF_02686787	650	Putative glycosyl hydrolase of unknown function (DUF1680)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2470	PATRIC.2.9855.2.9855.con.0001.CDS.2590866.2591762.fwd	PATRIC	CDS	2590866	2591762	897	+	PGF_10433935	298	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2471	PATRIC.2.9855.2.9855.con.0001.CDS.2591965.2592888.fwd	PATRIC	CDS	2591965	2592888	924	+	PGF_08030842	307	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2472	PATRIC.2.9855.2.9855.con.0001.CDS.2593226.2594743.rev	PATRIC	CDS	2593226	2594743	1518	-	PGF_00046611	505	alpha-L-arabinofuranosidase (EC 3.2.1.55)	GO:0046556|alpha-L-arabinofuranosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2473	PATRIC.2.9855.2.9855.con.0001.CDS.2594807.2595697.rev	PATRIC	CDS	2594807	2595697	891	-	PGF_00047141	296	Alpha-arabinosides ABC transport system, permease protein AraQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2474	PATRIC.2.9855.2.9855.con.0001.CDS.2595699.2596589.rev	PATRIC	CDS	2595699	2596589	891	-	PGF_07596169	296	Alpha-arabinosides ABC transport system, permease protein AraP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2475	PATRIC.2.9855.2.9855.con.0001.CDS.2596686.2598032.rev	PATRIC	CDS	2596686	2598032	1347	-	PGF_08187963	448	N-acetyl-D-glucosamine ABC transporter, substrate-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2477	PATRIC.2.9855.2.9855.con.0001.CDS.2599332.2600090.rev	PATRIC	CDS	2599332	2600090	759	-	PGF_07420523	252	Exodeoxyribonuclease III (EC 3.1.11.2)	GO:0008853|exodeoxyribonuclease III activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2478	PATRIC.2.9855.2.9855.con.0001.CDS.2600352.2601263.rev	PATRIC	CDS	2600352	2601263	912	-	PGF_12835329	303	Auxin efflux carrier family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2479	PATRIC.2.9855.2.9855.con.0001.CDS.2601530.2603509.rev	PATRIC	CDS	2601530	2603509	1980	-	PGF_00342563	659	UPF0313 [4Fe-4S] protein YgiQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.225	PATRIC.2.9855.2.9855.con.0001.CDS.260222.261061.fwd	PATRIC	CDS	260222	261061	840	+	PGF_07274539	279	MSM (multiple sugar metabolism) operon regulatory protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2481	PATRIC.2.9855.2.9855.con.0001.CDS.2604174.2605529.rev	PATRIC	CDS	2604174	2605529	1356	-	PGF_00075770	451	FIG00519347: Ribonucleotide reductase-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2482	PATRIC.2.9855.2.9855.con.0001.CDS.2605542.2605811.rev	PATRIC	CDS	2605542	2605811	270	-	PGF_02787188	89	ACT domain protein CAC_0478	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2484	PATRIC.2.9855.2.9855.con.0001.CDS.2606024.2606938.rev	PATRIC	CDS	2606024	2606938	915	-	PGF_03731575	304	Carbohydrate Esterase Family 4	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2489	PATRIC.2.9855.2.9855.con.0001.CDS.2610086.2610292.rev	PATRIC	CDS	2610086	2610292	207	-	PGF_00053039	68	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.226	PATRIC.2.9855.2.9855.con.0001.CDS.261211.261732.fwd	PATRIC	CDS	261211	261732	522	+	PGF_00026045	173	Nitroreductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.32	PATRIC.2.9855.2.9855.con.0001.CDS.26126.26914.fwd	PATRIC	CDS	26126	26914	789	+	PGF_00426471	262	5-deoxy-glucuronate isomerase (EC 5.3.1.30)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2494	PATRIC.2.9855.2.9855.con.0001.CDS.2612632.2613084.rev	PATRIC	CDS	2612632	2613084	453	-	PGF_01656966	150	Transcriptional regulator, AsnC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2495	PATRIC.2.9855.2.9855.con.0001.CDS.2613790.2615220.fwd	PATRIC	CDS	2613790	2615220	1431	+	PGF_00066854	476	Aspartate ammonia-lyase (EC 4.3.1.1)	GO:0008797|aspartate ammonia-lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2498	PATRIC.2.9855.2.9855.con.0001.CDS.2616678.2617223.rev	PATRIC	CDS	2616678	2617223	546	-	PGF_06833838	181	putative membrane-associated phospholipid phosphatase, PAP2 superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2499	PATRIC.2.9855.2.9855.con.0001.CDS.2617550.2617939.fwd	PATRIC	CDS	2617550	2617939	390	+	PGF_03751069	129	Hemerythrin domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2500	PATRIC.2.9855.2.9855.con.0001.CDS.2618113.2618568.rev	PATRIC	CDS	2618113	2618568	456	-	PGF_00417736	151	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2501	PATRIC.2.9855.2.9855.con.0001.CDS.2618847.2619254.fwd	PATRIC	CDS	2618847	2619254	408	+	PGF_03440867	135	UPF0047 protein Bsu YugU	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2502	PATRIC.2.9855.2.9855.con.0001.CDS.2619349.2619552.rev	PATRIC	CDS	2619349	2619552	204	-	PGF_01307847	67	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2503	PATRIC.2.9855.2.9855.con.0001.CDS.2619845.2620411.rev	PATRIC	CDS	2619845	2620411	567	-	PGF_00601415	188	Uncharacterized nitroreductase family protein CT0345	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2504	PATRIC.2.9855.2.9855.con.0001.CDS.2620425.2621105.rev	PATRIC	CDS	2620425	2621105	681	-	PGF_00007007	226	GTP pyrophosphokinase (EC 2.7.6.5)	GO:0008728|GTP diphosphokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.227	PATRIC.2.9855.2.9855.con.0001.CDS.262176.263111.fwd	PATRIC	CDS	262176	263111	936	+	PGF_04405923	311	Cysteine synthase (EC 2.5.1.47)	GO:0004124|cysteine synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2507	PATRIC.2.9855.2.9855.con.0001.CDS.2623206.2624342.rev	PATRIC	CDS	2623206	2624342	1137	-	PGF_09054074	378	Methionine synthase II (cobalamin-independent)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2508	PATRIC.2.9855.2.9855.con.0001.CDS.2624692.2625825.rev	PATRIC	CDS	2624692	2625825	1134	-	PGF_09054074	377	Methionine synthase II (cobalamin-independent)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2509	PATRIC.2.9855.2.9855.con.0001.CDS.2625834.2626766.rev	PATRIC	CDS	2625834	2626766	933	-	PGF_00020739	310	Methionine biosynthesis and transport regulator MtaR, LysR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2510	PATRIC.2.9855.2.9855.con.0001.CDS.2626822.2627997.rev	PATRIC	CDS	2626822	2627997	1176	-	PGF_08932911	391	Alanine racemase (EC 5.1.1.1)	GO:0008784|alanine racemase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2511	PATRIC.2.9855.2.9855.con.0001.CDS.2628490.2628672.rev	PATRIC	CDS	2628490	2628672	183	-	PGF_00158423	60	Uncharacterized protein CPF_2956	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2512	PATRIC.2.9855.2.9855.con.0001.CDS.2628864.2629517.rev	PATRIC	CDS	2628864	2629517	654	-	PGF_10460277	217	Phosphoglycolate phosphatase (EC 3.1.3.18)	GO:0008967|phosphoglycolate phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2513	PATRIC.2.9855.2.9855.con.0001.CDS.2629710.2630255.fwd	PATRIC	CDS	2629710	2630255	546	+	PGF_02930287	181	Reverse rubrerythrin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2516	PATRIC.2.9855.2.9855.con.0001.CDS.2631234.2631725.rev	PATRIC	CDS	2631234	2631725	492	-	PGF_05676885	163	HD superfamily hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.228	PATRIC.2.9855.2.9855.con.0001.CDS.263188.263598.rev	PATRIC	CDS	263188	263598	411	-	PGF_01285062	136	Hemerythrin domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2517	PATRIC.2.9855.2.9855.con.0001.CDS.2632062.2633714.rev	PATRIC	CDS	2632062	2633714	1653	-	PGF_00990926	550	Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	GO:0008788|alpha,alpha-phosphotrehalase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2518	PATRIC.2.9855.2.9855.con.0001.CDS.2633733.2635151.rev	PATRIC	CDS	2633733	2635151	1419	-	PGF_03446029	472	PTS system, trehalose-specific IIB component (EC 2.7.1.201) / PTS system, trehalose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2519	PATRIC.2.9855.2.9855.con.0001.CDS.2635933.2636652.fwd	PATRIC	CDS	2635933	2636652	720	+	PGF_02032393	239	Trehalose operon transcriptional repressor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2521	PATRIC.2.9855.2.9855.con.0001.CDS.2637565.2638698.rev	PATRIC	CDS	2637565	2638698	1134	-	PGF_00418278	377	Cobalt-precorrin 5A hydrolase (EC 3.7.1.12)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2522	PATRIC.2.9855.2.9855.con.0001.CDS.2638685.2639455.rev	PATRIC	CDS	2638685	2639455	771	-	PGF_00418291	256	Cobalt-precorrin-4 C(11)-methyltransferase (EC 2.1.1.271)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2523	PATRIC.2.9855.2.9855.con.0001.CDS.2639505.2640170.rev	PATRIC	CDS	2639505	2640170	666	-	PGF_00717752	221	Cobalt-precorrin-2 C(20)-methyltransferase (EC 2.1.1.151)	GO:0043781|cobalt-factor II C20-methyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.229	PATRIC.2.9855.2.9855.con.0001.CDS.263969.265099.fwd	PATRIC	CDS	263969	265099	1131	+	PGF_00420756	376	1,3-propanediol dehydrogenase (EC 1.1.1.202)	GO:0047516|1,3-propanediol dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2524	PATRIC.2.9855.2.9855.con.0001.CDS.2640318.2640890.rev	PATRIC	CDS	2640318	2640890	573	-	PGF_00418301	190	Cobalt-precorrin-6B C15-methyltransferase [decarboxylating] (EC 2.1.1.196)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2525	PATRIC.2.9855.2.9855.con.0001.CDS.2640957.2641571.rev	PATRIC	CDS	2640957	2641571	615	-	PGF_00418304	204	Cobalt-precorrin-7 (C5)-methyltransferase (EC 2.1.1.289)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2526	PATRIC.2.9855.2.9855.con.0001.CDS.2641683.2642867.rev	PATRIC	CDS	2641683	2642867	1185	-	PGF_00418292	394	Cobalt-precorrin-5B (C1)-methyltransferase (EC 2.1.1.195)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2527	PATRIC.2.9855.2.9855.con.0001.CDS.2642925.2643548.rev	PATRIC	CDS	2642925	2643548	624	-	PGF_00418309	207	Cobalt-precorrin-8 methylmutase (EC 5.4.99.60)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2529	PATRIC.2.9855.2.9855.con.0001.CDS.2644385.2645767.rev	PATRIC	CDS	2644385	2645767	1383	-	PGF_00418379	460	Cobyrinic acid a,c-diamide synthetase (EC 6.3.5.11)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2530	PATRIC.2.9855.2.9855.con.0001.CDS.2645849.2646673.rev	PATRIC	CDS	2645849	2646673	825	-	PGF_00324246	274	Sirohydrochlorin cobaltochelatase CbiK (EC 4.99.1.3) @ Sirohydrochlorin ferrochelatase activity of CbiK (EC 4.99.1.4)	GO:0016852|sirohydrochlorin cobaltochelatase activity;GO:0051266|sirohydrochlorin ferrochelatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2532	PATRIC.2.9855.2.9855.con.0001.CDS.2647892.2648260.fwd	PATRIC	CDS	2647892	2648260	369	+	PGF_01258559	122	Metal chaperone, involved in Zn homeostasis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2536	PATRIC.2.9855.2.9855.con.0001.CDS.2651653.2651790.rev	PATRIC	CDS	2651653	2651790	138	-	PGF_04664292	45	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)	GO:0003964|RNA-directed DNA polymerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.230	PATRIC.2.9855.2.9855.con.0001.CDS.265207.266652.fwd	PATRIC	CDS	265207	266652	1446	+	PGF_00778630	481	Uncharacterized amino acid permease, GabP family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2540	PATRIC.2.9855.2.9855.con.0001.CDS.2654207.2655883.rev	PATRIC	CDS	2654207	2655883	1677	-	PGF_10447617	558	Ribonuclease J (endonuclease and 5' exonuclease)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2541	PATRIC.2.9855.2.9855.con.0001.CDS.2656478.2657737.rev	PATRIC	CDS	2656478	2657737	1260	-	PGF_10449899	419	UDP-glucose:sterol glucosyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2546	PATRIC.2.9855.2.9855.con.0001.CDS.2659776.2659964.fwd	PATRIC	CDS	2659776	2659964	189	+	PGF_03281009	62	Uncharacterized protein Bsu3320.5	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2548	PATRIC.2.9855.2.9855.con.0001.CDS.2660890.2661576.rev	PATRIC	CDS	2660890	2661576	687	-	PGF_09666309	228	Two-component transcriptional response regulator, LuxR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2551	PATRIC.2.9855.2.9855.con.0001.CDS.2662660.2663739.rev	PATRIC	CDS	2662660	2663739	1080	-	PGF_02620852	359	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2552	PATRIC.2.9855.2.9855.con.0001.CDS.2663736.2664419.rev	PATRIC	CDS	2663736	2664419	684	-	PGF_07420062	227	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2553	PATRIC.2.9855.2.9855.con.0001.CDS.2664797.2665354.rev	PATRIC	CDS	2664797	2665354	558	-	PGF_08585032	185	Ribosomal RNA adenine dimethylase domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2554	PATRIC.2.9855.2.9855.con.0001.CDS.2665757.2665909.fwd	PATRIC	CDS	2665757	2665909	153	+	PGF_03281009	50	Uncharacterized protein Bsu3320.5	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.231	PATRIC.2.9855.2.9855.con.0001.CDS.266606.267424.fwd	PATRIC	CDS	266606	267424	819	+	PGF_00426217	272	5-aminopentanamidase (EC 3.5.1.30)	GO:0047588|5-aminopentanamidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2555	PATRIC.2.9855.2.9855.con.0001.CDS.2666104.2666439.rev	PATRIC	CDS	2666104	2666439	336	-	PGF_00422423	111	DSBH domain containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2557	PATRIC.2.9855.2.9855.con.0001.CDS.2666988.2667344.rev	PATRIC	CDS	2666988	2667344	357	-	PGF_03320197	118	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2558	PATRIC.2.9855.2.9855.con.0001.CDS.2667489.2668526.fwd	PATRIC	CDS	2667489	2668526	1038	+	PGF_02007855	345	Zinc-type alcohol dehydrogenase-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2559	PATRIC.2.9855.2.9855.con.0001.CDS.2669084.2669347.fwd	PATRIC	CDS	2669084	2669347	264	+	PGF_03320197	87	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2560	PATRIC.2.9855.2.9855.con.0001.CDS.2669412.2669852.rev	PATRIC	CDS	2669412	2669852	441	-	PGF_01285249	146	Auxin-binding protein, putative	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2562	PATRIC.2.9855.2.9855.con.0001.CDS.2670520.2670915.fwd	PATRIC	CDS	2670520	2670915	396	+	PGF_00025678	131	NimC/NimA family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2563	PATRIC.2.9855.2.9855.con.0001.CDS.2671236.2672681.rev	PATRIC	CDS	2671236	2672681	1446	-	PGF_09996723	481	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2565	PATRIC.2.9855.2.9855.con.0001.CDS.2673666.2675732.fwd	PATRIC	CDS	2673666	2675732	2067	+	PGF_01011695	688	ErIC-type fluoride/proton exchange protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2567	PATRIC.2.9855.2.9855.con.0001.CDS.2676924.2677496.fwd	PATRIC	CDS	2676924	2677496	573	+	PGF_00046564	190	RNA polymerase sigma factor RpoE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.232	PATRIC.2.9855.2.9855.con.0001.CDS.267706.268431.fwd	PATRIC	CDS	267706	268431	726	+	PGF_12854651	241	Glutamine ABC transporter, ATP-binding protein GlnQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2569	PATRIC.2.9855.2.9855.con.0001.CDS.2678495.2678680.fwd	PATRIC	CDS	2678495	2678680	186	+	PGF_03281009	61	Uncharacterized protein Bsu3320.5	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2570	PATRIC.2.9855.2.9855.con.0001.CDS.2678677.2679246.rev	PATRIC	CDS	2678677	2679246	570	-	PGF_08155688	189	Bifunctional deaminase-reductase domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2571	PATRIC.2.9855.2.9855.con.0001.CDS.2679384.2681084.rev	PATRIC	CDS	2679384	2681084	1701	-	PGF_07849456	566	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2572	PATRIC.2.9855.2.9855.con.0001.CDS.2681675.2682883.rev	PATRIC	CDS	2681675	2682883	1209	-	PGF_00016225	402	L-serine dehydratase, beta subunit (EC 4.3.1.17) / L-serine dehydratase, alpha subunit (EC 4.3.1.17)	GO:0003941|L-serine ammonia-lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2573	PATRIC.2.9855.2.9855.con.0001.CDS.2683024.2683860.rev	PATRIC	CDS	2683024	2683860	837	-	PGF_00037054	278	Probable enoyl-CoA hydratase (EC 4.2.1.17)	GO:0004300|enoyl-CoA hydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2574	PATRIC.2.9855.2.9855.con.0001.CDS.2684003.2684833.rev	PATRIC	CDS	2684003	2684833	831	-	PGF_00037054	276	Probable enoyl-CoA hydratase (EC 4.2.1.17)	GO:0004300|enoyl-CoA hydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2575	PATRIC.2.9855.2.9855.con.0001.CDS.2684865.2686079.rev	PATRIC	CDS	2684865	2686079	1215	-	PGF_10459810	404	Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate, subunit A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.233	PATRIC.2.9855.2.9855.con.0001.CDS.268513.269397.fwd	PATRIC	CDS	268513	269397	885	+	PGF_05873585	294	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2576	PATRIC.2.9855.2.9855.con.0001.CDS.2686315.2687628.fwd	PATRIC	CDS	2686315	2687628	1314	+	PGF_00047242	437	Regulatory protein (induces abgABT, used to catabolize p-aminobenzoyl-glutamate)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2577	PATRIC.2.9855.2.9855.con.0001.CDS.2687686.2688510.rev	PATRIC	CDS	2687686	2688510	825	-	PGF_02868448	274	Uncharacterized transcriptional regulator YrhO, TrmB family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2578	PATRIC.2.9855.2.9855.con.0001.CDS.2688651.2689568.fwd	PATRIC	CDS	2688651	2689568	918	+	PGF_12667083	305	Permease of the drug/metabolite transporter (DMT) superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2579	PATRIC.2.9855.2.9855.con.0001.CDS.2689708.2689914.rev	PATRIC	CDS	2689708	2689914	207	-	PGF_00053039	68	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2582	PATRIC.2.9855.2.9855.con.0001.CDS.2691092.2691694.rev	PATRIC	CDS	2691092	2691694	603	-	PGF_07324755	200	Undecaprenyl-diphosphatase BcrC (EC 3.6.1.27), conveys bacitracin resistance	GO:0050380|undecaprenyl-diphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2583	PATRIC.2.9855.2.9855.con.0001.CDS.2691951.2693345.rev	PATRIC	CDS	2691951	2693345	1395	-	PGF_02620852	464	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.33	PATRIC.2.9855.2.9855.con.0001.CDS.26929.28860.fwd	PATRIC	CDS	26929	28860	1932	+	PGF_00424627	643	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (EC 3.7.1.22)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2584	PATRIC.2.9855.2.9855.con.0001.CDS.2693350.2694030.rev	PATRIC	CDS	2693350	2694030	681	-	PGF_12898141	226	Putative response regulator ArlR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.234	PATRIC.2.9855.2.9855.con.0001.CDS.269456.270163.fwd	PATRIC	CDS	269456	270163	708	+	PGF_00970618	235	Glutamine ABC transporter, permease protein GlnP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2586	PATRIC.2.9855.2.9855.con.0001.CDS.2695315.2696712.rev	PATRIC	CDS	2695315	2696712	1398	-	PGF_08913741	465	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2587	PATRIC.2.9855.2.9855.con.0001.CDS.2696797.2697210.rev	PATRIC	CDS	2696797	2697210	414	-	PGF_00049228	137	Rrf2 family transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2588	PATRIC.2.9855.2.9855.con.0001.CDS.2697547.2697789.rev	PATRIC	CDS	2697547	2697789	243	-	PGF_05632115	80	Transition state regulatory protein AbrB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2589	PATRIC.2.9855.2.9855.con.0001.CDS.2698008.2698634.rev	PATRIC	CDS	2698008	2698634	627	-	PGF_00421821	208	DNA replication helicase loader DnaC/DnaI	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2590	PATRIC.2.9855.2.9855.con.0001.CDS.2698684.2700048.rev	PATRIC	CDS	2698684	2700048	1365	-	PGF_12690820	454	Phage replication initiation	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2593	PATRIC.2.9855.2.9855.con.0001.CDS.2701052.2701411.fwd	PATRIC	CDS	2701052	2701411	360	+	PGF_01280795	119	Repressor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2594	PATRIC.2.9855.2.9855.con.0001.CDS.2701983.2702837.rev	PATRIC	CDS	2701983	2702837	855	-	PGF_03558774	284	Peptidase M48, Ste24p precursor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2595	PATRIC.2.9855.2.9855.con.0001.CDS.2703335.2703844.fwd	PATRIC	CDS	2703335	2703844	510	+	PGF_03292196	169	Membrane protein, TerC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2596	PATRIC.2.9855.2.9855.con.0001.CDS.2704502.2705158.rev	PATRIC	CDS	2704502	2705158	657	-	PGF_02278882	218	Iron-sulfur flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.235	PATRIC.2.9855.2.9855.con.0001.CDS.270471.271697.fwd	PATRIC	CDS	270471	271697	1227	+	PGF_01303627	408	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2597	PATRIC.2.9855.2.9855.con.0001.CDS.2705299.2705679.fwd	PATRIC	CDS	2705299	2705679	381	+	PGF_03320197	126	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2602	PATRIC.2.9855.2.9855.con.0001.CDS.2708601.2709356.fwd	PATRIC	CDS	2708601	2709356	756	+	PGF_09978608	251	Transposase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2604	PATRIC.2.9855.2.9855.con.0001.CDS.2710230.2710682.rev	PATRIC	CDS	2710230	2710682	453	-	PGF_03031267	150	Uncharacterized N-acetyltransferase YhfO, GNAT-family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2605	PATRIC.2.9855.2.9855.con.0001.CDS.2710906.2712024.rev	PATRIC	CDS	2710906	2712024	1119	-	PGF_02434611	372	Pleiotropic regulatory protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2606	PATRIC.2.9855.2.9855.con.0001.CDS.2712416.2712787.rev	PATRIC	CDS	2712416	2712787	372	-	PGF_00045876	123	Pyridoxamine 5'-phosphate oxidase-related, FMN-binding	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2607	PATRIC.2.9855.2.9855.con.0001.CDS.2712962.2714386.fwd	PATRIC	CDS	2712962	2714386	1425	+	PGF_02617052	474	Transcriptional regulator of pyridoxine metabolism / Pyridoxamine phosphate aminotransferase (EC 2.6.1.54)	GO:0019163|pyridoxamine-phosphate transaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2608	PATRIC.2.9855.2.9855.con.0001.CDS.2714661.2715251.rev	PATRIC	CDS	2714661	2715251	591	-	PGF_07182652	196	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2609	PATRIC.2.9855.2.9855.con.0001.CDS.2715263.2715961.rev	PATRIC	CDS	2715263	2715961	699	-	PGF_01088286	232	Efflux ABC transporter, permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2610	PATRIC.2.9855.2.9855.con.0001.CDS.2715958.2716881.rev	PATRIC	CDS	2715958	2716881	924	-	PGF_00884706	307	Efflux ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2611	PATRIC.2.9855.2.9855.con.0001.CDS.2717164.2717793.rev	PATRIC	CDS	2717164	2717793	630	-	PGF_00730641	209	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)	GO:0008700|4-hydroxy-2-oxoglutarate aldolase activity;GO:0008675|2-dehydro-3-deoxy-phosphogluconate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2612	PATRIC.2.9855.2.9855.con.0001.CDS.2717793.2718878.rev	PATRIC	CDS	2717793	2718878	1086	-	PGF_06985891	361	Mannonate dehydratase (EC 4.2.1.8)	GO:0008927|mannonate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2613	PATRIC.2.9855.2.9855.con.0001.CDS.2718891.2719343.rev	PATRIC	CDS	2718891	2719343	453	-	PGF_01191217	150	PTS system, gluconate-specific IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.236	PATRIC.2.9855.2.9855.con.0001.CDS.271991.273331.fwd	PATRIC	CDS	271991	273331	1341	+	PGF_04337880	446	Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.6.1.19)	GO:0003867|4-aminobutyrate transaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2615	PATRIC.2.9855.2.9855.con.0001.CDS.2720348.2720851.rev	PATRIC	CDS	2720348	2720851	504	-	PGF_01189382	167	PTS system, gluconate-specific IIB component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2616	PATRIC.2.9855.2.9855.con.0001.CDS.2720873.2721730.rev	PATRIC	CDS	2720873	2721730	858	-	PGF_00029709	285	PTS system, gluconate-specific IID component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2617	PATRIC.2.9855.2.9855.con.0001.CDS.2721743.2722573.rev	PATRIC	CDS	2721743	2722573	831	-	PGF_00029706	276	PTS system, gluconate-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2618	PATRIC.2.9855.2.9855.con.0001.CDS.2722584.2723687.rev	PATRIC	CDS	2722584	2723687	1104	-	PGF_03456354	367	Glycerol dehydrogenase (EC 1.1.1.6)	GO:0008888|glycerol dehydrogenase [NAD+] activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2619	PATRIC.2.9855.2.9855.con.0001.CDS.2723698.2724699.rev	PATRIC	CDS	2723698	2724699	1002	-	PGF_00012987	333	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	GO:0004617|phosphoglycerate dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2620	PATRIC.2.9855.2.9855.con.0001.CDS.2724702.2725604.rev	PATRIC	CDS	2724702	2725604	903	-	PGF_00427299	300	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	GO:0004616|phosphogluconate dehydrogenase (decarboxylating) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2621	PATRIC.2.9855.2.9855.con.0001.CDS.2726127.2726975.fwd	PATRIC	CDS	2726127	2726975	849	+	PGF_09655255	282	Transcriptional regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2622	PATRIC.2.9855.2.9855.con.0001.CDS.2727453.2728742.rev	PATRIC	CDS	2727453	2728742	1290	-	PGF_02818638	429	Hemolysins and related proteins containing CBS domains	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2623	PATRIC.2.9855.2.9855.con.0001.CDS.2729100.2729660.rev	PATRIC	CDS	2729100	2729660	561	-	PGF_10153092	186	Nitroreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2624	PATRIC.2.9855.2.9855.con.0001.CDS.2729942.2730754.fwd	PATRIC	CDS	2729942	2730754	813	+	PGF_01281247	270	CorA, CorA-like Mg2+ transporter protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2625	PATRIC.2.9855.2.9855.con.0001.CDS.2730981.2731385.rev	PATRIC	CDS	2730981	2731385	405	-	PGF_12906306	134	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2627	PATRIC.2.9855.2.9855.con.0001.CDS.2732721.2734433.rev	PATRIC	CDS	2732721	2734433	1713	-	PGF_01282257	570	Methyl-accepting chemotaxis protein tlpA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.237	PATRIC.2.9855.2.9855.con.0001.CDS.273551.274486.fwd	PATRIC	CDS	273551	274486	936	+	PGF_01258344	311	Predicted deacylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2630	PATRIC.2.9855.2.9855.con.0001.CDS.2735964.2737175.rev	PATRIC	CDS	2735964	2737175	1212	-	PGF_01259951	403	alternate gene name: comB, yufA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2631	PATRIC.2.9855.2.9855.con.0001.CDS.2737728.2739110.rev	PATRIC	CDS	2737728	2739110	1383	-	PGF_01421686	460	NADH-dependent reduced ferredoxin:NADP+ oxidoreductase subunit B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2632	PATRIC.2.9855.2.9855.con.0001.CDS.2739116.2740006.rev	PATRIC	CDS	2739116	2740006	891	-	PGF_01480798	296	NADH-dependent reduced ferredoxin:NADP+ oxidoreductase subunit A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2633	PATRIC.2.9855.2.9855.con.0001.CDS.2740391.2741557.rev	PATRIC	CDS	2740391	2741557	1167	-	PGF_00552739	388	NADPH-dependent butanol dehydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2634	PATRIC.2.9855.2.9855.con.0001.CDS.2741938.2743902.rev	PATRIC	CDS	2741938	2743902	1965	-	PGF_00052097	654	Sigma-54-dependent transcriptional activator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.238	PATRIC.2.9855.2.9855.con.0001.CDS.274483.275418.fwd	PATRIC	CDS	274483	275418	936	+	PGF_00007754	311	Gll3979 protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2639	PATRIC.2.9855.2.9855.con.0001.CDS.2746205.2746540.rev	PATRIC	CDS	2746205	2746540	336	-	PGF_03022389	111	Protein of unknown function UPF0060	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2640	PATRIC.2.9855.2.9855.con.0001.CDS.2747117.2749120.rev	PATRIC	CDS	2747117	2749120	2004	-	PGF_12694106	667	2-isopropylmalate synthase (EC 2.3.3.13)	GO:0003852|2-isopropylmalate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2641	PATRIC.2.9855.2.9855.con.0001.CDS.2749480.2749845.rev	PATRIC	CDS	2749480	2749845	366	-	PGF_00577145	121	FIG138056: a glutathione-dependent thiol reductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2644	PATRIC.2.9855.2.9855.con.0001.CDS.2751827.2754925.rev	PATRIC	CDS	2751827	2754925	3099	-	PGF_01282281	1032	Sensory box sensor histidine kinase/response regulator VC0622	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.239	PATRIC.2.9855.2.9855.con.0001.CDS.275682.277085.fwd	PATRIC	CDS	275682	277085	1404	+	PGF_00045039	467	Putative transmembrane symporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2650	PATRIC.2.9855.2.9855.con.0001.CDS.2758441.2758842.rev	PATRIC	CDS	2758441	2758842	402	-	PGF_03751069	133	Hemerythrin domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2655	PATRIC.2.9855.2.9855.con.0001.CDS.2760976.2761305.fwd	PATRIC	CDS	2760976	2761305	330	+	PGF_01285111	109	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2657	PATRIC.2.9855.2.9855.con.0001.CDS.2762609.2765839.rev	PATRIC	CDS	2762609	2765839	3231	-	PGF_10416542	1076	Sensory box histidine kinase/response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2658	PATRIC.2.9855.2.9855.con.0001.CDS.2766240.2767328.rev	PATRIC	CDS	2766240	2767328	1089	-	PGF_12899499	362	Chromosome partition protein smc	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2659	PATRIC.2.9855.2.9855.con.0001.CDS.2767553.2767888.fwd	PATRIC	CDS	2767553	2767888	336	+	PGF_01284176	111	Rubrerythrin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2660	PATRIC.2.9855.2.9855.con.0001.CDS.2768007.2768369.rev	PATRIC	CDS	2768007	2768369	363	-	PGF_01306430	120	Glyoxalase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2661	PATRIC.2.9855.2.9855.con.0001.CDS.2768523.2769545.rev	PATRIC	CDS	2768523	2769545	1023	-	PGF_05595534	340	DNA polymerase I 5'-3' exonuclease domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2663	PATRIC.2.9855.2.9855.con.0001.CDS.2771187.2772617.rev	PATRIC	CDS	2771187	2772617	1431	-	PGF_09996723	476	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.240	PATRIC.2.9855.2.9855.con.0001.CDS.277245.277625.fwd	PATRIC	CDS	277245	277625	381	+	PGF_06916656	126	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2664	PATRIC.2.9855.2.9855.con.0001.CDS.2773189.2773641.rev	PATRIC	CDS	2773189	2773641	453	-	PGF_10423881	150	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2665	PATRIC.2.9855.2.9855.con.0001.CDS.2773800.2774879.rev	PATRIC	CDS	2773800	2774879	1080	-	PGF_00406002	359	putative NADH-dependent flavin oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2666	PATRIC.2.9855.2.9855.con.0001.CDS.2776081.2776785.rev	PATRIC	CDS	2776081	2776785	705	-	PGF_01281702	234	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2667	PATRIC.2.9855.2.9855.con.0001.CDS.2777313.2777702.rev	PATRIC	CDS	2777313	2777702	390	-	PGF_00033417	129	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), subunit DhaM; DHA-specific IIA component	GO:0047324|phosphoenolpyruvate-glycerone phosphotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2668	PATRIC.2.9855.2.9855.con.0001.CDS.2777752.2778381.rev	PATRIC	CDS	2777752	2778381	630	-	PGF_00719345	209	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), ADP-binding subunit DhaL	GO:0047324|phosphoenolpyruvate-glycerone phosphotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.241	PATRIC.2.9855.2.9855.con.0001.CDS.277803.278657.fwd	PATRIC	CDS	277803	278657	855	+	PGF_10425579	284	ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2669	PATRIC.2.9855.2.9855.con.0001.CDS.2778534.2779532.rev	PATRIC	CDS	2778534	2779532	999	-	PGF_01979610	332	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), dihydroxyacetone binding subunit DhaK	GO:0047324|phosphoenolpyruvate-glycerone phosphotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2670	PATRIC.2.9855.2.9855.con.0001.CDS.2780032.2782101.rev	PATRIC	CDS	2780032	2782101	2070	-	PGF_01281234	689	AAA superfamily ATPases with N-terminal receiver domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2671	PATRIC.2.9855.2.9855.con.0001.CDS.2782546.2783466.rev	PATRIC	CDS	2782546	2783466	921	-	PGF_00406657	306	putative deacetylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2672	PATRIC.2.9855.2.9855.con.0001.CDS.2783610.2785349.rev	PATRIC	CDS	2783610	2785349	1740	-	PGF_08128839	579	Heterodimeric efflux ABC transporter, permease/ATP-binding subunit 2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2673	PATRIC.2.9855.2.9855.con.0001.CDS.2785350.2787083.rev	PATRIC	CDS	2785350	2787083	1734	-	PGF_10540665	577	Heterodimeric efflux ABC transporter, permease/ATP-binding subunit 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2674	PATRIC.2.9855.2.9855.con.0001.CDS.2787224.2788090.fwd	PATRIC	CDS	2787224	2788090	867	+	PGF_07987589	288	Transcriptional regulator, LysR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.242	PATRIC.2.9855.2.9855.con.0001.CDS.278816.279475.fwd	PATRIC	CDS	278816	279475	660	+	PGF_01282226	219	ABC transporter, permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2675	PATRIC.2.9855.2.9855.con.0001.CDS.2788414.2789634.rev	PATRIC	CDS	2788414	2789634	1221	-	PGF_09996723	406	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2676	PATRIC.2.9855.2.9855.con.0001.CDS.2789636.2790424.rev	PATRIC	CDS	2789636	2790424	789	-	PGF_10567400	262	Ferrichrome transport ATP-binding protein FhuC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2677	PATRIC.2.9855.2.9855.con.0001.CDS.2790425.2791432.rev	PATRIC	CDS	2790425	2791432	1008	-	PGF_00004586	335	Ferrichrome transport system permease protein FhuG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2678	PATRIC.2.9855.2.9855.con.0001.CDS.2791434.2792426.rev	PATRIC	CDS	2791434	2792426	993	-	PGF_01756633	330	Ferrichrome transport system permease protein FhuB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2679	PATRIC.2.9855.2.9855.con.0001.CDS.2792413.2793363.rev	PATRIC	CDS	2792413	2793363	951	-	PGF_00004601	316	Ferrichrome-binding periplasmic protein precursor (TC 3.A.1.14.3)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2680	PATRIC.2.9855.2.9855.con.0001.CDS.2793731.2795350.rev	PATRIC	CDS	2793731	2795350	1620	-	PGF_00417743	539	Choline binding protein PcpA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2681	PATRIC.2.9855.2.9855.con.0001.CDS.2795565.2796566.fwd	PATRIC	CDS	2795565	2796566	1002	+	PGF_10339052	333	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2682	PATRIC.2.9855.2.9855.con.0001.CDS.2796726.2797289.fwd	PATRIC	CDS	2796726	2797289	564	+	PGF_00041794	187	Alkyl hydroperoxide reductase protein C (EC 1.11.1.15)	GO:0051920|peroxiredoxin activity

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2683	PATRIC.2.9855.2.9855.con.0001.CDS.2797301.2798830.fwd	PATRIC	CDS	2797301	2798830	1530	+	PGF_09969389	509	Alkyl hydroperoxide reductase protein F	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2685	PATRIC.2.9855.2.9855.con.0001.CDS.2799239.2799874.rev	PATRIC	CDS	2799239	2799874	636	-	PGF_08237337	211	Ankyrin repeat protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2686	PATRIC.2.9855.2.9855.con.0001.CDS.2801361.2802026.rev	PATRIC	CDS	2801361	2802026	666	-	PGF_00417736	221	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2688	PATRIC.2.9855.2.9855.con.0001.CDS.2804495.2805934.rev	PATRIC	CDS	2804495	2805934	1440	-	PGF_00067554	479	Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.7)	GO:0050566|asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity;GO:0050567|glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2689	PATRIC.2.9855.2.9855.con.0001.CDS.2805948.2807387.rev	PATRIC	CDS	2805948	2807387	1440	-	PGF_06522349	479	Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7)	GO:0050566|asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity;GO:0050567|glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2690	PATRIC.2.9855.2.9855.con.0001.CDS.2807403.2807687.rev	PATRIC	CDS	2807403	2807687	285	-	PGF_07836795	94	Aspartyl-tRNA(Asn) amidotransferase subunit C (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.7)	GO:0050566|asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity;GO:0050567|glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2691	PATRIC.2.9855.2.9855.con.0001.CDS.2807945.2809234.rev	PATRIC	CDS	2807945	2809234	1290	-	PGF_00982259	429	Aspartyl-tRNA synthetase (EC 6.1.1.12) @ Aspartyl-tRNA(Asn) synthetase (EC 6.1.1.23)	GO:0004815|aspartate-tRNA ligase activity;GO:0050560|aspartate-tRNA(Asn) ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.244	PATRIC.2.9855.2.9855.con.0001.CDS.280969.281760.fwd	PATRIC	CDS	280969	281760	792	+	PGF_00026487	263	Nucleotidyl transferase/aminotransferase, class V	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2693	PATRIC.2.9855.2.9855.con.0001.CDS.2810534.2811646.rev	PATRIC	CDS	2810534	2811646	1113	-	PGF_00404569	370	probable secreted protein homolog of yjcM/yhbB B. subtilis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2694	PATRIC.2.9855.2.9855.con.0001.CDS.2811680.2812585.rev	PATRIC	CDS	2811680	2812585	906	-	PGF_00021563	301	MII3043 protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2695	PATRIC.2.9855.2.9855.con.0001.CDS.2812954.2814363.fwd	PATRIC	CDS	2812954	2814363	1410	+	PGF_02158779	469	Di-tripeptide/cation symporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2696	PATRIC.2.9855.2.9855.con.0001.CDS.2814427.2815524.rev	PATRIC	CDS	2814427	2815524	1098	-	PGF_05863337	365	Lysophospholipase L2 (EC 3.1.1.5)	GO:0004622|lysophospholipase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2699	PATRIC.2.9855.2.9855.con.0001.CDS.2816405.2818579.rev	PATRIC	CDS	2816405	2818579	2175	-	PGF_02620852	724	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2700	PATRIC.2.9855.2.9855.con.0001.CDS.2818566.2819270.rev	PATRIC	CDS	2818566	2819270	705	-	PGF_07420062	234	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.245	PATRIC.2.9855.2.9855.con.0001.CDS.281868.283166.fwd	PATRIC	CDS	281868	283166	1299	+	PGF_00420132	432	Cytidylyltransferase domain / Phosphoenolpyruvate phosphomutase (EC 5.4.2.9)	GO:0050188|phosphoenolpyruvate mutase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2702	PATRIC.2.9855.2.9855.con.0001.CDS.2821897.2823783.rev	PATRIC	CDS	2821897	2823783	1887	-	PGF_00418149	628	Clostridial MutS2-related protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2703	PATRIC.2.9855.2.9855.con.0001.CDS.2824408.2825916.rev	PATRIC	CDS	2824408	2825916	1509	-	PGF_10048015	502	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) / CBS domain	GO:0003938|IMP dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2705	PATRIC.2.9855.2.9855.con.0001.CDS.2826879.2827928.rev	PATRIC	CDS	2826879	2827928	1050	-	PGF_00065238	349	Arsenical-resistance protein ACR3	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2706	PATRIC.2.9855.2.9855.con.0001.CDS.2827957.2828370.rev	PATRIC	CDS	2827957	2828370	414	-	PGF_01899098	137	Arsenate reductase (EC 1.20.4.4) thioredoxin-coupled, LMWP family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2707	PATRIC.2.9855.2.9855.con.0001.CDS.2828397.2830145.rev	PATRIC	CDS	2828397	2830145	1749	-	PGF_08102229	582	Arsenite/antimonite pump-driving ATPase ArsA (EC 3.6.3.16)	GO:0015446|arsenite-transmembrane transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2708	PATRIC.2.9855.2.9855.con.0001.CDS.2830201.2830587.rev	PATRIC	CDS	2830201	2830587	387	-	PGF_02772315	128	Asenic metallochaperone ArsD, transfers trivalent metalloids to ArsAB pump	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2709	PATRIC.2.9855.2.9855.con.0001.CDS.2830660.2830977.rev	PATRIC	CDS	2830660	2830977	318	-	PGF_00065208	105	Arsenical resistance operon repressor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2711	PATRIC.2.9855.2.9855.con.0001.CDS.2832040.2832840.rev	PATRIC	CDS	2832040	2832840	801	-	PGF_00011989	266	Histidinol-phosphatase (EC 3.1.3.15)	GO:0004401|histidinol-phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.246	PATRIC.2.9855.2.9855.con.0001.CDS.283300.284433.fwd	PATRIC	CDS	283300	284433	1134	+	PGF_06269608	377	Phosphonopyruvate decarboxylase (EC 4.1.1.82)	GO:0033980|phosphonopyruvate decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2712	PATRIC.2.9855.2.9855.con.0001.CDS.2833278.2833754.rev	PATRIC	CDS	2833278	2833754	477	-	PGF_00028031	158	Acetyltransferase, GNAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2713	PATRIC.2.9855.2.9855.con.0001.CDS.2834223.2835026.rev	PATRIC	CDS	2834223	2835026	804	-	PGF_03679803	267	N-acyl homoserine lactone hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2714	PATRIC.2.9855.2.9855.con.0001.CDS.2835062.2836372.rev	PATRIC	CDS	2835062	2836372	1311	-	PGF_05689946	436	4-hydroxybutyrate coenzyme A transferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2716	PATRIC.2.9855.2.9855.con.0001.CDS.2836670.2836939.rev	PATRIC	CDS	2836670	2836939	270	-	PGF_01284143	89	Nitrogen fixation protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2717	PATRIC.2.9855.2.9855.con.0001.CDS.2836953.2838407.rev	PATRIC	CDS	2836953	2838407	1455	-	PGF_00424287	484	4-hydroxybutanoyl-CoA dehydratase (EC 4.2.1.120) / Vinylacetyl-CoA Delta-isomerase (EC 5.3.3.3)	GO:0043721|4-hydroxybutanoyl-CoA dehydratase activity;GO:0050393|vinylacetyl-CoA delta-isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2718	PATRIC.2.9855.2.9855.con.0001.CDS.2838866.2840638.rev	PATRIC	CDS	2838866	2840638	1773	-	PGF_00052096	590	Sigma-54-dependent transcriptional activator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2719	PATRIC.2.9855.2.9855.con.0001.CDS.2840750.2842045.rev	PATRIC	CDS	2840750	2842045	1296	-	PGF_00017707	431	LuxC, acyl-CoA reductase (EC 1.2.1.50)	GO:0050062|long-chain-fatty-acyl-CoA reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2720	PATRIC.2.9855.2.9855.con.0001.CDS.2842042.2843139.rev	PATRIC	CDS	2842042	2843139	1098	-	PGF_01281709	365	LuxE, long-chain-fatty-acid ligase (EC 6.2.1.19)	GO:0047474|long-chain fatty acid luciferin component ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2721	PATRIC.2.9855.2.9855.con.0001.CDS.2843136.2844611.rev	PATRIC	CDS	2843136	2844611	1476	-	PGF_00734739	491	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	GO:0004467|long-chain fatty acid-CoA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.247	PATRIC.2.9855.2.9855.con.0001.CDS.284488.285612.fwd	PATRIC	CDS	284488	285612	1125	+	PGF_00053509	374	2-aminoethylphosphonate:pyruvate aminotransferase (EC 2.6.1.37)	GO:0047304|2-aminoethylphosphonate-pyruvate transaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2723	PATRIC.2.9855.2.9855.con.0001.CDS.2845576.2847504.rev	PATRIC	CDS	2845576	2847504	1929	-	PGF_02008990	642	Efflux ABC transporter, permease/ATP-binding protein BLI02169	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2724	PATRIC.2.9855.2.9855.con.0001.CDS.2847501.2849276.rev	PATRIC	CDS	2847501	2849276	1776	-	PGF_06927169	591	Efflux ABC transporter, permease/ATP-binding protein BLI02168	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2725	PATRIC.2.9855.2.9855.con.0001.CDS.2849290.2849733.rev	PATRIC	CDS	2849290	2849733	444	-	PGF_01282225	147	5-carboxymethyl-2-oxo-hex-3- ene-1,7-dioate decarboxylase (EC 4.1.1.68)	GO:0018800|5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2726	PATRIC.2.9855.2.9855.con.0001.CDS.2850571.2851575.rev	PATRIC	CDS	2850571	2851575	1005	-	PGF_00012956	334	Hydroxymethylpyrimidine ABC transporter, substrate-binding component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2727	PATRIC.2.9855.2.9855.con.0001.CDS.2851556.2852338.rev	PATRIC	CDS	2851556	2852338	783	-	PGF_04149001	260	Hydroxymethylpyrimidine ABC transporter, transmembrane component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2728	PATRIC.2.9855.2.9855.con.0001.CDS.2852340.2853101.rev	PATRIC	CDS	2852340	2853101	762	-	PGF_01281235	253	ABC-type multidrug/protein/lipid transport system, ATPase component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2729	PATRIC.2.9855.2.9855.con.0001.CDS.2853102.2853770.rev	PATRIC	CDS	2853102	2853770	669	-	PGF_00867759	222	Thiaminase II (EC 3.5.99.2) involved in salvage of thiamin pyrimidine moiety, TenA subgroup with Cys in active site	GO:0050334|thiaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2730	PATRIC.2.9855.2.9855.con.0001.CDS.2854012.2855946.rev	PATRIC	CDS	2854012	2855946	1935	-	PGF_02620852	644	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2731	PATRIC.2.9855.2.9855.con.0001.CDS.2856154.2857350.rev	PATRIC	CDS	2856154	2857350	1197	-	PGF_02753825	398	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9), FabV => refractory to triclosan	GO:0004318|enoyl-[acyl-carrier-protein] reductase (NADH) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.248	PATRIC.2.9855.2.9855.con.0001.CDS.285629.286429.rev	PATRIC	CDS	285629	286429	801	-	PGF_04150742	266	Zinc ABC transporter, permease protein ZnuB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2733	PATRIC.2.9855.2.9855.con.0001.CDS.2857967.2858923.rev	PATRIC	CDS	2857967	2858923	957	-	PGF_03696321	318	tRNA-dihydrouridine synthase BT3326	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2734	PATRIC.2.9855.2.9855.con.0001.CDS.2859568.2860185.rev	PATRIC	CDS	2859568	2860185	618	-	PGF_00016160	205	L-lysine permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2735	PATRIC.2.9855.2.9855.con.0001.CDS.2860294.2861769.rev	PATRIC	CDS	2860294	2861769	1476	-	PGF_09985786	491	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	GO:0004069|L-aspartate:2-oxoglutarate aminotransferase activity;GO:0004069|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2736	PATRIC.2.9855.2.9855.con.0001.CDS.2862422.2863654.rev	PATRIC	CDS	2862422	2863654	1233	-	PGF_01703470	410	Adenylosuccinate synthetase-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.249	PATRIC.2.9855.2.9855.con.0001.CDS.286463.287134.rev	PATRIC	CDS	286463	287134	672	-	PGF_08228852	223	Zinc ABC transporter, ATP-binding protein ZnuC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2740	PATRIC.2.9855.2.9855.con.0001.CDS.2866710.2868179.rev	PATRIC	CDS	2866710	2868179	1470	-	PGF_00025578	489	Nicotinamide phosphoribosyltransferase (EC 2.4.2.12)	GO:0047280|nicotinamide phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2741	PATRIC.2.9855.2.9855.con.0001.CDS.2868191.2868730.rev	PATRIC	CDS	2868191	2868730	540	-	PGF_01935566	179	Nicotinamidase (EC 3.5.1.19)	GO:0008936|nicotinamidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2742	PATRIC.2.9855.2.9855.con.0001.CDS.2869228.2870028.rev	PATRIC	CDS	2869228	2870028	801	-	PGF_00048787	266	Ribose-phosphate pyrophosphokinase, possible alternative form	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2743	PATRIC.2.9855.2.9855.con.0001.CDS.2870098.2870991.rev	PATRIC	CDS	2870098	2870991	894	-	PGF_06745520	297	Nudix-related transcriptional regulator NrtR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2744	PATRIC.2.9855.2.9855.con.0001.CDS.2871740.2872276.fwd	PATRIC	CDS	2871740	2872276	537	+	PGF_10519603	178	Acetyltransferase, GNAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2746	PATRIC.2.9855.2.9855.con.0001.CDS.2872963.2874297.rev	PATRIC	CDS	2872963	2874297	1335	-	PGF_01288664	444	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.250	PATRIC.2.9855.2.9855.con.0001.CDS.287416.288600.fwd	PATRIC	CDS	287416	288600	1185	+	PGF_04947330	394	Poly(glycerophosphate chain) D-alanine transfer protein DltD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2747	PATRIC.2.9855.2.9855.con.0001.CDS.2874796.2875659.fwd	PATRIC	CDS	2874796	2875659	864	+	PGF_05873585	287	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2748	PATRIC.2.9855.2.9855.con.0001.CDS.2875843.2876133.fwd	PATRIC	CDS	2875843	2876133	291	+	PGF_01312163	96	Protein CotJA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2749	PATRIC.2.9855.2.9855.con.0001.CDS.2876143.2876406.fwd	PATRIC	CDS	2876143	2876406	264	+	PGF_00940841	87	Polypeptide composition of the spore coat protein CotJB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2750	PATRIC.2.9855.2.9855.con.0001.CDS.2876413.2876979.fwd	PATRIC	CDS	2876413	2876979	567	+	PGF_03254598	188	Manganese catalase (EC 1.11.1.6) => Spore coat protein CotJC	GO:0004096|catalase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2751	PATRIC.2.9855.2.9855.con.0001.CDS.2877205.2878968.rev	PATRIC	CDS	2877205	2878968	1764	-	PGF_02620852	587	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2758	PATRIC.2.9855.2.9855.con.0001.CDS.2884800.2884979.rev	PATRIC	CDS	2884800	2884979	180	-	PGF_01265835	59	Iron-sulfur cluster assembly scaffold protein NifU	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.251	PATRIC.2.9855.2.9855.con.0001.CDS.288566.288706.fwd	PATRIC	CDS	288566	288706	141	+	PGF_06988845	46	Component involved in D-alanylation of teichoic acids	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.252	PATRIC.2.9855.2.9855.con.0001.CDS.288721.290235.fwd	PATRIC	CDS	288721	290235	1515	+	PGF_00420806	504	D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13)	GO:0047473|D-alanine-poly(phosphoribitol) ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.34	PATRIC.2.9855.2.9855.con.0001.CDS.28875.29888.fwd	PATRIC	CDS	28875	29888	1014	+	PGF_00023555	337	Myo-inositol 2-dehydrogenase 1 (EC 1.1.1.18)	GO:0050112|inositol 2-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2767	PATRIC.2.9855.2.9855.con.0001.CDS.2889925.2890425.rev	PATRIC	CDS	2889925	2890425	501	-	PGF_02705755	166	FIG045374: Type II restriction enzyme, methylase subunit YeeA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2768	PATRIC.2.9855.2.9855.con.0001.CDS.2890422.2891915.rev	PATRIC	CDS	2890422	2891915	1494	-	PGF_02705755	497	FIG045374: Type II restriction enzyme, methylase subunit YeeA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2769	PATRIC.2.9855.2.9855.con.0001.CDS.2892416.2893765.rev	PATRIC	CDS	2892416	2893765	1350	-	PGF_03587816	449	FAD-linked oxidoreductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2771	PATRIC.2.9855.2.9855.con.0001.CDS.2894067.2896721.rev	PATRIC	CDS	2894067	2896721	2655	-	PGF_05965846	884	Pyruvate-utilizing enzyme, similar to phosphoenolpyruvate synthase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2772	PATRIC.2.9855.2.9855.con.0001.CDS.2896736.2897350.rev	PATRIC	CDS	2896736	2897350	615	-	PGF_10311426	204	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2773	PATRIC.2.9855.2.9855.con.0001.CDS.2897659.2898246.fwd	PATRIC	CDS	2897659	2898246	588	+	PGF_07182652	195	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2774	PATRIC.2.9855.2.9855.con.0001.CDS.2898305.2900929.fwd	PATRIC	CDS	2898305	2900929	2625	+	PGF_05965846	874	Pyruvate-utilizing enzyme, similar to phosphoenolpyruvate synthase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2776	PATRIC.2.9855.2.9855.con.0001.CDS.2902006.2903250.rev	PATRIC	CDS	2902006	2903250	1245	-	PGF_06614457	414	Ammonium transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.253	PATRIC.2.9855.2.9855.con.0001.CDS.290235.291389.fwd	PATRIC	CDS	290235	291389	1155	+	PGF_00420819	384	D-alanyl transfer protein DltB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2780	PATRIC.2.9855.2.9855.con.0001.CDS.2906525.2907250.rev	PATRIC	CDS	2906525	2907250	726	-	PGF_00213073	241	2-hydroxychromene-2-carboxylate isomerase/DsbA-like thioredoxin domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2781	PATRIC.2.9855.2.9855.con.0001.CDS.2907873.2910296.rev	PATRIC	CDS	2907873	2910296	2424	-	PGF_10550392	807	flavoprotein subunit related to the succinate dehydrogenases and fumarate reductases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2782	PATRIC.2.9855.2.9855.con.0001.CDS.2910311.2910910.rev	PATRIC	CDS	2910311	2910910	600	-	PGF_01581821	199	FMN reductase-like protein EF_1226	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2783	PATRIC.2.9855.2.9855.con.0001.CDS.2911420.2912367.fwd	PATRIC	CDS	2911420	2912367	948	+	PGF_00658541	315	Transcriptional regulator, LysR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2784	PATRIC.2.9855.2.9855.con.0001.CDS.2912360.2913298.fwd	PATRIC	CDS	2912360	2913298	939	+	PGF_06832396	312	FAD:protein FMN transferase (EC 2.7.1.180) @ FAD:protein FMN transferase (EC 2.7.1.180), EF_1226/7-associated	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2785	PATRIC.2.9855.2.9855.con.0001.CDS.2913409.2916003.rev	PATRIC	CDS	2913409	2916003	2595	-	PGF_06434787	864	ABC transporter-coupled two-component system, fused permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.254	PATRIC.2.9855.2.9855.con.0001.CDS.291444.291671.fwd	PATRIC	CDS	291444	291671	228	+	PGF_00420810	75	D-alanine--poly(phosphoribitol) ligase ACP subunit (EC 6.1.1.13)	GO:0047473|D-alanine-poly(phosphoribitol) ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2786	PATRIC.2.9855.2.9855.con.0001.CDS.2916000.2916683.rev	PATRIC	CDS	2916000	2916683	684	-	PGF_03247871	227	ABC transporter-coupled two-component system, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2787	PATRIC.2.9855.2.9855.con.0001.CDS.2916819.2917820.rev	PATRIC	CDS	2916819	2917820	1002	-	PGF_00027629	333	ABC transporter-coupled two-component system, signal transduction histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2788	PATRIC.2.9855.2.9855.con.0001.CDS.2917822.2918499.rev	PATRIC	CDS	2917822	2918499	678	-	PGF_00740556	225	ABC transporter-coupled two-component system, LuxR family response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2789	PATRIC.2.9855.2.9855.con.0001.CDS.2919205.2919327.rev	PATRIC	CDS	2919205	2919327	123	-	PGF_04664292	40	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)	GO:0003964|RNA-directed DNA polymerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2790	PATRIC.2.9855.2.9855.con.0001.CDS.2919485.2920327.rev	PATRIC	CDS	2919485	2920327	843	-	PGF_06672158	280	Nitroreductase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2793	PATRIC.2.9855.2.9855.con.0001.CDS.2921714.2921905.rev	PATRIC	CDS	2921714	2921905	192	-	PGF_01448568	63	Uncharacterized protein YwbE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2794	PATRIC.2.9855.2.9855.con.0001.CDS.2922012.2922791.rev	PATRIC	CDS	2922012	2922791	780	-	PGF_08447472	259	Protein-L-isoD(D-D) O-methyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2795	PATRIC.2.9855.2.9855.con.0001.CDS.2923935.2924810.rev	PATRIC	CDS	2923935	2924810	876	-	PGF_08603671	291	Uncharacterized transcriptional regulator YdeE, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2797	PATRIC.2.9855.2.9855.con.0001.CDS.2925855.2927249.rev	PATRIC	CDS	2925855	2927249	1395	-	PGF_05940986	464	D-beta-hydroxybutyrate permease	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2798	PATRIC.2.9855.2.9855.con.0001.CDS.2927438.2928994.rev	PATRIC	CDS	2927438	2928994	1557	-	PGF_07834560	518	Coenzyme A transferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2799	PATRIC.2.9855.2.9855.con.0001.CDS.2929428.2931134.rev	PATRIC	CDS	2929428	2931134	1707	-	PGF_08174272	568	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2800	PATRIC.2.9855.2.9855.con.0001.CDS.2931453.2931878.rev	PATRIC	CDS	2931453	2931878	426	-	PGF_03241496	141	MaoC-like dehydratase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2801	PATRIC.2.9855.2.9855.con.0001.CDS.2931951.2932958.rev	PATRIC	CDS	2931951	2932958	1008	-	PGF_01308514	335	Electron bifurcating butyryl-CoA dehydrogenase, electron transfer flavoprotein alpha	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2802	PATRIC.2.9855.2.9855.con.0001.CDS.2932981.2933760.rev	PATRIC	CDS	2932981	2933760	780	-	PGF_00424111	259	Electron bifurcating butyryl-CoA dehydrogenase, electron transfer flavoprotein beta	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2803	PATRIC.2.9855.2.9855.con.0001.CDS.2933774.2934913.rev	PATRIC	CDS	2933774	2934913	1140	-	PGF_00424109	379	Electron bifurcating butyryl-CoA dehydrogenase (NAD+, ferredoxin)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2804	PATRIC.2.9855.2.9855.con.0001.CDS.2934988.2935773.rev	PATRIC	CDS	2934988	2935773	786	-	PGF_12694858	261	3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55)	GO:0003859|3-hydroxybutyryl-CoA dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2807	PATRIC.2.9855.2.9855.con.0001.CDS.2937242.2939245.rev	PATRIC	CDS	2937242	2939245	2004	-	PGF_04734234	667	Kup system potassium uptake protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.257	PATRIC.2.9855.2.9855.con.0001.CDS.293906.295690.fwd	PATRIC	CDS	293906	295690	1785	+	PGF_00401883	594	Oligoendopeptidase F	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2808	PATRIC.2.9855.2.9855.con.0001.CDS.2939373.2940071.rev	PATRIC	CDS	2939373	2940071	699	-	PGF_10469496	232	DNA-binding response regulator KdpE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2809	PATRIC.2.9855.2.9855.con.0001.CDS.2940061.2942646.rev	PATRIC	CDS	2940061	2942646	2586	-	PGF_02938414	861	Osmosensitive K+ channel histidine kinase KdpD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2812	PATRIC.2.9855.2.9855.con.0001.CDS.2944015.2944704.rev	PATRIC	CDS	2944015	2944704	690	-	PGF_00410190	229	putative plasmid-related protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2813	PATRIC.2.9855.2.9855.con.0001.CDS.2945467.2946177.rev	PATRIC	CDS	2945467	2946177	711	-	PGF_04019463	236	Repair of Iron Centers di-iron protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2815	PATRIC.2.9855.2.9855.con.0001.CDS.2947309.2947659.fwd	PATRIC	CDS	2947309	2947659	351	+	PGF_00072334	116	Bacterocin transport accessory protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2816	PATRIC.2.9855.2.9855.con.0001.CDS.2948092.2948484.rev	PATRIC	CDS	2948092	2948484	393	-	PGF_00057506	130	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2819	PATRIC.2.9855.2.9855.con.0001.CDS.2950266.2953196.rev	PATRIC	CDS	2950266	2953196	2931	-	PGF_00423472	976	DinG family ATP-dependent helicase YoaA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2822	PATRIC.2.9855.2.9855.con.0001.CDS.2954795.2955577.rev	PATRIC	CDS	2954795	2955577	783	-	PGF_00072326	260	Homocitrate synthase (EC 2.3.3.14)	GO:0004410|homocitrate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2823	PATRIC.2.9855.2.9855.con.0001.CDS.2955599.2956513.rev	PATRIC	CDS	2955599	2956513	915	-	PGF_01257073	304	Homocitrate synthase omega subunit (EC 2.3.3.14)	GO:0004410|homocitrate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2824	PATRIC.2.9855.2.9855.con.0001.CDS.2956731.2957198.rev	PATRIC	CDS	2956731	2957198	468	-	PGF_00052833	155	Siroheme decarboxylase AhbB, alternate heme biosynthesis pathway	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2825	PATRIC.2.9855.2.9855.con.0001.CDS.2957191.2957658.rev	PATRIC	CDS	2957191	2957658	468	-	PGF_00052829	155	Siroheme decarboxylase AhbA, alternate heme biosynthesis pathway	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2826	PATRIC.2.9855.2.9855.con.0001.CDS.2957710.2958693.rev	PATRIC	CDS	2957710	2958693	984	-	PGF_00047026	327	Radical SAM heme biosynthesis protein AhbD, Fe-coproporphyrin III decarboxylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2827	PATRIC.2.9855.2.9855.con.0001.CDS.2958743.2959912.rev	PATRIC	CDS	2958743	2959912	1170	-	PGF_08631162	389	Radical SAM heme biosynthesis protein AhbC, 12,18-didecarboxysirohaem deacetylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2828	PATRIC.2.9855.2.9855.con.0001.CDS.2960282.2960590.rev	PATRIC	CDS	2960282	2960590	309	-	PGF_02295498	102	Ferredoxin, 2Fe-2S	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2830	PATRIC.2.9855.2.9855.con.0001.CDS.2960916.2963606.rev	PATRIC	CDS	2960916	2963606	2691	-	PGF_00025974	896	Nitrogenase FeMo-cofactor scaffold and assembly protein NifN / Nitrogenase FeMo-cofactor synthesis FeS core scaffold and assembly protein NifB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.258	PATRIC.2.9855.2.9855.con.0001.CDS.296143.297183.fwd	PATRIC	CDS	296143	297183	1041	+	PGF_00807568	346	FIG056164: rhomboid family serine protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2831	PATRIC.2.9855.2.9855.con.0001.CDS.2963593.2964957.rev	PATRIC	CDS	2963593	2964957	1365	-	PGF_00025964	454	Nitrogenase FeMo-cofactor scaffold and assembly protein NifE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2833	PATRIC.2.9855.2.9855.con.0001.CDS.2966139.2967503.rev	PATRIC	CDS	2966139	2967503	1365	-	PGF_00025953	454	Nitrogenase (molybdenum-iron) beta chain (EC 1.18.6.1)	GO:0016163|nitrogenase activity;GO:0016163|carbonyl sulfide nitrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2834	PATRIC.2.9855.2.9855.con.0001.CDS.2967503.2969089.rev	PATRIC	CDS	2967503	2969089	1587	-	PGF_00025951	528	Nitrogenase (molybdenum-iron) alpha chain (EC 1.18.6.1)	GO:0016163|nitrogenase activity;GO:0016163|carbonyl sulfide nitrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2835	PATRIC.2.9855.2.9855.con.0001.CDS.2969108.2969491.rev	PATRIC	CDS	2969108	2969491	384	-	PGF_00025933	127	Nitrogen regulatory protein P-II, nitrogen-fixation associated, subunit B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2836	PATRIC.2.9855.2.9855.con.0001.CDS.2969516.2969842.rev	PATRIC	CDS	2969516	2969842	327	-	PGF_00025932	108	Nitrogen regulatory protein P-II, nitrogen-fixation associated, subunit A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2838	PATRIC.2.9855.2.9855.con.0001.CDS.2970132.2970953.rev	PATRIC	CDS	2970132	2970953	822	-	PGF_00025954	273	Nitrogenase (molybdenum-iron) reductase and maturation protein NifH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2840	PATRIC.2.9855.2.9855.con.0001.CDS.2972376.2972984.rev	PATRIC	CDS	2972376	2972984	609	-	PGF_00055817	202	AnfO protein, required for Mo- and V-independent nitrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2841	PATRIC.2.9855.2.9855.con.0001.CDS.2973141.2974106.rev	PATRIC	CDS	2973141	2974106	966	-	PGF_12723297	321	Predicted molybdate-responsive regulator YygK in bacilli	[illegible]|alpha-1,2-mannosyltransferase activity;GO:0000009|alpha-1,2-mannosyltransferase activity;GO:0000009|mannosyltransferase activity;GO:0000009|alpha-1,3-mannosyltransferase activity;GO:0000009|alpha-1,3-galactosyltransferase activity;GO:0000009|UDP-glucose:glycoprotein glucosyltransferase activity;GO:0000009|glycolipid mannosyltransferase activity;GO:0000009|oligosaccharyl transferase activity;GO:0000009|dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase activity;GO:0000009|acetylglucosaminyltransferase activity;GO:0000009|acetylgalactosaminyltransferase activity;GO:0000009|galactosyltransferase activity;GO:0000009|fucosyltransferase activity;GO:0000009|O antigen polymerase activity;GO:0000009|lipopolysaccharide-1,6-galactosyltransferase activity;GO:0000009|cellulose synthase activity;GO:0000009|9-phenanthrol UDP-glucuronosyltransferase activity;GO:0000009|1-phenanthrol glycosyltransferase activity;GO:0000009|9-phenanthrol glycosyltransferase activity;GO:0000009|1,2-dihydroxy-phenanthrene glycosyltransferase activity;GO:0000009|phenanthrol glycosyltransferase activity;GO:0000009|beta-1,4-mannosyltransferase activity;GO:0000009|alpha-1,2-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man7GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|lipopolysaccharide-1,5-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|inositol phosphoceramide synthase activity;GO:0000009|glucosyltransferase activity;GO:0000009|alpha-(1->3)-fucosyltransferase activity;GO:0000009|alpha-(1->6)-fucosyltransferase activity;GO:0000009|indole-3-butyrate beta-glucosyltransferase activity;GO:0000009|salicylic acid glucosyltransferase (ester-forming) activity;GO:0000009|salicylic acid glucosyltransferase (glucoside-forming) activity;GO:0000009|benzoic acid glucosyltransferase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.259	PATRIC.2.9855.2.9855.con.0001.CDS.297399.298787.fwd	PATRIC	CDS	297399	298787	1389	+	PGF_00023812	462	N-acetylglucosaminyltransferase (EC 2.4.1.-)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2842	PATRIC.2.9855.2.9855.con.0001.CDS.2974168.2975130.rev	PATRIC	CDS	2974168	2975130	963	-	PGF_02282857	320	Spermidine/putrescine-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2843	PATRIC.2.9855.2.9855.con.0001.CDS.2975341.2976858.rev	PATRIC	CDS	2975341	2976858	1518	-	PGF_00025486	505	Ni2+-binding GTPase involved in regulation of expression and maturation of hydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2844	PATRIC.2.9855.2.9855.con.0001.CDS.2977183.2977389.rev	PATRIC	CDS	2977183	2977389	207	-	PGF_04289125	68	Molybdate-binding domain of ModE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2845	PATRIC.2.9855.2.9855.con.0001.CDS.2978023.2978826.fwd	PATRIC	CDS	2978023	2978826	804	+	PGF_05572422	267	Molybdenum ABC transporter, substrate-binding protein ModA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2846	PATRIC.2.9855.2.9855.con.0001.CDS.2978883.2979317.rev	PATRIC	CDS	2978883	2979317	435	-	PGF_00003238	144	FIG060329: MOSC domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2847	PATRIC.2.9855.2.9855.con.0001.CDS.2979314.2979793.rev	PATRIC	CDS	2979314	2979793	480	-	PGF_00419913	159	Cyclic pyranopterin monophosphate synthase (EC 4.6.1.17)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2848	PATRIC.2.9855.2.9855.con.0001.CDS.2979873.2980847.rev	PATRIC	CDS	2979873	2980847	975	-	PGF_10244701	324	GTP 3',8-cyclase (EC 4.1.99.22)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2849	PATRIC.2.9855.2.9855.con.0001.CDS.2981017.2981796.rev	PATRIC	CDS	2981017	2981796	780	-	PGF_09188652	259	Molybdopterin molybdenumtransferase (EC 2.10.1.1)	GO:0061599|molybdopterin molybdotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2850	PATRIC.2.9855.2.9855.con.0001.CDS.2981793.2982038.rev	PATRIC	CDS	2981793	2982038	246	-	PGF_09188652	81	Molybdopterin molybdenumtransferase (EC 2.10.1.1)	GO:0061599|molybdopterin molybdotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2851	PATRIC.2.9855.2.9855.con.0001.CDS.2982246.2982560.rev	PATRIC	CDS	2982246	2982560	315	-	PGF_00022473	104	Molybdenum cofactor cytidylyltransferase (EC 2.7.7.76) / DNA-binding transcriptional regulator ModE	GO:0061602|molybdenum cofactor cytidylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2852	PATRIC.2.9855.2.9855.con.0001.CDS.2982520.2983176.rev	PATRIC	CDS	2982520	2983176	657	-	PGF_00022473	218	Molybdenum cofactor cytidylyltransferase (EC 2.7.7.76) / DNA-binding transcriptional regulator ModE	GO:0061602|molybdenum cofactor cytidylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2853	PATRIC.2.9855.2.9855.con.0001.CDS.2983597.2984415.rev	PATRIC	CDS	2983597	2984415	819	-	PGF_10555148	272	Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4)	GO:0004854|xanthine dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2854	PATRIC.2.9855.2.9855.con.0001.CDS.2984409.2984876.rev	PATRIC	CDS	2984409	2984876	468	-	PGF_02314677	155	Xanthine dehydrogenase iron-sulfur subunit (EC 1.17.1.4)	GO:0004854|xanthine dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2855	PATRIC.2.9855.2.9855.con.0001.CDS.2984876.2986990.rev	PATRIC	CDS	2984876	2986990	2115	-	PGF_10370701	704	Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)	GO:0004854|xanthine dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2856	PATRIC.2.9855.2.9855.con.0001.CDS.2987121.2987732.rev	PATRIC	CDS	2987121	2987732	612	-	PGF_10338075	203	Molybdenum cofactor cytidylyltransferase (EC 2.7.7.76)	GO:0061602|molybdenum cofactor cytidylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2857	PATRIC.2.9855.2.9855.con.0001.CDS.2987797.2990352.rev	PATRIC	CDS	2987797	2990352	2556	-	PGF_01252304	851	Xanthine dehydrogenase iron-sulfur subunit (EC 1.17.1.4) / Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)	GO:0004854|xanthine dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2858	PATRIC.2.9855.2.9855.con.0001.CDS.2990777.2992123.rev	PATRIC	CDS	2990777	2992123	1347	-	PGF_03066353	448	Xanthine-uracil permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.35	PATRIC.2.9855.2.9855.con.0001.CDS.29908.30804.fwd	PATRIC	CDS	29908	30804	897	+	PGF_00812877	298	Inosose dehydratase (EC 4.2.1.44)	GO:0050114|myo-inosose-2 dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.260	PATRIC.2.9855.2.9855.con.0001.CDS.299129.301078.fwd	PATRIC	CDS	299129	301078	1950	+	PGF_06005188	649	DNA topoisomerase IV subunit B (EC 5.99.1.3)	GO:0003918|DNA topoisomerase type II (ATP-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2859	PATRIC.2.9855.2.9855.con.0001.CDS.2992179.2993246.rev	PATRIC	CDS	2992179	2993246	1068	-	PGF_00734221	355	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2860	PATRIC.2.9855.2.9855.con.0001.CDS.2993327.2993704.rev	PATRIC	CDS	2993327	2993704	378	-	PGF_02690675	125	RidA/YER057c/UK114 superfamily protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2861	PATRIC.2.9855.2.9855.con.0001.CDS.2993789.2995117.rev	PATRIC	CDS	2993789	2995117	1329	-	PGF_12948555	442	Previously annotated as SsnA protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2862	PATRIC.2.9855.2.9855.con.0001.CDS.2995212.2996414.rev	PATRIC	CDS	2995212	2996414	1203	-	PGF_00423101	400	Diaminopropionate ammonia-lyase (EC 4.3.1.15)	GO:0008838|diaminopropionate ammonia-lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2863	PATRIC.2.9855.2.9855.con.0001.CDS.2996461.2997072.rev	PATRIC	CDS	2996461	2997072	612	-	PGF_00057994	203	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2864	PATRIC.2.9855.2.9855.con.0001.CDS.2997460.2998884.rev	PATRIC	CDS	2997460	2998884	1425	-	PGF_00066964	474	Xanthine/uracil/thiamine/ascorbate permease family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2865	PATRIC.2.9855.2.9855.con.0001.CDS.2999031.3002048.rev	PATRIC	CDS	2999031	3002048	3018	-	PGF_04489370	1005	Uncharacterized [4Fe4S] protein YgfK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1	PATRIC.2.9855.2.9855.con.0001.CDS.3.155.fwd	PATRIC	CDS	3	155	153	+	PGF_00417840	50	Chorismate synthase (EC 4.2.3.5)	GO:0004107|chorismate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3	PATRIC.2.9855.2.9855.con.0001.CDS.300.731.fwd	PATRIC	CDS	300	731	432	+	PGF_00417840	143	Chorismate synthase (EC 4.2.3.5)	GO:0004107|chorismate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2866	PATRIC.2.9855.2.9855.con.0001.CDS.3002195.3003478.rev	PATRIC	CDS	3002195	3003478	1284	-	PGF_00010332	427	Guanine deaminase (EC 3.5.4.3)	GO:0008892|guanine deaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2867	PATRIC.2.9855.2.9855.con.0001.CDS.3004078.3004719.rev	PATRIC	CDS	3004078	3004719	642	-	PGF_01013156	213	YheO-like PAS domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2868	PATRIC.2.9855.2.9855.con.0001.CDS.3004843.3006219.rev	PATRIC	CDS	3004843	3006219	1377	-	PGF_05131265	458	D-phenylhydantoinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2869	PATRIC.2.9855.2.9855.con.0001.CDS.3007166.3008086.rev	PATRIC	CDS	3007166	3008086	921	-	PGF_10347501	306	Carbamate kinase-like protein YqeA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2870	PATRIC.2.9855.2.9855.con.0001.CDS.3008257.3009450.rev	PATRIC	CDS	3008257	3009450	1194	-	PGF_10531984	397	Aspartate/ornithine carbamoyltransferase family protein protein YgeW	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2871	PATRIC.2.9855.2.9855.con.0001.CDS.3009487.3010839.rev	PATRIC	CDS	3009487	3010839	1353	-	PGF_00040527	450	Putative deacetylase YgeY	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2872	PATRIC.2.9855.2.9855.con.0001.CDS.3011356.3012033.fwd	PATRIC	CDS	3011356	3012033	678	+	PGF_09402727	225	Molybdenum ABC transporter permease protein ModB	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2873	PATRIC.2.9855.2.9855.con.0001.CDS.3012033.3013082.fwd	PATRIC	CDS	3012033	3013082	1050	+	PGF_06842926	349	Molybdenum ABC transporter ATP-binding protein ModC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.261	PATRIC.2.9855.2.9855.con.0001.CDS.301213.304125.fwd	PATRIC	CDS	301213	304125	2913	+	PGF_00057270	970	DNA topoisomerase IV subunit A (EC 5.99.1.3)	GO:0003918|DNA topoisomerase type II (ATP-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2874	PATRIC.2.9855.2.9855.con.0001.CDS.3013289.3014233.rev	PATRIC	CDS	3013289	3014233	945	-	PGF_00037043	314	Probable endo-1,4-beta-xylanase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2879	PATRIC.2.9855.2.9855.con.0001.CDS.3016116.3016994.rev	PATRIC	CDS	3016116	3016994	879	-	PGF_00052943	292	Site-specific tyrosine recombinase XerD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2880	PATRIC.2.9855.2.9855.con.0001.CDS.3017077.3017709.rev	PATRIC	CDS	3017077	3017709	633	-	PGF_00054013	210	Stage II sporulation protein M (SpoIIM)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2881	PATRIC.2.9855.2.9855.con.0001.CDS.3017875.3018285.rev	PATRIC	CDS	3017875	3018285	411	-	PGF_10532194	136	Oxidoreductase, short-chain dehydrogenase/reductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2882	PATRIC.2.9855.2.9855.con.0001.CDS.3018408.3018665.rev	PATRIC	CDS	3018408	3018665	258	-	PGF_10532194	85	Oxidoreductase, short-chain dehydrogenase/reductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2883	PATRIC.2.9855.2.9855.con.0001.CDS.3018877.3019800.rev	PATRIC	CDS	3018877	3019800	924	-	PGF_07730014	307	2-dehydropantoate 2-reductase (EC 1.1.1.169)	GO:0008677|2-dehydropantoate 2-reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2884	PATRIC.2.9855.2.9855.con.0001.CDS.3019933.3020814.fwd	PATRIC	CDS	3019933	3020814	882	+	PGF_07987589	293	Transcriptional regulator, LysR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2886	PATRIC.2.9855.2.9855.con.0001.CDS.3021502.3021915.rev	PATRIC	CDS	3021502	3021915	414	-	PGF_00424236	137	4-hydroxybenzoyl-CoA thioesterase family active site	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2887	PATRIC.2.9855.2.9855.con.0001.CDS.3022947.3023273.fwd	PATRIC	CDS	3022947	3023273	327	+	PGF_03495000	108	Mobile element protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2892	PATRIC.2.9855.2.9855.con.0001.CDS.3028348.3028791.fwd	PATRIC	CDS	3028348	3028791	444	+	PGF_10459236	147	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2893	PATRIC.2.9855.2.9855.con.0001.CDS.3028873.3030042.fwd	PATRIC	CDS	3028873	3030042	1170	+	PGF_09996723	389	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2894	PATRIC.2.9855.2.9855.con.0001.CDS.3030227.3031627.rev	PATRIC	CDS	3030227	3031627	1401	-	PGF_07597988	466	Aldehyde dehydrogenase (EC 1.2.1.3)	GO:0004029|aldehyde dehydrogenase (NAD) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2896	PATRIC.2.9855.2.9855.con.0001.CDS.3034361.3034744.fwd	PATRIC	CDS	3034361	3034744	384	+	PGF_03495000	127	Mobile element protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2898	PATRIC.2.9855.2.9855.con.0001.CDS.3039406.3040509.rev	PATRIC	CDS	3039406	3040509	1104	-	PGF_02157877	367	Membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2900	PATRIC.2.9855.2.9855.con.0001.CDS.3042342.3042989.rev	PATRIC	CDS	3042342	3042989	648	-	PGF_01282231	215	AnfO protein, required for Mo- and V-independent nitrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2903	PATRIC.2.9855.2.9855.con.0001.CDS.3045181.3046137.rev	PATRIC	CDS	3045181	3046137	957	-	PGF_02983928	318	Hydroxypyruvate reductase (EC 1.1.1.81)	GO:0016618|hydroxypyruvate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2904	PATRIC.2.9855.2.9855.con.0001.CDS.3046418.3046852.fwd	PATRIC	CDS	3046418	3046852	435	+	PGF_10514242	144	CBS domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2905	PATRIC.2.9855.2.9855.con.0001.CDS.3046962.3048182.rev	PATRIC	CDS	3046962	3048182	1221	-	PGF_03226829	406	Beta-ureidopropionase (EC 3.5.1.6)	GO:0003837|beta-ureidopropionase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.262	PATRIC.2.9855.2.9855.con.0001.CDS.304717.305268.fwd	PATRIC	CDS	304717	305268	552	+	PGF_07489704	183	DJ-1/YajL/Pfpl superfamily, includes chaperone protein YajL (former ThiJ), parkinsonism-associated protein DJ-1, peptidases Pfpl, Hsp31	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2906	PATRIC.2.9855.2.9855.con.0001.CDS.3048215.3049714.rev	PATRIC	CDS	3048215	3049714	1500	-	PGF_00024414	499	NAD-dependent dihydropyrimidine dehydrogenase subunit PreA (EC 1.3.1.1)	GO:0004159|dihydrouracil dehydrogenase (NAD+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2907	PATRIC.2.9855.2.9855.con.0001.CDS.3049858.3051225.rev	PATRIC	CDS	3049858	3051225	1368	-	PGF_06686458	455	Dihydropyrimidinase (EC 3.5.2.2) @ D-hydantoinase (EC 3.5.2.2)	GO:0004157|dihydropyrimidinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2908	PATRIC.2.9855.2.9855.con.0001.CDS.3051466.3052527.rev	PATRIC	CDS	3051466	3052527	1062	-	PGF_00045904	353	Pyrimidine ABC transporter, substrate-binding component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2909	PATRIC.2.9855.2.9855.con.0001.CDS.3052683.3053450.rev	PATRIC	CDS	3052683	3053450	768	-	PGF_00004842	255	Pyrimidine ABC transporter, transmembrane component 2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2910	PATRIC.2.9855.2.9855.con.0001.CDS.3053463.3054239.rev	PATRIC	CDS	3053463	3054239	777	-	PGF_03788523	258	Pyrimidine ABC transporter, transmembrane component 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.263	PATRIC.2.9855.2.9855.con.0001.CDS.305407.307173.fwd	PATRIC	CDS	305407	307173	1767	+	PGF_07058357	588	Single-stranded-DNA-specific exonuclease RecJ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2911	PATRIC.2.9855.2.9855.con.0001.CDS.3054242.3055075.rev	PATRIC	CDS	3054242	3055075	834	-	PGF_03031372	277	Pyrimidine ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2912	PATRIC.2.9855.2.9855.con.0001.CDS.3055148.3056299.rev	PATRIC	CDS	3055148	3056299	1152	-	PGF_03572345	383	Alcohol dehydrogenase (EC 1.1.1.1)	GO:0004022|alcohol dehydrogenase (NAD) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2913	PATRIC.2.9855.2.9855.con.0001.CDS.3056313.3057638.rev	PATRIC	CDS	3056313	3057638	1326	-	PGF_05382760	441	Aminotransferase, class III	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2914	PATRIC.2.9855.2.9855.con.0001.CDS.3057826.3058980.rev	PATRIC	CDS	3057826	3058980	1155	-	PGF_01303627	384	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2916	PATRIC.2.9855.2.9855.con.0001.CDS.3059878.3061155.rev	PATRIC	CDS	3059878	3061155	1278	-	PGF_00006334	425	Fragment flavodoxin oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2917	PATRIC.2.9855.2.9855.con.0001.CDS.3061356.3062534.rev	PATRIC	CDS	3061356	3062534	1179	-	PGF_04133028	392	NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	GO:0000252|C-3 sterol dehydrogenase (C-4 sterol decarboxylase) activity;GO:0000252|aldo-keto reductase (NADP) activity;GO:0000252|isocitrate dehydrogenase activity;GO:0000252|mevaldate reductase activity;GO:0000252|gluconate dehydrogenase activity;GO:0000252|steroid dehydrogenase activity;GO:0000252|epoxide dehydrogenase activity;GO:0000252|5-exo-hydroxycamphor dehydrogenase activity;GO:0000252|2-hydroxytetrahydrofuran dehydrogenase activity;GO:0000252|acetoin dehydrogenase activity;GO:0000252|phenylcoumaran benzylic ether reductase activity;GO:0000252|D-xylose:NADP reductase activity;GO:0000252|L-arabinose:NADP reductase activity;GO:0000252|D-arabinitol dehydrogenase, D-ribulose forming (NADP+) activity;GO:0000252|steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000252|steroid dehydrogenase activity, acting on the CH-CH group of donors;GO:0000252|(R)-(-)-1,2,3,4-tetrahydronaphthol dehydrogenase activity;GO:0000252|3-hydroxymenthone dehydrogenase activity;GO:0000252|very long-chain-3-hydroxyacyl-CoA dehydrogenase activity;GO:0000252|dihydrotestosterone 17-beta-dehydrogenase activity;GO:0000252|(R)-2-hydroxyisocaproate dehydrogenase activity;GO:0000252|L-arabinose 1-dehydrogenase (NADP+) activity;GO:0000252|L-xylulose reductase (NAD+) activity;GO:0000252|3-ketoglucose-reductase activity;GO:0000252|(R)-2-hydroxyglutarate dehydrogenase activity;GO:0000252|D-arabinitol dehydrogenase, D-xylulose forming (NADP+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2920	PATRIC.2.9855.2.9855.con.0001.CDS.3064302.3065777.fwd	PATRIC	CDS	3064302	3065777	1476	+	PGF_04165443	491	Serine/threonine protein kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2922	PATRIC.2.9855.2.9855.con.0001.CDS.3067192.3069186.rev	PATRIC	CDS	3067192	3069186	1995	-	PGF_00909019	664	2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)	GO:0008670|2,4-dienoyl-CoA reductase (NADPH) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2923	PATRIC.2.9855.2.9855.con.0001.CDS.3069396.3069941.fwd	PATRIC	CDS	3069396	3069941	546	+	PGF_00025416	181	Negative regulator of phenolic acid metabolism PadR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2925	PATRIC.2.9855.2.9855.con.0001.CDS.3070777.3072414.rev	PATRIC	CDS	3070777	3072414	1638	-	PGF_00016061	545	L-aspartate-beta-decarboxylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.264	PATRIC.2.9855.2.9855.con.0001.CDS.307261.308340.fwd	PATRIC	CDS	307261	308340	1080	+	PGF_03295331	359	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)	GO:0050511|undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase activity;GO:0050511|UDP-N-acetyl-D-glucosamine:N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelyl-D-alanyl-D-alanine-diphosphoundecaprenol 4-beta-N-acetylglucosaminlytransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2926	PATRIC.2.9855.2.9855.con.0001.CDS.3073186.3074391.rev	PATRIC	CDS	3073186	3074391	1206	-	PGF_01613113	401	Uncharacterized MFS-type transporter YnfM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2927	PATRIC.2.9855.2.9855.con.0001.CDS.3074724.3075767.fwd	PATRIC	CDS	3074724	3075767	1044	+	PGF_00037006	347	Agmatine deiminase (EC 3.5.3.12)	GO:0047632|agmatine deiminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2928	PATRIC.2.9855.2.9855.con.0001.CDS.3075790.3076668.fwd	PATRIC	CDS	3075790	3076668	879	+	PGF_01481375	292	N-carbamoylputrescine amidase (EC 3.5.1.53)	GO:0050126|N-carbamoylputrescine amidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2929	PATRIC.2.9855.2.9855.con.0001.CDS.3077172.3078017.rev	PATRIC	CDS	3077172	3078017	846	-	PGF_02146256	281	Sialic acid utilization regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2930	PATRIC.2.9855.2.9855.con.0001.CDS.3078056.3079129.rev	PATRIC	CDS	3078056	3079129	1074	-	PGF_00028476	357	Outer surface protein of unknown function, cellobiose operon	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2931	PATRIC.2.9855.2.9855.con.0001.CDS.3079272.3080633.rev	PATRIC	CDS	3079272	3080633	1362	-	PGF_02648683	453	PTS system, N-acetylmuramic acid-specific IIB component (EC 2.7.1.192) / PTS system, N-acetylmuramic acid-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2932	PATRIC.2.9855.2.9855.con.0001.CDS.3080648.3081562.rev	PATRIC	CDS	3080648	3081562	915	-	PGF_00023835	304	N-acetylmuramic acid 6-phosphate etherase (EC 4.2.1.126)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2933	PATRIC.2.9855.2.9855.con.0001.CDS.3082255.3082932.rev	PATRIC	CDS	3082255	3082932	678	-	PGF_00402141	225	outer membrane protein CC2294	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2935	PATRIC.2.9855.2.9855.con.0001.CDS.3083942.3084892.fwd	PATRIC	CDS	3083942	3084892	951	+	PGF_01400330	316	Biotin synthase (EC 2.8.1.6)	GO:0004076|biotin synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.265	PATRIC.2.9855.2.9855.con.0001.CDS.308490.308921.fwd	PATRIC	CDS	308490	308921	432	+	PGF_08946513	143	Flavodoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2936	PATRIC.2.9855.2.9855.con.0001.CDS.3084940.3085488.fwd	PATRIC	CDS	3084940	3085488	549	+	PGF_00054343	182	Substrate-specific component BioY of biotin ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2942	PATRIC.2.9855.2.9855.con.0001.CDS.3089835.3091235.rev	PATRIC	CDS	3089835	3091235	1401	-	PGF_00804040	466	Uncharacterized membrane protein YhfA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.266	PATRIC.2.9855.2.9855.con.0001.CDS.309072.312581.fwd	PATRIC	CDS	309072	312581	3510	+	PGF_00046007	1169	Pyruvate-flavodoxin oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2944	PATRIC.2.9855.2.9855.con.0001.CDS.3091886.3092002.rev	PATRIC	CDS	3091886	3092002	117	-	PGF_01740148	38	CoA-disulfide reductase (EC 1.8.1.14) / Disulfide bond regulator	GO:0050451|CoA-disulfide reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2945	PATRIC.2.9855.2.9855.con.0001.CDS.3092193.3092348.rev	PATRIC	CDS	3092193	3092348	156	-	PGF_00067473	51	Zinc-ribbon domain Caur_1000.N	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2946	PATRIC.2.9855.2.9855.con.0001.CDS.3092492.3092989.rev	PATRIC	CDS	3092492	3092989	498	-	PGF_03072132	165	CarD-like transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2947	PATRIC.2.9855.2.9855.con.0001.CDS.3093495.3094361.fwd	PATRIC	CDS	3093495	3094361	867	+	PGF_10143857	288	Fructose-bisphosphate aldolase class II (EC 4.1.2.13)	GO:0004332|fructose-bisphosphate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2949	PATRIC.2.9855.2.9855.con.0001.CDS.3095046.3096395.fwd	PATRIC	CDS	3095046	3096395	1350	+	PGF_00030905	449	[FeFe] hydrogenase (EC 1.12.7.2)	GO:0008901|ferredoxin hydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2950	PATRIC.2.9855.2.9855.con.0001.CDS.3096533.3098566.rev	PATRIC	CDS	3096533	3098566	2034	-	PGF_06875694	677	Penicillin-binding protein 3	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2951	PATRIC.2.9855.2.9855.con.0001.CDS.3098744.3099121.rev	PATRIC	CDS	3098744	3099121	378	-	PGF_00016546	125	Lactoylglutathione lyase (EC 4.4.1.5)	GO:0004462|lactoylglutathione lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2952	PATRIC.2.9855.2.9855.con.0001.CDS.3099459.3100505.fwd	PATRIC	CDS	3099459	3100505	1047	+	PGF_03362160	348	Ca(2+)/H(+) antiporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2953	PATRIC.2.9855.2.9855.con.0001.CDS.3100583.3101503.rev	PATRIC	CDS	3100583	3101503	921	-	PGF_04846590	306	Magnesium and cobalt transport protein CorA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2954	PATRIC.2.9855.2.9855.con.0001.CDS.3101786.3102352.fwd	PATRIC	CDS	3101786	3102352	567	+	PGF_01416568	188	LemA family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2955	PATRIC.2.9855.2.9855.con.0001.CDS.3102349.3103143.fwd	PATRIC	CDS	3102349	3103143	795	+	PGF_05672678	264	Beta-propeller domains of methanol dehydrogenase type	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2957	PATRIC.2.9855.2.9855.con.0001.CDS.3103736.3104695.rev	PATRIC	CDS	3103736	3104695	960	-	PGF_07849456	319	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.36	PATRIC.2.9855.2.9855.con.0001.CDS.31059.32489.fwd	PATRIC	CDS	31059	32489	1431	+	PGF_00018906	476	Major myo-inositol transporter IolT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2959	PATRIC.2.9855.2.9855.con.0001.CDS.3106007.3107338.rev	PATRIC	CDS	3106007	3107338	1332	-	PGF_08398205	443	CCA tRNA nucleotidyltransferase (EC 2.7.7.72)	GO:0001680|tRNA 3'-terminal CCA addition;GO:0001680|CTP:tRNA cytidylyltransferase activity;GO:0001680|CTP:3'-cytidine-tRNA cytidylyltransferase activity;GO:0001680|ATP:3'-cytidine-cytidine-tRNA adenylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2960	PATRIC.2.9855.2.9855.con.0001.CDS.3107445.3108341.rev	PATRIC	CDS	3107445	3108341	897	-	PGF_09655255	298	Transcriptional regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2961	PATRIC.2.9855.2.9855.con.0001.CDS.3108556.3109266.rev	PATRIC	CDS	3108556	3109266	711	-	PGF_00048829	236	LSU rRNA pseudouridine(2605) synthase (EC 5.4.99.22)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2962	PATRIC.2.9855.2.9855.con.0001.CDS.3109460.3109720.rev	PATRIC	CDS	3109460	3109720	261	-	PGF_01282544	86	keratin associated protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2964	PATRIC.2.9855.2.9855.con.0001.CDS.3110939.3111835.rev	PATRIC	CDS	3110939	3111835	897	-	PGF_00884706	298	Efflux ABC transporter, ATP-binding protein	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2965	PATRIC.2.9855.2.9855.con.0001.CDS.3111819.3112217.rev	PATRIC	CDS	3111819	3112217	399	-	PGF_02983874	132	Transcriptional repressor YtrA, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2967	PATRIC.2.9855.2.9855.con.0001.CDS.3112940.3114436.rev	PATRIC	CDS	3112940	3114436	1497	-	PGF_00014290	498	Inner membrane transporter YjeM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2969	PATRIC.2.9855.2.9855.con.0001.CDS.3115633.3116910.rev	PATRIC	CDS	3115633	3116910	1278	-	PGF_00006334	425	Fragment flavodoxin oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2970	PATRIC.2.9855.2.9855.con.0001.CDS.3116907.3117896.rev	PATRIC	CDS	3116907	3117896	990	-	PGF_00424129	329	Electron transfer subunit protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2971	PATRIC.2.9855.2.9855.con.0001.CDS.3118097.3118951.rev	PATRIC	CDS	3118097	3118951	855	-	PGF_06594113	284	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	GO:0009002|serine-type D-Ala-D-Ala carboxypeptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2973	PATRIC.2.9855.2.9855.con.0001.CDS.3119659.3120129.fwd	PATRIC	CDS	3119659	3120129	471	+	PGF_00053909	156	Spore protein GerW (YtfJ), not involved in spore germination	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2974	PATRIC.2.9855.2.9855.con.0001.CDS.3120297.3120887.rev	PATRIC	CDS	3120297	3120887	591	-	PGF_06649360	196	Segregation and condensation protein B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2975	PATRIC.2.9855.2.9855.con.0001.CDS.3120880.3121476.rev	PATRIC	CDS	3120880	3121476	597	-	PGF_02517283	198	Segregation and condensation protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2976	PATRIC.2.9855.2.9855.con.0001.CDS.3121454.3121627.rev	PATRIC	CDS	3121454	3121627	174	-	PGF_02517283	57	Segregation and condensation protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2977	PATRIC.2.9855.2.9855.con.0001.CDS.3122045.3122161.rev	PATRIC	CDS	3122045	3122161	117	-	PGF_06594113	38	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	GO:0009002|serine-type D-Ala-D-Ala carboxypeptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2978	PATRIC.2.9855.2.9855.con.0001.CDS.3122214.3123236.rev	PATRIC	CDS	3122214	3123236	1023	-	PGF_06594113	340	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	GO:0009002|serine-type D-Ala-D-Ala carboxypeptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2979	PATRIC.2.9855.2.9855.con.0001.CDS.3123413.3125602.rev	PATRIC	CDS	3123413	3125602	2190	-	PGF_10013075	729	DNA topoisomerase III (EC 5.99.1.2)	GO:0003917|DNA topoisomerase type I activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2981	PATRIC.2.9855.2.9855.con.0001.CDS.3126783.3126938.fwd	PATRIC	CDS	3126783	3126938	156	+	PGF_00401760	51	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2983	PATRIC.2.9855.2.9855.con.0001.CDS.3127473.3127988.rev	PATRIC	CDS	3127473	3127988	516	-	PGF_01282230	171	Amidase from nicotinamidase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2984	PATRIC.2.9855.2.9855.con.0001.CDS.3128209.3129444.rev	PATRIC	CDS	3128209	3129444	1236	-	PGF_05622318	411	Serine hydroxymethyltransferase (EC 2.1.2.1)	GO:0004372|glycine hydroxymethyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2986	PATRIC.2.9855.2.9855.con.0001.CDS.3130615.3131064.fwd	PATRIC	CDS	3130615	3131064	450	+	PGF_00549405	149	Putative membrane-spanning protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2990	PATRIC.2.9855.2.9855.con.0001.CDS.3133235.3135583.rev	PATRIC	CDS	3133235	3135583	2349	-	PGF_00008457	782	Glutathione biosynthesis bifunctional protein gshF (EC 6.3.2.2)(EC 6.3.2.3)	GO:0004357|glutamate-cysteine ligase activity;GO:0004363|glutathione synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2991	PATRIC.2.9855.2.9855.con.0001.CDS.3135629.3135991.rev	PATRIC	CDS	3135629	3135991	363	-	PGF_06257310	120	Na+-driven multidrug efflux pump	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2992	PATRIC.2.9855.2.9855.con.0001.CDS.3135948.3136592.rev	PATRIC	CDS	3135948	3136592	645	-	PGF_06257310	214	Na+-driven multidrug efflux pump	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2993	PATRIC.2.9855.2.9855.con.0001.CDS.3136570.3136944.rev	PATRIC	CDS	3136570	3136944	375	-	PGF_06257310	124	Na+-driven multidrug efflux pump	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.268	PATRIC.2.9855.2.9855.con.0001.CDS.313684.314877.fwd	PATRIC	CDS	313684	314877	1194	+	PGF_04544396	397	Aspartate aminotransferase (EC 2.6.1.1)	GO:0004069|L-aspartate:2-oxoglutarate aminotransferase activity;GO:0004069|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2994	PATRIC.2.9855.2.9855.con.0001.CDS.3137041.3137364.rev	PATRIC	CDS	3137041	3137364	324	-	PGF_12748067	107	Transcriptional regulator, ArsR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2995	PATRIC.2.9855.2.9855.con.0001.CDS.3137841.3138707.rev	PATRIC	CDS	3137841	3138707	867	-	PGF_10532194	288	Oxidoreductase, short-chain dehydrogenase/reductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2996	PATRIC.2.9855.2.9855.con.0001.CDS.3138852.3139703.rev	PATRIC	CDS	3138852	3139703	852	-	PGF_00845945	283	DegV family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2997	PATRIC.2.9855.2.9855.con.0001.CDS.3139875.3140519.rev	PATRIC	CDS	3139875	3140519	645	-	PGF_10538468	214	Pentapeptide repeat family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2998	PATRIC.2.9855.2.9855.con.0001.CDS.3140688.3141308.rev	PATRIC	CDS	3140688	3141308	621	-	PGF_00473519	206	Superoxide dismutase [Mn] (EC 1.15.1.1)	GO:0004784|superoxide dismutase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2999	PATRIC.2.9855.2.9855.con.0001.CDS.3141442.3143448.rev	PATRIC	CDS	3141442	3143448	2007	-	PGF_00051221	668	Serine phosphatase RsbU, regulator of sigma subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3000	PATRIC.2.9855.2.9855.con.0001.CDS.3143668.3145404.rev	PATRIC	CDS	3143668	3145404	1737	-	PGF_00051161	578	Ser-type protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3001	PATRIC.2.9855.2.9855.con.0001.CDS.3145672.3149187.rev	PATRIC	CDS	3145672	3149187	3516	-	PGF_00046007	1171	Pyruvate-flavodoxin oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3002	PATRIC.2.9855.2.9855.con.0001.CDS.3149493.3149918.rev	PATRIC	CDS	3149493	3149918	426	-	PGF_00041788	141	Putative iron-sulfur cluster assembly scaffold protein for SUF system, SufE2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3003	PATRIC.2.9855.2.9855.con.0001.CDS.3149924.3151153.rev	PATRIC	CDS	3149924	3151153	1230	-	PGF_07583562	409	Cysteine desulfurase (EC 2.8.1.7) => SufS	GO:0031071|cysteine desulfurase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3004	PATRIC.2.9855.2.9855.con.0001.CDS.3151146.3152243.rev	PATRIC	CDS	3151146	3152243	1098	-	PGF_00015517	365	Iron-sulfur cluster assembly protein SufD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3005	PATRIC.2.9855.2.9855.con.0001.CDS.3152253.3153662.rev	PATRIC	CDS	3152253	3153662	1410	-	PGF_00015514	469	Iron-sulfur cluster assembly protein SufB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3006	PATRIC.2.9855.2.9855.con.0001.CDS.3153678.3154430.rev	PATRIC	CDS	3153678	3154430	753	-	PGF_00015510	250	Iron-sulfur cluster assembly ATPase protein SufC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3007	PATRIC.2.9855.2.9855.con.0001.CDS.3154676.3155068.fwd	PATRIC	CDS	3154676	3155068	393	+	PGF_03147273	130	Nitrite-sensitive transcriptional repressor NsrR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3008	PATRIC.2.9855.2.9855.con.0001.CDS.3155311.3155862.rev	PATRIC	CDS	3155311	3155862	552	-	PGF_04019463	183	Repair of Iron Centers di-iron protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3009	PATRIC.2.9855.2.9855.con.0001.CDS.3155980.3156618.rev	PATRIC	CDS	3155980	3156618	639	-	PGF_00082519	212	hypothetical co-occurring with RIC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3010	PATRIC.2.9855.2.9855.con.0001.CDS.3156959.3158881.rev	PATRIC	CDS	3156959	3158881	1923	-	PGF_00960048	640	PTS system, fructose-specific IIA component (EC 2.7.1.202) / PTS system, fructose-specific IIB component (EC 2.7.1.202) / PTS system, fructose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3011	PATRIC.2.9855.2.9855.con.0001.CDS.3159006.3159908.rev	PATRIC	CDS	3159006	3159908	903	-	PGF_04655384	300	1-phosphofructokinase (EC 2.7.1.56)	GO:0008662|1-phosphofructokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.271	PATRIC.2.9855.2.9855.con.0001.CDS.315934.316572.fwd	PATRIC	CDS	315934	316572	639	+	PGF_00885992	212	Phosphoserine phosphatase (EC 3.1.3.3)	GO:0004647|phosphoserine phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3012	PATRIC.2.9855.2.9855.con.0001.CDS.3159901.3160653.rev	PATRIC	CDS	3159901	3160653	753	-	PGF_03379955	250	Transcriptional repressor of the fructose operon, DeoR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3013	PATRIC.2.9855.2.9855.con.0001.CDS.3160782.3161639.rev	PATRIC	CDS	3160782	3161639	858	-	PGF_03846068	285	Pyridoxal kinase (EC 2.7.1.35)	GO:0008478|pyridoxal kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3014	PATRIC.2.9855.2.9855.con.0001.CDS.3161889.3162380.rev	PATRIC	CDS	3161889	3162380	492	-	PGF_08661804	163	PTS system, mannose-specific IIB component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3015	PATRIC.2.9855.2.9855.con.0001.CDS.3162882.3164369.rev	PATRIC	CDS	3162882	3164369	1488	-	PGF_09453574	495	Altronate dehydratase (EC 4.2.1.7)	GO:0008789|altronate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3016	PATRIC.2.9855.2.9855.con.0001.CDS.3164462.3165910.rev	PATRIC	CDS	3164462	3165910	1449	-	PGF_00049721	482	Altronate oxidoreductase (EC 1.1.1.58)	GO:0009026|tagaturonate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3017	PATRIC.2.9855.2.9855.con.0001.CDS.3166243.3167193.rev	PATRIC	CDS	3166243	3167193	951	-	PGF_05097244	316	2-dehydro-3-deoxygluconokinase (EC 2.7.1.45)	GO:0008673|2-dehydro-3-deoxygluconokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3018	PATRIC.2.9855.2.9855.con.0001.CDS.3167195.3167842.rev	PATRIC	CDS	3167195	3167842	648	-	PGF_00730641	215	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)	GO:0008700|4-hydroxy-2-oxoglutarate aldolase activity;GO:0008675|2-dehydro-3-deoxy-phosphogluconate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.272	PATRIC.2.9855.2.9855.con.0001.CDS.316839.317573.fwd	PATRIC	CDS	316839	317573	735	+	PGF_02757207	244	aminotransferase, class IV	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3019	PATRIC.2.9855.2.9855.con.0001.CDS.3168512.3169918.rev	PATRIC	CDS	3168512	3169918	1407	-	PGF_00008043	468	Glucuronide transporter UidB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3020	PATRIC.2.9855.2.9855.con.0001.CDS.3169972.3170394.rev	PATRIC	CDS	3169972	3170394	423	-	PGF_04001818	140	HIT family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3021	PATRIC.2.9855.2.9855.con.0001.CDS.3170474.3171922.rev	PATRIC	CDS	3170474	3171922	1449	-	PGF_00049721	482	Altronate oxidoreductase (EC 1.1.1.58)	GO:0009026|tagaturonate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3022	PATRIC.2.9855.2.9855.con.0001.CDS.3172010.3173410.rev	PATRIC	CDS	3172010	3173410	1401	-	PGF_00066263	466	Uronate isomerase (EC 5.3.1.12)	GO:0008880|glucuronate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3023	PATRIC.2.9855.2.9855.con.0001.CDS.3173605.3174603.rev	PATRIC	CDS	3173605	3174603	999	-	PGF_00011616	332	Hexuronate utilization operon transcriptional repressor ExuR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3024	PATRIC.2.9855.2.9855.con.0001.CDS.3174781.3176022.rev	PATRIC	CDS	3174781	3176022	1242	-	PGF_03093523	413	NADH-dependent reduced ferredoxin:NADP+ oxidoreductase subunit B related protein CAC0764	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3026	PATRIC.2.9855.2.9855.con.0001.CDS.3176804.3178585.rev	PATRIC	CDS	3176804	3178585	1782	-	PGF_00426057	593	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) / Homolog of homocysteine-binding domain	GO:0004489|methylenetetrahydrofolate reductase (NAD(P)H) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.273	PATRIC.2.9855.2.9855.con.0001.CDS.317691.319640.fwd	PATRIC	CDS	317691	319640	1950	+	PGF_00051221	649	Serine phosphatase RsbU, regulator of sigma subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3028	PATRIC.2.9855.2.9855.con.0001.CDS.3179922.3180587.rev	PATRIC	CDS	3179922	3180587	666	-	PGF_06241294	221	SigI-like RNA polymerase sigma factor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3029	PATRIC.2.9855.2.9855.con.0001.CDS.3181181.3181684.rev	PATRIC	CDS	3181181	3181684	504	-	PGF_03042545	167	Molecular chaperone, DnaJ family (contain C-term. Zn finger domain)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3030	PATRIC.2.9855.2.9855.con.0001.CDS.3181806.3183491.rev	PATRIC	CDS	3181806	3183491	1686	-	PGF_02030844	561	ATP-dependent DNA helicase RecQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3031	PATRIC.2.9855.2.9855.con.0001.CDS.3183564.3184256.rev	PATRIC	CDS	3183564	3184256	693	-	PGF_02030844	230	ATP-dependent DNA helicase RecQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3032	PATRIC.2.9855.2.9855.con.0001.CDS.3184340.3185209.rev	PATRIC	CDS	3184340	3185209	870	-	PGF_06629251	289	Methionine aminopeptidase (EC 3.4.11.18)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3033	PATRIC.2.9855.2.9855.con.0001.CDS.3185522.3186964.rev	PATRIC	CDS	3185522	3186964	1443	-	PGF_00017863	480	ATP-dependent RNA helicase YxiN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3034	PATRIC.2.9855.2.9855.con.0001.CDS.3187281.3188489.fwd	PATRIC	CDS	3187281	3188489	1209	+	PGF_02434074	402	ATP-dependent RNA helicase YfmL	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3036	PATRIC.2.9855.2.9855.con.0001.CDS.3189669.3190412.rev	PATRIC	CDS	3189669	3190412	744	-	PGF_07495635	247	Uncharacterized membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3037	PATRIC.2.9855.2.9855.con.0001.CDS.3190465.3191463.rev	PATRIC	CDS	3190465	3191463	999	-	PGF_03342342	332	Uncharacterized membrane protein, YraQ family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3038	PATRIC.2.9855.2.9855.con.0001.CDS.3191460.3192128.rev	PATRIC	CDS	3191460	3192128	669	-	PGF_01258559	222	Metal chaperone, involved in Zn homeostasis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3039	PATRIC.2.9855.2.9855.con.0001.CDS.3192171.3193133.rev	PATRIC	CDS	3192171	3193133	963	-	PGF_01258559	320	Metal chaperone, involved in Zn homeostasis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3040	PATRIC.2.9855.2.9855.con.0001.CDS.3193437.3194912.rev	PATRIC	CDS	3193437	3194912	1476	-	PGF_00055348	491	Surface protein pspA precursor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3041	PATRIC.2.9855.2.9855.con.0001.CDS.3195042.3195698.rev	PATRIC	CDS	3195042	3195698	657	-	PGF_00012820	218	Hydrolase, haloacid dehalogenase-like family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3043	PATRIC.2.9855.2.9855.con.0001.CDS.3196085.3197122.rev	PATRIC	CDS	3196085	3197122	1038	-	PGF_00422645	345	Deblocking aminopeptidase (EC 3.4.11.-)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.274	PATRIC.2.9855.2.9855.con.0001.CDS.319655.320104.fwd	PATRIC	CDS	319655	320104	450	+	PGF_07311230	149	Positive regulator of CheA protein activity (CheW)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3044	PATRIC.2.9855.2.9855.con.0001.CDS.3197352.3198416.rev	PATRIC	CDS	3197352	3198416	1065	-	PGF_03811905	354	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	GO:0004400|histidinol-phosphate transaminase activity;GO:0004400|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3045	PATRIC.2.9855.2.9855.con.0001.CDS.3198646.3199272.fwd	PATRIC	CDS	3198646	3199272	627	+	PGF_01281941	208	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3046	PATRIC.2.9855.2.9855.con.0001.CDS.3199658.3200281.fwd	PATRIC	CDS	3199658	3200281	624	+	PGF_01284170	207	Putative membrane-spanning protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3047	PATRIC.2.9855.2.9855.con.0001.CDS.3200375.3201844.rev	PATRIC	CDS	3200375	3201844	1470	-	PGF_01889881	489	ABC-type antimicrobial peptide transport system, permease component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.275	PATRIC.2.9855.2.9855.con.0001.CDS.320114.320602.fwd	PATRIC	CDS	320114	320602	489	+	PGF_01481272	162	Chemotaxis protein CheD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3048	PATRIC.2.9855.2.9855.con.0001.CDS.3201835.3202578.rev	PATRIC	CDS	3201835	3202578	744	-	PGF_10347576	247	ABC-type antimicrobial peptide transport system, ATPase component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3049	PATRIC.2.9855.2.9855.con.0001.CDS.3202586.3204061.rev	PATRIC	CDS	3202586	3204061	1476	-	PGF_01283050	491	ABC transporter, RND-adapter-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3052	PATRIC.2.9855.2.9855.con.0001.CDS.3205629.3206327.rev	PATRIC	CDS	3205629	3206327	699	-	PGF_10382251	232	Two-component response regulator yycF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.276	PATRIC.2.9855.2.9855.con.0001.CDS.320634.321740.fwd	PATRIC	CDS	320634	321740	1107	+	PGF_00417580	368	Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)	GO:0008984|protein-glutamate methylesterase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3053	PATRIC.2.9855.2.9855.con.0001.CDS.3206369.3207814.rev	PATRIC	CDS	3206369	3207814	1446	-	PGF_02620852	481	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3055	PATRIC.2.9855.2.9855.con.0001.CDS.3208358.3209203.rev	PATRIC	CDS	3208358	3209203	846	-	PGF_00048836	281	LSU rRNA pseudouridine(604) synthase (EC 5.4.99.21)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3057	PATRIC.2.9855.2.9855.con.0001.CDS.3210148.3211029.rev	PATRIC	CDS	3210148	3211029	882	-	PGF_10462808	293	33 kDa chaperonin HslO	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3059	PATRIC.2.9855.2.9855.con.0001.CDS.3211895.3212113.rev	PATRIC	CDS	3211895	3212113	219	-	PGF_01528271	72	Small acid-soluble spore protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3060	PATRIC.2.9855.2.9855.con.0001.CDS.3212556.3213548.fwd	PATRIC	CDS	3212556	3213548	993	+	PGF_00067188	330	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	GO:0004073|aspartate-semialdehyde dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3061	PATRIC.2.9855.2.9855.con.0001.CDS.3213578.3214456.fwd	PATRIC	CDS	3213578	3214456	879	+	PGF_00549380	292	4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7)	GO:0008840|4-hydroxy-tetrahydrodipicolinate synthase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3062	PATRIC.2.9855.2.9855.con.0001.CDS.3214466.3215221.fwd	PATRIC	CDS	3214466	3215221	756	+	PGF_01176589	251	4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)	GO:0008839|4-hydroxy-tetrahydrodipicolinate reductase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3063	PATRIC.2.9855.2.9855.con.0001.CDS.3215456.3215764.rev	PATRIC	CDS	3215456	3215764	309	-	PGF_12775196	102	Methylated-DNA--protein-cysteine methyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3064	PATRIC.2.9855.2.9855.con.0001.CDS.3216072.3216389.rev	PATRIC	CDS	3216072	3216389	318	-	PGF_01285309	105	UPF0345 protein LIC_12681	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3065	PATRIC.2.9855.2.9855.con.0001.CDS.3216474.3217619.rev	PATRIC	CDS	3216474	3217619	1146	-	PGF_00023719	381	N-acetyl-L,L-diaminopimelate aminotransferase (EC 2.6.1.-)	GO:0010326|methionine-oxo-acid transaminase activity;GO:0010326|6-aminohexanoate transaminase activity;GO:0010326|N2-acetyl-L-lysine aminotransferase activity;GO:0010326|acetyldiaminopimelate aminotransferase activity;GO:0010326|branched-chain amino acid:2-keto-4-methylthiobutyrate aminotransferase activity;GO:0010326|D-lysine transaminase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.277	PATRIC.2.9855.2.9855.con.0001.CDS.321749.322516.fwd	PATRIC	CDS	321749	322516	768	+	PGF_08449066	255	Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)	GO:0008983|protein-glutamate O-methyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3066	PATRIC.2.9855.2.9855.con.0001.CDS.3217775.3218485.fwd	PATRIC	CDS	3217775	3218485	711	+	PGF_00019563	236	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase (EC 2.3.1.89)	GO:0047200|tetrahydrodipicolinate N-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3067	PATRIC.2.9855.2.9855.con.0001.CDS.3218712.3219362.rev	PATRIC	CDS	3218712	3219362	651	-	PGF_12882669	216	Single-stranded DNA-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3068	PATRIC.2.9855.2.9855.con.0001.CDS.3219468.3220229.rev	PATRIC	CDS	3219468	3220229	762	-	PGF_00417626	253	Chitooligosaccharide deacetylase (EC 3.5.1.-)	GO:0008418|protein-N-terminal asparagine amidohydrolase activity;GO:0008418|UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity;GO:0008418|iprodione amidohydrolase activity;GO:0008418|[3,5-dichlorophenylurea]acetate amidohydrolase activity;GO:0008418|4'-(2-hydroxyisopropyl)phenylurea amidohydrolase activity;GO:0008418|didemethylisoproturon amidohydrolase activity;GO:0008418|N-isopropylacetanilide amidohydrolase activity;GO:0008418|N-cyclohexylformamide amidohydrolase activity;GO:0008418|isonicotinic acid hydrazide hydrolase activity;GO:0008418|cis-aconitamide amidase activity;GO:0008418|gamma-N-formylaminovinylacetate hydrolase activity;GO:0008418|N2-acetyl-L-lysine deacetylase activity;GO:0008418|O-succinylbenzoate synthase activity;GO:0008418|indoleacetamide hydrolase activity;GO:0008418|N-acetylcitrulline deacetylase activity;GO:0008418|N-acetylgalactosamine-6-phosphate deacetylase activity;GO:0008418|diacetylchitobiose deacetylase
Bacteria DY20 complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3070	PATRIC.2.9855.2.9855.con.0001.CDS.3221165.3222043.rev	PATRIC	CDS	3221165	3222043	879	-	PGF 00055305	292	Surface antigen	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3073	PATRIC.2.9855.2.9855.con.0001.CDS.3224738.3226051.rev	PATRIC	CDS	3224738	3226051	1314	-	PGF_04485073	437	Dihydrofolate synthase (EC 6.3.2.12) @ Folylpolyglutamate synthase (EC 6.3.2.17)	GO:0008841|dihydrofolate synthase activity;GO:0004326|tetrahydrofolylpolyglutamate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.278	PATRIC.2.9855.2.9855.con.0001.CDS.322530.324593.fwd	PATRIC	CDS	322530	324593	2064	+	PGF_08121553	687	Signal transduction histidine kinase CheA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3074	PATRIC.2.9855.2.9855.con.0001.CDS.3226268.3227119.rev	PATRIC	CDS	3226268	3227119	852	-	PGF_00040053	283	Alkaline induced inner membrane protein Alx	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3075	PATRIC.2.9855.2.9855.con.0001.CDS.3227393.3230038.rev	PATRIC	CDS	3227393	3230038	2646	-	PGF_05500127	881	Valyl-tRNA synthetase (EC 6.1.1.9)	GO:0004832|valine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3076	PATRIC.2.9855.2.9855.con.0001.CDS.3231034.3232224.rev	PATRIC	CDS	3231034	3232224	1191	-	PGF_02817932	396	Cystathionine beta-lyase (EC 4.4.1.8)	GO:0004121|cystathionine beta-lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3077	PATRIC.2.9855.2.9855.con.0001.CDS.3232265.3232645.rev	PATRIC	CDS	3232265	3232645	381	-	PGF_00013273	126	Uncharacterized protein YaeR with similarity to glyoxylase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3080	PATRIC.2.9855.2.9855.con.0001.CDS.3233479.3234327.rev	PATRIC	CDS	3233479	3234327	849	-	PGF_01874253	282	Phosphoesterase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3082	PATRIC.2.9855.2.9855.con.0001.CDS.3235738.3236736.rev	PATRIC	CDS	3235738	3236736	999	-	PGF_00037171	332	Probable low-affinity inorganic phosphate transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3083	PATRIC.2.9855.2.9855.con.0001.CDS.3236729.3237352.rev	PATRIC	CDS	3236729	3237352	624	-	PGF_02787494	207	Phosphate transport regulator (distant homolog of PhoU)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3084	PATRIC.2.9855.2.9855.con.0001.CDS.3238086.3240020.rev	PATRIC	CDS	3238086	3240020	1935	-	PGF_02316562	644	Periplasmic [FeFe] hydrogenase large subunit (EC 1.12.7.2)	GO:0008901|ferredoxin hydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3085	PATRIC.2.9855.2.9855.con.0001.CDS.3240524.3241189.rev	PATRIC	CDS	3240524	3241189	666	-	PGF_00791500	221	CbbY family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3086	PATRIC.2.9855.2.9855.con.0001.CDS.3241289.3241759.rev	PATRIC	CDS	3241289	3241759	471	-	PGF_00055054	156	Sulfite reductase, assimilatory-type (EC 1.8.-.-)	GO:0032441|pheophorbide a oxygenase activity;GO:0032441|sulfite reductase (coenzyme F420) activity;GO:0032441|aflatoxin reductase (coenzyme F420) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3087	PATRIC.2.9855.2.9855.con.0001.CDS.3241799.3241948.rev	PATRIC	CDS	3241799	3241948	150	-	PGF_00055054	49	Sulfite reductase, assimilatory-type (EC 1.8.-.-)	GO:0032441|pheophorbide a oxygenase activity;GO:0032441|sulfite reductase (coenzyme F420) activity;GO:0032441|aflatoxin reductase (coenzyme F420) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3088	PATRIC.2.9855.2.9855.con.0001.CDS.3242292.3243521.fwd	PATRIC	CDS	3242292	3243521	1230	+	PGF_09996723	409	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3089	PATRIC.2.9855.2.9855.con.0001.CDS.3243650.3245131.rev	PATRIC	CDS	3243650	3245131	1482	-	PGF_10656094	493	diguanylate cyclase (GGDEF domain) with PAS/PAC sensor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3090	PATRIC.2.9855.2.9855.con.0001.CDS.3245089.3245190.rev	PATRIC	CDS	3245089	3245190	102	-	PGF_10656094	33	diguanylate cyclase (GGDEF domain) with PAS/PAC sensor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3092	PATRIC.2.9855.2.9855.con.0001.CDS.3246094.3247170.rev	PATRIC	CDS	3246094	3247170	1077	-	PGF_10343884	358	Branched-chain amino acid ABC transporter, substrate-binding protein LivJ (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3093	PATRIC.2.9855.2.9855.con.0001.CDS.3247452.3248165.rev	PATRIC	CDS	3247452	3248165	714	-	PGF_00700305	237	Branched-chain amino acid ABC transporter, ATP-binding protein LivF (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.279	PATRIC.2.9855.2.9855.con.0001.CDS.324788.325390.fwd	PATRIC	CDS	324788	325390	603	+	PGF_00717613	200	Chemotaxis protein CheC -- inhibitor of MCP methylation	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3094	PATRIC.2.9855.2.9855.con.0001.CDS.3248158.3248928.rev	PATRIC	CDS	3248158	3248928	771	-	PGF_01726878	256	Branched-chain amino acid ABC transporter, ATP-binding protein LivG (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3095	PATRIC.2.9855.2.9855.con.0001.CDS.3248928.3249986.rev	PATRIC	CDS	3248928	3249986	1059	-	PGF_03231750	352	Branched-chain amino acid ABC transporter, permease protein LivM (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3096	PATRIC.2.9855.2.9855.con.0001.CDS.3249989.3250891.rev	PATRIC	CDS	3249989	3250891	903	-	PGF_06868199	300	Branched-chain amino acid ABC transporter, permease protein LivH (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3097	PATRIC.2.9855.2.9855.con.0001.CDS.3250906.3252072.rev	PATRIC	CDS	3250906	3252072	1167	-	PGF_10343884	388	Branched-chain amino acid ABC transporter, substrate-binding protein LivJ (TC 3.A.1.4.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.7	PATRIC.2.9855.2.9855.con.0001.CDS.3251.3760.fwd	PATRIC	CDS	3251	3760	510	+	PGF_02838109	169	Shikimate kinase I (EC 2.7.1.71)	GO:0004765|shikimate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3098	PATRIC.2.9855.2.9855.con.0001.CDS.3252659.3253399.rev	PATRIC	CDS	3252659	3253399	741	-	PGF_01277352	246	GTP cyclohydrolase III (methanopterin)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3099	PATRIC.2.9855.2.9855.con.0001.CDS.3253982.3255382.rev	PATRIC	CDS	3253982	3255382	1401	-	PGF_08913741	466	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	
Bacteria DY20 complete	2.9855	2.9855.con.0001	fig|2.9855.peg.280	PATRIC.2.9855.2.9855.con.0001.CDS.325410.325769.fwd	PATRIC	CDS	325410	325769	360	+	PGF 10238627	119	Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3100	PATRIC.2.9855.2.9855.con.0001.CDS.3255696.3256394.rev	PATRIC	CDS	3255696	3256394	699	-	PGF_02703381	232	Phosphoglycerate mutase (EC 5.4.2.11)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.281	PATRIC.2.9855.2.9855.con.0001.CDS.325900.326301.fwd	PATRIC	CDS	325900	326301	402	+	PGF_07311230	133	Positive regulator of CheA protein activity (CheW)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.282	PATRIC.2.9855.2.9855.con.0001.CDS.326324.327322.fwd	PATRIC	CDS	326324	327322	999	+	PGF_01900675	332	Flagellar motor switch protein FliM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3105	PATRIC.2.9855.2.9855.con.0001.CDS.3264407.3265183.rev	PATRIC	CDS	3264407	3265183	777	-	PGF_00062023	258	Tryptophan synthase alpha chain (EC 4.2.1.20)	GO:0004834|tryptophan synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3106	PATRIC.2.9855.2.9855.con.0001.CDS.3265183.3266358.rev	PATRIC	CDS	3265183	3266358	1176	-	PGF_00062027	391	Tryptophan synthase beta chain (EC 4.2.1.20)	GO:0004834|tryptophan synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3107	PATRIC.2.9855.2.9855.con.0001.CDS.3266380.3267069.rev	PATRIC	CDS	3266380	3267069	690	-	PGF_00033941	229	Phosphoribosylanthranilate isomerase (EC 5.3.1.24)	GO:0004640|phosphoribosylanthranilate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3108	PATRIC.2.9855.2.9855.con.0001.CDS.3267112.3267915.rev	PATRIC	CDS	3267112	3267915	804	-	PGF_00014051	267	Indole-3-glycerol phosphate synthase (EC 4.1.1.48)	GO:0004425|indole-3-glycerol-phosphate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3109	PATRIC.2.9855.2.9855.con.0001.CDS.3267940.3268959.rev	PATRIC	CDS	3267940	3268959	1020	-	PGF_00056662	339	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	GO:0004048|anthranilate phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3110	PATRIC.2.9855.2.9855.con.0001.CDS.3269039.3269626.rev	PATRIC	CDS	3269039	3269626	588	-	PGF_00743561	195	Anthranilate synthase, amidotransferase component (EC 4.1.3.27)	GO:0004049|anthranilate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3111	PATRIC.2.9855.2.9855.con.0001.CDS.3269623.3271014.rev	PATRIC	CDS	3269623	3271014	1392	-	PGF_00056814	463	Anthranilate synthase, aminase component (EC 4.1.3.27)	GO:0004049|anthranilate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3114	PATRIC.2.9855.2.9855.con.0001.CDS.3272005.3272484.rev	PATRIC	CDS	3272005	3272484	480	-	PGF_08230303	159	Predicted transcriptional regulator of cysteine synthase, Rrf2 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3115	PATRIC.2.9855.2.9855.con.0001.CDS.3272757.3273866.fwd	PATRIC	CDS	3272757	3273866	1110	+	PGF_00017439	369	ATP-dependent RNA helicase BA2475	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.283	PATRIC.2.9855.2.9855.con.0001.CDS.327306.328520.fwd	PATRIC	CDS	327306	328520	1215	+	PGF_09438139	404	Flagellar motor switch protein FliN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3116	PATRIC.2.9855.2.9855.con.0001.CDS.3274127.3274774.rev	PATRIC	CDS	3274127	3274774	648	-	PGF_03122406	215	Predicted N-ribosylNicotinamide CRP-like regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3117	PATRIC.2.9855.2.9855.con.0001.CDS.3274947.3275369.fwd	PATRIC	CDS	3274947	3275369	423	+	PGF_02996831	140	Possible membrane-spanning protein	
Bacteria DY20 complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3118	PATRIC.2.9855.2.9855.con.0001.CDS.3275391.3275852.fwd	PATRIC	CDS	3275391	3275852	462	+	PGF 12693594	153	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3119	PATRIC.2.9855.2.9855.con.0001.CDS.3275946.3276725.rev	PATRIC	CDS	3275946	3276725	780	-	PGF_00970735	259	Putative predicted metal-dependent hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3120	PATRIC.2.9855.2.9855.con.0001.CDS.3276811.3278847.rev	PATRIC	CDS	3276811	3278847	2037	-	PGF_00982352	678	Ribosome protection-type tetracycline resistance related proteins, group 2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.37	PATRIC.2.9855.2.9855.con.0001.CDS.32781.33557.fwd	PATRIC	CDS	32781	33557	777	+	PGF_12694858	258	3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55)	GO:0003859|3-hydroxybutyryl-CoA dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3121	PATRIC.2.9855.2.9855.con.0001.CDS.3279129.3279830.rev	PATRIC	CDS	3279129	3279830	702	-	PGF_04252606	233	Acyl-CoA:1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	GO:0003841|1-acylglycerol-3-phosphate O-acyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3122	PATRIC.2.9855.2.9855.con.0001.CDS.3280097.3281023.rev	PATRIC	CDS	3280097	3281023	927	-	PGF_07097873	308	Ribonuclease Z (EC 3.1.26.11)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3123	PATRIC.2.9855.2.9855.con.0001.CDS.3281093.3281875.rev	PATRIC	CDS	3281093	3281875	783	-	PGF_00064270	260	UPF0246 protein YaaA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3124	PATRIC.2.9855.2.9855.con.0001.CDS.3282009.3282164.rev	PATRIC	CDS	3282009	3282164	156	-	PGF_01281928	51	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3125	PATRIC.2.9855.2.9855.con.0001.CDS.3282471.3283067.rev	PATRIC	CDS	3282471	3283067	597	-	PGF 10547233	198	FMN-dependent NADH-azoreductase (EC 1.7.1.6)	GO:0050446|azobenzene reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3126	PATRIC.2.9855.2.9855.con.0001.CDS.3283431.3283919.fwd	PATRIC	CDS	3283431	3283919	489	+	PGF_00896280	162	RNA polymerase ECF-type sigma factor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3127	PATRIC.2.9855.2.9855.con.0001.CDS.3283912.3285300.fwd	PATRIC	CDS	3283912	3285300	1389	+	PGF_01283475	462	no hits	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3130	PATRIC.2.9855.2.9855.con.0001.CDS.3287590.3289104.rev	PATRIC	CDS	3287590	3289104	1515	-	PGF_02620852	504	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.284	PATRIC.2.9855.2.9855.con.0001.CDS.328910.329716.fwd	PATRIC	CDS	328910	329716	807	+	PGF_12690820	268	Phage replication initiation	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3131	PATRIC.2.9855.2.9855.con.0001.CDS.3289107.3289784.rev	PATRIC	CDS	3289107	3289784	678	-	PGF_07420062	225	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3132	PATRIC.2.9855.2.9855.con.0001.CDS.3289933.3290439.rev	PATRIC	CDS	3289933	3290439	507	-	PGF_06598531	168	Nudix hydrolase-like protein	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3133	PATRIC.2.9855.2.9855.con.0001.CDS.3290695.3291918.rev	PATRIC	CDS	3290695	3291918	1224	-	PGF_03278601	407	Macrolide glycosyltransferase (EC 2.4.1.-)	GO:0000030|alpha-1,6-mannosyltransferase activity;GO:0000835|alpha-1,2-mannosyltransferase activity;GO:0000009|mannosyltransferase activity;GO:0000009|alpha-1,3-mannosyltransferase activity;GO:0000009|alpha-1,3-galactosyltransferase activity;GO:0000009|UDP-glucose:glycoprotein glucosyltransferase activity;GO:0000009|glycolipid mannosyltransferase activity;GO:0000009|oligosaccharyl transferase activity;GO:0000009|dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase activity;GO:0000009|acetylglucosaminyltransferase activity;GO:0000009|acetylgalactosaminyltransferase activity;GO:0000009|galactosyltransferase activity;GO:0000009|fucosyltransferase activity;GO:0000009|O antigen polymerase activity;GO:0000009|lipopolysaccharide-1,6-galactosyltransferase activity;GO:0000009|cellulose synthase activity;GO:0000009|9-phenanthrol UDP-glucuronosyltransferase activity;GO:0000009|1-phenanthrol glycosyltransferase activity;GO:0000009|9-phenanthrol glycosyltransferase activity;GO:0000009|1,2-dihydroxy-phenanthrene glycosyltransferase activity;GO:0000009|phenanthrol glycosyltransferase activity;GO:0000009|beta-1,4-mannosyltransferase activity;GO:0000009|alpha-1,2-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man7GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|lipopolysaccharide-1,5-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|inositol phosphoceramide synthase activity;GO:0000009|glucosyltransferase activity;GO:0000009|alpha-(1->3)-fucosyltransferase activity;GO:0000009|alpha-(1->6)-fucosyltransferase activity;GO:0000009|indole-3-butyrate beta-glucosyltransferase activity;GO:0000009|salicylic acid glucosyltransferase (ester-forming) activity;GO:0000009|salicylic acid glucosyltransferase (glucoside-forming) activity;GO:0000009|benzoic acid glucosyltransferase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3134	PATRIC.2.9855.2.9855.con.0001.CDS.3292079.3292531.rev	PATRIC	CDS	3292079	3292531	453	-	PGF_01281272	150	Parvulin-like peptidyl-prolyl isomerase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3135	PATRIC.2.9855.2.9855.con.0001.CDS.3292713.3293603.rev	PATRIC	CDS	3292713	3293603	891	-	PGF_00064393	296	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	GO:0003983|UTP:glucose-1-phosphate uridylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3137	PATRIC.2.9855.2.9855.con.0001.CDS.3295646.3297865.rev	PATRIC	CDS	3295646	3297865	2220	-	PGF_00014617	739	Integral membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3138	PATRIC.2.9855.2.9855.con.0001.CDS.3297879.3298865.rev	PATRIC	CDS	3297879	3298865	987	-	PGF_04305571	328	Glycosyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.285	PATRIC.2.9855.2.9855.con.0001.CDS.329880.330170.fwd	PATRIC	CDS	329880	330170	291	+	PGF_01766973	96	Negative regulator of flagellin synthesis FlgM (anti-sigma28)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3139	PATRIC.2.9855.2.9855.con.0001.CDS.3299170.3300888.rev	PATRIC	CDS	3299170	3300888	1719	-	PGF_02910829	572	Membrane assosiated methyl-accepting chemotaxis protein with HAMP domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3140	PATRIC.2.9855.2.9855.con.0001.CDS.3301310.3302476.rev	PATRIC	CDS	3301310	3302476	1167	-	PGF_00552739	388	NADPH-dependent butanol dehydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.286	PATRIC.2.9855.2.9855.con.0001.CDS.330173.330583.fwd	PATRIC	CDS	330173	330583	411	+	PGF_01287018	136	Flagellar biosynthesis protein FlgN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3141	PATRIC.2.9855.2.9855.con.0001.CDS.3302952.3303899.rev	PATRIC	CDS	3302952	3303899	948	-	PGF_10318549	315	Phosphoesterase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3142	PATRIC.2.9855.2.9855.con.0001.CDS.3304287.3304898.rev	PATRIC	CDS	3304287	3304898	612	-	PGF_03741671	203	Phosphoglycerate mutase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3143	PATRIC.2.9855.2.9855.con.0001.CDS.3304924.3305934.rev	PATRIC	CDS	3304924	3305934	1011	-	PGF_01281278	336	Prophage ps3 protein 01	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3145	PATRIC.2.9855.2.9855.con.0001.CDS.3306558.3307199.rev	PATRIC	CDS	3306558	3307199	642	-	PGF_01256206	213	Collagen adhesion protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3146	PATRIC.2.9855.2.9855.con.0001.CDS.3307379.3308671.rev	PATRIC	CDS	3307379	3308671	1293	-	PGF_00066935	430	Uracil permease @ Uracil:proton symporter UraA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.287	PATRIC.2.9855.2.9855.con.0001.CDS.330749.332728.fwd	PATRIC	CDS	330749	332728	1980	+	PGF_00005454	659	Flagellar hook-associated protein FlgK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3148	PATRIC.2.9855.2.9855.con.0001.CDS.3309661.3310068.rev	PATRIC	CDS	3309661	3310068	408	-	PGF_00011385	135	Hemerythrin domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3151	PATRIC.2.9855.2.9855.con.0001.CDS.3310954.3311775.rev	PATRIC	CDS	3310954	3311775	822	-	PGF_00053997	273	Stage 0 sporulation two-component response regulator (Spo0A)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3152	PATRIC.2.9855.2.9855.con.0001.CDS.3312383.3313573.rev	PATRIC	CDS	3312383	3313573	1191	-	PGF_00054088	396	Stage IV sporulation protein B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3153	PATRIC.2.9855.2.9855.con.0001.CDS.3313802.3315490.rev	PATRIC	CDS	3313802	3315490	1689	-	PGF_00421796	562	DNA repair protein RecN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3154	PATRIC.2.9855.2.9855.con.0001.CDS.3315510.3315962.rev	PATRIC	CDS	3315510	3315962	453	-	PGF_02156631	150	Arginine pathway regulatory protein ArgR, repressor of arg regulon	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3155	PATRIC.2.9855.2.9855.con.0001.CDS.3315959.3316813.rev	PATRIC	CDS	3315959	3316813	855	-	PGF_08421732	284	NAD kinase (EC 2.7.1.23)	GO:0003951|NAD+ kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3156	PATRIC.2.9855.2.9855.con.0001.CDS.3316830.3317639.rev	PATRIC	CDS	3316830	3317639	810	-	PGF_00011463	269	RNA binding methyltransferase FtsJ like	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3157	PATRIC.2.9855.2.9855.con.0001.CDS.3317652.3319508.rev	PATRIC	CDS	3317652	3319508	1857	-	PGF_00426115	618	1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)	GO:0008661|1-deoxy-D-xylulose-5-phosphate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3158	PATRIC.2.9855.2.9855.con.0001.CDS.3319526.3320395.rev	PATRIC	CDS	3319526	3320395	870	-	PGF_06784545	289	(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10)	GO:0004337|geranyltranstransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3159	PATRIC.2.9855.2.9855.con.0001.CDS.3320382.3320606.rev	PATRIC	CDS	3320382	3320606	225	-	PGF_05076104	74	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	GO:0008855|exodeoxyribonuclease VII activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3160	PATRIC.2.9855.2.9855.con.0001.CDS.3320619.3321818.rev	PATRIC	CDS	3320619	3321818	1200	-	PGF_00425024	399	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	GO:0008855|exodeoxyribonuclease VII activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3161	PATRIC.2.9855.2.9855.con.0001.CDS.3321808.3322656.rev	PATRIC	CDS	3321808	3322656	849	-	PGF_00020984	282	Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) / Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)	GO:0004477|methenyltetrahydrofolate cyclohydrolase activity;GO:0004488|methylenetetrahydrofolate dehydrogenase (NADP+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3162	PATRIC.2.9855.2.9855.con.0001.CDS.3322784.3323185.rev	PATRIC	CDS	3322784	3323185	402	-	PGF_10450086	133	Transcription termination protein NusB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3163	PATRIC.2.9855.2.9855.con.0001.CDS.3323317.3323697.rev	PATRIC	CDS	3323317	3323697	381	-	PGF_01676425	126	Alkaline shock protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3164	PATRIC.2.9855.2.9855.con.0001.CDS.3323799.3324314.rev	PATRIC	CDS	3323799	3324314	516	-	PGF_00054069	171	Stage III sporulation protein AH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3165	PATRIC.2.9855.2.9855.con.0001.CDS.3324354.3324974.rev	PATRIC	CDS	3324354	3324974	621	-	PGF_10377869	206	Stage III sporulation protein AG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3166	PATRIC.2.9855.2.9855.con.0001.CDS.3324986.3325585.rev	PATRIC	CDS	3324986	3325585	600	-	PGF_00054060	199	Stage III sporulation protein AF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3167	PATRIC.2.9855.2.9855.con.0001.CDS.3325592.3325711.rev	PATRIC	CDS	3325592	3325711	120	-	PGF_00054051	39	Stage III sporulation protein AE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3168	PATRIC.2.9855.2.9855.con.0001.CDS.3326030.3326881.rev	PATRIC	CDS	3326030	3326881	852	-	PGF_00054051	283	Stage III sporulation protein AE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3169	PATRIC.2.9855.2.9855.con.0001.CDS.3326892.3327275.rev	PATRIC	CDS	3326892	3327275	384	-	PGF_00054049	127	Stage III sporulation protein AD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3170	PATRIC.2.9855.2.9855.con.0001.CDS.3327287.3327484.rev	PATRIC	CDS	3327287	3327484	198	-	PGF_00054046	65	Stage III sporulation protein AC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.288	PATRIC.2.9855.2.9855.con.0001.CDS.332740.333969.fwd	PATRIC	CDS	332740	333969	1230	+	PGF_09162729	409	Flagellar hook-associated protein FlgL	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3171	PATRIC.2.9855.2.9855.con.0001.CDS.3327549.3328067.rev	PATRIC	CDS	3327549	3328067	519	-	PGF_10482126	172	Stage III sporulation protein AB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3172	PATRIC.2.9855.2.9855.con.0001.CDS.3328055.3328975.rev	PATRIC	CDS	3328055	3328975	921	-	PGF_00054038	306	Stage III sporulation protein AA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3174	PATRIC.2.9855.2.9855.con.0001.CDS.3329586.3330143.rev	PATRIC	CDS	3329586	3330143	558	-	PGF_03799365	185	Translation elongation factor P	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3182	PATRIC.2.9855.2.9855.con.0001.CDS.3333649.3334764.rev	PATRIC	CDS	3333649	3334764	1116	-	PGF_00016749	371	Late competence protein ComGB, access of DNA to ComEA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3183	PATRIC.2.9855.2.9855.con.0001.CDS.3334757.3335209.rev	PATRIC	CDS	3334757	3335209	453	-	PGF_02473679	150	Type IV fimbrial assembly, ATPase PilB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3185	PATRIC.2.9855.2.9855.con.0001.CDS.3336007.3336612.rev	PATRIC	CDS	3336007	3336612	606	-	PGF_03810679	201	SOS-response repressor and protease LexA (EC 3.4.21.88)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3189	PATRIC.2.9855.2.9855.con.0001.CDS.3338042.3338986.rev	PATRIC	CDS	3338042	3338986	945	-	PGF_02626858	314	Metallo-beta-lactamase superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3190	PATRIC.2.9855.2.9855.con.0001.CDS.3339147.3339587.rev	PATRIC	CDS	3339147	3339587	441	-	PGF_03510298	146	Surface protein PspC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.289	PATRIC.2.9855.2.9855.con.0001.CDS.333987.334406.fwd	PATRIC	CDS	333987	334406	420	+	PGF_00005291	139	Flagellar assembly factor FliW	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3197	PATRIC.2.9855.2.9855.con.0001.CDS.3342132.3343013.rev	PATRIC	CDS	3342132	3343013	882	-		293	Chromosome (plasmid) partitioning protein ParA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.290	PATRIC.2.9855.2.9855.con.0001.CDS.334418.334636.fwd	PATRIC	CDS	334418	334636	219	+	PGF_02174988	72	Carbon storage regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3200	PATRIC.2.9855.2.9855.con.0001.CDS.3345076.3345861.rev	PATRIC	CDS	3345076	3345861	786	-	PGF_05179218	261	Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (EC 3.2.1.17)	GO:0003796|lysozyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.291	PATRIC.2.9855.2.9855.con.0001.CDS.334678.335058.fwd	PATRIC	CDS	334678	335058	381	+	PGF_10343437	126	Flagellar protein FlaG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3207	PATRIC.2.9855.2.9855.con.0001.CDS.3348519.3349139.rev	PATRIC	CDS	3348519	3349139	621	-	PGF_00032950	206	Phage-like element PBSX protein xkdU	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3208	PATRIC.2.9855.2.9855.con.0001.CDS.3349141.3351420.rev	PATRIC	CDS	3349141	3351420	2280	-	PGF_00044323	759	Putative tail fiber protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3209	PATRIC.2.9855.2.9855.con.0001.CDS.3351423.3352484.rev	PATRIC	CDS	3351423	3352484	1062	-	PGF_01011503	353	Phage-like element PBSX protein xkdT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.293	PATRIC.2.9855.2.9855.con.0001.CDS.335392.335766.fwd	PATRIC	CDS	335392	335766	375	+	PGF_03774796	124	Flagellar biosynthesis protein FliS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.294	PATRIC.2.9855.2.9855.con.0001.CDS.335904.338300.fwd	PATRIC	CDS	335904	338300	2397	+	PGF_03233642	798	Flagellar cap protein FliD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.38	PATRIC.2.9855.2.9855.con.0001.CDS.33608.35161.fwd	PATRIC	CDS	33608	35161	1554	+	PGF_07834560	517	Coenzyme A transferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3224	PATRIC.2.9855.2.9855.con.0001.CDS.3361759.3362709.rev	PATRIC	CDS	3361759	3362709	951	-	PGF_00400892	316	main capsid protein Gp34	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3244	PATRIC.2.9855.2.9855.con.0001.CDS.3378090.3380723.rev	PATRIC	CDS	3378090	3380723	2634	-	PGF_00421679	877	DNA primase DnaG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3249	PATRIC.2.9855.2.9855.con.0001.CDS.3382012.3382641.rev	PATRIC	CDS	3382012	3382641	630	-	PGF_00032596	209	Phage protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3252	PATRIC.2.9855.2.9855.con.0001.CDS.3383670.3384443.rev	PATRIC	CDS	3383670	3384443	774	-	PGF_00037703	257	Prophage Lp1 protein 19	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3261	PATRIC.2.9855.2.9855.con.0001.CDS.3387150.3387875.rev	PATRIC	CDS	3387150	3387875	726	-		241	Phage antirepressor protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.296	PATRIC.2.9855.2.9855.con.0001.CDS.338935.340563.fwd	PATRIC	CDS	338935	340563	1629	+	PGF_00005653	542	Flagellin protein FlaA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3271	PATRIC.2.9855.2.9855.con.0001.CDS.3393539.3393757.rev	PATRIC	CDS	3393539	3393757	219	-	PGF_04857106	72	Transcriptional regulator, Xre family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3273	PATRIC.2.9855.2.9855.con.0001.CDS.3394539.3395489.rev	PATRIC	CDS	3394539	3395489	951	-	PGF_02626858	316	Metallo-beta-lactamase superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3274	PATRIC.2.9855.2.9855.con.0001.CDS.3395651.3396100.rev	PATRIC	CDS	3395651	3396100	450	-	PGF_03510298	149	Surface protein PspC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3278	PATRIC.2.9855.2.9855.con.0001.CDS.3398087.3398872.rev	PATRIC	CDS	3398087	3398872	786	-	PGF_05179218	261	Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (EC 3.2.1.17)	GO:0003796|lysozyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3281	PATRIC.2.9855.2.9855.con.0001.CDS.3399759.3400940.rev	PATRIC	CDS	3399759	3400940	1182	-	PGF_00038056	393	Protein containing cell adhesion domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3286	PATRIC.2.9855.2.9855.con.0001.CDS.3403788.3404918.rev	PATRIC	CDS	3403788	3404918	1131	-	PGF_01011503	376	Phage-like element PBSX protein xkdT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3287	PATRIC.2.9855.2.9855.con.0001.CDS.3404923.3405363.rev	PATRIC	CDS	3404923	3405363	441	-	PGF_00032947	146	Phage-like element PBSX protein xkdS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3289	PATRIC.2.9855.2.9855.con.0001.CDS.3405696.3406712.rev	PATRIC	CDS	3405696	3406712	1017	-	PGF_00032941	338	Phage-like element PBSX protein xkdQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3290	PATRIC.2.9855.2.9855.con.0001.CDS.3406717.3407403.rev	PATRIC	CDS	3406717	3407403	687	-	PGF_00032938	228	Phage-like element PBSX protein xkdP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.297	PATRIC.2.9855.2.9855.con.0001.CDS.340688.342751.fwd	PATRIC	CDS	340688	342751	2064	+	PGF_00009518	687	Glycosyl transferase, group 2 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3292	PATRIC.2.9855.2.9855.con.0001.CDS.3408050.3411697.rev	PATRIC	CDS	3408050	3411697	3648	-	PGF_05015217	1215	Phage tail length tape-measure protein T	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3295	PATRIC.2.9855.2.9855.con.0001.CDS.3412373.3412789.rev	PATRIC	CDS	3412373	3412789	417	-	PGF_00032927	138	Phage-like element PBSX protein xkdM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3296	PATRIC.2.9855.2.9855.con.0001.CDS.3412809.3414251.rev	PATRIC	CDS	3412809	3414251	1443	-	PGF_00032924	480	Phage-like element PBSX protein xkdK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3307	PATRIC.2.9855.2.9855.con.0001.CDS.3422038.3423450.rev	PATRIC	CDS	3422038	3423450	1413	-	PGF_00413418	470	terminase B protein, putative	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3308	PATRIC.2.9855.2.9855.con.0001.CDS.3423443.3424252.rev	PATRIC	CDS	3423443	3424252	810	-	PGF_07220970	269	Phage terminase, small subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3312	PATRIC.2.9855.2.9855.con.0001.CDS.3426004.3427236.rev	PATRIC	CDS	3426004	3427236	1233	-	PGF_07888543	410	DNA modification methylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.298	PATRIC.2.9855.2.9855.con.0001.CDS.342768.346235.fwd	PATRIC	CDS	342768	346235	3468	+	PGF_00009518	1155	Glycosyl transferase, group 2 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3323	PATRIC.2.9855.2.9855.con.0001.CDS.3433836.3434543.rev	PATRIC	CDS	3433836	3434543	708	-	PGF_00020531	235	Metallo-beta-lactamase superfamily domain protein in prophage	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3324	PATRIC.2.9855.2.9855.con.0001.CDS.3434543.3435463.rev	PATRIC	CDS	3434543	3435463	921	-	PGF_01956796	306	Recombinational DNA repair protein RecT (prophage associated)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3326	PATRIC.2.9855.2.9855.con.0001.CDS.3435934.3437925.rev	PATRIC	CDS	3435934	3437925	1992	-	PGF_00022045	663	ATPase involved in DNA repair, phage associated	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3333	PATRIC.2.9855.2.9855.con.0001.CDS.3439956.3440327.fwd	PATRIC	CDS	3439956	3440327	372	+	PGF_01304739	123	HTH-type transcriptional regulator AnsR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3337	PATRIC.2.9855.2.9855.con.0001.CDS.3443998.3445155.rev	PATRIC	CDS	3443998	3445155	1158	-		385	Phage protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3350	PATRIC.2.9855.2.9855.con.0001.CDS.3457295.3459016.fwd	PATRIC	CDS	3457295	3459016	1722	+	PGF_01324157	573	Cassette chromosome recombinase B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3355	PATRIC.2.9855.2.9855.con.0001.CDS.3461906.3462733.rev	PATRIC	CDS	3461906	3462733	828	-	PGF_00853991	275	Diaminopimelate epimerase (EC 5.1.1.7)	GO:0008837|diaminopimelate epimerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3356	PATRIC.2.9855.2.9855.con.0001.CDS.3463163.3464896.fwd	PATRIC	CDS	3463163	3464896	1734	+	PGF_09945387	577	Fibronectin/fibrinogen-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3357	PATRIC.2.9855.2.9855.con.0001.CDS.3464969.3465814.rev	PATRIC	CDS	3464969	3465814	846	-	PGF_00458499	281	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3358	PATRIC.2.9855.2.9855.con.0001.CDS.3466171.3467331.rev	PATRIC	CDS	3466171	3467331	1161	-	PGF_00415407	386	23S rRNA (guanine(2445)-N(2))-methyltransferase (EC 2.1.1.173)	GO:0052915|23S rRNA (guanine(2445)-N(2))-methyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3359	PATRIC.2.9855.2.9855.con.0001.CDS.3467355.3467891.rev	PATRIC	CDS	3467355	3467891	537	-	PGF_00066124	178	Pyrimidine operon regulatory protein PyrR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3360	PATRIC.2.9855.2.9855.con.0001.CDS.3467909.3468826.rev	PATRIC	CDS	3467909	3468826	918	-	PGF_10569727	305	LSU rRNA pseudouridine(1911/1915/1917) synthase (EC 5.4.99.23)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3361	PATRIC.2.9855.2.9855.con.0001.CDS.3469121.3469894.fwd	PATRIC	CDS	3469121	3469894	774	+	PGF_04321257	257	Flagellar motor rotation protein MotA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3362	PATRIC.2.9855.2.9855.con.0001.CDS.3469907.3470662.fwd	PATRIC	CDS	3469907	3470662	756	+	PGF_01899924	251	Flagellar motor rotation protein MotB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3363	PATRIC.2.9855.2.9855.con.0001.CDS.3470811.3471443.rev	PATRIC	CDS	3470811	3471443	633	-	PGF_09044927	210	Cell division initiation protein DivIVA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3364	PATRIC.2.9855.2.9855.con.0001.CDS.3471457.3472221.rev	PATRIC	CDS	3471457	3472221	765	-	PGF_00425720	254	Putative RNA-binding protein YlmH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3365	PATRIC.2.9855.2.9855.con.0001.CDS.3472225.3472479.rev	PATRIC	CDS	3472225	3472479	255	-	PGF_03081665	84	Cell division integral membrane protein, YggT and half-length relatives	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3366	PATRIC.2.9855.2.9855.con.0001.CDS.3472492.3472944.rev	PATRIC	CDS	3472492	3472944	453	-	PGF_03021263	150	SepF, FtsZ-interacting protein related to cell division	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3367	PATRIC.2.9855.2.9855.con.0001.CDS.3472937.3473617.rev	PATRIC	CDS	3472937	3473617	681	-	PGF_04498026	226	Pyridoxal phosphate-containing protein YggS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3368	PATRIC.2.9855.2.9855.con.0001.CDS.3473710.3474444.rev	PATRIC	CDS	3473710	3474444	735	-	PGF_07858968	244	Uncharacterized protein YlxW	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3369	PATRIC.2.9855.2.9855.con.0001.CDS.3474457.3474849.rev	PATRIC	CDS	3474457	3474849	393	-	PGF_05608844	130	Small basic protein Sbp	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3370	PATRIC.2.9855.2.9855.con.0001.CDS.3474862.3475590.rev	PATRIC	CDS	3474862	3475590	729	-	PGF_07858968	242	Uncharacterized protein YlxW	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3371	PATRIC.2.9855.2.9855.con.0001.CDS.3475598.3476290.rev	PATRIC	CDS	3475598	3476290	693	-	PGF_01306034	230	Cell division protein FtsQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3372	PATRIC.2.9855.2.9855.con.0001.CDS.3476550.3477686.rev	PATRIC	CDS	3476550	3477686	1137	-	PGF_00417069	378	Peptidoglycan glycosyltransferase FtsW (EC 2.4.1.129) @ Stage V sporulation protein E	GO:0008955|peptidoglycan glycosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3373	PATRIC.2.9855.2.9855.con.0001.CDS.3477716.3478696.rev	PATRIC	CDS	3477716	3478696	981	-	PGF_00033359	326	Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)	GO:0008963|phospho-N-acetylmuramoyl-pentapeptide-transferase activity;GO:0008963|UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelyl-D-alanyl-D-alanine:undecaprenyl-phosphate transferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3374	PATRIC.2.9855.2.9855.con.0001.CDS.3478800.3480152.rev	PATRIC	CDS	3478800	3480152	1353	-	PGF_04521913	450	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10)	GO:0047480|UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3375	PATRIC.2.9855.2.9855.con.0001.CDS.3480249.3481709.rev	PATRIC	CDS	3480249	3481709	1461	-	PGF_07096769	486	UDP-N-acetylmuramoyl-dipeptide--2,6-diaminopimelate ligase (EC 6.3.2.13)	GO:0008765|UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3376	PATRIC.2.9855.2.9855.con.0001.CDS.3482008.3484272.rev	PATRIC	CDS	3482008	3484272	2265	-	PGF_00730148	754	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) @ Sporulation peptidoglycan synthetase SpoVD	GO:0008955|peptidoglycan glycosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.301	PATRIC.2.9855.2.9855.con.0001.CDS.348228.349316.fwd	PATRIC	CDS	348228	349316	1089	+		362	Deblocking aminopeptidase (EC 3.4.11.-)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3377	PATRIC.2.9855.2.9855.con.0001.CDS.3484505.3486772.rev	PATRIC	CDS	3484505	3486772	2268	-	PGF_00730148	755	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) @ Sporulation peptidoglycan synthetase SpoVD	GO:0008955|peptidoglycan glycosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3378	PATRIC.2.9855.2.9855.con.0001.CDS.3486884.3487402.rev	PATRIC	CDS	3486884	3487402	519	-	PGF_03016292	172	Cell division protein FtsL	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3379	PATRIC.2.9855.2.9855.con.0001.CDS.3487432.3488364.rev	PATRIC	CDS	3487432	3488364	933	-	PGF_02390924	310	16S rRNA (cytosine(1402)-N(4))-methyltransferase (EC 2.1.1.199)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3380	PATRIC.2.9855.2.9855.con.0001.CDS.3488377.3488805.rev	PATRIC	CDS	3488377	3488805	429	-	PGF_01420802	142	Transcriptional regulator MraZ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3382	PATRIC.2.9855.2.9855.con.0001.CDS.3489023.3491401.rev	PATRIC	CDS	3489023	3491401	2379	-	PGF_00033095	792	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	GO:0004826|phenylalanine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3383	PATRIC.2.9855.2.9855.con.0001.CDS.3491778.3492797.rev	PATRIC	CDS	3491778	3492797	1020	-	PGF_02019462	339	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	GO:0004826|phenylalanine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3384	PATRIC.2.9855.2.9855.con.0001.CDS.3493498.3494280.rev	PATRIC	CDS	3493498	3494280	783	-	PGF_07411046	260	Uncharacterized RNA methyltransferase YsgA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3385	PATRIC.2.9855.2.9855.con.0001.CDS.3494381.3494740.rev	PATRIC	CDS	3494381	3494740	360	-	PGF_00016358	119	LSU ribosomal protein L20p	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3386	PATRIC.2.9855.2.9855.con.0001.CDS.3494769.3494966.rev	PATRIC	CDS	3494769	3494966	198	-	PGF_03818138	65	LSU ribosomal protein L35p	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3387	PATRIC.2.9855.2.9855.con.0001.CDS.3494987.3495544.rev	PATRIC	CDS	3494987	3495544	558	-	PGF_00060478	185	Translation initiation factor 3	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3391	PATRIC.2.9855.2.9855.con.0001.CDS.3498097.3498648.rev	PATRIC	CDS	3498097	3498648	552	-	PGF_10519603	183	Acetyltransferase, GNAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3392	PATRIC.2.9855.2.9855.con.0001.CDS.3499114.3500670.fwd	PATRIC	CDS	3499114	3500670	1557	+	PGF_03244749	518	Bis-ABC ATPase SPy1206	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3393	PATRIC.2.9855.2.9855.con.0001.CDS.3500994.3501413.fwd	PATRIC	CDS	3500994	3501413	420	+	PGF_05736193	139	Uncharacterized protein DUF2992, B. subtilis YjdF ortholog	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3394	PATRIC.2.9855.2.9855.con.0001.CDS.3501744.3502964.fwd	PATRIC	CDS	3501744	3502964	1221	+	PGF_01557745	406	Threonine dehydratase, catabolic (EC 4.3.1.19) @ L-serine dehydratase, (PLP)-dependent (EC 4.3.1.17)	GO:0004794|L-threonine ammonia-lyase activity;GO:0003941|L-serine ammonia-lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3396	PATRIC.2.9855.2.9855.con.0001.CDS.3503740.3504405.rev	PATRIC	CDS	3503740	3504405	666	-	PGF_00791500	221	CbbY family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3397	PATRIC.2.9855.2.9855.con.0001.CDS.3504530.3505150.rev	PATRIC	CDS	3504530	3505150	621	-	PGF_01776925	206	Uridine kinase (EC 2.7.1.48)	GO:0004849|uridine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3399	PATRIC.2.9855.2.9855.con.0001.CDS.3506504.3506983.fwd	PATRIC	CDS	3506504	3506983	480	+	PGF_03072132	159	CarD-like transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.304	PATRIC.2.9855.2.9855.con.0001.CDS.350691.351818.fwd	PATRIC	CDS	350691	351818	1128	+	PGF_00070457	375	dTDP-4-amino-4,6-dideoxygalactose transaminase (EC 2.6.1.59)	GO:0019180|dTDP-4-amino-4,6-dideoxygalactose transaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3400	PATRIC.2.9855.2.9855.con.0001.CDS.3507216.3507368.fwd	PATRIC	CDS	3507216	3507368	153	+	PGF_00401763	50	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3401	PATRIC.2.9855.2.9855.con.0001.CDS.3507465.3507620.rev	PATRIC	CDS	3507465	3507620	156	-	PGF_00067473	51	Zinc-ribbon domain Caur_1000.N	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3402	PATRIC.2.9855.2.9855.con.0001.CDS.3507786.3509402.rev	PATRIC	CDS	3507786	3509402	1617	-	PGF_00417168	538	Cell shape-determining protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3403	PATRIC.2.9855.2.9855.con.0001.CDS.3510001.3511842.rev	PATRIC	CDS	3510001	3511842	1842	-	PGF_02620852	613	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3405	PATRIC.2.9855.2.9855.con.0001.CDS.3513536.3514831.rev	PATRIC	CDS	3513536	3514831	1296	-	PGF_00492707	431	Homoserine dehydrogenase (EC 1.1.1.3)	GO:0004412|homoserine dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3406	PATRIC.2.9855.2.9855.con.0001.CDS.3515037.3515642.rev	PATRIC	CDS	3515037	3515642	606	-	PGF_00599208	201	Integral membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3407	PATRIC.2.9855.2.9855.con.0001.CDS.3515701.3516399.rev	PATRIC	CDS	3515701	3516399	699	-	PGF_01024695	232	Uncharacterized DUF554 membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3408	PATRIC.2.9855.2.9855.con.0001.CDS.3516719.3517315.fwd	PATRIC	CDS	3516719	3517315	597	+	PGF_00049893	198	SSU ribosomal protein S4p (S9e) @ SSU ribosomal protein S4p (S9e), zinc-independent	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3410	PATRIC.2.9855.2.9855.con.0001.CDS.3518228.3520027.rev	PATRIC	CDS	3518228	3520027	1800	-	PGF_06589185	599	Aspartyl-tRNA synthetase (EC 6.1.1.12)	GO:0004815|aspartate-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.305	PATRIC.2.9855.2.9855.con.0001.CDS.351895.352950.fwd	PATRIC	CDS	351895	352950	1056	+	PGF_03056683	351	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	GO:0008460|dTDP-glucose 4,6-dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3411	PATRIC.2.9855.2.9855.con.0001.CDS.3520059.3521312.rev	PATRIC	CDS	3520059	3521312	1254	-	PGF_03004613	417	Histidyl-tRNA synthetase (EC 6.1.1.21)	GO:0004821|histidine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3412	PATRIC.2.9855.2.9855.con.0001.CDS.3521372.3522799.rev	PATRIC	CDS	3521372	3522799	1428	-	PGF_00013418	475	Oxygen-independent coproporphyrinogen-III oxidase-like protein HemZ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3413	PATRIC.2.9855.2.9855.con.0001.CDS.3522845.3523441.rev	PATRIC	CDS	3522845	3523441	597	-	PGF_10420457	198	MBL-fold metallo-hydrolase superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3414	PATRIC.2.9855.2.9855.con.0001.CDS.3523454.3523903.rev	PATRIC	CDS	3523454	3523903	450	-	PGF_00421071	149	D-aminoacyl-tRNA deacylase (EC 3.1.1.96)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3415	PATRIC.2.9855.2.9855.con.0001.CDS.3523935.3526151.rev	PATRIC	CDS	3523935	3526151	2217	-	PGF_00010349	738	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (EC 3.1.7.2) / GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase II	GO:0008893|guanosine-3',5'-bis(diphosphate) 3'-diphosphatase activity;GO:0008728|GTP diphosphokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3416	PATRIC.2.9855.2.9855.con.0001.CDS.3526496.3527014.rev	PATRIC	CDS	3526496	3527014	519	-	PGF_00034972	172	Adenine phosphoribosyltransferase (EC 2.4.2.7)	GO:0003999|adenine phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.39	PATRIC.2.9855.2.9855.con.0001.CDS.35271.36410.fwd	PATRIC	CDS	35271	36410	1140	+	PGF_00792111	379	Butyryl-CoA dehydrogenase (EC 1.3.8.1)	GO:0004085|butyryl-CoA dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3417	PATRIC.2.9855.2.9855.con.0001.CDS.3527105.3527980.rev	PATRIC	CDS	3527105	3527980	876	-	PGF_00052817	291	Single-stranded-DNA-specific exonuclease RecJ, clostridial paralog	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3418	PATRIC.2.9855.2.9855.con.0001.CDS.3528104.3528979.rev	PATRIC	CDS	3528104	3528979	876	-	PGF_03589438	291	Protein translocase subunit SecF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3419	PATRIC.2.9855.2.9855.con.0001.CDS.3528972.3530237.rev	PATRIC	CDS	3528972	3530237	1266	-	PGF_05949521	421	Protein translocase subunit SecD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.306	PATRIC.2.9855.2.9855.con.0001.CDS.352962.353828.fwd	PATRIC	CDS	352962	353828	867	+	PGF_08108653	288	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	GO:0008879|glucose-1-phosphate thymidylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3421	PATRIC.2.9855.2.9855.con.0001.CDS.3531029.3531307.rev	PATRIC	CDS	3531029	3531307	279	-	PGF_00685189	92	Protein translocase subunit YajC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3422	PATRIC.2.9855.2.9855.con.0001.CDS.3531468.3532604.rev	PATRIC	CDS	3531468	3532604	1137	-	PGF_02061452	378	Queuine tRNA-ribosyltransferase (EC 2.4.2.29)	GO:0008479|queuine tRNA-ribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3423	PATRIC.2.9855.2.9855.con.0001.CDS.3532798.3533823.rev	PATRIC	CDS	3532798	3533823	1026	-	PGF_00049362	341	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3424	PATRIC.2.9855.2.9855.con.0001.CDS.3533952.3534995.rev	PATRIC	CDS	3533952	3534995	1044	-	PGF_05049118	347	Holliday junction ATP-dependent DNA helicase RuvB (EC 3.6.4.12)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3425	PATRIC.2.9855.2.9855.con.0001.CDS.3535061.3535657.rev	PATRIC	CDS	3535061	3535657	597	-	PGF_03189552	198	Holliday junction ATP-dependent DNA helicase RuvA (EC 3.6.4.12)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3426	PATRIC.2.9855.2.9855.con.0001.CDS.3535862.3536431.rev	PATRIC	CDS	3535862	3536431	570	-	PGF_00003000	189	FIG033889: YebC paralog in Clostridia	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3428	PATRIC.2.9855.2.9855.con.0001.CDS.3537301.3538170.rev	PATRIC	CDS	3537301	3538170	870	-	PGF_00022465	289	Molybdenum cofactor biosynthesis enzyme and related Fe-S oxidoreductases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3429	PATRIC.2.9855.2.9855.con.0001.CDS.3538781.3539278.rev	PATRIC	CDS	3538781	3539278	498	-	PGF_10339949	165	cell surface protein, ErfK family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3430	PATRIC.2.9855.2.9855.con.0001.CDS.3539342.3539956.rev	PATRIC	CDS	3539342	3539956	615	-	PGF_01285423	204	motif=eukaryotic putative RNA-binding region RNP-1 signature	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3432	PATRIC.2.9855.2.9855.con.0001.CDS.3541007.3542278.fwd	PATRIC	CDS	3541007	3542278	1272	+	PGF_00008168	423	Glutamate-aspartate carrier protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3433	PATRIC.2.9855.2.9855.con.0001.CDS.3542425.3542889.rev	PATRIC	CDS	3542425	3542889	465	-	PGF_01014387	154	CBS domain protein sometimes clustered with YjeE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3434	PATRIC.2.9855.2.9855.con.0001.CDS.3543050.3544579.rev	PATRIC	CDS	3543050	3544579	1530	-	PGF_09996723	509	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3435	PATRIC.2.9855.2.9855.con.0001.CDS.3544866.3545516.fwd	PATRIC	CDS	3544866	3545516	651	+	PGF_10434120	216	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3436	PATRIC.2.9855.2.9855.con.0001.CDS.3545692.3546852.rev	PATRIC	CDS	3545692	3546852	1161	-	PGF_00069740	386	2-iminoacetate synthase (ThiH) (EC 4.1.99.19)	GO:0036355|2-iminoacetate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3437	PATRIC.2.9855.2.9855.con.0001.CDS.3546863.3547633.rev	PATRIC	CDS	3546863	3547633	771	-	PGF_04175327	256	Thiazole synthase (EC 2.8.1.10)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3439	PATRIC.2.9855.2.9855.con.0001.CDS.3547839.3548036.rev	PATRIC	CDS	3547839	3548036	198	-	PGF_00055115	65	Sulfur carrier protein ThiS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3440	PATRIC.2.9855.2.9855.con.0001.CDS.3548359.3549996.rev	PATRIC	CDS	3548359	3549996	1638	-	PGF_08234189	545	ABC transporter, permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3441	PATRIC.2.9855.2.9855.con.0001.CDS.3549989.3550714.rev	PATRIC	CDS	3549989	3550714	726	-	PGF_00884706	241	Efflux ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3442	PATRIC.2.9855.2.9855.con.0001.CDS.3550970.3553012.rev	PATRIC	CDS	3550970	3553012	2043	-	PGF_05864899	680	Uncharacterized protein YyaL	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3445	PATRIC.2.9855.2.9855.con.0001.CDS.3553864.3554544.fwd	PATRIC	CDS	3553864	3554544	681	+	PGF_06916656	226	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3446	PATRIC.2.9855.2.9855.con.0001.CDS.3554610.3555548.fwd	PATRIC	CDS	3554610	3555548	939	+	PGF_00018962	312	Malate permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3448	PATRIC.2.9855.2.9855.con.0001.CDS.3556361.3557047.fwd	PATRIC	CDS	3556361	3557047	687	+	PGF_06916656	228	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3449	PATRIC.2.9855.2.9855.con.0001.CDS.3557189.3558859.fwd	PATRIC	CDS	3557189	3558859	1671	+	PGF_05070366	556	Dihydroxy-acid dehydratase (EC 4.2.1.9)	GO:0004160|dihydroxy-acid dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3450	PATRIC.2.9855.2.9855.con.0001.CDS.3559427.3560143.fwd	PATRIC	CDS	3559427	3560143	717	+	PGF_00336763	238	Uncharacterized protein MJ0935	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3452	PATRIC.2.9855.2.9855.con.0001.CDS.3561466.3562080.rev	PATRIC	CDS	3561466	3562080	615	-	PGF_00473519	204	Superoxide dismutase [Mn] (EC 1.15.1.1)	GO:0004784|superoxide dismutase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3453	PATRIC.2.9855.2.9855.con.0001.CDS.3562173.3563156.rev	PATRIC	CDS	3562173	3563156	984	-	PGF_06713057	327	D-lactate dehydrogenase (EC 1.1.1.28)	GO:0008720|D-lactate dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3454	PATRIC.2.9855.2.9855.con.0001.CDS.3563512.3564756.rev	PATRIC	CDS	3563512	3564756	1245	-	PGF_00905234	414	Manganese transport protein MntH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3455	PATRIC.2.9855.2.9855.con.0001.CDS.3565017.3565814.rev	PATRIC	CDS	3565017	3565814	798	-	PGF_00422446	265	DUF124 domain-containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3458	PATRIC.2.9855.2.9855.con.0001.CDS.3566661.3567797.rev	PATRIC	CDS	3566661	3567797	1137	-	PGF_00597585	378	Uncharacterized zinc-type alcohol dehydrogenase-like protein AdhB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.310	PATRIC.2.9855.2.9855.con.0001.CDS.356745.357149.fwd	PATRIC	CDS	356745	357149	405	+	PGF_01555804	134	Flagellar basal-body rod protein FlgB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3459	PATRIC.2.9855.2.9855.con.0001.CDS.3567817.3568179.rev	PATRIC	CDS	3567817	3568179	363	-	PGF_00821259	120	Spore coat protein F	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3460	PATRIC.2.9855.2.9855.con.0001.CDS.3568235.3568444.rev	PATRIC	CDS	3568235	3568444	210	-	PGF_00053839	69	Uncharacterized protein YraG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3461	PATRIC.2.9855.2.9855.con.0001.CDS.3568724.3570433.fwd	PATRIC	CDS	3568724	3570433	1710	+	PGF_06837078	569	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3463	PATRIC.2.9855.2.9855.con.0001.CDS.3571784.3572104.rev	PATRIC	CDS	3571784	3572104	321	-	PGF_00069548	106	carboxymuconolactone decarboxylase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3464	PATRIC.2.9855.2.9855.con.0001.CDS.3572129.3572362.rev	PATRIC	CDS	3572129	3572362	234	-	PGF_01281729	77	Putative glycosyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.311	PATRIC.2.9855.2.9855.con.0001.CDS.357232.357639.fwd	PATRIC	CDS	357232	357639	408	+	PGF_00005354	135	Flagellar basal-body rod protein FlgC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3465	PATRIC.2.9855.2.9855.con.0001.CDS.3572454.3572978.rev	PATRIC	CDS	3572454	3572978	525	-	PGF_01662006	174	Transcriptional regulator, PadR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.312	PATRIC.2.9855.2.9855.con.0001.CDS.357651.357968.fwd	PATRIC	CDS	357651	357968	318	+	PGF_03936597	105	Flagellar hook-basal body complex protein FliE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3473	PATRIC.2.9855.2.9855.con.0001.CDS.3578644.3579645.rev	PATRIC	CDS	3578644	3579645	1002	-	PGF_00401757	333	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3474	PATRIC.2.9855.2.9855.con.0001.CDS.3579671.3580363.rev	PATRIC	CDS	3579671	3580363	693	-	PGF_03126194	230	Iron-sulfur cluster assembly scaffold protein IscU/NifU-like	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.313	PATRIC.2.9855.2.9855.con.0001.CDS.357990.359558.fwd	PATRIC	CDS	357990	359558	1569	+	PGF_00005284	522	Flagellar M-ring protein FliF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3476	PATRIC.2.9855.2.9855.con.0001.CDS.3582507.3583427.fwd	PATRIC	CDS	3582507	3583427	921	+	PGF_07201805	306	Permease of the drug/metabolite transporter (DMT) superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3477	PATRIC.2.9855.2.9855.con.0001.CDS.3583801.3585039.rev	PATRIC	CDS	3583801	3585039	1239	-	PGF_00027383	412	Acetyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3478	PATRIC.2.9855.2.9855.con.0001.CDS.3585593.3586444.fwd	PATRIC	CDS	3585593	3586444	852	+	PGF_12840497	283	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3480	PATRIC.2.9855.2.9855.con.0001.CDS.3587117.3588103.fwd	PATRIC	CDS	3587117	3588103	987	+	PGF_00650532	328	UPF0365 protein YqfA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3482	PATRIC.2.9855.2.9855.con.0001.CDS.3588544.3589287.fwd	PATRIC	CDS	3588544	3589287	744	+	PGF_00735941	247	Autolysis response regulater LytR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3483	PATRIC.2.9855.2.9855.con.0001.CDS.3589427.3590185.rev	PATRIC	CDS	3589427	3590185	759	-	PGF_02146256	252	Sialic acid utilization regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3484	PATRIC.2.9855.2.9855.con.0001.CDS.3590349.3591677.rev	PATRIC	CDS	3590349	3591677	1329	-	PGF_00029610	442	PTS system, cellobiose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3485	PATRIC.2.9855.2.9855.con.0001.CDS.3591806.3593215.rev	PATRIC	CDS	3591806	3593215	1410	-	PGF_08148954	469	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3486	PATRIC.2.9855.2.9855.con.0001.CDS.3593257.3593562.rev	PATRIC	CDS	3593257	3593562	306	-	PGF_05148511	101	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3487	PATRIC.2.9855.2.9855.con.0001.CDS.3593632.3593955.rev	PATRIC	CDS	3593632	3593955	324	-	PGF_01629422	107	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3488	PATRIC.2.9855.2.9855.con.0001.CDS.3594631.3595989.fwd	PATRIC	CDS	3594631	3595989	1359	+	PGF_00069345	452	Na(+)-dependent branched-chain amino acid transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.314	PATRIC.2.9855.2.9855.con.0001.CDS.359564.360580.fwd	PATRIC	CDS	359564	360580	1017	+	PGF_02109968	338	Flagellar motor switch protein FliG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3489	PATRIC.2.9855.2.9855.con.0001.CDS.3596818.3597417.rev	PATRIC	CDS	3596818	3597417	600	-	PGF_00026050	199	Nitroreductase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3490	PATRIC.2.9855.2.9855.con.0001.CDS.3597746.3598054.rev	PATRIC	CDS	3597746	3598054	309	-	PGF_00650519	102	Transcriptional regulator YodB, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3493	PATRIC.2.9855.2.9855.con.0001.CDS.3599683.3600552.rev	PATRIC	CDS	3599683	3600552	870	-	PGF_04493258	289	Cobalt-zinc-cadmium resistance protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3494	PATRIC.2.9855.2.9855.con.0001.CDS.3600942.3601724.rev	PATRIC	CDS	3600942	3601724	783	-	PGF_00020445	260	Metal-dependent phosphohydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3495	PATRIC.2.9855.2.9855.con.0001.CDS.3601943.3603337.rev	PATRIC	CDS	3601943	3603337	1395	-	PGF_01421686	464	NADH-dependent reduced ferredoxin:NADP+ oxidoreductase subunit B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3496	PATRIC.2.9855.2.9855.con.0001.CDS.3603337.3604227.rev	PATRIC	CDS	3603337	3604227	891	-	PGF_01480798	296	NADH-dependent reduced ferredoxin:NADP+ oxidoreductase subunit A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3497	PATRIC.2.9855.2.9855.con.0001.CDS.3604379.3605461.rev	PATRIC	CDS	3604379	3605461	1083	-	PGF_01992064	360	2,3-butanediol dehydrogenase, R-alcohol forming, (R)- and (S)-acetoin-specific (EC 1.1.1.4)	GO:0000721|(R,R)-butanediol dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.315	PATRIC.2.9855.2.9855.con.0001.CDS.360564.361349.fwd	PATRIC	CDS	360564	361349	786	+	PGF_00005305	261	Flagellar assembly protein FliH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3498	PATRIC.2.9855.2.9855.con.0001.CDS.3605702.3607648.rev	PATRIC	CDS	3605702	3607648	1947	-	PGF_00057529	648	Transcriptional activator of acetoin dehydrogenase operon AcoR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3503	PATRIC.2.9855.2.9855.con.0001.CDS.3610274.3610852.fwd	PATRIC	CDS	3610274	3610852	579	+	PGF_00010471	192	HAD-superfamily hydrolase-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3505	PATRIC.2.9855.2.9855.con.0001.CDS.3611613.3615131.fwd	PATRIC	CDS	3611613	3615131	3519	+	PGF_00046007	1172	Pyruvate-flavodoxin oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.316	PATRIC.2.9855.2.9855.con.0001.CDS.361370.362686.fwd	PATRIC	CDS	361370	362686	1317	+	PGF_03474542	438	Flagellum-specific ATP synthase FliI	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3506	PATRIC.2.9855.2.9855.con.0001.CDS.3615477.3615641.rev	PATRIC	CDS	3615477	3615641	165	-	PGF_03744661	54	Uncharacterized protein CLJU_c29350	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3507	PATRIC.2.9855.2.9855.con.0001.CDS.3615879.3617717.rev	PATRIC	CDS	3615879	3617717	1839	-	PGF_00051161	612	Ser-type protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3508	PATRIC.2.9855.2.9855.con.0001.CDS.3618211.3619425.rev	PATRIC	CDS	3618211	3619425	1215	-	PGF_03510298	404	Surface protein PspC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3509	PATRIC.2.9855.2.9855.con.0001.CDS.3619600.3621429.rev	PATRIC	CDS	3619600	3621429	1830	-	PGF_00051161	609	Ser-type protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3510	PATRIC.2.9855.2.9855.con.0001.CDS.3622043.3622909.fwd	PATRIC	CDS	3622043	3622909	867	+	PGF_00402549	288	Beta-lysine acetyltransferase (EC 2.3.1.-)	activity;GO:0004147|sterol O-acyltransferase activity;GO:0004147|N-acetyltransferase activity;GO:0004147|O-acyltransferase activity;GO:0004147|palmitoleoyl [acyl-carrier-protein]-dependent acyltransferase activity;GO:0004147|carnitine O-acyltransferase activity;GO:0004147|acetyltransferase activity;GO:0004147|C-acyltransferase activity;GO:0004147|palmitoyltransferase activity;GO:0004147|N-acyltransferase activity;GO:0004147|acylglycerol O-acyltransferase activity;GO:0004147|serine O-acyltransferase activity;GO:0004147|O-acetyltransferase activity;GO:0004147|O-octanoyltransferase activity;GO:0004147|octanoyltransferase activity;GO:0004147|O-palmitoyltransferase activity;GO:0004147|S-acyltransferase activity;GO:0004147|S-acetyltransferase activity;GO:0004147|S-malonyltransferase activity;GO:0004147|malonyltransferase activity;GO:0004147|C-palmitoyltransferase activity;GO:0004147|succinyltransferase activity;GO:0004147|N-succinyltransferase activity;GO:0004147|O-succinyltransferase activity;GO:0004147|S-succinyltransferase activity;GO:0004147|sinapoyltransferase activity;GO:0004147|O-sinapoyltransferase activity;GO:0004147|peptidyl-lysine N6-myristoyltransferase activity;GO:0004147|peptidyl-lysine N6-palmitoyltransferase activity;GO:0004147|benzoyl acetate-CoA thiolase activity;GO:0004147|3-hydroxybutyryl-CoA thiolase activity;GO:0004147|3-ketopimelyl-CoA thiolase activity;GO:0004147|N-palmitoyltransferase activity;GO:0004147|myristoyltransferase activity;GO:0004147|acyl-CoA N-acyltransferase activity;GO:0004147|protein-cysteine S-myristoyltransferase activity;GO:0004147|protein-cysteine S-acyltransferase activity;GO:0004147|dihydrolipoamide S-acyltransferase activity;GO:0004147|glucosaminyl-phosphotidylinositol O-acyltransferase activity;GO:0004147|ergosterol O-acyltransferase activity;GO:0004147|lanosterol O-
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3512	PATRIC.2.9855.2.9855.con.0001.CDS.3623424.3623744.rev	PATRIC	CDS	3623424	3623744	321	-	PGF_04713899	106	Rhodanese-like domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3513	PATRIC.2.9855.2.9855.con.0001.CDS.3623784.3624476.rev	PATRIC	CDS	3623784	3624476	693	-	PGF_10276960	230	Transcriptional regulator, Crp/Fnr family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3514	PATRIC.2.9855.2.9855.con.0001.CDS.3624602.3627022.rev	PATRIC	CDS	3624602	3627022	2421	-	PGF_00440579	806	Cadmium, zinc and cobalt-transporting P-type ATPase (EC 3.6.3.3) (EC 3.6.3.5)	GO:0008551|cadmium-exporting ATPase activity;GO:0016463|zinc-exporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.317	PATRIC.2.9855.2.9855.con.0001.CDS.362700.363137.fwd	PATRIC	CDS	362700	363137	438	+	PGF_00005603	145	Flagellar protein FliJ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3515	PATRIC.2.9855.2.9855.con.0001.CDS.3627045.3627410.rev	PATRIC	CDS	3627045	3627410	366	-	PGF_00416152	121	Cadmium efflux system accessory protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3516	PATRIC.2.9855.2.9855.con.0001.CDS.3627948.3628154.rev	PATRIC	CDS	3627948	3628154	207	-	PGF_00053039	68	Small acid-soluble spore protein, alpha-type SASP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3517	PATRIC.2.9855.2.9855.con.0001.CDS.3628339.3629541.rev	PATRIC	CDS	3628339	3629541	1203	-	PGF_06945838	400	Na+/H+ antiporter NhaA type	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3518	PATRIC.2.9855.2.9855.con.0001.CDS.3629859.3630746.rev	PATRIC	CDS	3629859	3630746	888	-	PGF_02829859	295	Uncharacterized protein YpuA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3519	PATRIC.2.9855.2.9855.con.0001.CDS.3630964.3632628.rev	PATRIC	CDS	3630964	3632628	1665	-	PGF_00004040	554	Family 13 glycosyl hydrolase, row 724	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.318	PATRIC.2.9855.2.9855.con.0001.CDS.363231.364574.fwd	PATRIC	CDS	363231	364574	1344	+	PGF_00005487	447	Flagellar hook-length control protein FliK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3520	PATRIC.2.9855.2.9855.con.0001.CDS.3632663.3635035.rev	PATRIC	CDS	3632663	3635035	2373	-	PGF_00047556	790	Alpha-glucosidase (EC 3.2.1.20)	GO:0004558|alpha-1,4-glucosidase activity;GO:0004558|maltose alpha-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3521	PATRIC.2.9855.2.9855.con.0001.CDS.3635155.3636012.rev	PATRIC	CDS	3635155	3636012	858	-	PGF_06874321	285	Multiple sugar ABC transporter, permease protein MsmG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3522	PATRIC.2.9855.2.9855.con.0001.CDS.3636012.3637052.rev	PATRIC	CDS	3636012	3637052	1041	-	PGF_02876233	346	ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3523	PATRIC.2.9855.2.9855.con.0001.CDS.3637215.3638507.rev	PATRIC	CDS	3637215	3638507	1293	-	PGF_07870324	430	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3524	PATRIC.2.9855.2.9855.con.0001.CDS.3638954.3639988.fwd	PATRIC	CDS	3638954	3639988	1035	+	PGF_09774558	344	Transcriptional regulator, LacI family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3527	PATRIC.2.9855.2.9855.con.0001.CDS.3642017.3643276.rev	PATRIC	CDS	3642017	3643276	1260	-	PGF_01269642	419	cell wall-associated protein precursor (CWBP23, CWBP52)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3528	PATRIC.2.9855.2.9855.con.0001.CDS.3643607.3645430.rev	PATRIC	CDS	3643607	3645430	1824	-	PGF_00344969	607	Heavy-metal-associated domain (N-terminus) and membrane-bounded cytochrome biogenesis cycZ-like domain, possible membrane copper tolerance protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.319	PATRIC.2.9855.2.9855.con.0001.CDS.364586.365596.fwd	PATRIC	CDS	364586	365596	1011	+	PGF_01602421	336	Flagellar basal-body rod modification protein FlgD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3529	PATRIC.2.9855.2.9855.con.0001.CDS.3646560.3648263.rev	PATRIC	CDS	3646560	3648263	1704	-	PGF_00736089	567	Hydroxylamine reductase (EC 1.7.99.1)	GO:0050418|hydroxylamine reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3530	PATRIC.2.9855.2.9855.con.0001.CDS.3648561.3649316.rev	PATRIC	CDS	3648561	3649316	756	-	PGF_01257694	251	Sensory box protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3531	PATRIC.2.9855.2.9855.con.0001.CDS.3649530.3650168.rev	PATRIC	CDS	3649530	3650168	639	-	PGF_00055396	212	Anaerobic nitric oxide reductase flavorubredoxin	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3533	PATRIC.2.9855.2.9855.con.0001.CDS.3650794.3652071.rev	PATRIC	CDS	3650794	3652071	1278	-	PGF_00051525	425	Seryl-tRNA synthetase (EC 6.1.1.11)	GO:0004828|serine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3534	PATRIC.2.9855.2.9855.con.0001.CDS.3652700.3653356.rev	PATRIC	CDS	3652700	3653356	657	-	PGF_01257472	218	Membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3535	PATRIC.2.9855.2.9855.con.0001.CDS.3653794.3655203.rev	PATRIC	CDS	3653794	3655203	1410	-	PGF_09996723	469	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3536	PATRIC.2.9855.2.9855.con.0001.CDS.3655350.3655919.rev	PATRIC	CDS	3655350	3655919	570	-	PGF_07182652	189	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.320	PATRIC.2.9855.2.9855.con.0001.CDS.365597.365995.fwd	PATRIC	CDS	365597	365995	399	+	PGF_00846939	132	Flagellar operon protein CA_C2155	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3537	PATRIC.2.9855.2.9855.con.0001.CDS.3656244.3657905.fwd	PATRIC	CDS	3656244	3657905	1662	+	PGF_00008326	553	Glutaminyl-tRNA synthetase (EC 6.1.1.18)	GO:0004819|glutamine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3538	PATRIC.2.9855.2.9855.con.0001.CDS.3658171.3659934.fwd	PATRIC	CDS	3658171	3659934	1764	+	PGF_06837078	587	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3539	PATRIC.2.9855.2.9855.con.0001.CDS.3660017.3661678.rev	PATRIC	CDS	3660017	3661678	1662	-	PGF_00008337	553	Glutamyl-tRNA synthetase (EC 6.1.1.17) @ Glutamyl-tRNA(Gln) synthetase (EC 6.1.1.24)	GO:0004818|glutamate-tRNA ligase activity;GO:0050561|glutamate-tRNA(Gln) ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.321	PATRIC.2.9855.2.9855.con.0001.CDS.366141.367232.fwd	PATRIC	CDS	366141	367232	1092	+	PGF_00005450	363	Flagellar hook protein FlgE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3541	PATRIC.2.9855.2.9855.con.0001.CDS.3663275.3663853.fwd	PATRIC	CDS	3663275	3663853	579	+	PGF_02936222	192	Serine/threonine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3542	PATRIC.2.9855.2.9855.con.0001.CDS.3663942.3664718.rev	PATRIC	CDS	3663942	3664718	777	-	PGF_05621995	258	Prolipoprotein diacylglyceryl transferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3545	PATRIC.2.9855.2.9855.con.0001.CDS.3666421.3667455.rev	PATRIC	CDS	3666421	3667455	1035	-	PGF_00023916	344	N-acetylmuramoyl-L-alanine amidase/putative S-layer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3546	PATRIC.2.9855.2.9855.con.0001.CDS.3667654.3669021.rev	PATRIC	CDS	3667654	3669021	1368	-	PGF_04035638	455	Adhesin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3548	PATRIC.2.9855.2.9855.con.0001.CDS.3670406.3671050.fwd	PATRIC	CDS	3670406	3671050	645	+	PGF_06724323	214	O-acetyl-ADP-ribose deacetylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3549	PATRIC.2.9855.2.9855.con.0001.CDS.3671154.3671696.rev	PATRIC	CDS	3671154	3671696	543	-	PGF_02930287	180	Reverse rubrerythrin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.40	PATRIC.2.9855.2.9855.con.0001.CDS.36715.38676.rev	PATRIC	CDS	36715	38676	1962	-	PGF_00006377	653	Fructose-1,6-bisphosphatase, Bacillus type (EC 3.1.3.11)	GO:0042132|fructose 1,6-bisphosphate 1-phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3551	PATRIC.2.9855.2.9855.con.0001.CDS.3673011.3673616.fwd	PATRIC	CDS	3673011	3673616	606	+	PGF_03042545	201	Molecular chaperone, DnaJ family (contain C-term. Zn finger domain)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3552	PATRIC.2.9855.2.9855.con.0001.CDS.3673800.3674294.fwd	PATRIC	CDS	3673800	3674294	495	+	PGF_01309485	164	Predicted membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.322	PATRIC.2.9855.2.9855.con.0001.CDS.367479.367670.fwd	PATRIC	CDS	367479	367670	192	+	PGF_01170345	63	Flagellar protein FlbD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3555	PATRIC.2.9855.2.9855.con.0001.CDS.3676360.3677199.fwd	PATRIC	CDS	3676360	3677199	840	+	PGF_01737397	279	FIG00031715: Predicted metal-dependent phosphoesterases (PHP family)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3556	PATRIC.2.9855.2.9855.con.0001.CDS.3677286.3678683.rev	PATRIC	CDS	3677286	3678683	1398	-	PGF_00036814	465	Probable M18-family aminopeptidase 1 (EC 3.4.11.-)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3557	PATRIC.2.9855.2.9855.con.0001.CDS.3678783.3679691.rev	PATRIC	CDS	3678783	3679691	909	-	PGF_04645019	302	HPr kinase/phosphorylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.323	PATRIC.2.9855.2.9855.con.0001.CDS.367900.368385.fwd	PATRIC	CDS	367900	368385	486	+	PGF_00005329	161	Flagellar basal body-associated protein FliL	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3562	PATRIC.2.9855.2.9855.con.0001.CDS.3681782.3682330.rev	PATRIC	CDS	3681782	3682330	549	-	PGF_00054381	182	Substrate-specific component NiaX of predicted niacin ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3563	PATRIC.2.9855.2.9855.con.0001.CDS.3682579.3683382.fwd	PATRIC	CDS	3682579	3683382	804	+	PGF_00048598	267	Ribonuclease Z (EC 3.1.26.11)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3564	PATRIC.2.9855.2.9855.con.0001.CDS.3683493.3685823.rev	PATRIC	CDS	3683493	3685823	2331	-	PGF_00426722	776	5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	GO:0008705|methionine synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.324	PATRIC.2.9855.2.9855.con.0001.CDS.368395.368793.fwd	PATRIC	CDS	368395	368793	399	+	PGF_08239180	132	Flagellar biosynthesis protein FliO	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3565	PATRIC.2.9855.2.9855.con.0001.CDS.3685813.3686496.rev	PATRIC	CDS	3685813	3686496	684	-	PGF_00020759	227	Methionine synthase activation domain (EC 2.1.1.13)	GO:0008705|methionine synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3566	PATRIC.2.9855.2.9855.con.0001.CDS.3686866.3687816.rev	PATRIC	CDS	3686866	3687816	951	-	PGF_00780840	316	Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.33)	GO:0036380|UDP-N-acetylglucosamine-undecaprenyl-phosphate N-acetylglucosaminephosphotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.325	PATRIC.2.9855.2.9855.con.0001.CDS.368783.369562.fwd	PATRIC	CDS	368783	369562	780	+	PGF_06326847	259	Flagellar biosynthesis protein FliP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3567	PATRIC.2.9855.2.9855.con.0001.CDS.3687979.3689442.rev	PATRIC	CDS	3687979	3689442	1464	-	PGF_09996723	487	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3568	PATRIC.2.9855.2.9855.con.0001.CDS.3689515.3689886.rev	PATRIC	CDS	3689515	3689886	372	-	PGF_06902558	123	Transcriptional regulator AdhR, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3569	PATRIC.2.9855.2.9855.con.0001.CDS.3690351.3690488.rev	PATRIC	CDS	3690351	3690488	138	-	PGF_00033396	45	Acyl-CoA thioesterase 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3570	PATRIC.2.9855.2.9855.con.0001.CDS.3690858.3692516.rev	PATRIC	CDS	3690858	3692516	1659	-	PGF_00004169	552	Fe-S oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3572	PATRIC.2.9855.2.9855.con.0001.CDS.3693201.3694505.rev	PATRIC	CDS	3693201	3694505	1305	-	PGF_10535179	434	putative lipoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3573	PATRIC.2.9855.2.9855.con.0001.CDS.3694755.3695585.rev	PATRIC	CDS	3694755	3695585	831	-	PGF_07849456	276	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.326	PATRIC.2.9855.2.9855.con.0001.CDS.369574.369843.fwd	PATRIC	CDS	369574	369843	270	+	PGF_07525202	89	Flagellar biosynthesis protein FliQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3574	PATRIC.2.9855.2.9855.con.0001.CDS.3695814.3696644.rev	PATRIC	CDS	3695814	3696644	831	-	PGF_07849456	276	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3575	PATRIC.2.9855.2.9855.con.0001.CDS.3696832.3698331.rev	PATRIC	CDS	3696832	3698331	1500	+	PGF_10468640	499	Stage V sporulation protein B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3576	PATRIC.2.9855.2.9855.con.0001.CDS.3698505.3700121.rev	PATRIC	CDS	3698505	3700121	1617	-	PGF_10409443	538	FIG006789: Stage V sporulation protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.327	PATRIC.2.9855.2.9855.con.0001.CDS.369857.371698.fwd	PATRIC	CDS	369857	371698	1842	+	PGF_08070154	613	Flagellar biosynthesis protein FliR / Flagellar biosynthesis protein FlhB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3577	PATRIC.2.9855.2.9855.con.0001.CDS.3700131.3701105.rev	PATRIC	CDS	3700131	3701105	975	-	PGF_02996782	324	LSU rRNA pseudouridine(955/2504/2580) synthase (EC 5.4.99.24)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3578	PATRIC.2.9855.2.9855.con.0001.CDS.3701199.3702380.rev	PATRIC	CDS	3701199	3702380	1182	-	PGF_02454442	393	N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)	GO:0050118|N-acetyldiaminopimelate deacetylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3579	PATRIC.2.9855.2.9855.con.0001.CDS.3702534.3704627.rev	PATRIC	CDS	3702534	3704627	2094	-	PGF_12727396	697	Cell division protein FtsA, extended form	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3581	PATRIC.2.9855.2.9855.con.0001.CDS.3706026.3707768.rev	PATRIC	CDS	3706026	3707768	1743	-	PGF_03971086	580	Sodium-Choline Symporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3582	PATRIC.2.9855.2.9855.con.0001.CDS.3708219.3709958.fwd	PATRIC	CDS	3708219	3709958	1740	+	PGF_12782145	579	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3583	PATRIC.2.9855.2.9855.con.0001.CDS.3710018.3711643.fwd	PATRIC	CDS	3710018	3711643	1626	+	PGF_00062533	541	Two-component response regulator yesN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3584	PATRIC.2.9855.2.9855.con.0001.CDS.3711710.3712705.fwd	PATRIC	CDS	3711710	3712705	996	+	PGF_01281262	331	ABC transporter, substrate-binding protein (cluster 2, ribose/xylose/arabinose/galactose)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3585	PATRIC.2.9855.2.9855.con.0001.CDS.3712800.3714815.rev	PATRIC	CDS	3712800	3714815	2016	-	PGF_01296054	671	putative ATP-dependent DNA helicase YjcD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3586	PATRIC.2.9855.2.9855.con.0001.CDS.3715115.3716599.fwd	PATRIC	CDS	3715115	3716599	1485	+	PGF_00025600	494	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3588	PATRIC.2.9855.2.9855.con.0001.CDS.3717121.3717447.rev	PATRIC	CDS	3717121	3717447	327	-	PGF_01305534	108	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.328	PATRIC.2.9855.2.9855.con.0001.CDS.371759.373825.fwd	PATRIC	CDS	371759	373825	2067	+	PGF_00005384	688	Flagellar biosynthesis protein FlhA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3589	PATRIC.2.9855.2.9855.con.0001.CDS.3717861.3718268.fwd	PATRIC	CDS	3717861	3718268	408	+	PGF_00031568	135	Peroxide stress regulator PerR, FUR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3594	PATRIC.2.9855.2.9855.con.0001.CDS.3721254.3721850.rev	PATRIC	CDS	3721254	3721850	597	-	PGF_00007026	198	GTP-binding protein EngB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3595	PATRIC.2.9855.2.9855.con.0001.CDS.3721840.3724170.rev	PATRIC	CDS	3721840	3724170	2331	-	PGF_04438983	776	ATP-dependent protease La (EC 3.4.21.53) Type I	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3596	PATRIC.2.9855.2.9855.con.0001.CDS.3724478.3724747.rev	PATRIC	CDS	3724478	3724747	270	-	PGF_00019536	89	ATP-dependent protease La (EC 3.4.21.53) LonB Type I	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3597	PATRIC.2.9855.2.9855.con.0001.CDS.3724777.3725358.rev	PATRIC	CDS	3724777	3725358	582	-	PGF_00019536	193	ATP-dependent protease La (EC 3.4.21.53) LonB Type I	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3598	PATRIC.2.9855.2.9855.con.0001.CDS.3725343.3726158.rev	PATRIC	CDS	3725343	3726158	816	-	PGF_00019536	271	ATP-dependent protease La (EC 3.4.21.53) LonB Type I	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3600	PATRIC.2.9855.2.9855.con.0001.CDS.3726404.3727693.rev	PATRIC	CDS	3726404	3727693	1290	-	PGF_00016338	429	ATP-dependent Clp protease ATP-binding subunit ClpX	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3601	PATRIC.2.9855.2.9855.con.0001.CDS.3727736.3728335.rev	PATRIC	CDS	3727736	3728335	600	-	PGF_00285620	199	ATP-dependent Clp protease proteolytic subunit ClpP (EC 3.4.21.92)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3602	PATRIC.2.9855.2.9855.con.0001.CDS.3728491.3729774.rev	PATRIC	CDS	3728491	3729774	1284	-	PGF_02452671	427	Cell division trigger factor (EC 5.2.1.8)	GO:0003755|peptidyl-prolyl cis-trans isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3605	PATRIC.2.9855.2.9855.con.0001.CDS.3731649.3731975.rev	PATRIC	CDS	3731649	3731975	327	-	PGF_01172431	108	Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	GO:0004636|phosphoribosyl-ATP diphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3606	PATRIC.2.9855.2.9855.con.0001.CDS.3732007.3732336.rev	PATRIC	CDS	3732007	3732336	330	-	PGF_02776739	109	Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19)	GO:0004635|phosphoribosyl-AMP cyclohydrolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3607	PATRIC.2.9855.2.9855.con.0001.CDS.3732394.3733155.rev	PATRIC	CDS	3732394	3733155	762	-	PGF_02011760	253	Imidazole glycerol phosphate synthase cyclase subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3608	PATRIC.2.9855.2.9855.con.0001.CDS.3733160.3733882.rev	PATRIC	CDS	3733160	3733882	723	-	PGF_00033946	240	Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16)	GO:0003949|1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3609	PATRIC.2.9855.2.9855.con.0001.CDS.3733879.3734499.rev	PATRIC	CDS	3733879	3734499	621	-	PGF_04867467	206	Imidazole glycerol phosphate synthase amidotransferase subunit HisH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3610	PATRIC.2.9855.2.9855.con.0001.CDS.3734627.3735214.rev	PATRIC	CDS	3734627	3735214	588	-	PGF_00013803	195	Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	GO:0004424|imidazoleglycerol-phosphate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3611	PATRIC.2.9855.2.9855.con.0001.CDS.3735432.3736472.rev	PATRIC	CDS	3735432	3736472	1041	-	PGF_03811905	346	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	GO:0004400|histidinol-phosphate transaminase activity;GO:0004400|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3612	PATRIC.2.9855.2.9855.con.0001.CDS.3736459.3737757.rev	PATRIC	CDS	3736459	3737757	1299	-	PGF_05760069	432	Histidinol dehydrogenase (EC 1.1.1.23)	GO:0004399|histidinol dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3613	PATRIC.2.9855.2.9855.con.0001.CDS.3737890.3738519.rev	PATRIC	CDS	3737890	3738519	630	-	PGF_03287477	209	ATP phosphoribosyltransferase (EC 2.4.2.17) => HisGs	GO:0003879|ATP phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.329	PATRIC.2.9855.2.9855.con.0001.CDS.373826.375172.fwd	PATRIC	CDS	373826	375172	1347	+	PGF_01169833	448	Flagellar biosynthesis protein FlhF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3614	PATRIC.2.9855.2.9855.con.0001.CDS.3738522.3739667.rev	PATRIC	CDS	3738522	3739667	1146	-	PGF_02224568	381	ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17)	GO:0003879|ATP phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3616	PATRIC.2.9855.2.9855.con.0001.CDS.3740754.3741911.rev	PATRIC	CDS	3740754	3741911	1158	-	PGF_06115957	385	tRNA 4-thiouridine synthase (EC 2.8.1.4)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3617	PATRIC.2.9855.2.9855.con.0001.CDS.3741911.3743059.rev	PATRIC	CDS	3741911	3743059	1149	-	PGF_02788759	382	Cysteine desulfurase (EC 2.8.1.7), associated with tRNA 4-thiouridine synthase	GO:0031071|cysteine desulfurase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3618	PATRIC.2.9855.2.9855.con.0001.CDS.3743288.3744163.rev	PATRIC	CDS	3743288	3744163	876	-	PGF_10097632	291	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	GO:0008679|2-hydroxy-3-oxopropionate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3619	PATRIC.2.9855.2.9855.con.0001.CDS.3744229.3745053.rev	PATRIC	CDS	3744229	3745053	825	-	PGF_00007004	274	GTP pyrophosphokinase (EC 2.7.6.5)	GO:0008728|GTP diphosphokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3620	PATRIC.2.9855.2.9855.con.0001.CDS.3745497.3746717.rev	PATRIC	CDS	3745497	3746717	1221	-	PGF_00038867	406	Proton/sodium-glutamate symport protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3621	PATRIC.2.9855.2.9855.con.0001.CDS.3746764.3748233.rev	PATRIC	CDS	3746764	3748233	1470	-	PGF_07096769	489	UDP-N-acetylmuramoyl-dipeptide--2,6-diaminopimelate ligase (EC 6.3.2.13)	GO:0008765|UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3622	PATRIC.2.9855.2.9855.con.0001.CDS.3748554.3749414.rev	PATRIC	CDS	3748554	3749414	861	+	PGF_00058797	286	Transcriptional regulator of rhamnose utilization, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3623	PATRIC.2.9855.2.9855.con.0001.CDS.3749481.3749954.rev	PATRIC	CDS	3749481	3749954	474	-	PGF_05083865	157	Peptide-methionine (S)-S-oxide reductase MsrA (EC 1.8.4.11)	GO:0008113|peptide-methionine (S)-S-oxide reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3624	PATRIC.2.9855.2.9855.con.0001.CDS.3750130.3751077.rev	PATRIC	CDS	3750130	3751077	948	-	PGF_10512761	315	Lysophospholipase (EC 3.1.1.5); Monoglyceride lipase (EC 3.1.1.23)	GO:0004622|lysophospholipase activity;GO:0047372|acylglycerol lipase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.330	PATRIC.2.9855.2.9855.con.0001.CDS.375166.376026.fwd	PATRIC	CDS	375166	376026	861	+	PGF_03070510	286	Flagellar synthesis regulator FleN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3627	PATRIC.2.9855.2.9855.con.0001.CDS.3752788.3754029.rev	PATRIC	CDS	3752788	3754029	1242	-	PGF_01284137	413	Membrane associated protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3628	PATRIC.2.9855.2.9855.con.0001.CDS.3754031.3754585.rev	PATRIC	CDS	3754031	3754585	555	-	PGF_08137168	184	RNA polymerase sigma factor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3630	PATRIC.2.9855.2.9855.con.0001.CDS.3756450.3756590.rev	PATRIC	CDS	3756450	3756590	141	-	PGF_01272197	46	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.331	PATRIC.2.9855.2.9855.con.0001.CDS.376039.376680.fwd	PATRIC	CDS	376039	376680	642	+	PGF_00034313	213	PilZ domain-containing protein associated with flagellar synthesis TM0905	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3635	PATRIC.2.9855.2.9855.con.0001.CDS.3761401.3761841.rev	PATRIC	CDS	3761401	3761841	441	-	PGF_00012657	146	ACT domain-containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3636	PATRIC.2.9855.2.9855.con.0001.CDS.3761838.3762734.rev	PATRIC	CDS	3761838	3762734	897	-	PGF_00012356	298	Homoserine kinase (EC 2.7.1.39)	GO:0004413|homoserine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3637	PATRIC.2.9855.2.9855.con.0001.CDS.3762746.3764203.rev	PATRIC	CDS	3762746	3764203	1458	-	PGF_03316046	485	Threonine synthase (EC 4.2.3.1)	GO:0004795|threonine synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3639	PATRIC.2.9855.2.9855.con.0001.CDS.3765689.3766663.fwd	PATRIC	CDS	3765689	3766663	975	+	PGF_01301460	324	Probable lipase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3641	PATRIC.2.9855.2.9855.con.0001.CDS.3767952.3768593.rev	PATRIC	CDS	3767952	3768593	642	-	PGF_03751326	213	Epoxyqueuosine reductase (EC 1.17.99.6) QueH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.332	PATRIC.2.9855.2.9855.con.0001.CDS.376800.377528.fwd	PATRIC	CDS	376800	377528	729	+	PGF_00046377	242	RNA polymerase sigma factor for flagellar operon	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3642	PATRIC.2.9855.2.9855.con.0001.CDS.3768634.3769929.rev	PATRIC	CDS	3768634	3769929	1296	-	PGF_09019918	431	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)	GO:0042286|glutamate-1-semialdehyde 2,1-aminomutase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3643	PATRIC.2.9855.2.9855.con.0001.CDS.3770167.3771165.rev	PATRIC	CDS	3770167	3771165	999	-	PGF_00489714	332	Porphobilinogen synthase (EC 4.2.1.24)	GO:0004655|porphobilinogen synthase activity

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3644	PATRIC.2.9855.2.9855.con.0001.CDS.3771230.3772693.rev	PATRIC	CDS	3771230	3772693	1464	-	PGF_00066286	487	Uroporphyrinogen-III methyltransferase (EC 2.1.1.107) / Uroporphyrinogen-III synthase (EC 4.2.1.75)	GO:0004851|uroporphyrin-III C-methyltransferase activity;GO:0004852|uroporphyrinogen-III synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3645	PATRIC.2.9855.2.9855.con.0001.CDS.3772706.3773608.rev	PATRIC	CDS	3772706	3773608	903	-	PGF_10097367	300	Porphobilinogen deaminase (EC 2.5.1.61)	GO:0004418|hydroxymethylbilane synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3646	PATRIC.2.9855.2.9855.con.0001.CDS.3773625.3774305.rev	PATRIC	CDS	3773625	3774305	681	-	PGF_00035452	226	Precorrin-2 oxidase (EC 1.3.1.76) @ Sirohydrochlorin ferrochelatase activity of CysG (EC 4.99.1.4)	GO:0043115|precorrin-2 dehydrogenase activity;GO:0051266|sirohydrochlorin ferrochelatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3647	PATRIC.2.9855.2.9855.con.0001.CDS.3774263.3775468.rev	PATRIC	CDS	3774263	3775468	1206	-	PGF_00008334	401	Glutamyl-tRNA reductase (EC 1.2.1.70)	GO:0008883|glutamyl-tRNA reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3648	PATRIC.2.9855.2.9855.con.0001.CDS.3776608.3777249.fwd	PATRIC	CDS	3776608	3777249	642	+	PGF_02280759	213	Undecaprenyl diphosphate synthase (EC 2.5.1.31)	GO:0008834|di-trans,poly-cis-decaprenylcistransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3649	PATRIC.2.9855.2.9855.con.0001.CDS.3777395.3777661.fwd	PATRIC	CDS	3777395	3777661	267	+	PGF_01462289	88	Uncharacterized membrane protein YsdA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3651	PATRIC.2.9855.2.9855.con.0001.CDS.3778394.3779308.rev	PATRIC	CDS	3778394	3779308	915	-	PGF_00012336	304	Homoserine O-succinyltransferase (EC 2.3.1.46)	GO:0008899|homoserine O-succinyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3653	PATRIC.2.9855.2.9855.con.0001.CDS.3781134.3782903.fwd	PATRIC	CDS	3781134	3782903	1770	+	PGF_00068000	589	Adenine deaminase (EC 3.5.4.2)	GO:0000034|adenine deaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3654	PATRIC.2.9855.2.9855.con.0001.CDS.3782949.3784055.rev	PATRIC	CDS	3782949	3784055	1107	-	PGF_01137083	368	HD-GYP hydrolase domain containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3655	PATRIC.2.9855.2.9855.con.0001.CDS.3784519.3785331.rev	PATRIC	CDS	3784519	3785331	813	-	PGF_00035900	270	Predicted hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3656	PATRIC.2.9855.2.9855.con.0001.CDS.3785642.3786268.fwd	PATRIC	CDS	3785642	3786268	627	+	PGF_06292183	208	Integral membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3658	PATRIC.2.9855.2.9855.con.0001.CDS.3787001.3788500.rev	PATRIC	CDS	3787001	3788500	1500	-	PGF_05554840	499	Cobyric acid synthase (EC 6.3.5.10)	GO:0051921|adenosylcobyric acid synthase (glutamine-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.335	PATRIC.2.9855.2.9855.con.0001.CDS.378724.379494.fwd	PATRIC	CDS	378724	379494	771	+	PGF_07179577	256	Flagellar basal-body rod protein FlgF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3659	PATRIC.2.9855.2.9855.con.0001.CDS.3788607.3789269.rev	PATRIC	CDS	3788607	3789269	663	-	PGF_02930291	220	COG2102: Predicted ATPases of PP-loop superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3660	PATRIC.2.9855.2.9855.con.0001.CDS.3789290.3790027.rev	PATRIC	CDS	3789290	3790027	738	-	PGF_00417736	245	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3661	PATRIC.2.9855.2.9855.con.0001.CDS.3790104.3791189.rev	PATRIC	CDS	3790104	3791189	1086	-	PGF_05579323	361	L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)	GO:0048472|threonine-phosphate decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3662	PATRIC.2.9855.2.9855.con.0001.CDS.3791377.3792324.rev	PATRIC	CDS	3791377	3792324	948	-	PGF_00035334	315	Adenosylcobinamide-phosphate synthase (EC 6.3.1.10)	GO:0043757|adenosylcobinamide-phosphate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3663	PATRIC.2.9855.2.9855.con.0001.CDS.3792381.3792989.rev	PATRIC	CDS	3792381	3792989	609	-	PGF_00368502	202	Alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.73)	GO:0043755|alpha-ribazole phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3665	PATRIC.2.9855.2.9855.con.0001.CDS.3793446.3794204.rev	PATRIC	CDS	3793446	3794204	759	-	PGF_00662997	252	Cobalamin synthase (EC 2.7.8.26)	GO:0051073|adenosylcobinamide-GDP ribazoletransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3666	PATRIC.2.9855.2.9855.con.0001.CDS.3794201.3794740.rev	PATRIC	CDS	3794201	3794740	540	-	PGF_02790700	179	Adenosylcobinamide kinase (EC 2.7.1.156) / Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)	GO:0043752|adenosylcobinamide kinase activity;GO:0008820|cobinamide phosphate guanylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3667	PATRIC.2.9855.2.9855.con.0001.CDS.3794779.3795309.rev	PATRIC	CDS	3794779	3795309	531	-	PGF_00418244	176	Cob(I)alamin adenosyltransferase (EC 2.5.1.17) @ Cob(I)alamin adenosyltransferase (EC 2.5.1.17), clustered with cobalamin synthesis	GO:0008817|cob(I)yrinic acid a,c-diamide adenosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3668	PATRIC.2.9855.2.9855.con.0001.CDS.3795729.3796820.rev	PATRIC	CDS	3795729	3796820	1092	-	PGF_00025623	363	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21)	GO:0008939|nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.336	PATRIC.2.9855.2.9855.con.0001.CDS.379581.380348.fwd	PATRIC	CDS	379581	380348	768	+	PGF_00005358	255	Flagellar basal-body rod protein FlgG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3669	PATRIC.2.9855.2.9855.con.0001.CDS.3796894.3797859.rev	PATRIC	CDS	3796894	3797859	966	-	PGF_00032911	321	Phage-associated cell wall hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3671	PATRIC.2.9855.2.9855.con.0001.CDS.3798393.3798572.rev	PATRIC	CDS	3798393	3798572	180	-	PGF_00035500	59	Uncharacterized protein CAC2259	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3674	PATRIC.2.9855.2.9855.con.0001.CDS.3799780.3800544.rev	PATRIC	CDS	3799780	3800544	765	-	PGF_00418294	254	Cobalt-precorrin-6A reductase (EC 1.3.1.106)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3675	PATRIC.2.9855.2.9855.con.0001.CDS.3800674.3801396.rev	PATRIC	CDS	3800674	3801396	723	-	PGF_00418285	240	Cobalt-precorrin-3 C(17)-methyltransferase (EC 2.1.1.272)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3676	PATRIC.2.9855.2.9855.con.0001.CDS.3801583.3802137.rev	PATRIC	CDS	3801583	3802137	555	-	PGF_02879212	184	Transcriptional regulator, Xre-family with cupin domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3677	PATRIC.2.9855.2.9855.con.0001.CDS.3802288.3803223.fwd	PATRIC	CDS	3802288	3803223	936	+	PGF_00409480	311	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3678	PATRIC.2.9855.2.9855.con.0001.CDS.3803395.3805782.rev	PATRIC	CDS	3803395	3805782	2388	-	PGF_04438983	795	ATP-dependent protease La (EC 3.4.21.53) Type I	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3679	PATRIC.2.9855.2.9855.con.0001.CDS.3805908.3806471.rev	PATRIC	CDS	3805908	3806471	564	-	PGF_00057460	187	Transcription regulator of multidrug efflux pump operon, TetR (AcrR) family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3680	PATRIC.2.9855.2.9855.con.0001.CDS.3806748.3807119.rev	PATRIC	CDS	3806748	3807119	372	-	PGF_04996095	123	Uncharacterized cysteine-rich DUF326 protein bsYhjQ/STM1261	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3684	PATRIC.2.9855.2.9855.con.0001.CDS.3808316.3808756.rev	PATRIC	CDS	3808316	3808756	441	-	PGF_00012082	146	Histone acetyltransferase HPA2 and related acetyltransferases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3685	PATRIC.2.9855.2.9855.con.0001.CDS.3808959.3809660.fwd	PATRIC	CDS	3808959	3809660	702	+	PGF_01259724	233	Uncharacterized protein MJ1433	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.337	PATRIC.2.9855.2.9855.con.0001.CDS.380962.382608.fwd	PATRIC	CDS	380962	382608	1647	+	PGF_00019248	548	Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	GO:0004427|inorganic diphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3686	PATRIC.2.9855.2.9855.con.0001.CDS.3809733.3810719.rev	PATRIC	CDS	3809733	3810719	987	-	PGF_03683722	328	COG1180: Radical SAM, Pyruvate-formate lyase-activating enzyme like	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3687	PATRIC.2.9855.2.9855.con.0001.CDS.3810820.3812226.rev	PATRIC	CDS	3810820	3812226	1407	-	PGF_00425417	468	Extradiol ring-cleavage dioxygenase, class III subunit B-like domain / COG2078: Uncharacterized ACR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3690	PATRIC.2.9855.2.9855.con.0001.CDS.3813146.3815146.fwd	PATRIC	CDS	3813146	3815146	2001	+	PGF_04734234	666	Kup system potassium uptake protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3692	PATRIC.2.9855.2.9855.con.0001.CDS.3815960.3817291.rev	PATRIC	CDS	3815960	3817291	1332	-	PGF_00025007	443	NLP/P60 family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3693	PATRIC.2.9855.2.9855.con.0001.CDS.3817730.3819019.rev	PATRIC	CDS	3817730	3819019	1290	-	PGF_00057866	429	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3695	PATRIC.2.9855.2.9855.con.0001.CDS.3819772.3821694.rev	PATRIC	CDS	3819772	3821694	1923	-	PGF_01282261	640	Oligopeptide transporter, OPT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3696	PATRIC.2.9855.2.9855.con.0001.CDS.3822027.3822614.rev	PATRIC	CDS	3822027	3822614	588	-	PGF_06454307	195	Acyl carrier protein phosphodiesterase (EC 3.1.4.14)	GO:0008770|[acyl-carrier-protein] phosphodiesterase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3697	PATRIC.2.9855.2.9855.con.0001.CDS.3822945.3823424.fwd	PATRIC	CDS	3822945	3823424	480	+	PGF_00049433	159	S-ribosylhomocysteine lyase (EC 4.4.1.21) @ Autoinducer-2 production protein LuxS	GO:0043768|S-ribosylhomocysteine lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3698	PATRIC.2.9855.2.9855.con.0001.CDS.3823568.3823864.rev	PATRIC	CDS	3823568	3823864	297	-	PGF_00660064	98	Galactoside O-acetyltransferase (EC 2.3.1.18)	GO:0008870|galactoside O-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3700	PATRIC.2.9855.2.9855.con.0001.CDS.3824264.3827290.rev	PATRIC	CDS	3824264	3827290	3027	-	PGF_04836613	1008	beta-galactosidase (EC 3.2.1.23)	GO:0004565|beta-galactosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3701	PATRIC.2.9855.2.9855.con.0001.CDS.3827690.3829243.fwd	PATRIC	CDS	3827690	3829243	1554	+	PGF_00062533	517	Two-component response regulator yesN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3702	PATRIC.2.9855.2.9855.con.0001.CDS.3829274.3831064.fwd	PATRIC	CDS	3829274	3831064	1791	+	PGF_10464866	596	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3703	PATRIC.2.9855.2.9855.con.0001.CDS.3831197.3832129.rev	PATRIC	CDS	3831197	3832129	933	-	PGF_07730014	310	2-dehydropantoate 2-reductase (EC 1.1.1.169)	GO:0008677|2-dehydropantoate 2-reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3704	PATRIC.2.9855.2.9855.con.0001.CDS.3832369.3834462.rev	PATRIC	CDS	3832369	3834462	2094	-	PGF_04836613	697	beta-galactosidase (EC 3.2.1.23)	GO:0004565|beta-galactosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.338	PATRIC.2.9855.2.9855.con.0001.CDS.383240.385825.fwd	PATRIC	CDS	383240	385825	2586	+	PGF_03248819	861	P-type Ca(2+)-transport ATPase (EC 3.6.3.8)	GO:0005388|calcium-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3705	PATRIC.2.9855.2.9855.con.0001.CDS.3834573.3835406.rev	PATRIC	CDS	3834573	3835406	834	-	PGF_04081265	277	beta-galactoside ABC transporter, permease protein LacG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3706	PATRIC.2.9855.2.9855.con.0001.CDS.3835396.3836292.rev	PATRIC	CDS	3835396	3836292	897	-	PGF_00716434	298	beta-galactoside ABC transporter, permease protein LacF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3707	PATRIC.2.9855.2.9855.con.0001.CDS.3836406.3837719.rev	PATRIC	CDS	3836406	3837719	1314	-	PGF_05572832	437	beta-galactoside ABC transporter, substrate-binding protein LacE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3708	PATRIC.2.9855.2.9855.con.0001.CDS.3838180.3839184.rev	PATRIC	CDS	3838180	3839184	1005	-	PGF_10656017	334	beta-galactoside operon transcriptional repressor LacI	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3709	PATRIC.2.9855.2.9855.con.0001.CDS.3840244.3840708.rev	PATRIC	CDS	3840244	3840708	465	-	PGF_00426932	154	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3710	PATRIC.2.9855.2.9855.con.0001.CDS.3840875.3842068.rev	PATRIC	CDS	3840875	3842068	1194	-	PGF_00416674	397	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25)	GO:0008686|3,4-dihydroxy-2-butanone-4-phosphate synthase activity;GO:0003935|GTP cyclohydrolase II activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3711	PATRIC.2.9855.2.9855.con.0001.CDS.3842133.3842783.rev	PATRIC	CDS	3842133	3842783	651	-	PGF_03751076	216	Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)	GO:0004746|riboflavin synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3712	PATRIC.2.9855.2.9855.con.0001.CDS.3842810.3843895.rev	PATRIC	CDS	3842810	3843895	1086	-	PGF_00423089	361	Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)	GO:0008835|diaminohydroxyphosphoribosylaminopyrimidine deaminase activity;GO:0008703|5-amino-6-(5-phosphoribosylamino)uracil reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3715	PATRIC.2.9855.2.9855.con.0001.CDS.3847552.3848982.rev	PATRIC	CDS	3847552	3848982	1431	-	PGF_01054379	476	Adenylosuccinate lyase (EC 4.3.2.2) @ SAICAR lyase (EC 4.3.2.2)	GO:0004018|N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity;GO:0004018|(S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido)succinate AMP-lyase (fumarate-forming) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3716	PATRIC.2.9855.2.9855.con.0001.CDS.3849184.3849402.fwd	PATRIC	CDS	3849184	3849402	219	+	PGF_05313742	72	Uncharacterized membrane protein YuzA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3717	PATRIC.2.9855.2.9855.con.0001.CDS.3849530.3849790.rev	PATRIC	CDS	3849530	3849790	261	-	PGF_08051111	86	Phosphotransferase system, phosphocarrier protein HPr	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3718	PATRIC.2.9855.2.9855.con.0001.CDS.3849913.3850173.rev	PATRIC	CDS	3849913	3850173	261	-	PGF_00054118	86	Spore core dehydratation and coat assembly protein SpoVS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3719	PATRIC.2.9855.2.9855.con.0001.CDS.3850394.3851935.rev	PATRIC	CDS	3850394	3851935	1542	-	PGF_03000099	513	Ribonuclease Y	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3720	PATRIC.2.9855.2.9855.con.0001.CDS.3852230.3853315.rev	PATRIC	CDS	3852230	3853315	1086	-	PGF_00047078	361	RecA protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3721	PATRIC.2.9855.2.9855.con.0001.CDS.3853487.3854077.rev	PATRIC	CDS	3853487	3854077	591	-	PGF_03295678	196	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	GO:0008444|CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3722	PATRIC.2.9855.2.9855.con.0001.CDS.3854061.3855458.rev	PATRIC	CDS	3854061	3855458	1398	-	PGF_00048846	465	Ribosomal protein S12p Asp88 (E. coli) methylthiotransferase (EC 2.8.4.4)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3723	PATRIC.2.9855.2.9855.con.0001.CDS.3855673.3858042.rev	PATRIC	CDS	3855673	3858042	2370	-	PGF_08155727	789	DNA translocase FtsK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3724	PATRIC.2.9855.2.9855.con.0001.CDS.3858157.3858864.rev	PATRIC	CDS	3858157	3858864	708	-	PGF_00060487	235	Translocation-enhancing protein TepA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3725	PATRIC.2.9855.2.9855.con.0001.CDS.3859133.3860329.rev	PATRIC	CDS	3859133	3860329	1197	-	PGF_00862519	398	Aspartokinase (EC 2.7.2.4)	GO:0004072|aspartate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3727	PATRIC.2.9855.2.9855.con.0001.CDS.3860695.3862002.rev	PATRIC	CDS	3860695	3862002	1308	-	PGF_05572316	435	FIG007959: peptidase, M16 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3728	PATRIC.2.9855.2.9855.con.0001.CDS.3862052.3864157.rev	PATRIC	CDS	3862052	3864157	2106	-	PGF_03104485	701	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)	GO:0004654|polyribonucleotide nucleotidyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3729	PATRIC.2.9855.2.9855.con.0001.CDS.3864264.3864527.rev	PATRIC	CDS	3864264	3864527	264	-	PGF_00049847	87	SSU ribosomal protein S15p (S13e)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3730	PATRIC.2.9855.2.9855.con.0001.CDS.3864647.3865582.rev	PATRIC	CDS	3864647	3865582	936	-	PGF_02623406	311	FMN adenylyltransferase (EC 2.7.7.2) / Riboflavin kinase (EC 2.7.1.26)	GO:0003919|FMN adenylyltransferase activity;GO:0008531|riboflavin kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3731	PATRIC.2.9855.2.9855.con.0001.CDS.3865640.3866539.rev	PATRIC	CDS	3865640	3866539	900	-	PGF_00413295	299	tRNA pseudouridine(55) synthase (EC 5.4.99.25)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3732	PATRIC.2.9855.2.9855.con.0001.CDS.3866610.3867590.rev	PATRIC	CDS	3866610	3867590	981	-	PGF_01833449	326	3'-to-5' oligoribonuclease A, Bacillus type	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.340	PATRIC.2.9855.2.9855.con.0001.CDS.386729.387775.fwd	PATRIC	CDS	386729	387775	1047	+	PGF_03787622	348	DNA polymerase IV (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3733	PATRIC.2.9855.2.9855.con.0001.CDS.3867583.3867939.rev	PATRIC	CDS	3867583	3867939	357	-	PGF_09452281	118	Ribosome-binding factor A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3734	PATRIC.2.9855.2.9855.con.0001.CDS.3867957.3870044.rev	PATRIC	CDS	3867957	3870044	2088	-	PGF_10525419	695	Translation initiation factor 2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3735	PATRIC.2.9855.2.9855.con.0001.CDS.3870071.3870382.rev	PATRIC	CDS	3870071	3870382	312	-	PGF_00411944	103	Ribosomal protein L7Ae family protein YlxQ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3736	PATRIC.2.9855.2.9855.con.0001.CDS.3870375.3870641.rev	PATRIC	CDS	3870375	3870641	267	-	PGF_00415631	88	COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3737	PATRIC.2.9855.2.9855.con.0001.CDS.3870655.3871851.rev	PATRIC	CDS	3870655	3871851	1197	-	PGF_07063065	398	Transcription termination protein NusA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3738	PATRIC.2.9855.2.9855.con.0001.CDS.3871868.3872326.rev	PATRIC	CDS	3871868	3872326	459	-	PGF_01682834	152	Bacterial ribosome SSU maturation protein RimP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3739	PATRIC.2.9855.2.9855.con.0001.CDS.3872861.3873940.rev	PATRIC	CDS	3872861	3873940	1080	-	PGF_00426236	359	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase (flavodoxin) (EC 1.17.7.3)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3740	PATRIC.2.9855.2.9855.con.0001.CDS.3874275.3875285.rev	PATRIC	CDS	3874275	3875285	1011	-	PGF_03752718	336	Intramembrane protease RasP/YluC, implicated in cell division based on FtsL cleavage	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3741	PATRIC.2.9855.2.9855.con.0001.CDS.3875303.3876466.rev	PATRIC	CDS	3875303	3876466	1164	-	PGF_09077460	387	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	GO:0030604|1-deoxy-D-xylulose-5-phosphate reductoisomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3742	PATRIC.2.9855.2.9855.con.0001.CDS.3876591.3877406.rev	PATRIC	CDS	3876591	3877406	816	-	PGF_00769248	271	Sporulation integral membrane protein Ytvl	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3743	PATRIC.2.9855.2.9855.con.0001.CDS.3877997.3878791.rev	PATRIC	CDS	3877997	3878791	795	-	PGF_02450432	264	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	GO:0004605|phosphatidate cytidylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3744	PATRIC.2.9855.2.9855.con.0001.CDS.3878807.3879565.rev	PATRIC	CDS	3878807	3879565	759	-	PGF_02280759	252	Undecaprenyl diphosphate synthase (EC 2.5.1.31)	GO:0008834|di-trans,poly-cis-decaprenylcistransferase activity

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3745	PATRIC.2.9855.2.9855.con.0001.CDS.3879978.3880535.rev	PATRIC	CDS	3879978	3880535	558	-	PGF_00048926	185	Ribosome recycling factor		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3746	PATRIC.2.9855.2.9855.con.0001.CDS.3880767.3881489.rev	PATRIC	CDS	3880767	3881489	723	-	PGF_02923127	240	Uridylate kinase (EC 2.7.4.22)	GO:0033862|UMP kinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3747	PATRIC.2.9855.2.9855.con.0001.CDS.3881598.3882515.rev	PATRIC	CDS	3881598	3882515	918	-	PGF_06936561	305	Translation elongation factor Ts		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.41	PATRIC.2.9855.2.9855.con.0001.CDS.38826.39386.rev	PATRIC	CDS	38826	39386	561	-	PGF_00035508	186	Adenylate cyclase (EC 4.6.1.1)	GO:0004016|adenylate cyclase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3748	PATRIC.2.9855.2.9855.con.0001.CDS.3882611.3883312.rev	PATRIC	CDS	3882611	3883312	702	-	PGF_04505269	233	SSU ribosomal protein S2p (SAe)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.341	PATRIC.2.9855.2.9855.con.0001.CDS.388356.389129.rev	PATRIC	CDS	388356	389129	774	-	PGF_00035907	257	Predicted hydrolase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3749	PATRIC.2.9855.2.9855.con.0001.CDS.3883853.3884629.rev	PATRIC	CDS	3883853	3884629	777	-	PGF_00007045	258	GTP-sensing transcriptional pleiotropic repressor CodY		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3750	PATRIC.2.9855.2.9855.con.0001.CDS.3884838.3886931.rev	PATRIC	CDS	3884838	3886931	2094	-	PGF_10300474	697	DNA topoisomerase I (EC 5.99.1.2)	GO:0003917|DNA topoisomerase type I activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3751	PATRIC.2.9855.2.9855.con.0001.CDS.3886978.3888033.rev	PATRIC	CDS	3886978	3888033	1056	-	PGF_09432500	351	Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3752	PATRIC.2.9855.2.9855.con.0001.CDS.3888056.3889576.rev	PATRIC	CDS	3888056	3889576	1521	-	PGF_05877811	506	AAA+ ATPase superfamily protein YifB/ComM, associated with DNA recombination		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3753	PATRIC.2.9855.2.9855.con.0001.CDS.3889738.3890109.fwd	PATRIC	CDS	3889738	3890109	372	+	PGF_02501663	123	UPF0102 protein YraN		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3754	PATRIC.2.9855.2.9855.con.0001.CDS.3890301.3891113.rev	PATRIC	CDS	3890301	3891113	813	-	PGF_00048556	270	Ribonuclease HII (EC 3.1.26.4)	GO:0004523|RNA-DNA hybrid ribonuclease activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3755	PATRIC.2.9855.2.9855.con.0001.CDS.3891100.3891963.rev	PATRIC	CDS	3891100	3891963	864	-	PGF_00426877	287	LSU ribosomal maturation GTPase RbgA (B. subtilis YlqF)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3756	PATRIC.2.9855.2.9855.con.0001.CDS.3892181.3892531.rev	PATRIC	CDS	3892181	3892531	351	-	PGF_04845029	116	LSU ribosomal protein L19p		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3757	PATRIC.2.9855.2.9855.con.0001.CDS.3892648.3893367.rev	PATRIC	CDS	3892648	3893367	720	-	PGF_00413208	239	tRNA (guanine(37)-N(1))-methyltransferase (EC 2.1.1.228)	GO:0052906|tRNA (guanine(37)-N(1))-methyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.342	PATRIC.2.9855.2.9855.con.0001.CDS.389323.390801.fwd	PATRIC	CDS	389323	390801	1479	+	PGF_00019898	492	Membrane protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3758	PATRIC.2.9855.2.9855.con.0001.CDS.3893357.3893854.rev	PATRIC	CDS	3893357	3893854	498	-	PGF_06000821	165	16S rRNA processing protein RimM		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3759	PATRIC.2.9855.2.9855.con.0001.CDS.3894256.3894483.rev	PATRIC	CDS	3894256	3894483	228	-	PGF_04388239	75	KH domain RNA binding protein YlqC		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3760	PATRIC.2.9855.2.9855.con.0001.CDS.3894532.3894777.rev	PATRIC	CDS	3894532	3894777	246	-	PGF_00178044	81	SSU ribosomal protein S16p		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3761	PATRIC.2.9855.2.9855.con.0001.CDS.3894830.3896182.rev	PATRIC	CDS	3894830	3896182	1353	-	PGF_00052238	450	Signal recognition particle protein Ffh		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3762	PATRIC.2.9855.2.9855.con.0001.CDS.3896195.3896524.rev	PATRIC	CDS	3896195	3896524	330	-	PGF_06632167	109	Signal recognition particle associated protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3763	PATRIC.2.9855.2.9855.con.0001.CDS.3896933.3897841.rev	PATRIC	CDS	3896933	3897841	909	-	PGF_08905885	302	Signal recognition particle receptor FtsY		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3764	PATRIC.2.9855.2.9855.con.0001.CDS.3897980.3901537.rev	PATRIC	CDS	3897980	3901537	3558	-	PGF_09950730	1185	Chromosome partition protein smc		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3766	PATRIC.2.9855.2.9855.con.0001.CDS.3901778.3902809.rev	PATRIC	CDS	3901778	3902809	1032	-	PGF_03754581	343	Radical SAM domain protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3767	PATRIC.2.9855.2.9855.con.0001.CDS.3902802.3903500.rev	PATRIC	CDS	3902802	3903500	699	-	PGF_03790040	232	Ribonuclease III (EC 3.1.26.3)	GO:0004525|ribonuclease III activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3768	PATRIC.2.9855.2.9855.con.0001.CDS.3903775.3904005.rev	PATRIC	CDS	3903775	3904005	231	-	PGF_07487229	76	Acyl carrier protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3769	PATRIC.2.9855.2.9855.con.0001.CDS.3904086.3905087.rev	PATRIC	CDS	3904086	3905087	1002	-	PGF_00033289	333	Phosphate:acyl-ACP acyltransferase PlsX (EC 2.3.1.n2)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3770	PATRIC.2.9855.2.9855.con.0001.CDS.3905334.3905516.rev	PATRIC	CDS	3905334	3905516	183	-	PGF_00016404	60	LSU ribosomal protein L32p @ LSU ribosomal protein L32p, zinc-dependent		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3771	PATRIC.2.9855.2.9855.con.0001.CDS.3905520.3906026.rev	PATRIC	CDS	3905520	3906026	507	-	PGF_02031353	168	FIG01269488: protein, clustered with ribosomal protein L32p		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3772	PATRIC.2.9855.2.9855.con.0001.CDS.3906375.3907577.rev	PATRIC	CDS	3906375	3907577	1203	-	PGF_09945671	400	Acetate kinase (EC 2.7.2.1)	GO:0008776|acetate kinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3773	PATRIC.2.9855.2.9855.con.0001.CDS.3907673.3908674.rev	PATRIC	CDS	3907673	3908674	1002	-	PGF_00033197	333	Phosphate acetyltransferase (EC 2.3.1.8)	GO:0008959|phosphate acetyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3774	PATRIC.2.9855.2.9855.con.0001.CDS.3909236.3910441.fwd	PATRIC	CDS	3909236	3910441	1206	+	PGF_00000196	401	UPF0348 protein family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3775	PATRIC.2.9855.2.9855.con.0001.CDS.3910494.3911675.fwd	PATRIC	CDS	3910494	3911675	1182	+	PGF_04040359	393	FIGfam003972: membrane protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3776	PATRIC.2.9855.2.9855.con.0001.CDS.3911655.3912197.rev	PATRIC	CDS	3911655	3912197	543	-	PGF_00000411	180	FIG00814129: Possible chaperone		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3777	PATRIC.2.9855.2.9855.con.0001.CDS.3912371.3912850.rev	PATRIC	CDS	3912371	3912850	480	-	PGF_04762552	159	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	GO:0004595|pantetheine-phosphate adenylyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3778	PATRIC.2.9855.2.9855.con.0001.CDS.3912854.3913411.rev	PATRIC	CDS	3912854	3913411	558	-	PGF_07133621	185	16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171)	GO:0052913|16S rRNA (guanine(966)-N(2))-methyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3779	PATRIC.2.9855.2.9855.con.0001.CDS.3913677.3915710.rev	PATRIC	CDS	3913677	3915710	2034	-	PGF_02226715	677	ATP-dependent DNA helicase RecG (EC 3.6.4.12)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3780	PATRIC.2.9855.2.9855.con.0001.CDS.3915771.3917411.rev	PATRIC	CDS	3915771	3917411	1641	-	PGF_00423429	546	Dihydroxyacetone kinase-like protein, phosphatase domain / Dihydroxyacetone kinase-like protein, kinase domain		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3781	PATRIC.2.9855.2.9855.con.0001.CDS.3917425.3917775.rev	PATRIC	CDS	3917425	3917775	351	-	PGF_05636025	116	FIG001802: Putative alkaline-shock protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3782	PATRIC.2.9855.2.9855.con.0001.CDS.3918671.3918862.fwd	PATRIC	CDS	3918671	3918862	192	+	PGF_00016387	63	LSU ribosomal protein L28p @ LSU ribosomal protein L28p, zinc-dependent		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3783	PATRIC.2.9855.2.9855.con.0001.CDS.3919351.3919986.rev	PATRIC	CDS	3919351	3919986	636	-	PGF_01719396	211	Thiamin pyrophosphokinase (EC 2.7.6.2)	GO:0004788|thiamine diphosphokinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3784	PATRIC.2.9855.2.9855.con.0001.CDS.3919991.3920635.rev	PATRIC	CDS	3919991	3920635	645	-	PGF_10245672	214	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	GO:0004750|ribulose-phosphate 3-epimerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3785	PATRIC.2.9855.2.9855.con.0001.CDS.3920629.3921501.rev	PATRIC	CDS	3920629	3921501	873	-	PGF_00048928	290	Ribosome small subunit biogenesis RbfA-release protein RsgA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.344	PATRIC.2.9855.2.9855.con.0001.CDS.392136.393416.fwd	PATRIC	CDS	392136	393416	1281	+	PGF_01283491	426	putative secreted protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3786	PATRIC.2.9855.2.9855.con.0001.CDS.3921870.3923813.rev	PATRIC	CDS	3921870	3923813	1944	-	PGF_06459503	647	Serine/threonine protein kinase PrkC, regulator of stationary phase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3787	PATRIC.2.9855.2.9855.con.0001.CDS.3923815.3924534.rev	PATRIC	CDS	3923815	3924534	720	-	PGF_01286574	239	Protein serine/threonine phosphatase PrpC, regulation of stationary phase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3788	PATRIC.2.9855.2.9855.con.0001.CDS.3924518.3925579.rev	PATRIC	CDS	3924518	3925579	1062	-	PGF_00618776	353	23S rRNA (adenine(2503)-C(2))-methyltransferase @ tRNA (adenine(37)-C(2))-methyltransferase (EC 2.1.1.192)	GO:0070040|rRNA (adenine-C2-)-methyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3789	PATRIC.2.9855.2.9855.con.0001.CDS.3925591.3926910.rev	PATRIC	CDS	3925591	3926910	1320	-	PGF_00769755	439	16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2.1.1.176)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3790	PATRIC.2.9855.2.9855.con.0001.CDS.3926925.3927617.rev	PATRIC	CDS	3926925	3927617	693	-	PGF_07723617	230	Putative membrane protease YugP		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3791	PATRIC.2.9855.2.9855.con.0001.CDS.3927633.3928559.rev	PATRIC	CDS	3927633	3928559	927	-	PGF_05165078	308	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	GO:0004479|methionyl-tRNA formyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3792	PATRIC.2.9855.2.9855.con.0001.CDS.3928582.3929040.rev	PATRIC	CDS	3928582	3929040	459	-	PGF_00030655	152	Peptide deformylase (EC 3.5.1.88)	GO:0042586|peptide deformylase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3793	PATRIC.2.9855.2.9855.con.0001.CDS.3929053.3930192.rev	PATRIC	CDS	3929053	3930192	1140	-	PGF_00011081	379	Helicase PriA essential for oriC/DnaA-independent DNA replication		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3794	PATRIC.2.9855.2.9855.con.0001.CDS.3930325.3931251.rev	PATRIC	CDS	3930325	3931251	927	-	PGF_00011081	308	Helicase PriA essential for oriC/DnaA-independent DNA replication		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3795	PATRIC.2.9855.2.9855.con.0001.CDS.3931432.3932616.rev	PATRIC	CDS	3931432	3932616	1185	-	PGF_09111052	394	Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36) / Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)	GO:0004633|phosphopantothenoylcysteine decarboxylase activity;GO:0004632|phosphopantothenate--cysteine ligase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3796	PATRIC.2.9855.2.9855.con.0001.CDS.3932618.3932836.rev	PATRIC	CDS	3932618	3932836	219	-	PGF_05906360	72	DNA-directed RNA polymerase omega subunit (EC 2.7.7.6)	GO:0003899|DNA-directed RNA polymerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3797	PATRIC.2.9855.2.9855.con.0001.CDS.3932817.3933455.rev	PATRIC	CDS	3932817	3933455	639	-	PGF_00689961	212	Guanylate kinase (EC 2.7.4.8)	GO:0004385|guanylate kinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3798	PATRIC.2.9855.2.9855.con.0001.CDS.3933455.3933727.rev	PATRIC	CDS	3933455	3933727	273	-	PGF_03021159	90	UPF0296 protein YlzA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3799	PATRIC.2.9855.2.9855.con.0001.CDS.3933742.3934623.rev	PATRIC	CDS	3933742	3934623	882	-	PGF_07102049	293	UPF0701 protein YicC		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.345	PATRIC.2.9855.2.9855.con.0001.CDS.393421.394674.fwd	PATRIC	CDS	393421	394674	1254	+	PGF_00009593	417	Uncharacterized glycosyltransferase YdaM		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3800	PATRIC.2.9855.2.9855.con.0001.CDS.3935199.3935792.fwd	PATRIC	CDS	3935199	3935792	594	+	PGF_01281703	197	FmtB protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3801	PATRIC.2.9855.2.9855.con.0001.CDS.3936079.3936504.rev	PATRIC	CDS	3936079	3936504	426	-	PGF_01296087	141	spbA protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3802	PATRIC.2.9855.2.9855.con.0001.CDS.3936945.3938423.rev	PATRIC	CDS	3936945	3938423	1479	-	PGF_00054087	492	Stage IV sporulation protein A		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3803	PATRIC.2.9855.2.9855.con.0001.CDS.3938933.3939925.rev	PATRIC	CDS	3938933	3939925	993	-	PGF_00008611	330	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	GO:0004367|glycerol-3-phosphate dehydrogenase [NAD+] activity;GO:0004367|glycerol-3-phosphate dehydrogenase [NADP+] activity;GO:0004367|glycerol-3-phosphate dehydrogenase [NAD(P)+] activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3804	PATRIC.2.9855.2.9855.con.0001.CDS.3939928.3941244.rev	PATRIC	CDS	3939928	3941244	1317	-	PGF_00007024	438	GTP-binding protein EngA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3805	PATRIC.2.9855.2.9855.con.0001.CDS.3941303.3942637.rev	PATRIC	CDS	3941303	3942637	1335	-	PGF_00004177	444	Fe-S oxidoreductase, related to NifB/MoaA family with PDZ N-terminal domain		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3806	PATRIC.2.9855.2.9855.con.0001.CDS.3942877.3943539.rev	PATRIC	CDS	3942877	3943539	663	-	PGF_00984073	220	Phosphate transport system regulatory protein PhoU		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3807	PATRIC.2.9855.2.9855.con.0001.CDS.3943851.3944513.rev	PATRIC	CDS	3943851	3944513	663	-	PGF_00984073	220	Phosphate transport system regulatory protein PhoU		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3808	PATRIC.2.9855.2.9855.con.0001.CDS.3944532.3945281.rev	PATRIC	CDS	3944532	3945281	750	-	PGF_06213055	249	Phosphate ABC transporter, ATP-binding protein PstB (TC 3.A.1.7.1)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3809	PATRIC.2.9855.2.9855.con.0001.CDS.3945291.3946175.rev	PATRIC	CDS	3945291	3946175	885	-	PGF_01072302	294	Phosphate ABC transporter, permease protein PstA (TC 3.A.1.7.1)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3810	PATRIC.2.9855.2.9855.con.0001.CDS.3946175.3947068.rev	PATRIC	CDS	3946175	3947068	894	-	PGF_02405545	297	Phosphate ABC transporter, permease protein PstC (TC 3.A.1.7.1)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3811	PATRIC.2.9855.2.9855.con.0001.CDS.3947092.3948000.rev	PATRIC	CDS	3947092	3948000	909	-	PGF_07668761	302	Phosphate ABC transporter, substrate-binding protein PstS (TC 3.A.1.7.1)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3812	PATRIC.2.9855.2.9855.con.0001.CDS.3948203.3949909.rev	PATRIC	CDS	3948203	3949909	1707	-	PGF_10125211	568	Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)	GO:0004673|protein histidine kinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3813	PATRIC.2.9855.2.9855.con.0001.CDS.3949912.3950613.rev	PATRIC	CDS	3949912	3950613	702	-	PGF_09160328	233	Phosphate regulon transcriptional regulatory protein PhoB (SphR)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3814	PATRIC.2.9855.2.9855.con.0001.CDS.3950629.3950829.rev	PATRIC	CDS	3950629	3950829	201	-	PGF_05501316	66	FIG00003370: Multicopper polyphenol oxidase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3815	PATRIC.2.9855.2.9855.con.0001.CDS.3950810.3951370.rev	PATRIC	CDS	3950810	3951370	561	-	PGF_05501316	186	FIG00003370: Multicopper polyphenol oxidase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3816	PATRIC.2.9855.2.9855.con.0001.CDS.3951643.3952086.rev	PATRIC	CDS	3951643	3952086	444	-	PGF_00048643	147	Ribonucleotide reductase transcriptional regulator NrdR		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3818	PATRIC.2.9855.2.9855.con.0001.CDS.3952467.3953240.rev	PATRIC	CDS	3952467	3953240	774	-	PGF_00046553	257	RNA polymerase sporulation specific sigma factor SigG		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3819	PATRIC.2.9855.2.9855.con.0001.CDS.3953323.3954030.rev	PATRIC	CDS	3953323	3954030	708	-	PGF_00046551	235	RNA polymerase sporulation specific sigma factor SigE		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3820	PATRIC.2.9855.2.9855.con.0001.CDS.3954005.3954847.rev	PATRIC	CDS	3954005	3954847	843	-	PGF_02629766	280	Sporulation sigma-E factor processing peptidase (SpoIIGA)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3821	PATRIC.2.9855.2.9855.con.0001.CDS.3955386.3956525.rev	PATRIC	CDS	3955386	3956525	1140	-	PGF_03520151	379	Cell division protein FtsZ		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3822	PATRIC.2.9855.2.9855.con.0001.CDS.3956540.3957793.rev	PATRIC	CDS	3956540	3957793	1254	-	PGF_00843497	417	Cell division protein FtsA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3823	PATRIC.2.9855.2.9855.con.0001.CDS.3957894.3958925.rev	PATRIC	CDS	3957894	3958925	1032	-	PGF_02204321	343	Twitching motility protein PilT		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3824	PATRIC.2.9855.2.9855.con.0001.CDS.3959185.3959883.rev	PATRIC	CDS	3959185	3959883	699	-	PGF_00591197	232	RNA polymerase sporulation specific sigma factor SigK		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3825	PATRIC.2.9855.2.9855.con.0001.CDS.3960193.3961995.rev	PATRIC	CDS	3960193	3961995	1803	-	PGF_12739364	600	MrdA-like protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3826	PATRIC.2.9855.2.9855.con.0001.CDS.3962060.3963280.rev	PATRIC	CDS	3962060	3963280	1221	-	PGF_09398028	406	Uncharacterized protease YrrO		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3827	PATRIC.2.9855.2.9855.con.0001.CDS.3963287.3963931.rev	PATRIC	CDS	3963287	3963931	645	-	PGF_08719117	214	FIG011945: O-methyltransferase family protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3828	PATRIC.2.9855.2.9855.con.0001.CDS.3964031.3965056.rev	PATRIC	CDS	3964031	3965056	1026	-	PGF_01534078	341	Murein endolytic transglycosylase MltG		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3829	PATRIC.2.9855.2.9855.con.0001.CDS.3965165.3966991.rev	PATRIC	CDS	3965165	3966991	1827	-	PGF_00007041	608	GTP-binding protein TypA/BipA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3830	PATRIC.2.9855.2.9855.con.0001.CDS.3967391.3968284.rev	PATRIC	CDS	3967391	3968284	894	-	PGF_06848757	297	Ribonuclease J2 (endoribonuclease in RNA processing)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3831	PATRIC.2.9855.2.9855.con.0001.CDS.3968294.3969058.rev	PATRIC	CDS	3968294	3969058	765	-	PGF_06848757	254	Ribonuclease J2 (endoribonuclease in RNA processing)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3832	PATRIC.2.9855.2.9855.con.0001.CDS.3969422.3969886.rev	PATRIC	CDS	3969422	3969886	465	-	PGF_10470343	154	Ferric uptake regulation protein FUR		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3835	PATRIC.2.9855.2.9855.con.0001.CDS.3970459.3970875.rev	PATRIC	CDS	3970459	3970875	417	-	PGF_10488938	138	Putative pre-16S rRNA nuclease YqgF		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3836	PATRIC.2.9855.2.9855.con.0001.CDS.3970984.3971241.rev	PATRIC	CDS	3970984	3971241	258	-	PGF_00013347	85	UPF0297 protein YrzL		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3837	PATRIC.2.9855.2.9855.con.0001.CDS.3971378.3974017.rev	PATRIC	CDS	3971378	3974017	2640	-	PGF_07830674	879	Alanyl-tRNA synthetase (EC 6.1.1.7)	GO:0004813|alanine-tRNA ligase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.347	PATRIC.2.9855.2.9855.con.0001.CDS.397414.398148.fwd	PATRIC	CDS	397414	398148	735	+	PGF_07900067	244	putative histidinol phosphatase and related hydrolases of the PHP family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3838	PATRIC.2.9855.2.9855.con.0001.CDS.3974824.3975852.rev	PATRIC	CDS	3974824	3975852	1029	-	PGF_06866315	342	Uncharacterized UPF0118 membrane protein		

Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3842	PATRIC.2.9855.2.9855.con.0001.CDS.3977623.3978699.rev	PATRIC	CDS	3977623	3978699	1077	-	PGF_07304022	358	tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.13)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3843	PATRIC.2.9855.2.9855.con.0001.CDS.3978711.3979148.rev	PATRIC	CDS	3978711	3979148	438	-	PGF_04198335	145	Iron-sulfur cluster assembly scaffold protein IscU/NifU-like	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3844	PATRIC.2.9855.2.9855.con.0001.CDS.3979150.3980331.rev	PATRIC	CDS	3979150	3980331	1182	-	PGF_10025016	393	Cysteine desulfurase (EC 2.8.1.7)	GO:0031071|cysteine desulfurase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.43	PATRIC.2.9855.2.9855.con.0001.CDS.39792.42542.fwd	PATRIC	CDS	39792	42542	2751	+	PGF_00026324	916	NtrC family Transcriptional regulator, ATPase domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3845	PATRIC.2.9855.2.9855.con.0001.CDS.3980334.3980786.rev	PATRIC	CDS	3980334	3980786	453	-	PGF_09345013	150	Iron-sulfur cluster regulator IscR	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3846	PATRIC.2.9855.2.9855.con.0001.CDS.3980909.3982153.rev	PATRIC	CDS	3980909	3982153	1245	-	PGF_05935795	414	Replication-associated recombination protein RarA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.348	PATRIC.2.9855.2.9855.con.0001.CDS.398221.398493.rev	PATRIC	CDS	398221	398493	273	-	PGF_10367439	90	Acylphosphate phosphohydrolase (EC 3.6.1.7)	GO:0003998|acylphosphatase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3852	PATRIC.2.9855.2.9855.con.0001.CDS.3985754.3987265.rev	PATRIC	CDS	3985754	3987265	1512	-	PGF_01316031	503	AMP-dependent synthetase and ligase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3854	PATRIC.2.9855.2.9855.con.0001.CDS.3988659.3990257.rev	PATRIC	CDS	3988659	3990257	1599	-	PGF_05144608	532	Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)	GO:0004147|dihydrolipoamide branched chain acyltransferase activity;GO:0004147|sterol O-acyltransferase activity;GO:0004147|N-acetyltransferase activity;GO:0004147|O-acyltransferase activity;GO:0004147|palmitoleoyl [acyl-carrier-protein]-dependent acyltransferase activity;GO:0004147|carnitine O-acyltransferase activity;GO:0004147|acetyltransferase activity;GO:0004147|C-acyltransferase activity;GO:0004147|palmitoyltransferase activity;GO:0004147|N-acyltransferase activity;GO:0004147|acylglycerol O-acyltransferase activity;GO:0004147|serine O-acyltransferase activity;GO:0004147|O-acetyltransferase activity;GO:0004147|O-octanoyltransferase activity;GO:0004147|octanoyltransferase activity;GO:0004147|O-palmitoyltransferase activity;GO:0004147|S-acyltransferase activity;GO:0004147|S-acetyltransferase activity;GO:0004147|S-malonyltransferase activity;GO:0004147|malonyltransferase activity;GO:0004147|C-palmitoyltransferase activity;GO:0004147|succinyltransferase activity;GO:0004147|N-succinyltransferase activity;GO:0004147|O-succinyltransferase activity;GO:0004147|S-succinyltransferase activity;GO:0004147|sinapoyltransferase activity;GO:0004147|O-sinapoyltransferase activity;GO:0004147|peptidyl-lysine N6-myristoyltransferase activity;GO:0004147|peptidyl-lysine N6-palmitoyltransferase activity;GO:0004147|benzoyl acetate-CoA thiolase activity;GO:0004147|3-hydroxybutyryl-CoA thiolase activity;GO:0004147|3-ketopimelyl-CoA thiolase activity;GO:0004147|N-palmitoyltransferase activity;GO:0004147|myristoyltransferase activity;GO:0004147|acyl-CoA N-acyltransferase activity;GO:0004147|protein-cysteine S-myristoyltransferase activity;GO:0004147|protein-cysteine S-acyltransferase activity;GO:0004147|dihydrolipoamide S-acyltransferase activity;GO:0004147|glucosaminyl-phosphotidylinositol O-acyltransferase activity;GO:0004147|ergosterol O-acyltransferase activity;GO:0004147|lanosterol O-
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.349	PATRIC.2.9855.2.9855.con.0001.CDS.398931.399338.fwd	PATRIC	CDS	398931	399338	408	+	PGF_03518570	135	Nucleoside diphosphate kinase (EC 2.7.4.6)	GO:0004550|nucleoside diphosphate kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3855	PATRIC.2.9855.2.9855.con.0001.CDS.3990831.3992726.rev	PATRIC	CDS	3990831	3992726	1896	-	PGF_01284125	631	Diguanylate cyclase/phosphodiesterase domain 1	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3858	PATRIC.2.9855.2.9855.con.0001.CDS.3994180.3995229.rev	PATRIC	CDS	3994180	3995229	1050	-	PGF_05728830	349	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3863	PATRIC.2.9855.2.9855.con.0001.CDS.3997733.3998527.rev	PATRIC	CDS	3997733	3998527	795	-	PGF_08407282	264	ABC transporter, ATP-binding protein (cluster 15, trp?)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3864	PATRIC.2.9855.2.9855.con.0001.CDS.3998493.3999395.rev	PATRIC	CDS	3998493	3999395	903	-	PGF_03204088	300	ABC transporter, permease protein (cluster 15, trp?)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3865	PATRIC.2.9855.2.9855.con.0001.CDS.3999395.4000411.rev	PATRIC	CDS	3999395	4000411	1017	-	PGF_07669258	338	ABC transporter, substrate-binding protein (cluster 15, trp?)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3866	PATRIC.2.9855.2.9855.con.0001.CDS.4000937.4001350.rev	PATRIC	CDS	4000937	4001350	414	-	PGF_00016134	137	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3867	PATRIC.2.9855.2.9855.con.0001.CDS.4001559.4002377.rev	PATRIC	CDS	4001559	4002377	819	-	PGF_05399159	272	Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)	GO:0003989|acetyl-CoA carboxylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3868	PATRIC.2.9855.2.9855.con.0001.CDS.4002380.4003243.rev	PATRIC	CDS	4002380	4003243	864	-	PGF_00026453	287	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)	GO:0003989|acetyl-CoA carboxylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3869	PATRIC.2.9855.2.9855.con.0001.CDS.4003236.4004588.rev	PATRIC	CDS	4003236	4004588	1353	-	PGF_07396749	450	Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)	GO:0004075|biotin carboxylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3870	PATRIC.2.9855.2.9855.con.0001.CDS.4004603.4005031.rev	PATRIC	CDS	4004603	4005031	429	-	PGF_07504595	142	3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form (EC 4.2.1.59)	GO:0019171|3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity;GO:0019171|3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3871	PATRIC.2.9855.2.9855.con.0001.CDS.4005035.4005550.rev	PATRIC	CDS	4005035	4005550	516	-	PGF_00648021	171	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3872	PATRIC.2.9855.2.9855.con.0001.CDS.4005821.4007056.rev	PATRIC	CDS	4005821	4007056	1236	-	PGF_06652053	411	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	GO:0033817|beta-ketoacyl-acyl-carrier-protein synthase II activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.351	PATRIC.2.9855.2.9855.con.0001.CDS.400657.401715.rev	PATRIC	CDS	400657	401715	1059	-	PGF_05982667	352	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)	GO:0008955|peptidoglycan glycosyltransferase activity;GO:0008234|cysteine-type peptidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3873	PATRIC.2.9855.2.9855.con.0001.CDS.4007074.4007814.rev	PATRIC	CDS	4007074	4007814	741	-	PGF_08693885	246	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100), FadG	GO:0004316|3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.8	PATRIC.2.9855.2.9855.con.0001.CDS.4008.4142.fwd	PATRIC	CDS	4008	4142	135	+	PGF_00417577	44	3-dehydroquinate dehydratase II (EC 4.2.1.10)	GO:0003855|3-dehydroquinate dehydratase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3874	PATRIC.2.9855.2.9855.con.0001.CDS.4008013.4008957.rev	PATRIC	CDS	4008013	4008957	945	-	PGF_06655223	314	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	GO:0004314|[acyl-carrier-protein] S-malonyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3875	PATRIC.2.9855.2.9855.con.0001.CDS.4008950.4009891.rev	PATRIC	CDS	4008950	4009891	942	-	PGF_02037786	313	Enoyl-[acyl-carrier-protein] reductase [FMN, NADH] (EC 1.3.1.9), FabK => refractory to triclosan	GO:0004318|enoyl-[acyl-carrier-protein] reductase (NADH) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3876	PATRIC.2.9855.2.9855.con.0001.CDS.4010246.4011217.rev	PATRIC	CDS	4010246	4011217	972	-	PGF_00420953	323	3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.180)	GO:0033818|beta-ketoacyl-acyl-carrier-protein synthase III activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3877	PATRIC.2.9855.2.9855.con.0001.CDS.4011232.4011681.rev	PATRIC	CDS	4011232	4011681	450	-	PGF_02278962	149	Transcriptional regulator of fatty acid biosynthesis FabT	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3880	PATRIC.2.9855.2.9855.con.0001.CDS.4014321.4015232.rev	PATRIC	CDS	4014321	4015232	912	-	PGF_00908432	303	TPR-repeat-containing protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3881	PATRIC.2.9855.2.9855.con.0001.CDS.4015489.4017798.rev	PATRIC	CDS	4015489	4017798	2310	-	PGF_01281691	769	Beta-lactamase regulatory sensor-transducer BlaR1	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.352	PATRIC.2.9855.2.9855.con.0001.CDS.401722.403131.rev	PATRIC	CDS	401722	403131	1410	-	PGF_05982667	469	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)	GO:0008955|peptidoglycan glycosyltransferase activity;GO:0008234|cysteine-type peptidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3882	PATRIC.2.9855.2.9855.con.0001.CDS.4017803.4018171.rev	PATRIC	CDS	4017803	4018171	369	-	PGF_01462000	122	Transcriptional repressor, BlaI/MecI family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3884	PATRIC.2.9855.2.9855.con.0001.CDS.4019415.4020665.rev	PATRIC	CDS	4019415	4020665	1251	-	PGF_07750515	416	Phosphoribosylamine--glycine ligase (EC 6.3.4.13)	GO:0004637|phosphoribosylamine-glycine ligase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3885	PATRIC.2.9855.2.9855.con.0001.CDS.4021081.4022589.rev	PATRIC	CDS	4021081	4022589	1509	-	PGF_00013509	502	IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	GO:0003937|IMP cyclohydrolase activity;GO:0004643|phosphoribosylaminoimidazolecarboxamide formyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3886	PATRIC.2.9855.2.9855.con.0001.CDS.4022603.4023214.rev	PATRIC	CDS	4022603	4023214	612	-	PGF_00033968	203	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	GO:0004644|phosphoribosylglycinamide formyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3887	PATRIC.2.9855.2.9855.con.0001.CDS.4023202.4024203.rev	PATRIC	CDS	4023202	4024203	1002	-	PGF_00033954	333	Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	GO:0004641|phosphoribosylformylglycinamidine cyclo-ligase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3888	PATRIC.2.9855.2.9855.con.0001.CDS.4024273.4025688.rev	PATRIC	CDS	4024273	4025688	1416	-	PGF_00050995	471	Amidophosphoribosyltransferase (EC 2.4.2.14)	GO:0004044|amidophosphoribosyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3889	PATRIC.2.9855.2.9855.con.0001.CDS.4025946.4026653.rev	PATRIC	CDS	4025946	4026653	708	-	PGF_00033936	235	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	GO:0004639|phosphoribosylaminoimidazolesuccinocarboxamide synthase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3890	PATRIC.2.9855.2.9855.con.0001.CDS.4026653.4027132.rev	PATRIC	CDS	4026653	4027132	480	-	PGF_05172785	159	N5-carboxyaminoimidazole ribonucleotide mutase (EC 5.4.99.18)	GO:0034023|5-(carboxyamino)imidazole ribonucleotide mutase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3891	PATRIC.2.9855.2.9855.con.0001.CDS.4027601.4031347.rev	PATRIC	CDS	4027601	4031347	3747	-	PGF_00033963	1248	Phosphoribosylformylglycinamidine synthase, synthetase subunit (EC 6.3.5.3) / Phosphoribosylformylglycinamidine synthase, glutamine amidotransferase subunit (EC 6.3.5.3)	GO:0004642|phosphoribosylformylglycinamidine synthase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3892	PATRIC.2.9855.2.9855.con.0001.CDS.4031855.4032022.rev	PATRIC	CDS	4031855	4032022	168	-	PGF_00067473	55	Zinc-ribbon domain Caur_1000.N	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3893	PATRIC.2.9855.2.9855.con.0001.CDS.4032289.4032975.rev	PATRIC	CDS	4032289	4032975	687	-	PGF_00008281	228	Glutamine ABC transporter, ATP-binding protein GlnQ	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3894	PATRIC.2.9855.2.9855.con.0001.CDS.4032991.4033632.rev	PATRIC	CDS	4032991	4033632	642	-	PGF_07804709	213	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3895	PATRIC.2.9855.2.9855.con.0001.CDS.4033696.4034529.rev	PATRIC	CDS	4033696	4034529	834	-	PGF_05873585	277	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3896	PATRIC.2.9855.2.9855.con.0001.CDS.4034678.4035193.rev	PATRIC	CDS	4034678	4035193	516	-	PGF_01272144	171	internalin, putative	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3898	PATRIC.2.9855.2.9855.con.0001.CDS.4036562.4037509.rev	PATRIC	CDS	4036562	4037509	948	-	PGF_00634936	315	Protein QmcA (possibly involved in integral membrane quality control)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3899	PATRIC.2.9855.2.9855.con.0001.CDS.4037513.4037944.rev	PATRIC	CDS	4037513	4037944	432	-	PGF_00926873	143	Putative activity regulator of membrane protease YbbK	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3900	PATRIC.2.9855.2.9855.con.0001.CDS.4038261.4040159.fwd	PATRIC	CDS	4038261	4040159	1899	+	PGF_06525160	632	NAD synthetase (EC 6.3.1.5) / Glutamine amidotransferase chain of NAD synthetase	GO:0008795|NAD+ synthase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3901	PATRIC.2.9855.2.9855.con.0001.CDS.4040481.4041509.fwd	PATRIC	CDS	4040481	4041509	1029	+	PGF_08376928	342	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	GO:0004084|branched-chain-amino-acid transaminase activity;GO:0004084|L-leucine transaminase activity;GO:0004084|L-valine transaminase activity;GO:0004084|L-isoleucine transaminase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3903	PATRIC.2.9855.2.9855.con.0001.CDS.4042204.4043910.rev	PATRIC	CDS	4042204	4043910	1707	-	PGF_01462537	568	Efflux ABC transporter, permease/ATP-binding protein YwjA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.354	PATRIC.2.9855.2.9855.con.0001.CDS.404226.404747.rev	PATRIC	CDS	404226	404747	522	-	PGF_00013490	173	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	GO:0004422|hypoxanthine phosphoribosyltransferase activity;GO:0004422|guanine phosphoribosyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3905	PATRIC.2.9855.2.9855.con.0001.CDS.4044298.4044966.rev	PATRIC	CDS	4044298	4044966	669	-	PGF_04580158	222	ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3906	PATRIC.2.9855.2.9855.con.0001.CDS.4044963.4045718.rev	PATRIC	CDS	4044963	4045718	756	-	PGF_10519324	251	ABC transporter, permease protein (cluster 10, nitrate/sulfonate/bicarbonate)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3907	PATRIC.2.9855.2.9855.con.0001.CDS.4045693.4046691.rev	PATRIC	CDS	4045693	4046691	999	-	PGF_08616437	332	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3908	PATRIC.2.9855.2.9855.con.0001.CDS.4047303.4047722.rev	PATRIC	CDS	4047303	4047722	420	-	PGF_02778011	139	DUF327 domain-containing protein CA_C1049	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3909	PATRIC.2.9855.2.9855.con.0001.CDS.4048041.4050653.fwd	PATRIC	CDS	4048041	4050653	2613	+	PGF_02952136	870	Cation-transporting ATPase, E1-E2 family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3911	PATRIC.2.9855.2.9855.con.0001.CDS.4051174.4053018.rev	PATRIC	CDS	4051174	4053018	1845	-	PGF_05423582	614	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)	GO:0004066|asparagine synthase (glutamine-hydrolyzing) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3912	PATRIC.2.9855.2.9855.con.0001.CDS.4053458.4054873.fwd	PATRIC	CDS	4053458	4054873	1416	+	PGF_00054103	471	Stage V sporulation protein AF (SpoVAF)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.355	PATRIC.2.9855.2.9855.con.0001.CDS.405443.407233.fwd	PATRIC	CDS	405443	407233	1791	+	PGF_00007028	596	Ribosome LSU-associated GTP-binding protein HflX	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3913	PATRIC.2.9855.2.9855.con.0001.CDS.4054961.4055797.rev	PATRIC	CDS	4054961	4055797	837	-	PGF_02026136	278	Uncharacterized S1 RNA binding domain protein YitL	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3914	PATRIC.2.9855.2.9855.con.0001.CDS.4056006.4056506.rev	PATRIC	CDS	4056006	4056506	501	-	PGF_00900330	166	Carbonic anhydrase-like protein MJ0304	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3917	PATRIC.2.9855.2.9855.con.0001.CDS.4058412.4058882.fwd	PATRIC	CDS	4058412	4058882	471	+	PGF_01424767	156	Transcriptional regulator, AsnC family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3918	PATRIC.2.9855.2.9855.con.0001.CDS.4058956.4059156.fwd	PATRIC	CDS	4058956	4059156	201	+	PGF_05313742	66	Uncharacterized membrane protein YuzA	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3919	PATRIC.2.9855.2.9855.con.0001.CDS.4059377.4060135.fwd	PATRIC	CDS	4059377	4060135	759	+	PGF_06535427	252	Uncharacterized DUF1113 membrane protein family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3920	PATRIC.2.9855.2.9855.con.0001.CDS.4060166.4061917.rev	PATRIC	CDS	4060166	4061917	1752	-	PGF_00779345	583	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)	GO:0004612|phosphoenolpyruvate carboxykinase (ATP) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3921	PATRIC.2.9855.2.9855.con.0001.CDS.4062316.4063197.fwd	PATRIC	CDS	4062316	4063197	882	+	PGF_10420457	293	MBL-fold metallo-hydrolase superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3923	PATRIC.2.9855.2.9855.con.0001.CDS.4064123.4064851.rev	PATRIC	CDS	4064123	4064851	729	-	PGF_03116802	242	Phosphoserine phosphatase (EC 3.1.3.3)	GO:0004647|phosphoserine phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3924	PATRIC.2.9855.2.9855.con.0001.CDS.4065113.4065649.rev	PATRIC	CDS	4065113	4065649	537	-	PGF_06672158	178	Nitroreductase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3925	PATRIC.2.9855.2.9855.con.0001.CDS.4065679.4066812.rev	PATRIC	CDS	4065679	4066812	1134	-	PGF_06866315	377	Uncharacterized UPF0118 membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3926	PATRIC.2.9855.2.9855.con.0001.CDS.4066965.4068656.rev	PATRIC	CDS	4066965	4068656	1692	-	PGF_00926109	563	Arginyl-tRNA synthetase (EC 6.1.1.19)	GO:0004814|arginine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3929	PATRIC.2.9855.2.9855.con.0001.CDS.4071358.4071645.rev	PATRIC	CDS	4071358	4071645	288	-	PGF_00023916	95	N-acetylmuramoyl-L-alanine amidase/putative S-layer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3930	PATRIC.2.9855.2.9855.con.0001.CDS.4071688.4072392.rev	PATRIC	CDS	4071688	4072392	705	-	PGF_00023916	234	N-acetylmuramoyl-L-alanine amidase/putative S-layer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3931	PATRIC.2.9855.2.9855.con.0001.CDS.4072578.4073549.fwd	PATRIC	CDS	4072578	4073549	972	+	PGF_04486278	323	Biotin operon repressor / Biotin--protein ligase (EC 6.3.4.9)(EC 6.3.4.10)(EC 6.3.4.11)(EC 6.3.4.15)	GO:0004079|biotin-[methylmalonyl-CoA-carboxytransferase] ligase activity;GO:0004080|biotin-[propionyl-CoA-carboxylase (ATP-hydrolyzing)] ligase activity;GO:0004078|biotin-[methylcrotonoyl-CoA-carboxylase] ligase activity;GO:0004077|biotin-[acetyl-CoA-carboxylase] ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3932	PATRIC.2.9855.2.9855.con.0001.CDS.4074307.4075257.rev	PATRIC	CDS	4074307	4075257	951	-	PGF_03941737	316	L-lactate dehydrogenase (EC 1.1.1.27)	GO:0004459|L-lactate dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3933	PATRIC.2.9855.2.9855.con.0001.CDS.4075520.4076149.fwd	PATRIC	CDS	4075520	4076149	630	+	PGF_12770045	209	DNA polymerase III epsilon subunit (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3934	PATRIC.2.9855.2.9855.con.0001.CDS.4076310.4076471.fwd	PATRIC	CDS	4076310	4076471	162	+	PGF_00929131	53	Rubredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3935	PATRIC.2.9855.2.9855.con.0001.CDS.4076705.4078936.rev	PATRIC	CDS	4076705	4078936	2232	-	PGF_06513690	743	Pyruvate formate-lyase (EC 2.3.1.54)	GO:0008861|formate C-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3936	PATRIC.2.9855.2.9855.con.0001.CDS.4079377.4080102.rev	PATRIC	CDS	4079377	4080102	726	-	PGF_08333365	241	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	GO:0043365|[formate-C-acetyltransferase]-activating enzyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3937	PATRIC.2.9855.2.9855.con.0001.CDS.4080446.4082677.rev	PATRIC	CDS	4080446	4082677	2232	-	PGF_06513690	743	Pyruvate formate-lyase (EC 2.3.1.54)	GO:0008861|formate C-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3939	PATRIC.2.9855.2.9855.con.0001.CDS.4084668.4085429.rev	PATRIC	CDS	4084668	4085429	762	-	PGF_02617142	253	5'-nucleotidase SurE (EC 3.1.3.5)	GO:0008253|5'-nucleotidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3940	PATRIC.2.9855.2.9855.con.0001.CDS.4086125.4086799.rev	PATRIC	CDS	4086125	4086799	675	-	PGF_10381714	224	Orotate phosphoribosyltransferase (EC 2.4.2.10)	GO:0004588|orotate phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3941	PATRIC.2.9855.2.9855.con.0001.CDS.4086899.4087795.rev	PATRIC	CDS	4086899	4087795	897	-	PGF_03029062	298	Dihydroorotate dehydrogenase (NAD(+)), catalytic subunit (EC 1.3.1.14)	GO:0004589|orotate reductase (NADH) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3942	PATRIC.2.9855.2.9855.con.0001.CDS.4087817.4088560.rev	PATRIC	CDS	4087817	4088560	744	-	PGF_01513923	247	Dihydroorotate dehydrogenase (NAD(+)), electron transfer subunit (EC 1.3.1.14)	GO:0004589|orotate reductase (NADH) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3943	PATRIC.2.9855.2.9855.con.0001.CDS.4088596.4089567.rev	PATRIC	CDS	4088596	4089567	972	-	PGF_06461498	323	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	GO:0004590|orotidine-5'-phosphate decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3944	PATRIC.2.9855.2.9855.con.0001.CDS.4089829.4091025.rev	PATRIC	CDS	4089829	4091025	1197	-	PGF_00423378	398	Dihydroorotase (EC 3.5.2.3)	GO:0004151|dihydroorotase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3945	PATRIC.2.9855.2.9855.con.0001.CDS.4091045.4091476.rev	PATRIC	CDS	4091045	4091476	432	-	PGF_00066960	143	Aspartate carbamoyltransferase regulatory chain (PyrI)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3946	PATRIC.2.9855.2.9855.con.0001.CDS.4091478.4092404.rev	PATRIC	CDS	4091478	4092404	927	-	PGF_00066906	308	Aspartate carbamoyltransferase (EC 2.1.3.2)	GO:0004070|aspartate carbamoyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3947	PATRIC.2.9855.2.9855.con.0001.CDS.4092707.4093483.rev	PATRIC	CDS	4092707	4093483	777	-	PGF_00918177	258	Beta-lactamase class A-like and penicillin binding proteins (PBPs) superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.358	PATRIC.2.9855.2.9855.con.0001.CDS.409332.410774.fwd	PATRIC	CDS	409332	410774	1443	+	PGF_09985786	480	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	GO:0004069|L-aspartate:2-oxoglutarate aminotransferase activity;GO:0004069|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3948	PATRIC.2.9855.2.9855.con.0001.CDS.4093578.4094675.rev	PATRIC	CDS	4093578	4094675	1098	-	PGF_07421229	365	6-phosphofructokinase (EC 2.7.1.11)	GO:0003872|6-phosphofructokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3949	PATRIC.2.9855.2.9855.con.0001.CDS.4095277.4096137.rev	PATRIC	CDS	4095277	4096137	861	-	PGF_00084324	286	Undecaprenyl-diphosphatase (EC 3.6.1.27)	GO:0050380|undecaprenyl-diphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3950	PATRIC.2.9855.2.9855.con.0001.CDS.4096468.4097445.rev	PATRIC	CDS	4096468	4097445	978	-	PGF_06400908	325	Mannose-6-phosphate isomerase (EC 5.3.1.8)	GO:0004476|mannose-6-phosphate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3951	PATRIC.2.9855.2.9855.con.0001.CDS.4097514.4099364.rev	PATRIC	CDS	4097514	4099364	1851	-	PGF_00419473	616	Conserved protein, tetratricopeptide repeat family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3952	PATRIC.2.9855.2.9855.con.0001.CDS.4099788.4100885.rev	PATRIC	CDS	4099788	4100885	1098	-	PGF_00007012	365	GTP-binding and nucleic acid-binding protein YchF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3953	PATRIC.2.9855.2.9855.con.0001.CDS.4101446.4102333.fwd	PATRIC	CDS	4101446	4102333	888	+	PGF_03462401	295	Peptidoglycan-N-acetylmuramic acid deacetylase PdaA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3956	PATRIC.2.9855.2.9855.con.0001.CDS.4103558.4104208.rev	PATRIC	CDS	4103558	4104208	651	-	PGF_01020154	216	Formiminotetrahydrofolate cyclodeaminase (EC 4.3.1.4)	GO:0030412|formimidoyltetrahydrofolate cyclodeaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3958	PATRIC.2.9855.2.9855.con.0001.CDS.4105471.4106634.rev	PATRIC	CDS	4105471	4106634	1164	-	PGF_00044330	387	Putative teichuronic acid biosynthesis glycosyl transferase TuaC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3959	PATRIC.2.9855.2.9855.con.0001.CDS.4106635.4107924.rev	PATRIC	CDS	4106635	4107924	1290	-	PGF_01285323	429	TPR/glycosyl transferase domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3960	PATRIC.2.9855.2.9855.con.0001.CDS.4107936.4109462.rev	PATRIC	CDS	4107936	4109462	1527	-	PGF_07235150	508	Peptidoglycan lipid II flippase MurJ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3961	PATRIC.2.9855.2.9855.con.0001.CDS.4109507.4110232.rev	PATRIC	CDS	4109507	4110232	726	-	PGF_03416607	241	N-acetylmannosaminyltransferase (EC 2.4.1.187)	GO:0047244|N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3962	PATRIC.2.9855.2.9855.con.0001.CDS.4110355.4111455.rev	PATRIC	CDS	4110355	4111455	1101	-	PGF_00055640	366	TPR repeats containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.359	PATRIC.2.9855.2.9855.con.0001.CDS.411151.411798.fwd	PATRIC	CDS	411151	411798	648	+	PGF_00425679	215	FIG000605: protein co-occurring with transport systems (COG1739)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3963	PATRIC.2.9855.2.9855.con.0001.CDS.4111993.4113720.rev	PATRIC	CDS	4111993	4113720	1728	-	PGF_00837639	575	Phosphoglucomutase (EC 5.4.2.2) @ Phosphomannomutase (EC 5.4.2.8)	GO:0004614|phosphoglucomutase activity;GO:0004615|phosphomannomutase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3964	PATRIC.2.9855.2.9855.con.0001.CDS.4114028.4114597.rev	PATRIC	CDS	4114028	4114597	570	-	PGF_07051332	189	LSU ribosomal protein L25p	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3965	PATRIC.2.9855.2.9855.con.0001.CDS.4114927.4118418.rev	PATRIC	CDS	4114927	4118418	3492	-	PGF_08690689	1163	Exonuclease SbcC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3966	PATRIC.2.9855.2.9855.con.0001.CDS.4118393.4119622.rev	PATRIC	CDS	4118393	4119622	1230	-	PGF_09155108	409	Exonuclease SbcD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3967	PATRIC.2.9855.2.9855.con.0001.CDS.4119901.4120449.fwd	PATRIC	CDS	4119901	4120449	549	+	PGF_00054401	182	Substrate-specific component PdxU2 of predicted pyridoxin-related ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3968	PATRIC.2.9855.2.9855.con.0001.CDS.4120790.4122244.rev	PATRIC	CDS	4120790	4122244	1455	-	PGF_09996723	484	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.360	PATRIC.2.9855.2.9855.con.0001.CDS.412177.412914.fwd	PATRIC	CDS	412177	412914	738	+	PGF_05767868	245	Probable transcriptional regulatory protein YebC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3969	PATRIC.2.9855.2.9855.con.0001.CDS.4122415.4123650.fwd	PATRIC	CDS	4122415	4123650	1236	+	PGF_02917027	411	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3970	PATRIC.2.9855.2.9855.con.0001.CDS.4123750.4124262.rev	PATRIC	CDS	4123750	4124262	513	-	PGF_10519603	170	Acetyltransferase, GNAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3971	PATRIC.2.9855.2.9855.con.0001.CDS.4124504.4125289.rev	PATRIC	CDS	4124504	4125289	786	-	PGF_02631779	261	Histidinol-phosphatase-related protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3972	PATRIC.2.9855.2.9855.con.0001.CDS.4125330.4126157.rev	PATRIC	CDS	4125330	4126157	828	-	PGF_00012589	275	Hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3973	PATRIC.2.9855.2.9855.con.0001.CDS.4126732.4127598.fwd	PATRIC	CDS	4126732	4127598	867	+	PGF_09655255	288	Transcriptional regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3974	PATRIC.2.9855.2.9855.con.0001.CDS.4127884.4130823.rev	PATRIC	CDS	4127884	4130823	2940	-	PGF_00049981	979	SWF/SNF family helicase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3975	PATRIC.2.9855.2.9855.con.0001.CDS.4131120.4131515.fwd	PATRIC	CDS	4131120	4131515	396	+	PGF_00960129	131	Transcriptional repressor, BlaI/MecI family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3976	PATRIC.2.9855.2.9855.con.0001.CDS.4131662.4133878.fwd	PATRIC	CDS	4131662	4133878	2217	+	PGF_00715121	738	Regulatory sensor-transducer, BlaR1/MecR1 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3977	PATRIC.2.9855.2.9855.con.0001.CDS.4134051.4134917.rev	PATRIC	CDS	4134051	4134917	867	-	PGF_00036472	288	Predicted transcriptional regulator, dicA/hipB/ansR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3978	PATRIC.2.9855.2.9855.con.0001.CDS.4135098.4136561.fwd	PATRIC	CDS	4135098	4136561	1464	+	PGF_02933248	487	Membrane protein involved in the export of O-antigen, teichoic acid lipoteichoic acids	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3979	PATRIC.2.9855.2.9855.con.0001.CDS.4136833.4137888.rev	PATRIC	CDS	4136833	4137888	1056	-	PGF_00773249	351	putative glucosamine-fructose-6-phosphate aminotransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3980	PATRIC.2.9855.2.9855.con.0001.CDS.4137917.4138717.rev	PATRIC	CDS	4137917	4138717	801	-	PGF_00644224	266	PTS system, mannose-specific IID component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3981	PATRIC.2.9855.2.9855.con.0001.CDS.4138710.4138895.rev	PATRIC	CDS	4138710	4138895	186	-	PGF_01653368	61	PTS system, mannose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3982	PATRIC.2.9855.2.9855.con.0001.CDS.4138849.4139502.rev	PATRIC	CDS	4138849	4139502	654	-	PGF_01653368	217	PTS system, mannose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3983	PATRIC.2.9855.2.9855.con.0001.CDS.4139521.4139988.rev	PATRIC	CDS	4139521	4139988	468	-	PGF_08661804	155	PTS system, mannose-specific IIB component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3984	PATRIC.2.9855.2.9855.con.0001.CDS.4139978.4140418.rev	PATRIC	CDS	4139978	4140418	441	-	PGF_06621789	146	PTS system, mannose-specific IIA component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3985	PATRIC.2.9855.2.9855.con.0001.CDS.4140530.4143289.rev	PATRIC	CDS	4140530	4143289	2760	-	PGF_00026324	919	NtrC family Transcriptional regulator, ATPase domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3986	PATRIC.2.9855.2.9855.con.0001.CDS.4143838.4144707.fwd	PATRIC	CDS	4143838	4144707	870	+	PGF_01737397	289	FIG00031715: Predicted metal-dependent phosphoesterases (PHP family)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3987	PATRIC.2.9855.2.9855.con.0001.CDS.4144914.4145777.rev	PATRIC	CDS	4144914	4145777	864	-	PGF_01971913	287	Uncharacterized sugar kinase, ribokinase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3988	PATRIC.2.9855.2.9855.con.0001.CDS.4145849.4146847.rev	PATRIC	CDS	4145849	4146847	999	-	PGF_03066827	332	Putative glucosamine-fructose-6-phosphate aminotransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3989	PATRIC.2.9855.2.9855.con.0001.CDS.4146915.4147754.rev	PATRIC	CDS	4146915	4147754	840	-	PGF_00644224	279	PTS system, mannose-specific IID component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3990	PATRIC.2.9855.2.9855.con.0001.CDS.4147741.4148505.rev	PATRIC	CDS	4147741	4148505	765	-	PGF_01653368	254	PTS system, mannose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3991	PATRIC.2.9855.2.9855.con.0001.CDS.4148520.4148990.rev	PATRIC	CDS	4148520	4148990	471	-	PGF_08661804	156	PTS system, mannose-specific IIB component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3992	PATRIC.2.9855.2.9855.con.0001.CDS.4149005.4149427.rev	PATRIC	CDS	4149005	4149427	423	-	PGF_06621789	140	PTS system, mannose-specific IIA component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3993	PATRIC.2.9855.2.9855.con.0001.CDS.4149550.4152324.rev	PATRIC	CDS	4149550	4152324	2775	-	PGF_00026324	924	NtrC family Transcriptional regulator, ATPase domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3994	PATRIC.2.9855.2.9855.con.0001.CDS.4152479.4155178.rev	PATRIC	CDS	4152479	4155178	2700	-	PGF_00026324	899	NtrC family Transcriptional regulator, ATPase domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3995	PATRIC.2.9855.2.9855.con.0001.CDS.4155378.4155716.rev	PATRIC	CDS	4155378	4155716	339	-	PGF_01629422	112	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3996	PATRIC.2.9855.2.9855.con.0001.CDS.4155730.4156038.rev	PATRIC	CDS	4155730	4156038	309	-	PGF_05148511	102	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3997	PATRIC.2.9855.2.9855.con.0001.CDS.4156089.4157345.rev	PATRIC	CDS	4156089	4157345	1257	-	PGF_00029610	418	PTS system, cellobiose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3998	PATRIC.2.9855.2.9855.con.0001.CDS.4158425.4159225.rev	PATRIC	CDS	4158425	4159225	801	-	PGF_01284118	266	Chitosanase precursor (EC 3.2.1.132)	GO:0016977|chitosanase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4000	PATRIC.2.9855.2.9855.con.0001.CDS.4160603.4161331.rev	PATRIC	CDS	4160603	4161331	729	-	PGF_09153377	242	Uncharacterized protein YbbK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4001	PATRIC.2.9855.2.9855.con.0001.CDS.4161506.4163866.rev	PATRIC	CDS	4161506	4163866	2361	-	PGF_06776852	786	Recombination inhibitory protein MutS2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4002	PATRIC.2.9855.2.9855.con.0001.CDS.4164020.4166380.rev	PATRIC	CDS	4164020	4166380	2361	-	PGF_01281052	786	Uncharacterized protease CPF_2136	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4003	PATRIC.2.9855.2.9855.con.0001.CDS.4166397.4168361.rev	PATRIC	CDS	4166397	4168361	1965	-	PGF_00023579	654	Myosin heavy chain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4004	PATRIC.2.9855.2.9855.con.0001.CDS.4168636.4169994.fwd	PATRIC	CDS	4168636	4169994	1359	+	PGF_02777905	452	proposed amino acid ligase found clustered with an amidotransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4005	PATRIC.2.9855.2.9855.con.0001.CDS.4170013.4170735.fwd	PATRIC	CDS	4170013	4170735	723	+	PGF_03801195	240	Putative amidotransferase similar to cobyric acid synthase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4006	PATRIC.2.9855.2.9855.con.0001.CDS.4170901.4172223.fwd	PATRIC	CDS	4170901	4172223	1323	+	PGF_06594113	440	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	GO:0009002|serine-type D-Ala-D-Ala carboxypeptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4007	PATRIC.2.9855.2.9855.con.0001.CDS.4172329.4172913.fwd	PATRIC	CDS	4172329	4172913	585	+	PGF_00809978	194	Flavoredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.365	PATRIC.2.9855.2.9855.con.0001.CDS.417263.417556.rev	PATRIC	CDS	417263	417556	294	-		97	Phage antirepressor protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4008	PATRIC.2.9855.2.9855.con.0001.CDS.4173087.4174136.fwd	PATRIC	CDS	4173087	4174136	1050	+	PGF_05728830	349	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4010	PATRIC.2.9855.2.9855.con.0001.CDS.4175782.4176495.rev	PATRIC	CDS	4175782	4176495	714	-	PGF_00017655	237	LrgA-associated membrane protein LrgB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4011	PATRIC.2.9855.2.9855.con.0001.CDS.4176535.4176891.rev	PATRIC	CDS	4176535	4176891	357	-	PGF_01151115	118	Antiholin-like protein LrgA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4012	PATRIC.2.9855.2.9855.con.0001.CDS.4177195.4178031.rev	PATRIC	CDS	4177195	4178031	837	-	PGF_04149001	278	Hydroxymethylpyrimidine ABC transporter, transmembrane component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4013	PATRIC.2.9855.2.9855.con.0001.CDS.4178018.4178785.rev	PATRIC	CDS	4178018	4178785	768	-	PGF_05587835	255	Hydroxymethylpyrimidine ABC transporter, ATPase component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4014	PATRIC.2.9855.2.9855.con.0001.CDS.4178820.4179296.rev	PATRIC	CDS	4178820	4179296	477	-	PGF_08616437	158	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4017	PATRIC.2.9855.2.9855.con.0001.CDS.4180989.4181777.rev	PATRIC	CDS	4180989	4181777	789	-	PGF_05179218	262	Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (EC 3.2.1.17)	GO:0003796|lysozyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4027	PATRIC.2.9855.2.9855.con.0001.CDS.4187180.4188865.rev	PATRIC	CDS	4187180	4188865	1686	-	PGF_12924161	561	Phage endopeptidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4034	PATRIC.2.9855.2.9855.con.0001.CDS.4194859.4195206.rev	PATRIC	CDS	4194859	4195206	348	-	PGF_07389431	115	Phage head-tail adaptor (ACLAME 40)	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4036	PATRIC.2.9855.2.9855.con.0001.CDS.4196390.4196983.rev	PATRIC	CDS	4196390	4196983	594	-	PGF_12901354	197	Phage head maturation protease		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4037	PATRIC.2.9855.2.9855.con.0001.CDS.4197000.4197281.rev	PATRIC	CDS	4197000	4197281	282	-	PGF_07445627	93	Phage DNA packaging		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4038	PATRIC.2.9855.2.9855.con.0001.CDS.4197262.4198524.rev	PATRIC	CDS	4197262	4198524	1263	-	PGF_01675198	420	Phage portal protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4040	PATRIC.2.9855.2.9855.con.0001.CDS.4198757.4200436.rev	PATRIC	CDS	4198757	4200436	1680	-	PGF_12737092	559	Phage terminase, large subunit		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4041	PATRIC.2.9855.2.9855.con.0001.CDS.4200436.4200900.rev	PATRIC	CDS	4200436	4200900	465	-	PGF_00032486	154	Phage terminase, small subunit		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4042	PATRIC.2.9855.2.9855.con.0001.CDS.4201017.4201445.rev	PATRIC	CDS	4201017	4201445	429	-	PGF_08270901	142	Phage-associated homing endonuclease		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4065	PATRIC.2.9855.2.9855.con.0001.CDS.4212174.4212512.fwd	PATRIC	CDS	4212174	4212512	339	+	PGF_06335969	112	Transcriptional regulator, Xre family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4069	PATRIC.2.9855.2.9855.con.0001.CDS.4216739.4217236.fwd	PATRIC	CDS	4216739	4217236	498	+	PGF_01282245	165	Gp23-like protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4070	PATRIC.2.9855.2.9855.con.0001.CDS.4217338.4218951.fwd	PATRIC	CDS	4217338	4218951	1614	+	PGF_01324157	537	Cassette chromosome recombinase B		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4071	PATRIC.2.9855.2.9855.con.0001.CDS.4218926.4219516.rev	PATRIC	CDS	4218926	4219516	591	-	PGF_08616437	196	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4072	PATRIC.2.9855.2.9855.con.0001.CDS.4219846.4221321.fwd	PATRIC	CDS	4219846	4221321	1476	+	PGF_00053479	491	Sodium/proline symporter		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4073	PATRIC.2.9855.2.9855.con.0001.CDS.4221429.4223537.rev	PATRIC	CDS	4221429	4223537	2109	-	PGF_07849456	702	Methyl-accepting chemotaxis protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4074	PATRIC.2.9855.2.9855.con.0001.CDS.4223573.4224307.rev	PATRIC	CDS	4223573	4224307	735	-	PGF_01286518	244	Acetyltransferase-like		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4075	PATRIC.2.9855.2.9855.con.0001.CDS.4225022.4225927.rev	PATRIC	CDS	4225022	4225927	906	-	PGF_00069433	301	calcineurin-like phosphoesterase family protein / contains Pfam profile: PF00149 calcineurin-like phosphoesterase; go_function: protein serine/threonine phosphatase activity [goid 0004722]		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4076	PATRIC.2.9855.2.9855.con.0001.CDS.4226186.4228186.rev	PATRIC	CDS	4226186	4228186	2001	-	PGF_07849456	666	Methyl-accepting chemotaxis protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4077	PATRIC.2.9855.2.9855.con.0001.CDS.4228660.4229892.rev	PATRIC	CDS	4228660	4229892	1233	-	PGF_06614457	410	Ammonium transporter		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4079	PATRIC.2.9855.2.9855.con.0001.CDS.4231478.4232368.fwd	PATRIC	CDS	4231478	4232368	891	+	PGF_10532194	296	Oxidoreductase, short-chain dehydrogenase/reductase family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4080	PATRIC.2.9855.2.9855.con.0001.CDS.4232432.4234600.rev	PATRIC	CDS	4232432	4234600	2169	-	PGF_10013075	722	DNA topoisomerase III (EC 5.99.1.2)	GO:0003917|DNA topoisomerase type I activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4082	PATRIC.2.9855.2.9855.con.0001.CDS.4235862.4236821.rev	PATRIC	CDS	4235862	4236821	960	-	PGF_00039182	319	Putative D-2-hydroxyacid dehydrogenase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4083	PATRIC.2.9855.2.9855.con.0001.CDS.4237150.4239510.rev	PATRIC	CDS	4237150	4239510	2361	-	PGF_00019063	786	Maltodextrin phosphorylase (EC 2.4.1.1)	GO:0004645|phosphorylase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4084	PATRIC.2.9855.2.9855.con.0001.CDS.4239513.4241000.rev	PATRIC	CDS	4239513	4241000	1488	-	PGF_03060077	495	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	GO:0004134|4-alpha-glucanotransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4085	PATRIC.2.9855.2.9855.con.0001.CDS.4241094.4242110.rev	PATRIC	CDS	4241094	4242110	1017	-	PGF_07008246	338	Maltose operon transcriptional repressor MalR, LacI family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4086	PATRIC.2.9855.2.9855.con.0001.CDS.4242521.4243465.rev	PATRIC	CDS	4242521	4243465	945	-	PGF_01267847	314	Regulator of polyketide synthase expression		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4087	PATRIC.2.9855.2.9855.con.0001.CDS.4243496.4244605.rev	PATRIC	CDS	4243496	4244605	1110	-	PGF_10491055	369	Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19); Maltodextrin ABC transporter, ATP-binding protein MsmX	GO:0015423|maltose-transporting ATPase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4088	PATRIC.2.9855.2.9855.con.0001.CDS.4244876.4245643.rev	PATRIC	CDS	4244876	4245643	768	-	PGF_01281733	255	Putative protease		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4089	PATRIC.2.9855.2.9855.con.0001.CDS.4246081.4246833.fwd	PATRIC	CDS	4246081	4246833	753	+	PGF_10294766	250	Glutamine amidotransferase, class I		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4090	PATRIC.2.9855.2.9855.con.0001.CDS.4246975.4248693.rev	PATRIC	CDS	4246975	4248693	1719	-	PGF_00051161	572	Ser-type protease		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4091	PATRIC.2.9855.2.9855.con.0001.CDS.4248690.4250540.rev	PATRIC	CDS	4248690	4250540	1851	-	PGF_00051161	616	Ser-type protease		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4092	PATRIC.2.9855.2.9855.con.0001.CDS.4250766.4252337.rev	PATRIC	CDS	4250766	4252337	1572	-	PGF_00917167	523	Xylan 1,4-beta-xylosidase (EC 3.2.1.37)	GO:0009044|xylan 1,4-beta-xylosidase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4096	PATRIC.2.9855.2.9855.con.0001.CDS.4257085.4258476.rev	PATRIC	CDS	4257085	4258476	1392	-	PGF_01350985	463	Xyloside transporter XynT		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4098	PATRIC.2.9855.2.9855.con.0001.CDS.4259965.4260756.rev	PATRIC	CDS	4259965	4260756	792	-	PGF_09020471	263	GTP cyclohydrolase 1 type 2 homolog YbgI		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4099	PATRIC.2.9855.2.9855.con.0001.CDS.4260768.4261460.rev	PATRIC	CDS	4260768	4261460	693	-	PGF_00413189	230	tRNA (adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4100	PATRIC.2.9855.2.9855.con.0001.CDS.4261690.4262820.rev	PATRIC	CDS	4261690	4262820	1131	-	PGF_07072582	376	RNA polymerase sigma factor RpoD		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4101	PATRIC.2.9855.2.9855.con.0001.CDS.4262826.4264616.rev	PATRIC	CDS	4262826	4264616	1791	-	PGF_00421679	596	DNA primase DnaG		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4102	PATRIC.2.9855.2.9855.con.0001.CDS.4264892.4265917.rev	PATRIC	CDS	4264892	4265917	1026	-	PGF_12771936	341	dNTP triphosphohydrolase, broad substrate specificity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4103	PATRIC.2.9855.2.9855.con.0001.CDS.4266247.4267314.fwd	PATRIC	CDS	4266247	4267314	1068	+	PGF_10665061	355	Spore coat protein S		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4104	PATRIC.2.9855.2.9855.con.0001.CDS.4267593.4270220.rev	PATRIC	CDS	4267593	4270220	2628	-	PGF_00045999	875	Pyruvate,phosphate dikinase (EC 2.7.9.1)	GO:0050242|pyruvate, phosphate dikinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4105	PATRIC.2.9855.2.9855.con.0001.CDS.4270303.4270941.rev	PATRIC	CDS	4270303	4270941	639	-	PGF_00412532	212	Transcriptional repressor CcpN, MarR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4106	PATRIC.2.9855.2.9855.con.0001.CDS.4271141.4271770.rev	PATRIC	CDS	4271141	4271770	630	-	PGF_00024248	209	N-terminal of elongation factor Ts		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4107	PATRIC.2.9855.2.9855.con.0001.CDS.4271777.4272526.rev	PATRIC	CDS	4271777	4272526	750	-	PGF_06216244	249	DNA recombination and repair protein RecO		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4108	PATRIC.2.9855.2.9855.con.0001.CDS.4272591.4273487.rev	PATRIC	CDS	4272591	4273487	897	-	PGF_00007027	298	GTP-binding protein Era		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.44	PATRIC.2.9855.2.9855.con.0001.CDS.42734.43045.fwd	PATRIC	CDS	42734	43045	312	+	PGF_05148511	103	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4109	PATRIC.2.9855.2.9855.con.0001.CDS.4273743.4274444.rev	PATRIC	CDS	4273743	4274444	702	-	PGF_08331244	233	Diacylglycerol kinase (EC 2.7.1.107)	GO:0004143|diacylglycerol kinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4110	PATRIC.2.9855.2.9855.con.0001.CDS.4274480.4274983.rev	PATRIC	CDS	4274480	4274983	504	-	PGF_00020361	167	Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4111	PATRIC.2.9855.2.9855.con.0001.CDS.4275010.4277094.rev	PATRIC	CDS	4275010	4277094	2085	-	PGF_03110657	694	Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4112	PATRIC.2.9855.2.9855.con.0001.CDS.4277155.4278282.rev	PATRIC	CDS	4277155	4278282	1128	-	PGF_00054082	375	Uncharacterized protein YqfD		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4114	PATRIC.2.9855.2.9855.con.0001.CDS.4278856.4279308.rev	PATRIC	CDS	4278856	4279308	453	-	PGF_10054809	150	Transamidase GatB domain protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4115	PATRIC.2.9855.2.9855.con.0001.CDS.4279339.4279515.rev	PATRIC	CDS	4279339	4279515	177	-	PGF_04034430	58	SSU ribosomal protein S21p		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4116	PATRIC.2.9855.2.9855.con.0001.CDS.4279658.4280002.rev	PATRIC	CDS	4279658	4280002	345	-	PGF_00404817	114	Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17)	GO:0004081|bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4117	PATRIC.2.9855.2.9855.con.0001.CDS.4280152.4281555.rev	PATRIC	CDS	4280152	4281555	1404	-	PGF_00413298	467	tRNA t(6)A37-methylthiotransferase (EC 2.8.4.5)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4118	PATRIC.2.9855.2.9855.con.0001.CDS.4281555.4282322.rev	PATRIC	CDS	4281555	4282322	768	-	PGF_10233208	255	16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4119	PATRIC.2.9855.2.9855.con.0001.CDS.4282529.4283473.rev	PATRIC	CDS	4282529	4283473	945	-	PGF_00048840	314	Ribosomal protein L11 methyltransferase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4120	PATRIC.2.9855.2.9855.con.0001.CDS.4284207.4284866.rev	PATRIC	CDS	4284207	4284866	660	-	PGF_06530721	219	tRNA (guanine(46)-N(7))-methyltransferase (EC 2.1.1.33)	GO:0008176|tRNA (guanine-N7-)-methyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4121	PATRIC.2.9855.2.9855.con.0001.CDS.4285289.4286839.rev	PATRIC	CDS	4285289	4286839	1551	-	PGF_00665441	516	Ferredoxin--sulfite reductase (EC 1.8.7.1)	GO:0050311|sulfite reductase (ferredoxin) activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4122	PATRIC.2.9855.2.9855.con.0001.CDS.4287000.4288133.rev	PATRIC	CDS	4287000	4288133	1134	-	PGF_10301134	377	Chaperone protein DnaJ		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4123	PATRIC.2.9855.2.9855.con.0001.CDS.4288244.4290088.rev	PATRIC	CDS	4288244	4290088	1845	-	PGF_10357457	614	Chaperone protein DnaK		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4124	PATRIC.2.9855.2.9855.con.0001.CDS.4290194.4290817.rev	PATRIC	CDS	4290194	4290817	624	-	PGF_03751823	207	Heat shock protein GrpE		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4125	PATRIC.2.9855.2.9855.con.0001.CDS.4290855.4291907.rev	PATRIC	CDS	4290855	4291907	1053	-	PGF_01867628	350	Heat-inducible transcription repressor HrcA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4126	PATRIC.2.9855.2.9855.con.0001.CDS.4292122.4293249.rev	PATRIC	CDS	4292122	4293249	1128	-	PGF_04991657	375	Oxygen-independent coproporphyrinogen-III oxidase-like protein YggW		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4128	PATRIC.2.9855.2.9855.con.0001.CDS.4294087.4295898.rev	PATRIC	CDS	4294087	4295898	1812	-	PGF_00060414	603	Translation elongation factor LepA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4130	PATRIC.2.9855.2.9855.con.0001.CDS.4296719.4297792.rev	PATRIC	CDS	4296719	4297792	1074	-	PGF_06533121	357	Stage II sporulation protein P		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.375	PATRIC.2.9855.2.9855.con.0001.CDS.429754.430767.fwd	PATRIC	CDS	429754	430767	1014	+	PGF_04642292	337	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)	GO:0003964|RNA-directed DNA polymerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4131	PATRIC.2.9855.2.9855.con.0001.CDS.4297999.4298982.rev	PATRIC	CDS	4297999	4298982	984	-	PGF_00053878	327	Spore germination endopeptidase Gpr (EC 3.4.24.78)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4132	PATRIC.2.9855.2.9855.con.0001.CDS.4299155.4299418.fwd	PATRIC	CDS	4299155	4299418	264	+	PGF_02454577	87	SSU ribosomal protein S20p		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4133	PATRIC.2.9855.2.9855.con.0001.CDS.4299471.4300505.rev	PATRIC	CDS	4299471	4300505	1035	-	PGF_09201380	344	DNA polymerase III delta subunit (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4134	PATRIC.2.9855.2.9855.con.0001.CDS.4300566.4302257.rev	PATRIC	CDS	4300566	4302257	1692	-	PGF_06887246	563	DNA internalization-related competence protein ComEC/Rec2		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4135	PATRIC.2.9855.2.9855.con.0001.CDS.4302262.4304781.rev	PATRIC	CDS	4302262	4304781	2520	-	PGF_08139201	839	Cation-transporting ATPase, E1-E2 family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4136	PATRIC.2.9855.2.9855.con.0001.CDS.4305016.4305372.rev	PATRIC	CDS	4305016	4305372	357	-	PGF_00054100	118	Stage V sporulation protein AE1 (SpoVAE1)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4137	PATRIC.2.9855.2.9855.con.0001.CDS.4305445.4306464.rev	PATRIC	CDS	4305445	4306464	1020	-	PGF_00054098	339	Stage V sporulation protein AD (SpoVAD)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4138	PATRIC.2.9855.2.9855.con.0001.CDS.4306567.4307034.rev	PATRIC	CDS	4306567	4307034	468	-	PGF_00054097	155	Stage V sporulation protein AC (SpoVAC)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.9	PATRIC.2.9855.2.9855.con.0001.CDS.4307.4447.fwd	PATRIC	CDS	4307	4447	141	+	PGF_00417577	46	3-dehydroquinate dehydratase II (EC 4.2.1.10)	GO:0003855|3-dehydroquinate dehydratase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4139	PATRIC.2.9855.2.9855.con.0001.CDS.4307236.4307991.rev	PATRIC	CDS	4307236	4307991	756	-	PGF_02177520	251	RNA polymerase sporulation specific sigma factor SigF		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4140	PATRIC.2.9855.2.9855.con.0001.CDS.4308002.4308433.rev	PATRIC	CDS	4308002	4308433	432	-	PGF_00057127	143	Anti-sigma F factor (EC 2.7.11.1)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4141	PATRIC.2.9855.2.9855.con.0001.CDS.4308448.4308783.rev	PATRIC	CDS	4308448	4308783	336	-	PGF_00057198	111	Anti-sigma F factor antagonist		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4142	PATRIC.2.9855.2.9855.con.0001.CDS.4309191.4311497.rev	PATRIC	CDS	4309191	4311497	2307	-	PGF_00019567	768	ATP-dependent protease La (EC 3.4.21.53) Type II		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4143	PATRIC.2.9855.2.9855.con.0001.CDS.4311810.4312310.rev	PATRIC	CDS	4311810	4312310	501	-	PGF_00400670	166	Benzodiazepine receptor TspO		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4144	PATRIC.2.9855.2.9855.con.0001.CDS.4312505.4314529.rev	PATRIC	CDS	4312505	4314529	2025	-	PGF_02620852	674	Two-component system sensor histidine kinase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4145	PATRIC.2.9855.2.9855.con.0001.CDS.4314532.4316442.rev	PATRIC	CDS	4314532	4316442	1911	-	PGF_02620852	636	Two-component system sensor histidine kinase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4146	PATRIC.2.9855.2.9855.con.0001.CDS.4316613.4318904.rev	PATRIC	CDS	4316613	4318904	2292	-	PGF_12779560	763	Phage infection protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4147	PATRIC.2.9855.2.9855.con.0001.CDS.4318939.4321236.rev	PATRIC	CDS	4318939	4321236	2298	-	PGF_00929740	765	phage infection protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4148	PATRIC.2.9855.2.9855.con.0001.CDS.4321524.4323233.rev	PATRIC	CDS	4321524	4323233	1710	-	PGF_07849456	569	Methyl-accepting chemotaxis protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4149	PATRIC.2.9855.2.9855.con.0001.CDS.4323815.4324450.rev	PATRIC	CDS	4323815	4324450	636	-	PGF_08109371	211	Membrane-bound lytic murein transglycosylase D		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4150	PATRIC.2.9855.2.9855.con.0001.CDS.4324465.4325064.rev	PATRIC	CDS	4324465	4325064	600	-	PGF_01135236	199	Dephospho-CoA kinase (EC 2.7.1.24)	GO:0004140|dephospho-CoA kinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4151	PATRIC.2.9855.2.9855.con.0001.CDS.4325101.4327704.rev	PATRIC	CDS	4325101	4327704	2604	-	PGF_10347756	867	DNA polymerase I (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4152	PATRIC.2.9855.2.9855.con.0001.CDS.4328018.4329244.fwd	PATRIC	CDS	4328018	4329244	1227	+	PGF_00053966	408	Aminopeptidase S (Leu, Val, Phe, Tyr preference) (EC 3.4.11.24)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4154	PATRIC.2.9855.2.9855.con.0001.CDS.4329785.4330804.rev	PATRIC	CDS	4329785	4330804	1020	-	PGF_00062045	339	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	GO:0004830|tryptophan-tRNA ligase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4156	PATRIC.2.9855.2.9855.con.0001.CDS.4331395.4331829.rev	PATRIC	CDS	4331395	4331829	435	-	PGF_00065080	144	Uncharacterized protein MJ0531		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4157	PATRIC.2.9855.2.9855.con.0001.CDS.4332050.4332784.rev	PATRIC	CDS	4332050	4332784	735	-	PGF_00004337	244	Ferredoxin 3 fused to uncharacterized domain		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4158	PATRIC.2.9855.2.9855.con.0001.CDS.4332960.4333805.rev	PATRIC	CDS	4332960	4333805	846	-	PGF_04828114	281	Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)	GO:0004514|nicotinate-nucleotide diphosphorylase (carboxylating) activity GO:0008734|L-aspartate oxidase activity;GO:0008734|L-aspartate:fumarate oxidoreductase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4159	PATRIC.2.9855.2.9855.con.0001.CDS.4333780.4335087.rev	PATRIC	CDS	4333780	4335087	1308	-	PGF_07459509	435	L-aspartate oxidase (EC 1.4.3.16)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4160	PATRIC.2.9855.2.9855.con.0001.CDS.4335095.4336024.rev	PATRIC	CDS	4335095	4336024	930	-	PGF_02278006	309	Quinolinate synthetase (EC 2.5.1.72)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4161	PATRIC.2.9855.2.9855.con.0001.CDS.4336242.4336610.fwd	PATRIC	CDS	4336242	4336610	369	+	PGF_06916656	122	Transcriptional regulator, GntR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4162	PATRIC.2.9855.2.9855.con.0001.CDS.4336610.4337389.fwd	PATRIC	CDS	4336610	4337389	780	+	PGF_00884706	259	Efflux ABC transporter, ATP-binding protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4164	PATRIC.2.9855.2.9855.con.0001.CDS.4338769.4340193.fwd	PATRIC	CDS	4338769	4340193	1425	+	PGF_00018016	474	Lysine-specific permease		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4165	PATRIC.2.9855.2.9855.con.0001.CDS.4340334.4341488.rev	PATRIC	CDS	4340334	4341488	1155	-	PGF_00778630	384	Uncharacterized amino acid permease, GabP family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4166	PATRIC.2.9855.2.9855.con.0001.CDS.4341501.4342172.rev	PATRIC	CDS	4341501	4342172	672	-	PGF_00778630	223	Uncharacterized amino acid permease, GabP family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.46	PATRIC.2.9855.2.9855.con.0001.CDS.43423.44325.fwd	PATRIC	CDS	43423	44325	903	+	PGF_05680688	300	Kinase similar to eukaryotic-like N-acetylglucosamine kinase		

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4167	PATRIC.2.9855.2.9855.con.0001.CDS.4342470.4344107.rev	PATRIC	CDS	4342470	4344107	1638	-	PGF_00736089	545	Hydroxylamine reductase (EC 1.7.99.1)	GO:0050418|hydroxylamine reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4168	PATRIC.2.9855.2.9855.con.0001.CDS.4344599.4345564.rev	PATRIC	CDS	4344599	4345564	966	-	PGF_00055735	321	Anaerobic sulfite reductase subunit C (EC 1.8.1.-)	GO:0008785|alkyl hydroperoxide reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4169	PATRIC.2.9855.2.9855.con.0001.CDS.4345577.4346371.rev	PATRIC	CDS	4345577	4346371	795	-	PGF_00055722	264	Anaerobic sulfite reductase subunit B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4170	PATRIC.2.9855.2.9855.con.0001.CDS.4346364.4347374.rev	PATRIC	CDS	4346364	4347374	1011	-	PGF_00055659	336	Anaerobic sulfite reductase subunit A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4171	PATRIC.2.9855.2.9855.con.0001.CDS.4347387.4348154.rev	PATRIC	CDS	4347387	4348154	768	-	PGF_06960029	255	Sulfite transporter, NirC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4172	PATRIC.2.9855.2.9855.con.0001.CDS.4348235.4348927.rev	PATRIC	CDS	4348235	4348927	693	-	PGF_02782442	230	Transcriptional regulator CPF_1694, Crp/Fnr family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4173	PATRIC.2.9855.2.9855.con.0001.CDS.4349074.4349754.rev	PATRIC	CDS	4349074	4349754	681	-	PGF_03752790	226	Hcp transcriptional regulator HcpR (Crp/Fnr family)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4174	PATRIC.2.9855.2.9855.con.0001.CDS.4349809.4350249.rev	PATRIC	CDS	4349809	4350249	441	-	PGF_00586606	146	Organic hydroperoxide resistance transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4175	PATRIC.2.9855.2.9855.con.0001.CDS.4350424.4351290.rev	PATRIC	CDS	4350424	4351290	867	-	PGF_01625234	288	Thioredoxin reductase (EC 1.8.1.9)	GO:0004791|thioredoxin-disulfide reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4176	PATRIC.2.9855.2.9855.con.0001.CDS.4351417.4351896.rev	PATRIC	CDS	4351417	4351896	480	-	PGF_08363070	159	Glutathione peroxidase (EC 1.11.1.9) @ Thioredoxin peroxidase (EC 1.11.1.15)	GO:0004602|glutathione peroxidase activity;GO:0051920|peroxiredoxin activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4177	PATRIC.2.9855.2.9855.con.0001.CDS.4352029.4352337.rev	PATRIC	CDS	4352029	4352337	309	-	PGF_10345259	102	Thioredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4179	PATRIC.2.9855.2.9855.con.0001.CDS.4353572.4354330.rev	PATRIC	CDS	4353572	4354330	759	-	PGF_08546938	252	Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4180	PATRIC.2.9855.2.9855.con.0001.CDS.4354419.4356194.rev	PATRIC	CDS	4354419	4356194	1776	-	PGF_05614715	591	Oligoendopeptidase F-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4181	PATRIC.2.9855.2.9855.con.0001.CDS.4356374.4358731.rev	PATRIC	CDS	4356374	4358731	2358	-	PGF_00068225	785	alpha-xylosidase (EC 3.2.1.177)	GO:0061634|alpha-D-xyloside xylohydrolase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4182	PATRIC.2.9855.2.9855.con.0001.CDS.4358861.4359688.rev	PATRIC	CDS	4358861	4359688	828	-	PGF_10552060	275	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4183	PATRIC.2.9855.2.9855.con.0001.CDS.4359688.4360566.rev	PATRIC	CDS	4359688	4360566	879	-	PGF_05110907	292	N-acetyl-D-glucosamine ABC transporter, permease protein 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4184	PATRIC.2.9855.2.9855.con.0001.CDS.4360633.4361961.rev	PATRIC	CDS	4360633	4361961	1329	-	PGF_07870324	442	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4185	PATRIC.2.9855.2.9855.con.0001.CDS.4362133.4364010.fwd	PATRIC	CDS	4362133	4364010	1878	+	PGF_00062721	625	Two-component sensor kinase YesM (EC 2.7.3.-)	GO:0000155|phosphorelay sensor kinase activity;GO:0000155|histone arginine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4186	PATRIC.2.9855.2.9855.con.0001.CDS.4363988.4364758.fwd	PATRIC	CDS	4363988	4364758	771	+	PGF_00062533	256	Two-component response regulator yesN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4187	PATRIC.2.9855.2.9855.con.0001.CDS.4364967.4366256.rev	PATRIC	CDS	4364967	4366256	1290	-	PGF_04792526	429	O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) @ O-succinylhomoserine sulfhydrylase (EC 2.5.1.48)	GO:0003961|O-acetylhomoserine aminocarboxypropyltransferase activity;GO:0003962|cystathionine gamma-synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4188	PATRIC.2.9855.2.9855.con.0001.CDS.4366802.4367269.fwd	PATRIC	CDS	4366802	4367269	468	+	PGF_00220548	155	Thiol peroxidase, Bcp-type (EC 1.11.1.15)	GO:0051920|peroxiredoxin activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4189	PATRIC.2.9855.2.9855.con.0001.CDS.4368133.4368423.fwd	PATRIC	CDS	4368133	4368423	291	+	PGF_03495000	96	Mobile element protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.387	PATRIC.2.9855.2.9855.con.0001.CDS.436938.437306.fwd	PATRIC	CDS	436938	437306	369	+	PGF_05767868	122	Probable transcriptional regulatory protein YebC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4193	PATRIC.2.9855.2.9855.con.0001.CDS.4373047.4374210.rev	PATRIC	CDS	4373047	4374210	1164	-	PGF_09996723	387	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4195	PATRIC.2.9855.2.9855.con.0001.CDS.4381543.4382463.rev	PATRIC	CDS	4381543	4382463	921	-	PGF_00042825	306	Putative oxidoreductase SCO7655	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4196	PATRIC.2.9855.2.9855.con.0001.CDS.4382549.4383400.rev	PATRIC	CDS	4382549	4383400	852	-	PGF_09655255	283	Transcriptional regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4197	PATRIC.2.9855.2.9855.con.0001.CDS.4383455.4384423.rev	PATRIC	CDS	4383455	4384423	969	-	PGF_12905405	322	Oxidoreductase, Gfo/Idh/MocA family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4198	PATRIC.2.9855.2.9855.con.0001.CDS.4384471.4385151.rev	PATRIC	CDS	4384471	4385151	681	-	PGF_05657253	226	Ribose-5-phosphate isomerase A (EC 5.3.1.6)	GO:0004751|ribose-5-phosphate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4199	PATRIC.2.9855.2.9855.con.0001.CDS.4385339.4385872.rev	PATRIC	CDS	4385339	4385872	534	-	PGF_00054401	177	Substrate-specific component PdxU2 of predicted pyridoxin-related ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4200	PATRIC.2.9855.2.9855.con.0001.CDS.4385911.4387065.rev	PATRIC	CDS	4385911	4387065	1155	-	PGF_02189378	384	Serine--glyoxylate aminotransferase (EC 2.6.1.45)	GO:0050281|serine-glyoxylate transaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4201	PATRIC.2.9855.2.9855.con.0001.CDS.4387347.4387658.rev	PATRIC	CDS	4387347	4387658	312	-	PGF_05148511	103	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4202	PATRIC.2.9855.2.9855.con.0001.CDS.4387977.4389359.rev	PATRIC	CDS	4387977	4389359	1383	-	PGF_00930759	460	L,D-transpeptidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.389	PATRIC.2.9855.2.9855.con.0001.CDS.438844.439296.fwd	PATRIC	CDS	438844	439296	453	+	PGF_03510298	150	Surface protein PspC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4203	PATRIC.2.9855.2.9855.con.0001.CDS.4389653.4390984.rev	PATRIC	CDS	4389653	4390984	1332	-	PGF_00930759	443	L,D-transpeptidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4204	PATRIC.2.9855.2.9855.con.0001.CDS.4391440.4392339.rev	PATRIC	CDS	4391440	4392339	900	-	PGF_01496598	299	Chemotaxis protein CheV (EC 2.7.3.-)	GO:0000155|phosphorelay sensor kinase activity;GO:0000155|histone arginine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4205	PATRIC.2.9855.2.9855.con.0001.CDS.4392674.4393819.rev	PATRIC	CDS	4392674	4393819	1146	-	PGF_04034434	381	Uncharacterized protein YaaN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4206	PATRIC.2.9855.2.9855.con.0001.CDS.4393847.4395046.rev	PATRIC	CDS	4393847	4395046	1200	-	PGF_01316804	399	P235 rhoptry protein E5	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4207	PATRIC.2.9855.2.9855.con.0001.CDS.4395447.4396283.rev	PATRIC	CDS	4395447	4396283	837	-	PGF_03514578	278	Beta-glucoside bgl operon antiterminator, BglG family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4208	PATRIC.2.9855.2.9855.con.0001.CDS.4396309.4398447.rev	PATRIC	CDS	4396309	4398447	2139	-	PGF_02516495	712	PTS system, IIC component / PTS system, IIB component / PTS system, IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4209	PATRIC.2.9855.2.9855.con.0001.CDS.4398753.4399217.fwd	PATRIC	CDS	4398753	4399217	465	+	PGF_01043799	154	Transcription elongation factor GreA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4210	PATRIC.2.9855.2.9855.con.0001.CDS.4399405.4400289.rev	PATRIC	CDS	4399405	4400289	885	-	PGF_02146256	294	Sialic acid utilization regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4211	PATRIC.2.9855.2.9855.con.0001.CDS.4400549.4401253.fwd	PATRIC	CDS	4400549	4401253	705	+	PGF_05026985	234	Deoxyribose-phosphate aldolase (EC 4.1.2.4)	GO:0004139|deoxyribose-phosphate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4212	PATRIC.2.9855.2.9855.con.0001.CDS.4401499.4403193.rev	PATRIC	CDS	4401499	4403193	1695	-	PGF_00036081	564	Predicted membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4214	PATRIC.2.9855.2.9855.con.0001.CDS.4403521.4404138.rev	PATRIC	CDS	4403521	4404138	618	-	PGF_01136590	205	Dolichyl-phosphate-mannose-protein mannosyltransferase-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4215	PATRIC.2.9855.2.9855.con.0001.CDS.4404181.4405101.rev	PATRIC	CDS	4404181	4405101	921	-	PGF_01136590	306	Dolichyl-phosphate-mannose-protein mannosyltransferase-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4216	PATRIC.2.9855.2.9855.con.0001.CDS.4405515.4407950.rev	PATRIC	CDS	4405515	4407950	2436	-	PGF_00006821	811	GGDEF domain protein	[illegible] activity;GO:0000179|protein C-terminal carboxyl O-methyltransferase activity;GO:0000179|tRNA (guanine-N2-)-methyltransferase activity;GO:0000179|C-methyltransferase activity;GO:0000179|N-methyltransferase activity;GO:0000179|O-methyltransferase activity;GO:0000179|S-methyltransferase activity;GO:0000179|RNA methyltransferase activity;GO:0000179|mRNA methyltransferase activity;GO:0000179|tRNA methyltransferase activity;GO:0000179|protein methyltransferase activity;GO:0000179|2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity;GO:0000179|rRNA methyltransferase activity;GO:0000179|rRNA (uridine-2'-O-)-methyltransferase activity;GO:0000179|rRNA (adenine-N6-)-methyltransferase activity;GO:0000179|DNA-methyltransferase activity;GO:0000179|tRNA (guanine-N1-)-methyltransferase activity;GO:0000179|rRNA (cytosine-C5-)-methyltransferase activity;GO:0000179|selenocysteine methyltransferase activity;GO:0000179|arginine N-methyltransferase activity;GO:0000179|protein-arginine N-methyltransferase activity;GO:0000179|lysine N-methyltransferase activity;GO:0000179|protein-lysine N-methyltransferase activity;GO:0000179|tRNA (uracil) methyltransferase activity;GO:0000179|tRNA (guanine) methyltransferase activity;GO:0000179|tRNA (adenine) methyltransferase activity;GO:0000179|tRNA (cytosine) methyltransferase activity;GO:0000179|tRNA (cytosine-5-)-methyltransferase activity;GO:0000179|tRNA (adenine-N1-)-methyltransferase activity;GO:0000179|rRNA (adenine) methyltransferase activity;GO:0000179|rRNA (cytosine) methyltransferase activity;GO:0000179|rRNA (guanine) methyltransferase activity;GO:0000179|rRNA (uridine) methyltransferase activity;GO:0000179|protein C-terminal leucine carboxyl O-methyltransferase activity;GO:0000179|1-phenanthrol methyltransferase activity;GO:0000179|protein-arginine NS-methyltransferase activity;GO:0000179|methylarsonite methyltransferase activity;GO:0000179|dimethylarsinite methyltransferase activity;GO:0000179|4,5-
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4217	PATRIC.2.9855.2.9855.con.0001.CDS.4408278.4409411.rev	PATRIC	CDS	4408278	4409411	1134	-	PGF_00018000	377	Lysine-N-methylase (EC 2.1.1.-)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4218	PATRIC.2.9855.2.9855.con.0001.CDS.4409702.4410916.rev	PATRIC	CDS	4409702	4410916	1215	-	PGF_01283111	404	Streptococcal hemagglutinin protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4219	PATRIC.2.9855.2.9855.con.0001.CDS.4411281.4411790.rev	PATRIC	CDS	4411281	4411790	510	-	PGF_03742559	169	Substrate-specific component QueT (COG4708) of predicted queuosine-regulated ECF transporter	

															GO:0008168|tRNA (adenine-N6,N6-)-dimethyltransferase activity;GO:0000179|protein C-terminal carboxyl O-methyltransferase activity;GO:0000179|tRNA (guanine-N2-)-methyltransferase activity;GO:0000179|C-methyltransferase activity;GO:0000179|N-methyltransferase activity;GO:0000179|O-methyltransferase activity;GO:0000179|S-methyltransferase activity;GO:0000179|RNA methyltransferase activity;GO:0000179|mRNA methyltransferase activity;GO:0000179|tRNA methyltransferase activity;GO:0000179|protein methyltransferase activity;GO:0000179|2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity;GO:0000179|rRNA methyltransferase activity;GO:0000179|rRNA (uridine-2'-O-)-methyltransferase activity;GO:0000179|rRNA (adenine-N6-)-methyltransferase activity;GO:0000179|DNA-methyltransferase activity;GO:0000179|tRNA (guanine-N1-)-methyltransferase activity;GO:0000179|rRNA (cytosine-C5-)-methyltransferase activity;GO:0000179|selenocysteine methyltransferase activity;GO:0000179|arginine N-methyltransferase activity;GO:0000179|protein-arginine N-methyltransferase activity;GO:0000179|lysine N-methyltransferase activity;GO:0000179|protein-lysine N-methyltransferase activity;GO:0000179|tRNA (uracil) methyltransferase activity;GO:0000179|tRNA (guanine) methyltransferase activity;GO:0000179|tRNA (adenine) methyltransferase activity;GO:0000179|tRNA (cytosine) methyltransferase activity;GO:0000179|tRNA (cytosine-5-)-methyltransferase activity;GO:0000179|tRNA (adenine-N1-)-methyltransferase activity;GO:0000179|rRNA (adenine) methyltransferase activity;GO:0000179|rRNA (cytosine) methyltransferase activity;GO:0000179|rRNA (guanine) methyltransferase activity;GO:0000179|rRNA (uridine) methyltransferase activity;GO:0000179|protein C-terminal leucine carboxyl O-methyltransferase activity;GO:0000179|1-phenanthrol methyltransferase activity;GO:0000179|protein-arginine N5-methyltransferase activity;GO:0000179|methylarsonite methyltransferase
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.391	PATRIC.2.9855.2.9855.con.0001.CDS.441219.441971.fwd	PATRIC	CDS	441219	441971	753	+	PGF_09449034	250	Leader peptidase (Prepilin peptidase) (EC 3.4.23.43) / N-methyltransferase (EC 2.1.1.-)	activity;GO:0000179|dimethylarsinite methyltransferase activity;GO:0000179|4,5-
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4220	PATRIC.2.9855.2.9855.con.0001.CDS.4412302.4412880.rev	PATRIC	CDS	4412302	4412880	579	-	PGF_00064569	192	Uncharacterized transcriptional regulator YdeS, TetR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4221	PATRIC.2.9855.2.9855.con.0001.CDS.4413268.4413903.fwd	PATRIC	CDS	4413268	4413903	636	+	PGF_00023289	211	Multimeric flavodoxin WrbA family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4222	PATRIC.2.9855.2.9855.con.0001.CDS.4414028.4415245.fwd	PATRIC	CDS	4414028	4415245	1218	+	PGF_09996723	405	Uncharacterized MFS-type transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4223	PATRIC.2.9855.2.9855.con.0001.CDS.4415386.4416420.rev	PATRIC	CDS	4415386	4416420	1035	-	PGF_00037810	344	Protease	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4226	PATRIC.2.9855.2.9855.con.0001.CDS.4418404.4420044.rev	PATRIC	CDS	4418404	4420044	1641	-	PGF_00007806	546	Glucan 1,6-alpha-glucosidase (EC 3.2.1.70)	GO:0043896|glucan 1,6-alpha-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4227	PATRIC.2.9855.2.9855.con.0001.CDS.4420098.4420922.rev	PATRIC	CDS	4420098	4420922	825	-	PGF_06874321	274	Multiple sugar ABC transporter, permease protein MsmG	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.392	PATRIC.2.9855.2.9855.con.0001.CDS.442086.443780.fwd	PATRIC	CDS	442086	443780	1695	+	PGF_02473679	564	Type IV fimbrial assembly, ATPase PilB	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4228	PATRIC.2.9855.2.9855.con.0001.CDS.4420919.4421782.rev	PATRIC	CDS	4420919	4421782	864	-	PGF_01074106	287	Multiple sugar ABC transporter, permease protein MsmF	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4229	PATRIC.2.9855.2.9855.con.0001.CDS.4421956.4423206.rev	PATRIC	CDS	4421956	4423206	1251	-	PGF_01673829	416	Multiple sugar ABC transporter, substrate-binding protein MsmE	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4230	PATRIC.2.9855.2.9855.con.0001.CDS.4423583.4424608.rev	PATRIC	CDS	4423583	4424608	1026	-	PGF_09774558	341	Transcriptional regulator, LacI family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4232	PATRIC.2.9855.2.9855.con.0001.CDS.4426692.4428182.rev	PATRIC	CDS	4426692	4428182	1491	-	PGF_04147121	496	Aldehyde dehydrogenase B (EC 1.2.1.22)	GO:0008911|lactaldehyde dehydrogenase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4233	PATRIC.2.9855.2.9855.con.0001.CDS.4428478.4429254.rev	PATRIC	CDS	4428478	4429254	777	-	PGF_06788576	258	SAM-dependent methyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4234	PATRIC.2.9855.2.9855.con.0001.CDS.4429369.4430823.rev	PATRIC	CDS	4429369	4430823	1455	-	PGF_07597988	484	Aldehyde dehydrogenase (EC 1.2.1.3)	GO:0004029|aldehyde dehydrogenase (NAD) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4235	PATRIC.2.9855.2.9855.con.0001.CDS.4430920.4431330.fwd	PATRIC	CDS	4430920	4431330	411	+	PGF_00057506	136	Transcriptional regulator, MerR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4236	PATRIC.2.9855.2.9855.con.0001.CDS.4431440.4432024.rev	PATRIC	CDS	4431440	4432024	585	-	PGF_00026045	194	Nitroreductase family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4237	PATRIC.2.9855.2.9855.con.0001.CDS.4432178.4433629.rev	PATRIC	CDS	4432178	4433629	1452	-	PGF_01325659	483	Permease, multidrug efflux	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4238	PATRIC.2.9855.2.9855.con.0001.CDS.4433814.4434686.fwd	PATRIC	CDS	4433814	4434686	873	+	PGF_07987589	290	Transcriptional regulator, LysR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4239	PATRIC.2.9855.2.9855.con.0001.CDS.4434793.4435575.rev	PATRIC	CDS	4434793	4435575	783	-	PGF_12690820	260	Phage replication initiation	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4240	PATRIC.2.9855.2.9855.con.0001.CDS.4435745.4436542.rev	PATRIC	CDS	4435745	4436542	798	-	PGF_03788625	265	Polysaccharide deacetylase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4242	PATRIC.2.9855.2.9855.con.0001.CDS.4437198.4438676.rev	PATRIC	CDS	4437198	4438676	1479	-	PGF_00046611	492	alpha-L-arabinofuranosidase (EC 3.2.1.55)	GO:0046556|alpha-L-arabinofuranosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4243	PATRIC.2.9855.2.9855.con.0001.CDS.4438769.4439623.rev	PATRIC	CDS	4438769	4439623	855	-	PGF_10552060	284	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.393	PATRIC.2.9855.2.9855.con.0001.CDS.443884.445086.fwd	PATRIC	CDS	443884	445086	1203	+	PGF_10309996	400	Type IV fimbrial assembly protein PilC	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4244	PATRIC.2.9855.2.9855.con.0001.CDS.4439648.4440454.rev	PATRIC	CDS	4439648	4440454	807	-	PGF_00067040	268	Xylose ABC transporter, permease component 2	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4245	PATRIC.2.9855.2.9855.con.0001.CDS.4440593.4441894.rev	PATRIC	CDS	4440593	4441894	1302	-	PGF_07870324	433	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.47	PATRIC.2.9855.2.9855.con.0001.CDS.44411.45697.fwd	PATRIC	CDS	44411	45697	1287	+	PGF_00029610	428	PTS system, cellobiose-specific IIC component	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4248	PATRIC.2.9855.2.9855.con.0001.CDS.4445891.4448176.rev	PATRIC	CDS	4445891	4448176	2286	-	PGF_04836613	761	beta-galactosidase (EC 3.2.1.23)	GO:0004565|beta-galactosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4249	PATRIC.2.9855.2.9855.con.0001.CDS.4448251.4449519.rev	PATRIC	CDS	4448251	4449519	1269	-	PGF_00029610	422	PTS system, cellobiose-specific IIC component	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4250	PATRIC.2.9855.2.9855.con.0001.CDS.4449562.4449867.rev	PATRIC	CDS	4449562	4449867	306	-	PGF_05148511	101	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4252	PATRIC.2.9855.2.9855.con.0001.CDS.4450473.4453172.rev	PATRIC	CDS	4450473	4453172	2700	-	PGF_00026324	899	NtrC family Transcriptional regulator, ATPase domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.394	PATRIC.2.9855.2.9855.con.0001.CDS.445163.445594.fwd	PATRIC	CDS	445163	445594	432	+	PGF_01304756	143	Type IV pilin PilA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4253	PATRIC.2.9855.2.9855.con.0001.CDS.4453500.4454387.rev	PATRIC	CDS	4453500	4454387	888	-	PGF_00012030	295	Histone acetyltransferase HPA2 and related acetyltransferases	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4255	PATRIC.2.9855.2.9855.con.0001.CDS.4455640.4456881.fwd	PATRIC	CDS	4455640	4456881	1242	+	PGF_09996723	413	Uncharacterized MFS-type transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4256	PATRIC.2.9855.2.9855.con.0001.CDS.4457159.4457950.fwd	PATRIC	CDS	4457159	4457950	792	+	PGF_00425232	263	4Fe-4S dicluster domain / Nitroreductase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4257	PATRIC.2.9855.2.9855.con.0001.CDS.4458160.4458537.rev	PATRIC	CDS	4458160	4458537	378	-	PGF_00043457	125	Putative regulator of the mannose operon, ManO	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.395	PATRIC.2.9855.2.9855.con.0001.CDS.445826.447004.fwd	PATRIC	CDS	445826	447004	1179	+	PGF_00063722	392	Type IV pilus biogenesis protein PilM	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4258	PATRIC.2.9855.2.9855.con.0001.CDS.4458691.4459602.rev	PATRIC	CDS	4458691	4459602	912	-	PGF_00644224	303	PTS system, mannose-specific IID component	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4259	PATRIC.2.9855.2.9855.con.0001.CDS.4459622.4460428.rev	PATRIC	CDS	4459622	4460428	807	-	PGF_01653368	268	PTS system, mannose-specific IIC component	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4260	PATRIC.2.9855.2.9855.con.0001.CDS.4460464.4461441.rev	PATRIC	CDS	4460464	4461441	978	-	PGF_00029812	325	PTS system, mannose-specific IIA component (EC 2.7.1.191) / PTS system, mannose-specific IIB component (EC 2.7.1.191)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4261	PATRIC.2.9855.2.9855.con.0001.CDS.4461920.4464022.rev	PATRIC	CDS	4461920	4464022	2103	-	PGF_00067000	700	Xylan alpha-1,2-glucuronosidase (EC 3.2.1.131)	GO:0033939|xylan alpha-1,2-glucuronosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4262	PATRIC.2.9855.2.9855.con.0001.CDS.4464060.4465190.rev	PATRIC	CDS	4464060	4465190	1131	-	PGF_06985891	376	Mannonate dehydratase (EC 4.2.1.8)	GO:0008927|mannonate dehydratase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4264	PATRIC.2.9855.2.9855.con.0001.CDS.4467507.4468346.rev	PATRIC	CDS	4467507	4468346	840	-	PGF_10552060	279	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4265	PATRIC.2.9855.2.9855.con.0001.CDS.4468346.4469281.rev	PATRIC	CDS	4468346	4469281	936	-	PGF_02876233	311	ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4266	PATRIC.2.9855.2.9855.con.0001.CDS.4469457.4470785.rev	PATRIC	CDS	4469457	4470785	1329	-	PGF_07870324	442	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.396	PATRIC.2.9855.2.9855.con.0001.CDS.447021.447578.fwd	PATRIC	CDS	447021	447578	558	+	PGF_00063737	185	Type IV pilus biogenesis protein PilN	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4270	PATRIC.2.9855.2.9855.con.0001.CDS.4475199.4475528.rev	PATRIC	CDS	4475199	4475528	330	-	PGF_10416542	109	Sensory box histidine kinase/response regulator	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4271	PATRIC.2.9855.2.9855.con.0001.CDS.4475575.4477545.rev	PATRIC	CDS	4475575	4477545	1971	-	PGF_10416542	656	Sensory box histidine kinase/response regulator	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.397	PATRIC.2.9855.2.9855.con.0001.CDS.447580.448914.fwd	PATRIC	CDS	447580	448914	1335	+	PGF_00063744	444	Type IV pilus biogenesis protein PilO	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4274	PATRIC.2.9855.2.9855.con.0001.CDS.4479635.4480813.fwd	PATRIC	CDS	4479635	4480813	1179	+	PGF_09996723	392	Uncharacterized MFS-type transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4275	PATRIC.2.9855.2.9855.con.0001.CDS.4481220.4481663.fwd	PATRIC	CDS	4481220	4481663	444	+	PGF_10423881	147	Transcriptional regulator, MarR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4276	PATRIC.2.9855.2.9855.con.0001.CDS.4481821.4484226.rev	PATRIC	CDS	4481821	4484226	2406	-	PGF_06513690	801	Pyruvate formate-lyase (EC 2.3.1.54)	GO:0008861|formate C-acetyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4277	PATRIC.2.9855.2.9855.con.0001.CDS.4484610.4484819.fwd	PATRIC	CDS	4484610	4484819	210	+	PGF_06335969	69	Transcriptional regulator, Xre family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4279	PATRIC.2.9855.2.9855.con.0001.CDS.4485674.4486426.rev	PATRIC	CDS	4485674	4486426	753	-	PGF_00059193	250	Transcriptional regulator, DeoR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4280	PATRIC.2.9855.2.9855.con.0001.CDS.4486750.4487652.fwd	PATRIC	CDS	4486750	4487652	903	+	PGF_08333365	300	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	GO:0043365|[formate-C-acetyltransferase]-activating enzyme activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4281	PATRIC.2.9855.2.9855.con.0001.CDS.4487878.4489302.rev	PATRIC	CDS	4487878	4489302	1425	-	PGF_08148954	474	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4282	PATRIC.2.9855.2.9855.con.0001.CDS.4489295.4490722.rev	PATRIC	CDS	4489295	4490722	1428	-	PGF_00029589	475	PTS system, arbutin-, cellobiose-, and salicin-specific IIB component / PTS system, arbutin-, cellobiose-, and salicin-specific IIC component	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4283	PATRIC.2.9855.2.9855.con.0001.CDS.4491035.4491778.rev	PATRIC	CDS	4491035	4491778	744	-	PGF_09655255	247	Transcriptional regulator, RpiR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4284	PATRIC.2.9855.2.9855.con.0001.CDS.4491866.4492150.rev	PATRIC	CDS	4491866	4492150	285	-	PGF_00399622	94	Barstar, ribonuclease (Barnase) inhibitor	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4285	PATRIC.2.9855.2.9855.con.0001.CDS.4492172.4492693.rev	PATRIC	CDS	4492172	4492693	522	-	PGF_00048499	173	Ribonuclease (Barnase), secreted	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4287	PATRIC.2.9855.2.9855.con.0001.CDS.4493264.4493944.fwd	PATRIC	CDS	4493264	4493944	681	+	PGF_04255142	226	ISSth1, transposase (orf1), IS3 family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4288	PATRIC.2.9855.2.9855.con.0001.CDS.4494032.4494514.fwd	PATRIC	CDS	4494032	4494514	483	+	PGF_07304485	160	Putative transposase InsK for insertion sequence element IS150	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4294	PATRIC.2.9855.2.9855.con.0001.CDS.4504241.4506064.rev	PATRIC	CDS	4504241	4506064	1824	-	PGF_12888289	607	Serine phosphatase RsbU, regulator of sigma subunit	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4295	PATRIC.2.9855.2.9855.con.0001.CDS.4506119.4506391.rev	PATRIC	CDS	4506119	4506391	273	-	PGF_12840096	90	Anti-sigma B factor antagonist RsbV	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4296	PATRIC.2.9855.2.9855.con.0001.CDS.4506403.4508403.rev	PATRIC	CDS	4506403	4508403	2001	-	PGF_07849456	666	Methyl-accepting chemotaxis protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4297	PATRIC.2.9855.2.9855.con.0001.CDS.4508465.4508860.rev	PATRIC	CDS	4508465	4508860	396	-	PGF_01283106	131	Serine-protein kinase RsbW (EC 2.7.11.1)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4298	PATRIC.2.9855.2.9855.con.0001.CDS.4509286.4511001.rev	PATRIC	CDS	4509286	4511001	1716	-	PGF_06837078	571	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4299	PATRIC.2.9855.2.9855.con.0001.CDS.4511668.4513668.fwd	PATRIC	CDS	4511668	4513668	2001	+	PGF_01295927	666	Alpha-amylase (EC 3.2.1.1)	GO:0004556|alpha-amylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4300	PATRIC.2.9855.2.9855.con.0001.CDS.4513831.4514550.rev	PATRIC	CDS	4513831	4514550	720	-	PGF_07035610	239	putative membrane protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4301	PATRIC.2.9855.2.9855.con.0001.CDS.4514920.4516314.rev	PATRIC	CDS	4514920	4516314	1395	-	PGF_01421686	464	NADH-dependent reduced ferredoxin:NADP+ oxidoreductase subunit B	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4302	PATRIC.2.9855.2.9855.con.0001.CDS.4516314.4517204.rev	PATRIC	CDS	4516314	4517204	891	-	PGF_01480798	296	NADH-dependent reduced ferredoxin:NADP+ oxidoreductase subunit A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4307	PATRIC.2.9855.2.9855.con.0001.CDS.4520820.4521260.rev	PATRIC	CDS	4520820	4521260	441	-	PGF_01430214	146	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	GO:0004170|dUTP diphosphatase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4309	PATRIC.2.9855.2.9855.con.0001.CDS.4522044.4527410.rev	PATRIC	CDS	4522044	4527410	5367	-	PGF_03060798	1788	diguanylate cyclase (GGDEF domain) with PAS/PAC sensor	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4310	PATRIC.2.9855.2.9855.con.0001.CDS.4527576.4528292.fwd	PATRIC	CDS	4527576	4528292	717	+	PGF_03970701	238	Polysaccharide deacetylase (EC 3.5.1.41)	GO:0004099|chitin deacetylase activity

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4311	PATRIC.2.9855.2.9855.con.0001.CDS.4528365.4528883.rev	PATRIC	CDS	4528365	4528883	519	-	PGF_00054425	172	Substrate-specific component TrpP of tryptophan ECF transporter		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4312	PATRIC.2.9855.2.9855.con.0001.CDS.4529338.4531083.rev	PATRIC	CDS	4529338	4531083	1746	-	PGF_08632970	581	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4314	PATRIC.2.9855.2.9855.con.0001.CDS.4531276.4531467.rev	PATRIC	CDS	4531276	4531467	192	-	PGF_01746393	63	Uncharacterized protein BT_4646		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4315	PATRIC.2.9855.2.9855.con.0001.CDS.4531557.4532423.rev	PATRIC	CDS	4531557	4532423	867	-	PGF_00413306	288	tRNA-(cytosine32)-2-thiocytidine synthetase TtcA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4316	PATRIC.2.9855.2.9855.con.0001.CDS.4532607.4533257.rev	PATRIC	CDS	4532607	4533257	651	-	PGF_00056545	216	Thiazole tautomerase TenI (EC 5.3.99.10)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4317	PATRIC.2.9855.2.9855.con.0001.CDS.4533265.4534068.rev	PATRIC	CDS	4533265	4534068	804	-	PGF_00055125	267	Sulfur carrier protein ThiS / Sulfur carrier protein ThiS adenylyltransferase (EC 2.7.7.73)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4318	PATRIC.2.9855.2.9855.con.0001.CDS.4534694.4535290.fwd	PATRIC	CDS	4534694	4535290	597	+	PGF_00054388	198	Substrate-specific component PanT of predicted pantothenate ECF transporter		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4319	PATRIC.2.9855.2.9855.con.0001.CDS.4535558.4538149.rev	PATRIC	CDS	4535558	4538149	2592	-	PGF_00529632	863	Chaperone protein ClpB (ATP-dependent unfoldase)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4320	PATRIC.2.9855.2.9855.con.0001.CDS.4538414.4538800.fwd	PATRIC	CDS	4538414	4538800	387	+	PGF_10407822	128	CBS domain protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4321	PATRIC.2.9855.2.9855.con.0001.CDS.4538958.4540232.rev	PATRIC	CDS	4538958	4540232	1275	-	PGF_00066995	424	Xre family DNA-binding domain and TPR-repeat-containing protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4322	PATRIC.2.9855.2.9855.con.0001.CDS.4540241.4541551.rev	PATRIC	CDS	4540241	4541551	1311	-	PGF_00066996	436	Xre family DNA-binding domain and TPR-repeat-containing protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4324	PATRIC.2.9855.2.9855.con.0001.CDS.4542200.4543150.rev	PATRIC	CDS	4542200	4543150	951	-	PGF_00048553	316	Ribonuclease HI-related protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4327	PATRIC.2.9855.2.9855.con.0001.CDS.4544967.4545362.rev	PATRIC	CDS	4544967	4545362	396	-	PGF_05366548	131	Methionine ABC transporter substrate-binding protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4328	PATRIC.2.9855.2.9855.con.0001.CDS.4545374.4546012.rev	PATRIC	CDS	4545374	4546012	639	-	PGF_02898176	212	Methionine ABC transporter permease protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4329	PATRIC.2.9855.2.9855.con.0001.CDS.4546012.4546977.rev	PATRIC	CDS	4546012	4546977	966	-	PGF_00020717	321	Methionine ABC transporter ATP-binding protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4330	PATRIC.2.9855.2.9855.con.0001.CDS.4547671.4550928.rev	PATRIC	CDS	4547671	4550928	3258	-	PGF_00425957	1085	5'-nucleotidase (EC 3.1.3.5); Thermonuclease	GO:0008253|5'-nucleotidase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4331	PATRIC.2.9855.2.9855.con.0001.CDS.4551147.4551620.rev	PATRIC	CDS	4551147	4551620	474	-	PGF_00413554	157	tmRNA-binding protein SmpB		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4332	PATRIC.2.9855.2.9855.con.0001.CDS.4551766.4553973.rev	PATRIC	CDS	4551766	4553973	2208	-	PGF_04962192	735	3'-to-5' exoribonuclease RNase R		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4333	PATRIC.2.9855.2.9855.con.0001.CDS.4554408.4555766.rev	PATRIC	CDS	4554408	4555766	1359	-	PGF_03197709	452	Nitrogenase molybdenum-iron protein beta chain (EC 1.18.6.1)	GO:0016163|nitrogenase activity;GO:0016163|carbonyl sulfide nitrogenase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4334	PATRIC.2.9855.2.9855.con.0001.CDS.4555792.4557324.rev	PATRIC	CDS	4555792	4557324	1533	-	PGF_03782075	510	Nitrogenase alpha chain paralog		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4335	PATRIC.2.9855.2.9855.con.0001.CDS.4557532.4558446.rev	PATRIC	CDS	4557532	4558446	915	-	PGF_00760084	304	Cystathionine beta-synthase (EC 4.2.1.22)	GO:0004122|cystathionine beta-synthase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4336	PATRIC.2.9855.2.9855.con.0001.CDS.4558443.4559603.rev	PATRIC	CDS	4558443	4559603	1161	-	PGF_05950073	386	Cystathionine gamma-lyase (EC 4.4.1.1)	GO:0004123|cystathionine gamma-lyase activity;GO:0004123|L-cystine L-cysteine-lyase (deaminating);GO:0004123|L-cysteine desulfhydrase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4337	PATRIC.2.9855.2.9855.con.0001.CDS.4559847.4560719.rev	PATRIC	CDS	4559847	4560719	873	-	PGF_06674514	290	Nitrogenase FeMo-cofactor synthesis FeS core scaffold and assembly protein NifB		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4338	PATRIC.2.9855.2.9855.con.0001.CDS.4560857.4561204.rev	PATRIC	CDS	4560857	4561204	348	-	PGF_00025630	115	NifB-domain protein, type 2		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4339	PATRIC.2.9855.2.9855.con.0001.CDS.4561218.4562063.rev	PATRIC	CDS	4561218	4562063	846	-	PGF_05366548	281	Methionine ABC transporter substrate-binding protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.402	PATRIC.2.9855.2.9855.con.0001.CDS.456143.456796.fwd	PATRIC	CDS	456143	456796	654	+	PGF_08055739	217	DedA protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4340	PATRIC.2.9855.2.9855.con.0001.CDS.4562080.4562748.rev	PATRIC	CDS	4562080	4562748	669	-	PGF_02898176	222	Methionine ABC transporter permease protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4341	PATRIC.2.9855.2.9855.con.0001.CDS.4562738.4563523.rev	PATRIC	CDS	4562738	4563523	786	-	PGF_00020717	261	Methionine ABC transporter ATP-binding protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4342	PATRIC.2.9855.2.9855.con.0001.CDS.4563601.4564455.rev	PATRIC	CDS	4563601	4564455	855	-	PGF_00025954	284	Nitrogenase (molybdenum-iron) reductase and maturation protein NifH		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4343	PATRIC.2.9855.2.9855.con.0001.CDS.4564576.4565874.rev	PATRIC	CDS	4564576	4565874	1299	-	PGF_04792526	432	O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) @ O-succinylhomoserine sulfhydrylase (EC 2.5.1.48)	GO:0003961|O-acetylhomoserine aminocarboxypropyltransferase activity;GO:0003962|cystathionine gamma-synthase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4344	PATRIC.2.9855.2.9855.con.0001.CDS.4566100.4567428.rev	PATRIC	CDS	4566100	4567428	1329	-	PGF_00026000	442	Nitrogenase vanadium-cofactor synthesis protein VnfN		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4345	PATRIC.2.9855.2.9855.con.0001.CDS.4567412.4568893.rev	PATRIC	CDS	4567412	4568893	1482	-	PGF_03782075	493	Nitrogenase alpha chain paralog		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4346	PATRIC.2.9855.2.9855.con.0001.CDS.4569176.4569328.rev	PATRIC	CDS	4569176	4569328	153	-	PGF_01656712	50	Uncharacterized protein Bsu1558.5		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4348	PATRIC.2.9855.2.9855.con.0001.CDS.4570203.4570829.rev	PATRIC	CDS	4570203	4570829	627	-	PGF_03097747	208	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4349	PATRIC.2.9855.2.9855.con.0001.CDS.4570851.4571003.rev	PATRIC	CDS	4570851	4571003	153	-	PGF_03097747	50	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4350	PATRIC.2.9855.2.9855.con.0001.CDS.4571000.4572052.rev	PATRIC	CDS	4571000	4572052	1053	-	PGF_00041527	350	Alkanesulfonates transport system permease protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.403	PATRIC.2.9855.2.9855.con.0001.CDS.457121.458434.rev	PATRIC	CDS	457121	458434	1314	-	PGF_00862519	437	Aspartokinase (EC 2.7.2.4)	GO:0004072|aspartate kinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4351	PATRIC.2.9855.2.9855.con.0001.CDS.4572073.4573071.rev	PATRIC	CDS	4572073	4573071	999	-	PGF_08616437	332	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4352	PATRIC.2.9855.2.9855.con.0001.CDS.4573704.4573937.rev	PATRIC	CDS	4573704	4573937	234	-	PGF_10456344	77	Protein translocase membrane subunit SecG		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4353	PATRIC.2.9855.2.9855.con.0001.CDS.4574165.4575457.rev	PATRIC	CDS	4574165	4575457	1293	-	PGF_02516909	430	Enolase (EC 4.2.1.11)	GO:0004634|phosphopyruvate hydratase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4354	PATRIC.2.9855.2.9855.con.0001.CDS.4575846.4576451.rev	PATRIC	CDS	4575846	4576451	606	-	PGF_02936222	201	Serine/threonine kinase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4355	PATRIC.2.9855.2.9855.con.0001.CDS.4576830.4578368.rev	PATRIC	CDS	4576830	4578368	1539	-	PGF_00021217	512	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4356	PATRIC.2.9855.2.9855.con.0001.CDS.4578698.4579444.rev	PATRIC	CDS	4578698	4579444	747	-	PGF_04574228	248	Triosephosphate isomerase (EC 5.3.1.1)	GO:0004807|triose-phosphate isomerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4357	PATRIC.2.9855.2.9855.con.0001.CDS.4579880.4581055.rev	PATRIC	CDS	4579880	4581055	1176	-	PGF_02277678	391	Phosphoglycerate kinase (EC 2.7.2.3)	GO:0004618|phosphoglycerate kinase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4358	PATRIC.2.9855.2.9855.con.0001.CDS.4581195.4582196.rev	PATRIC	CDS	4581195	4582196	1002	-	PGF_00024478	333	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	GO:0004365|glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4359	PATRIC.2.9855.2.9855.con.0001.CDS.4582268.4583317.rev	PATRIC	CDS	4582268	4583317	1050	-	PGF_00417381	349	Central glycolytic genes regulator		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4360	PATRIC.2.9855.2.9855.con.0001.CDS.4583700.4585091.rev	PATRIC	CDS	4583700	4585091	1392	-	PGF_00046403	463	RNA polymerase sigma-54 factor RpoN		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4361	PATRIC.2.9855.2.9855.con.0001.CDS.4585335.4586171.rev	PATRIC	CDS	4585335	4586171	837	-	PGF_00845945	278	DegV family protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4362	PATRIC.2.9855.2.9855.con.0001.CDS.4586192.4586653.rev	PATRIC	CDS	4586192	4586653	462	-	PGF_00413203	153	tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4363	PATRIC.2.9855.2.9855.con.0001.CDS.4586926.4588422.rev	PATRIC	CDS	4586926	4588422	1497	-	PGF_04746167	498	uncharacterized protein with VanW-like domain		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4364	PATRIC.2.9855.2.9855.con.0001.CDS.4588611.4589552.rev	PATRIC	CDS	4588611	4589552	942	-	PGF_12921518	313	Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (EC 3.2.1.17)	GO:0003796|lysozyme activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4365	PATRIC.2.9855.2.9855.con.0001.CDS.4589631.4591139.rev	PATRIC	CDS	4589631	4591139	1509	-	PGF_02620852	502	Two-component system sensor histidine kinase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4366	PATRIC.2.9855.2.9855.con.0001.CDS.4591129.4591836.rev	PATRIC	CDS	4591129	4591836	708	-	PGF_07420062	235	Two-component transcriptional response regulator, OmpR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4367	PATRIC.2.9855.2.9855.con.0001.CDS.4592188.4594107.rev	PATRIC	CDS	4592188	4594107	1920	-	PGF_00013003	639	Bis-ABC ATPase YheS		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4368	PATRIC.2.9855.2.9855.con.0001.CDS.4594368.4594982.fwd	PATRIC	CDS	4594368	4594982	615	+	PGF_07182652	204	Transcriptional regulator, AcrR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4370	PATRIC.2.9855.2.9855.con.0001.CDS.4595737.4597041.fwd	PATRIC	CDS	4595737	4597041	1305	+	PGF_10025016	434	Cysteine desulfurase (EC 2.8.1.7)	GO:0031071|cysteine desulfurase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4371	PATRIC.2.9855.2.9855.con.0001.CDS.4597206.4598084.rev	PATRIC	CDS	4597206	4598084	879	-	PGF_01264039	292	Pyrophosphate-dependent fructose 6-phosphate-1-kinase (EC 2.7.1.90)	GO:0047334|diphosphate-fructose-6-phosphate 1-phosphotransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4372	PATRIC.2.9855.2.9855.con.0001.CDS.4598211.4598423.rev	PATRIC	CDS	4598211	4598423	213	-	PGF_01264039	70	Pyrophosphate-dependent fructose 6-phosphate-1-kinase (EC 2.7.1.90)	GO:0047334|diphosphate-fructose-6-phosphate 1-phosphotransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4373	PATRIC.2.9855.2.9855.con.0001.CDS.4598612.4599163.fwd	PATRIC	CDS	4598612	4599163	552	+	PGF_01311373	183	Membrane protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.10	PATRIC.2.9855.2.9855.con.0001.CDS.4599.4805.fwd	PATRIC	CDS	4599	4805	207	+	PGF_00070550	68	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	GO:0003849|3-deoxy-7-phosphoheptulonate synthase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4374	PATRIC.2.9855.2.9855.con.0001.CDS.4599221.4599634.fwd	PATRIC	CDS	4599221	4599634	414	+	PGF_10470343	137	Ferric uptake regulation protein FUR		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.404	PATRIC.2.9855.2.9855.con.0001.CDS.459979.461310.fwd	PATRIC	CDS	459979	461310	1332	+	PGF_00275905	443	Glutamine synthetase type I (EC 6.3.1.2)	GO:0004356|glutamate-ammonia ligase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4375	PATRIC.2.9855.2.9855.con.0001.CDS.4599802.4600707.rev	PATRIC	CDS	4599802	4600707	906	-	PGF_10518532	301	D-alanine--D-alanine ligase (EC 6.3.2.4)	GO:0008716|D-alanine-D-alanine ligase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4376	PATRIC.2.9855.2.9855.con.0001.CDS.4600863.4601495.rev	PATRIC	CDS	4600863	4601495	633	-	PGF_08394843	210	Endonuclease III (EC 4.2.99.18)	GO:0003906|DNA-(apurinic or apyrimidinic site) lyase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4377	PATRIC.2.9855.2.9855.con.0001.CDS.4601512.4602216.rev	PATRIC	CDS	4601512	4602216	705	-	PGF_04252606	234	Acyl-CoA:1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	GO:0003841|1-acylglycerol-3-phosphate O-acyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4378	PATRIC.2.9855.2.9855.con.0001.CDS.4602973.4603563.rev	PATRIC	CDS	4602973	4603563	591	-	PGF_04695681	196	Serine acetyltransferase (EC 2.3.1.30)	GO:0009001|serine O-acetyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4379	PATRIC.2.9855.2.9855.con.0001.CDS.4603704.4604615.rev	PATRIC	CDS	4603704	4604615	912	-	PGF_04405923	303	Cysteine synthase (EC 2.5.1.47)	GO:0004124|cysteine synthase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4380	PATRIC.2.9855.2.9855.con.0001.CDS.4605188.4606435.rev	PATRIC	CDS	4605188	4606435	1248	-	PGF_04560429	415	Mg/Co/Ni transporter MgtE, CBS domain-containing		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4381	PATRIC.2.9855.2.9855.con.0001.CDS.4606996.4608996.fwd	PATRIC	CDS	4606996	4608996	2001	+	PGF_00342563	666	UPF0313 [4Fe-4S] protein YgiQ		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4382	PATRIC.2.9855.2.9855.con.0001.CDS.4609171.4609836.rev	PATRIC	CDS	4609171	4609836	666	-	PGF_01311865	221	Two-component system sensor histidine kinase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4383	PATRIC.2.9855.2.9855.con.0001.CDS.4609888.4610766.rev	PATRIC	CDS	4609888	4610766	879	-	PGF_02746079	292	Transcription regulator [contains diacylglycerol kinase catalytic domain]		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4385	PATRIC.2.9855.2.9855.con.0001.CDS.4611064.4611591.fwd	PATRIC	CDS	4611064	4611591	528	+	PGF_10373609	175	CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)	GO:0003882|CDP-diacylglycerol-serine O-phosphatidyltransferase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4388	PATRIC.2.9855.2.9855.con.0001.CDS.4612458.4613000.rev	PATRIC	CDS	4612458	4613000	543	-	PGF_01284176	180	Rubrerythrin		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4389	PATRIC.2.9855.2.9855.con.0001.CDS.4613151.4614521.rev	PATRIC	CDS	4613151	4614521	1371	-	PGF_00426231	456	FIG004684: SpoVR-like protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.48	PATRIC.2.9855.2.9855.con.0001.CDS.46134.46988.fwd	PATRIC	CDS	46134	46988	855	+	PGF_03514578	284	Beta-glucoside bgl operon antiterminator, BglG family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.405	PATRIC.2.9855.2.9855.con.0001.CDS.461352.461912.fwd	PATRIC	CDS	461352	461912	561	+	PGF_10368549	186	Glutamine synthetase-associated two-component response regulator		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4390	PATRIC.2.9855.2.9855.con.0001.CDS.4614526.4615698.rev	PATRIC	CDS	4614526	4615698	1173	-	PGF_05990709	390	UPF0229 protein YeaH		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4391	PATRIC.2.9855.2.9855.con.0001.CDS.4615707.4617635.rev	PATRIC	CDS	4615707	4617635	1929	-	PGF_00051320	642	Serine protein kinase (prkA protein), P-loop containing		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4395	PATRIC.2.9855.2.9855.con.0001.CDS.4619155.4620195.rev	PATRIC	CDS	4619155	4620195	1041	-	PGF_00024841	346	NADPH dehydrogenase (EC 1.6.99.1) (Xenobiotic reductase)	GO:0003959|NADPH dehydrogenase activity;GO:0003959|pentaerythritol trinitrate reductase activity;GO:0003959|trichloro-p-hydroquinone reductive dehalogenase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4396	PATRIC.2.9855.2.9855.con.0001.CDS.4620313.4621059.rev	PATRIC	CDS	4620313	4621059	747	-	PGF_00418088	248	Circadian phase modifier @ NCAIR mutase (PurE)-related protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.406	PATRIC.2.9855.2.9855.con.0001.CDS.462052.466662.fwd	PATRIC	CDS	462052	466662	4611	+	PGF_00008115	1536	Glutamate synthase [NADPH] large chain (EC 1.4.1.13)	GO:0004355|glutamate synthase (NADPH) activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4397	PATRIC.2.9855.2.9855.con.0001.CDS.4621128.4621952.rev	PATRIC	CDS	4621128	4621952	825	-	PGF_07213164	274	ATP-utilizing enzyme of the PP-loop superfamily		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4399	PATRIC.2.9855.2.9855.con.0001.CDS.4623598.4624755.rev	PATRIC	CDS	4623598	4624755	1158	-	PGF_00038846	385	Aldo/keto reductase, 4Fe-4S-containing, TM1183 family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4400	PATRIC.2.9855.2.9855.con.0001.CDS.4625064.4625432.fwd	PATRIC	CDS	4625064	4625432	369	+	PGF_00057506	122	Transcriptional regulator, MerR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4401	PATRIC.2.9855.2.9855.con.0001.CDS.4625661.4626419.rev	PATRIC	CDS	4625661	4626419	759	-	PGF_09666309	252	Two-component transcriptional response regulator, LuxR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4402	PATRIC.2.9855.2.9855.con.0001.CDS.4626447.4627640.rev	PATRIC	CDS	4626447	4627640	1194	-	PGF_08080265	397	Autolysis histidine kinase LytS		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4403	PATRIC.2.9855.2.9855.con.0001.CDS.4627861.4629657.fwd	PATRIC	CDS	4627861	4629657	1797	+	PGF_00416506	598	Carbon starvation protein A		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4404	PATRIC.2.9855.2.9855.con.0001.CDS.4629757.4630437.rev	PATRIC	CDS	4629757	4630437	681	-	PGF_09954313	226	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	GO:0003755|peptidyl-prolyl cis-trans isomerase activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4405	PATRIC.2.9855.2.9855.con.0001.CDS.4630611.4631444.rev	PATRIC	CDS	4630611	4631444	834	-	PGF_00424337	277	Endonuclease IV (EC 3.1.21.2)	GO:0008833|deoxyribonuclease IV (phage-T4-induced) activity	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4406	PATRIC.2.9855.2.9855.con.0001.CDS.4631837.4632493.rev	PATRIC	CDS	4631837	4632493	657	-	PGF_10245672	218	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	GO:0004750|ribulose-phosphate 3-epimerase activity	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4407	PATRIC.2.9855.2.9855.con.0001.CDS.4632561.4634096.rev	PATRIC	CDS	4632561	4634096	1536	-	PGF_00033474	511	Phosphoglucomutase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4408	PATRIC.2.9855.2.9855.con.0001.CDS.4634230.4634919.rev	PATRIC	CDS	4634230	4634919	690	-	PGF_05225955	229	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)		GO:0008742|L-ribulose-phosphate 4-epimerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4409	PATRIC.2.9855.2.9855.con.0001.CDS.4634946.4635389.rev	PATRIC	CDS	4634946	4635389	444	-	PGF_01724713	147	Ribose-5-phosphate isomerase B (EC 5.3.1.6)		GO:0004751|ribose-5-phosphate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4410	PATRIC.2.9855.2.9855.con.0001.CDS.4635421.4636080.rev	PATRIC	CDS	4635421	4636080	660	-	PGF_10245672	219	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)		GO:0004750|ribulose-phosphate 3-epimerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4411	PATRIC.2.9855.2.9855.con.0001.CDS.4636096.4637013.rev	PATRIC	CDS	4636096	4637013	918	-	PGF_00060399	305	Transketolase, C-terminal section (EC 2.2.1.1)		GO:0004802|transketolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4412	PATRIC.2.9855.2.9855.con.0001.CDS.4637013.4637831.rev	PATRIC	CDS	4637013	4637831	819	-	PGF_03267589	272	Transketolase, N-terminal section (EC 2.2.1.1)		GO:0004802|transketolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4413	PATRIC.2.9855.2.9855.con.0001.CDS.4637845.4638903.rev	PATRIC	CDS	4637845	4638903	1059	-	PGF_00007078	352	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)		GO:0008868|galactitol-1-phosphate 5-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4414	PATRIC.2.9855.2.9855.con.0001.CDS.4639298.4640716.rev	PATRIC	CDS	4639298	4640716	1419	-	PGF_00029677	472	PTS system, galactitol-specific IIC component		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4416	PATRIC.2.9855.2.9855.con.0001.CDS.4641109.4641555.rev	PATRIC	CDS	4641109	4641555	447	-	PGF_04724541	148	PTS system, galactitol-specific IIA component (EC 2.7.1.200)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4417	PATRIC.2.9855.2.9855.con.0001.CDS.4641574.4644456.rev	PATRIC	CDS	4641574	4644456	2883	-	PGF_00026324	960	NtrC family Transcriptional regulator, ATPase domain		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4420	PATRIC.2.9855.2.9855.con.0001.CDS.4646115.4646480.rev	PATRIC	CDS	4646115	4646480	366	-	PGF_10238627	121	Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4421	PATRIC.2.9855.2.9855.con.0001.CDS.4647209.4648588.rev	PATRIC	CDS	4647209	4648588	1380	-	PGF_08913741	459	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4422	PATRIC.2.9855.2.9855.con.0001.CDS.4648842.4649915.rev	PATRIC	CDS	4648842	4649915	1074	-	PGF_02620852	357	Two-component system sensor histidine kinase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4423	PATRIC.2.9855.2.9855.con.0001.CDS.4649912.4650589.rev	PATRIC	CDS	4649912	4650589	678	-	PGF_00062859	225	Two-component system response regulator DSY3639		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4424	PATRIC.2.9855.2.9855.con.0001.CDS.4650746.4652101.rev	PATRIC	CDS	4650746	4652101	1356	-	PGF_01469197	451	RNA methyltransferase, TrmA family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4427	PATRIC.2.9855.2.9855.con.0001.CDS.4653601.4654287.rev	PATRIC	CDS	4653601	4654287	687	-	PGF_07824136	228	Late competence protein ComEA, DNA receptor		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4428	PATRIC.2.9855.2.9855.con.0001.CDS.4654453.4655688.fwd	PATRIC	CDS	4654453	4655688	1236	+	PGF_06594113	411	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)		GO:0009002|serine-type D-Ala-D-Ala carboxypeptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4429	PATRIC.2.9855.2.9855.con.0001.CDS.4655752.4656837.rev	PATRIC	CDS	4655752	4656837	1086	-	PGF_00067188	361	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)		GO:0004073|aspartate-semialdehyde dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4430	PATRIC.2.9855.2.9855.con.0001.CDS.4656959.4657855.fwd	PATRIC	CDS	4656959	4657855	897	+	PGF_07987589	298	Transcriptional regulator, LysR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4431	PATRIC.2.9855.2.9855.con.0001.CDS.4657930.4658829.rev	PATRIC	CDS	4657930	4658829	900	-	PGF_10396914	299	Similar to ribosomal large subunit pseudouridine synthase D, Bacillus subtilis YjbO type		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4432	PATRIC.2.9855.2.9855.con.0001.CDS.4659031.4660323.rev	PATRIC	CDS	4659031	4660323	1293	-	PGF_02963397	430	Cell envelope-associated transcriptional attenuator LytR-CpsA-Psr, subfamily M		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4433	PATRIC.2.9855.2.9855.con.0001.CDS.4660423.4661001.rev	PATRIC	CDS	4660423	4661001	579	-	PGF_03117711	192	Hydrolase (HAD superfamily), YqeK		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4434	PATRIC.2.9855.2.9855.con.0001.CDS.4661088.4661702.rev	PATRIC	CDS	4661088	4661702	615	-	PGF_08432396	204	Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)		GO:0004515|nicotinate-nucleotide adenylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4435	PATRIC.2.9855.2.9855.con.0001.CDS.4661865.4662167.rev	PATRIC	CDS	4661865	4662167	303	-	PGF_04287303	100	RNA-binding protein YhbY		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4436	PATRIC.2.9855.2.9855.con.0001.CDS.4662315.4663607.rev	PATRIC	CDS	4662315	4663607	1293	-	PGF_02029783	430	GTP-binding protein Obg		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4437	PATRIC.2.9855.2.9855.con.0001.CDS.4663909.4664208.rev	PATRIC	CDS	4663909	4664208	300	-	PGF_00016385	99	LSU ribosomal protein L27p		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4438	PATRIC.2.9855.2.9855.con.0001.CDS.4664213.4664599.rev	PATRIC	CDS	4664213	4664599	387	-	PGF_00641077	128	FIG139598: Potential ribosomal protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4439	PATRIC.2.9855.2.9855.con.0001.CDS.4664607.4664918.rev	PATRIC	CDS	4664607	4664918	312	-	PGF_04978890	103	LSU ribosomal protein L21p		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4440	PATRIC.2.9855.2.9855.con.0001.CDS.4665094.4666542.rev	PATRIC	CDS	4665094	4666542	1449	-	PGF_01089656	482	Ribonuclease G		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.407	PATRIC.2.9855.2.9855.con.0001.CDS.466676.468148.fwd	PATRIC	CDS	466676	468148	1473	+	PGF_10440725	490	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)		GO:0004355|glutamate synthase (NADPH) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4442	PATRIC.2.9855.2.9855.con.0001.CDS.4667418.4669274.rev	PATRIC	CDS	4667418	4669274	1857	-	PGF_03752158	618	FIG092679: Fe-S oxidoreductase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4444	PATRIC.2.9855.2.9855.con.0001.CDS.4673929.4676019.rev	PATRIC	CDS	4673929	4676019	2091	-	PGF_01266515	696	N-acetylmuramoyl-L-alanine amidase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4446	PATRIC.2.9855.2.9855.con.0001.CDS.4677067.4677924.rev	PATRIC	CDS	4677067	4677924	858	-	PGF_07866963	285	Stage IV sporulation pro-sigma-K processing enzyme (SpoIVFB)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4449	PATRIC.2.9855.2.9855.con.0001.CDS.4678938.4680068.rev	PATRIC	CDS	4678938	4680068	1131	-	PGF_01126005	376	Rod shape-determining protein RodA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4450	PATRIC.2.9855.2.9855.con.0001.CDS.4680338.4680607.rev	PATRIC	CDS	4680338	4680607	270	-	PGF_05220786	89	Cell division topological specificity factor MinE		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4451	PATRIC.2.9855.2.9855.con.0001.CDS.4680622.4681422.rev	PATRIC	CDS	4680622	4681422	801	-	PGF_02950579	266	Septum site-determining protein MinD		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4452	PATRIC.2.9855.2.9855.con.0001.CDS.4681443.4682102.rev	PATRIC	CDS	4681443	4682102	660	-	PGF_00051120	219	Septum site-determining protein MinC		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4453	PATRIC.2.9855.2.9855.con.0001.CDS.4682302.4682982.rev	PATRIC	CDS	4682302	4682982	681	-	PGF_00054920	226	Sugar fermentation stimulation protein SfsA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4454	PATRIC.2.9855.2.9855.con.0001.CDS.4683140.4686037.rev	PATRIC	CDS	4683140	4686037	2898	-	PGF_10376398	965	Peptidoglycan D,D-transpeptidase MrdA (EC 3.4.16.4)		GO:0009002|serine-type D-Ala-D-Ala carboxypeptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4455	PATRIC.2.9855.2.9855.con.0001.CDS.4686034.4686525.rev	PATRIC	CDS	4686034	4686525	492	-	PGF_00049195	163	Rod shape-determining protein MreD		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4456	PATRIC.2.9855.2.9855.con.0001.CDS.4686535.4687383.rev	PATRIC	CDS	4686535	4687383	849	-	PGF_10369954	282	Rod shape-determining protein MreC		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.409	PATRIC.2.9855.2.9855.con.0001.CDS.468671.469588.fwd	PATRIC	CDS	468671	469588	918	+	PGF_01315021	305	CAAX amino terminal protease family protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4457	PATRIC.2.9855.2.9855.con.0001.CDS.4687386.4688402.rev	PATRIC	CDS	4687386	4688402	1017	-	PGF_00648450	338	Rod shape-determining protein MreB		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4458	PATRIC.2.9855.2.9855.con.0001.CDS.4688423.4689112.rev	PATRIC	CDS	4688423	4689112	690	-	PGF_10454652	229	UPF0758 family protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4459	PATRIC.2.9855.2.9855.con.0001.CDS.4689164.4689730.rev	PATRIC	CDS	4689164	4689730	567	-	PGF_08843714	188	Septum formation protein Maf		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4461	PATRIC.2.9855.2.9855.con.0001.CDS.4691042.4691635.rev	PATRIC	CDS	4691042	4691635	594	-	PGF_01275815	197	Cell wall-associated hydrolases		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4462	PATRIC.2.9855.2.9855.con.0001.CDS.4692000.4693457.rev	PATRIC	CDS	4692000	4693457	1458	-	PGF_00420732	485	Cytosol nonspecific dipeptidase (EC 3.4.13.18)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4463	PATRIC.2.9855.2.9855.con.0001.CDS.4693621.4695039.fwd	PATRIC	CDS	4693621	4695039	1419	+	PGF_07760799	472	Pyruvate kinase (EC 2.7.1.40)		GO:0004743|pyruvate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4464	PATRIC.2.9855.2.9855.con.0001.CDS.4695112.4696266.rev	PATRIC	CDS	4695112	4696266	1155	-	PGF_09939762	384	SSU ribosomal protein S1p		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4466	PATRIC.2.9855.2.9855.con.0001.CDS.4697333.4697983.fwd	PATRIC	CDS	4697333	4697983	651	+	PGF_00055295	216	Suppressor of sigma54-dependent transcription, PspA-like		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4468	PATRIC.2.9855.2.9855.con.0001.CDS.4698840.4699289.rev	PATRIC	CDS	4698840	4699289	450	-	PGF_00414866	149	CBS domain protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4469	PATRIC.2.9855.2.9855.con.0001.CDS.4699408.4700319.rev	PATRIC	CDS	4699408	4700319	912	-	PGF_08232787	303	Probable DNA polymerase III epsilon chain		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4470	PATRIC.2.9855.2.9855.con.0001.CDS.4700367.4702157.rev	PATRIC	CDS	4700367	4702157	1791	-	PGF_00023412	596	MutS-related protein, family 1		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4471	PATRIC.2.9855.2.9855.con.0001.CDS.4702662.4703273.rev	PATRIC	CDS	4702662	4703273	612	-	PGF_02486076	203	Zinc ABC transporter, substrate-binding protein ZnuA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4472	PATRIC.2.9855.2.9855.con.0001.CDS.4703316.4703558.rev	PATRIC	CDS	4703316	4703558	243	-	PGF_02486076	80	Zinc ABC transporter, substrate-binding protein ZnuA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.49	PATRIC.2.9855.2.9855.con.0001.CDS.47035.47532.rev	PATRIC	CDS	47035	47532	498	-	PGF_01309240	165	PTS system, glucose-specific IIA component (EC 2.7.1.199)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4473	PATRIC.2.9855.2.9855.con.0001.CDS.4703668.4706403.rev	PATRIC	CDS	4703668	4706403	2736	-	PGF_00421225	911	DNA double-strand break repair Rad50 ATPase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.412	PATRIC.2.9855.2.9855.con.0001.CDS.470449.471243.fwd	PATRIC	CDS	470449	471243	795	+	PGF_12690820	264	Phage replication initiation		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4475	PATRIC.2.9855.2.9855.con.0001.CDS.4706505.4707638.rev	PATRIC	CDS	4706505	4707638	1134	-	PGF_02278516	377	DNA double-strand break repair protein Mre11		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4476	PATRIC.2.9855.2.9855.con.0001.CDS.4707870.4708061.rev	PATRIC	CDS	4707870	4708061	192	-	PGF_00053039	63	Small acid-soluble spore protein, alpha-type SASP		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4478	PATRIC.2.9855.2.9855.con.0001.CDS.4709975.4711042.fwd	PATRIC	CDS	4709975	4711042	1068	+	PGF_00917689	355	Putative FabK-like enoyl-[acyl-carrier-protein] reductase		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4479	PATRIC.2.9855.2.9855.con.0001.CDS.4711140.4711520.rev	PATRIC	CDS	4711140	4711520	381	-	PGF_02690675	126	RidA/YER057c/UK114 superfamily protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4480	PATRIC.2.9855.2.9855.con.0001.CDS.4711991.4712893.rev	PATRIC	CDS	4711991	4712893	903	-	PGF_02486076	300	Zinc ABC transporter, substrate-binding protein ZnuA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4481	PATRIC.2.9855.2.9855.con.0001.CDS.4713341.4713802.fwd	PATRIC	CDS	4713341	4713802	462	+	PGF_03753407	153	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4482	PATRIC.2.9855.2.9855.con.0001.CDS.4713799.4714533.fwd	PATRIC	CDS	4713799	4714533	735	+	PGF_02792560	244	tRNA threonylcarbamoyladenosine biosynthesis protein TsaB		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4483	PATRIC.2.9855.2.9855.con.0001.CDS.4714533.4714973.fwd	PATRIC	CDS	4714533	4714973	441	+	PGF_01366266	146	Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.128)		GO:0008999|ribosomal-protein-alanine N-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4484	PATRIC.2.9855.2.9855.con.0001.CDS.4715126.4715890.rev	PATRIC	CDS	4715126	4715890	765	-	PGF_00008623	254	Glycerol-3-phosphate regulon repressor GlpR		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.413	PATRIC.2.9855.2.9855.con.0001.CDS.471568.472776.fwd	PATRIC	CDS	471568	472776	1209	+	PGF_00015699	402	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)		GO:0004450|isocitrate dehydrogenase (NADP+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4485	PATRIC.2.9855.2.9855.con.0001.CDS.4716087.4716248.rev	PATRIC	CDS	4716087	4716248	162	-	PGF_00929131	53	Rubredoxin		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4486	PATRIC.2.9855.2.9855.con.0001.CDS.4717028.4717609.rev	PATRIC	CDS	4717028	4717609	582	-	PGF_03751878	193	Substrate-specific component RibU of riboflavin ECF transporter		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4487	PATRIC.2.9855.2.9855.con.0001.CDS.4718079.4718468.rev	PATRIC	CDS	4718079	4718468	390	-	PGF_03751069	129	Hemerythrin domain protein		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4488	PATRIC.2.9855.2.9855.con.0001.CDS.4718785.4719411.rev	PATRIC	CDS	4718785	4719411	627	-	PGF_00730641	208	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)		GO:0008700|4-hydroxy-2-oxoglutarate aldolase activity;GO:0008675|2-dehydro-3-deoxy-phosphogluconate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4489	PATRIC.2.9855.2.9855.con.0001.CDS.4719501.4720421.rev	PATRIC	CDS	4719501	4720421	921	-	PGF_05097244	306	2-dehydro-3-deoxygluconokinase (EC 2.7.1.45)		GO:0008673|2-dehydro-3-deoxygluconokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4490	PATRIC.2.9855.2.9855.con.0001.CDS.4720585.4721367.rev	PATRIC	CDS	4720585	4721367	783	-	PGF_00061907	260	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase (EC 1.1.1.127) @ 2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)		GO:0047001|2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase activity;GO:0008678|2-deoxy-D-gluconate 3-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4491	PATRIC.2.9855.2.9855.con.0001.CDS.4721611.4722420.fwd	PATRIC	CDS	4721611	4722420	810	+	PGF_08238312	269	Transcriptional regulator, IclR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4492	PATRIC.2.9855.2.9855.con.0001.CDS.4722664.4723476.rev	PATRIC	CDS	4722664	4723476	813	-	PGF_02899915	270	Hydrolase, HAD superfamily		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4493	PATRIC.2.9855.2.9855.con.0001.CDS.4723608.4724225.rev	PATRIC	CDS	4723608	4724225	618	-	PGF_00010778	205	Transcriptional repressor GlcR, DeoR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4494	PATRIC.2.9855.2.9855.con.0001.CDS.4724460.4724927.rev	PATRIC	CDS	4724460	4724927	468	-	PGF_10483430	155	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)		GO:0003908|methylated-DNA-[protein]-cysteine S-methyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4495	PATRIC.2.9855.2.9855.con.0001.CDS.4725377.4726531.rev	PATRIC	CDS	4725377	4726531	1155	-	PGF_00016494	384	Lactaldehyde reductase (EC 1.1.1.77)		GO:0008912|lactaldehyde reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4496	PATRIC.2.9855.2.9855.con.0001.CDS.4726871.4727689.rev	PATRIC	CDS	4726871	4727689	819	-	PGF_00048285	272	Rhamnulose-1-phosphate aldolase (EC 4.1.2.19)		GO:0008994|rhamnulose-1-phosphate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4497	PATRIC.2.9855.2.9855.con.0001.CDS.4728061.4728819.rev	PATRIC	CDS	4728061	4728819	759	-	PGF_00065860	252	Uncharacterized transcriptional regulator YdjF, DeoR family		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4498	PATRIC.2.9855.2.9855.con.0001.CDS.4729055.4729369.fwd	PATRIC	CDS	4729055	4729369	315	+	PGF_00016202	104	L-rhamnose mutarotase (EC 5.1.3.32)		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4499	PATRIC.2.9855.2.9855.con.0001.CDS.4729528.4731066.rev	PATRIC	CDS	4729528	4731066	1539	-	PGF_00048271	512	Rhamnogalacturonide transporter RhiT		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4501	PATRIC.2.9855.2.9855.con.0001.CDS.4732991.4734118.fwd	PATRIC	CDS	4732991	4734118	1128	+	PGF_03081716	375	Rhamnogalacturonides degradation protein RhiN		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4502	PATRIC.2.9855.2.9855.con.0001.CDS.4734517.4735299.rev	PATRIC	CDS	4734517	4735299	783	-	PGF_00061907	260	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase (EC 1.1.1.127) @ 2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)		GO:0047001|2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase activity;GO:0008678|2-deoxy-D-gluconate 3-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4503	PATRIC.2.9855.2.9855.con.0001.CDS.4735324.4736160.rev	PATRIC	CDS	4735324	4736160	837	-	PGF_00423470	278	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)		GO:0008697|4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.414	PATRIC.2.9855.2.9855.con.0001.CDS.473587.473796.fwd	PATRIC	CDS	473587	473796	210	+	PGF_10078722	69	FeoA-like protein CKL_1603		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4504	PATRIC.2.9855.2.9855.con.0001.CDS.4736289.4737545.rev	PATRIC	CDS	4736289	4737545	1257	-	PGF_00016200	418	L-rhamnose isomerase (EC 5.3.1.14)		GO:0008740|L-rhamnose isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4505	PATRIC.2.9855.2.9855.con.0001.CDS.4737680.4739083.rev	PATRIC	CDS	4737680	4739083	1404	-	PGF_00048282	467	Rhamnulokinase (EC 2.7.1.5)		GO:0008993|rhamnulokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.415	PATRIC.2.9855.2.9855.con.0001.CDS.473810.474031.fwd	PATRIC	CDS	473810	474031	222	+	PGF_09238933	73	Ferrous iron transporter-associated protein FeoA		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4506	PATRIC.2.9855.2.9855.con.0001.CDS.4739815.4741908.fwd	PATRIC	CDS	4739815	4741908	2094	+	PGF_00008261	697	Glutamine synthetase type III, GlnN (EC 6.3.1.2)		GO:0004356|glutamate-ammonia ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.416	PATRIC.2.9855.2.9855.con.0001.CDS.474106.476256.rev	PATRIC	CDS	474106	476256	2151	+	PGF_01467683	716	Ferrous iron transporter FeoB		

																GO:0008443|phosphatidylcholine kinase activity;GO:0008443|phosphatidylinositol 4-kinase regulator activity;GO:0008443|cobinamide kinase activity;GO:0008443|phytol kinase activity;GO:0008443|phosphatidylinositol phosphate kinase activity;GO:0008443|cyclin-dependent protein serine/threonine kinase regulator activity;GO:0008443|phenol kinase activity;GO:0008443|cyclin-dependent protein kinase activating kinase regulator activity;GO:0008443|inositol tetrakisphosphate 2-kinase activity;GO:0008443|heptose 7-phosphate kinase activity;GO:0008443|aminoglycoside phosphotransferase activity;GO:0008443|phosphatidylinositol 3-kinase activity;GO:0008443|eukaryotic elongation factor-2 kinase regulator activity;GO:0008443|eukaryotic elongation factor-2 kinase activator activity;GO:0008443|LPPG:FO 2-phospho-L-lactate transferase activity;GO:0008443|cytidine kinase activity;GO:0008443|glycerate 2-kinase activity;GO:0008443|(S)-lactate 2-kinase activity;GO:0008443|phosphoserine:homoserine phosphotransferase activity;GO:0008443|L-seryl-tRNA(Sec) kinase activity;GO:0008443|phosphocholine transferase activity;GO:0008443|polynucleotide 5'-hydroxyl-kinase activity;GO:0008443|ATP-dependent polynucleotide kinase activity;GO:0008443|GTP-dependent polynucleotide kinase activity;GO:0008443|farnesol kinase activity;GO:0008443|CTP:2-trans,-6-trans-farnesol kinase activity;GO:0008443|geraniol kinase activity;GO:0008443|geranylgeraniol kinase activity;GO:0008443|CTP:geranylgeraniol kinase activity;GO:0008443|prenol kinase activity;GO:0008443|1-phosphatidylinositol-5-kinase activity;GO:0008443|1-phosphatidylinositol-3-phosphate 4-kinase activity;GO:0008443|phosphatidylinositol-3,4-bisphosphate 5-kinase activity;GO:0008443|phosphatidylinositol bisphosphate kinase activity;GO:0008443|inositol-3,4,6-trisphosphate 1-kinase activity;GO:0008443|inositol 5-diphosphate pentakisphosphate 5-kinase activity;GO:0008443|inositol diphosphate tetrakisphosphate kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4507	PATRIC.2.9855.2.9855.con.0001.CDS.4742064.4742957.rev	PATRIC	CDS	4742064	4742957	894	-	PGF_01066598	297	Sugar kinase and transcription regulator (EC 2.7.1.-)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4508	PATRIC.2.9855.2.9855.con.0001.CDS.4743304.4744284.rev	PATRIC	CDS	4743304	4744284	981	-	PGF_10523121	326	Transcriptional regulator of rhamnose utilization, AraC family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4509	PATRIC.2.9855.2.9855.con.0001.CDS.4744381.4745352.rev	PATRIC	CDS	4744381	4745352	972	-	PGF_00409474	323	putative membrane protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4510	PATRIC.2.9855.2.9855.con.0001.CDS.4745360.4746316.rev	PATRIC	CDS	4745360	4746316	957	-	PGF_02621158	318	Oxidoreductase, N-terminal:Oxidoreductase, C-terminal	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4511	PATRIC.2.9855.2.9855.con.0001.CDS.4746574.4748751.rev	PATRIC	CDS	4746574	4748751	2178	-	PGF_02906681	725	Transcription accessory protein (S1 RNA-binding domain)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4513	PATRIC.2.9855.2.9855.con.0001.CDS.4749260.4750171.rev	PATRIC	CDS	4749260	4750171	912	-	PGF_00019588	303	Membrane metalloprotease	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4514	PATRIC.2.9855.2.9855.con.0001.CDS.4750370.4751872.rev	PATRIC	CDS	4750370	4751872	1503	-	PGF_02620852	500	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4515	PATRIC.2.9855.2.9855.con.0001.CDS.4751862.4752557.rev	PATRIC	CDS	4751862	4752557	696	-	PGF_07420062	231	Two-component transcriptional response regulator, OmpR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4517	PATRIC.2.9855.2.9855.con.0001.CDS.4753219.4754193.rev	PATRIC	CDS	4753219	4754193	975	-	PGF_06759833	324	Peptide chain release factor 2	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4518	PATRIC.2.9855.2.9855.con.0001.CDS.4754488.4757055.rev	PATRIC	CDS	4754488	4757055	2568	-	PGF_10049811	855	Protein translocase subunit SecA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4519	PATRIC.2.9855.2.9855.con.0001.CDS.4757400.4757933.rev	PATRIC	CDS	4757400	4757933	534	-	PGF_01382519	177	Ribosome hibernation promoting factor Hpf	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4520	PATRIC.2.9855.2.9855.con.0001.CDS.4758349.4759005.rev	PATRIC	CDS	4758349	4759005	657	-	PGF_07275226	218	Competence protein F homolog, phosphoribosyltransferase domain; protein YhgH required for utilization of DNA as sole source of carbon and energy	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4521	PATRIC.2.9855.2.9855.con.0001.CDS.4758978.4759994.rev	PATRIC	CDS	4758978	4759994	1017	-	PGF_00871747	338	ComF operon protein A, DNA transporter ATPase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4522	PATRIC.2.9855.2.9855.con.0001.CDS.4760013.4762241.rev	PATRIC	CDS	4760013	4762241	2229	-	PGF_00047095	742	RecD-like DNA helicase YrrC	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4523	PATRIC.2.9855.2.9855.con.0001.CDS.4762693.4763868.rev	PATRIC	CDS	4762693	4763868	1176	-	PGF_03202156	391	S-adenosylmethionine synthetase (EC 2.5.1.6)	GO:0004478|methionine adenosyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4524	PATRIC.2.9855.2.9855.con.0001.CDS.4765138.4765542.rev	PATRIC	CDS	4765138	4765542	405	-	PGF_01283476	134	no significant homology Putative N-terminal signal sequence was found by PSORT	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4525	PATRIC.2.9855.2.9855.con.0001.CDS.4765643.4766179.fwd	PATRIC	CDS	4765643	4766179	537	+	PGF_10349657	178	Spore protease GPR related protein, YYAC B.subtilis ortholog	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4526	PATRIC.2.9855.2.9855.con.0001.CDS.4766247.4767281.rev	PATRIC	CDS	4766247	4767281	1035	-	PGF_00417319	344	MreB-like protein (Mbl protein)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4527	PATRIC.2.9855.2.9855.con.0001.CDS.4767361.4767615.rev	PATRIC	CDS	4767361	4767615	255	-	PGF_00054075	84	Stage III sporulation protein D	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4528	PATRIC.2.9855.2.9855.con.0001.CDS.4767723.4768460.rev	PATRIC	CDS	4767723	4768460	738	-	PGF_01299277	245	Stage II sporulation protein related to metaloproteases (SpoIIQ)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4529	PATRIC.2.9855.2.9855.con.0001.CDS.4768901.4769959.rev	PATRIC	CDS	4768901	4769959	1059	-	PGF_02888001	352	Stage II sporulation protein D (SpoIID)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4530	PATRIC.2.9855.2.9855.con.0001.CDS.4770560.4771822.rev	PATRIC	CDS	4770560	4771822	1263	-	PGF_00900122	420	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	GO:0008760|UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4532	PATRIC.2.9855.2.9855.con.0001.CDS.4772849.4773256.rev	PATRIC	CDS	4772849	4773256	408	-	PGF_07919746	135	ATP synthase epsilon chain (EC 3.6.3.14)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4533	PATRIC.2.9855.2.9855.con.0001.CDS.4773272.4774663.rev	PATRIC	CDS	4773272	4774663	1392	-	PGF_05195027	463	ATP synthase beta chain (EC 3.6.3.14)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4534	PATRIC.2.9855.2.9855.con.0001.CDS.4774678.4775529.rev	PATRIC	CDS	4774678	4775529	852	-	PGF_00015259	283	ATP synthase gamma chain (EC 3.6.3.14)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.419	PATRIC.2.9855.2.9855.con.0001.CDS.477540.478583.fwd	PATRIC	CDS	477540	478583	1044	+	PGF_05442739	347	Sulfate and thiosulfate binding protein CysP	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4535	PATRIC.2.9855.2.9855.con.0001.CDS.4775571.4777085.rev	PATRIC	CDS	4775571	4777085	1515	-	PGF_04569524	504	ATP synthase alpha chain (EC 3.6.3.14)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4536	PATRIC.2.9855.2.9855.con.0001.CDS.4777096.4777635.rev	PATRIC	CDS	4777096	4777635	540	-	PGF_06274006	179	ATP synthase delta chain (EC 3.6.3.14)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4537	PATRIC.2.9855.2.9855.con.0001.CDS.4777638.4778117.rev	PATRIC	CDS	4777638	4778117	480	-	PGF_10546429	159	ATP synthase F0 sector subunit b (EC 3.6.3.14)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4538	PATRIC.2.9855.2.9855.con.0001.CDS.4778170.4778385.rev	PATRIC	CDS	4778170	4778385	216	-	PGF_10444145	71	ATP synthase F0 sector subunit c (EC 3.6.3.14)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4539	PATRIC.2.9855.2.9855.con.0001.CDS.4778439.4779119.rev	PATRIC	CDS	4778439	4779119	681	-	PGF_08518355	226	ATP synthase F0 sector subunit a (EC 3.6.3.14)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4541	PATRIC.2.9855.2.9855.con.0001.CDS.4780206.4781387.rev	PATRIC	CDS	4780206	4781387	1182	-	PGF_10164212	393	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	GO:0003985|acetyl-CoA C-acetyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4542	PATRIC.2.9855.2.9855.con.0001.CDS.4781509.4782657.rev	PATRIC	CDS	4781509	4782657	1149	-	PGF_10317148	382	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)	GO:0008761|UDP-N-acetylglucosamine 2-epimerase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4543	PATRIC.2.9855.2.9855.con.0001.CDS.4782937.4783431.rev	PATRIC	CDS	4782937	4783431	495	-	PGF_02704803	164	dCMP deaminase (EC 3.5.4.12) @ Late competence protein ComEB	GO:0004132|dCMP deaminase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4544	PATRIC.2.9855.2.9855.con.0001.CDS.4783513.4784142.rev	PATRIC	CDS	4783513	4784142	630	-	PGF_00403095	209	Uracil phosphoribosyltransferase (EC 2.4.2.9)	GO:0004845|uracil phosphoribosyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4545	PATRIC.2.9855.2.9855.con.0001.CDS.4784292.4784741.rev	PATRIC	CDS	4784292	4784741	450	-	PGF_01724713	149	Ribose-5-phosphate isomerase B (EC 5.3.1.6)	GO:0004751|ribose-5-phosphate isomerase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4546	PATRIC.2.9855.2.9855.con.0001.CDS.4784792.4785841.rev	PATRIC	CDS	4784792	4785841	1050	-	PGF_09112178	349	Threonylcarbamoyl-AMP synthase (EC 2.7.7.87) / SUA5 domain with internal deletion	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4547	PATRIC.2.9855.2.9855.con.0001.CDS.4785897.4786484.rev	PATRIC	CDS	4785897	4786484	588	-	PGF_00408619	195	putative membrane protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4548	PATRIC.2.9855.2.9855.con.0001.CDS.4786550.4787632.rev	PATRIC	CDS	4786550	4787632	1083	-	PGF_00030640	360	Peptide chain release factor 1	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.420	PATRIC.2.9855.2.9855.con.0001.CDS.478783.479607.fwd	PATRIC	CDS	478783	479607	825	+	PGF_00054986	274	Sulfate transport system permease protein CysT	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4550	PATRIC.2.9855.2.9855.con.0001.CDS.4789554.4790138.rev	PATRIC	CDS	4789554	4790138	585	-	PGF_10401812	194	Thymidine kinase (EC 2.7.1.21)	GO:0004797|thymidine kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4551	PATRIC.2.9855.2.9855.con.0001.CDS.4790328.4790537.fwd	PATRIC	CDS	4790328	4790537	210	+	PGF_05770273	69	LSU ribosomal protein L31p @ LSU ribosomal protein L31p, zinc-dependent	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4552	PATRIC.2.9855.2.9855.con.0001.CDS.4790751.4791857.fwd	PATRIC	CDS	4790751	4791857	1107	+	PGF_00022608	368	Monogalactosyldiacylglycerol synthase precursor	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4553	PATRIC.2.9855.2.9855.con.0001.CDS.4791899.4793341.rev	PATRIC	CDS	4791899	4793341	1443	-	PGF_00057483	480	Transcription termination factor Rho	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4554	PATRIC.2.9855.2.9855.con.0001.CDS.4793652.4795262.rev	PATRIC	CDS	4793652	4795262	1611	-	PGF_00416129	536	CTP synthase (EC 6.3.4.2)	GO:0003883|CTP synthase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.50	PATRIC.2.9855.2.9855.con.0001.CDS.47941.49377.fwd	PATRIC	CDS	47941	49377	1437	+	PGF_03318742	478	PTS system, N-acetylglucosamine-specific IIC component / PTS system, N-acetylglucosamine-specific IIB component (EC 2.7.1.193)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4556	PATRIC.2.9855.2.9855.con.0001.CDS.4795841.4796257.rev	PATRIC	CDS	4795841	4796257	417	-	PGF_00422481	138	DUF1934 domain-containing protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.421	PATRIC.2.9855.2.9855.con.0001.CDS.479620.480450.fwd	PATRIC	CDS	479620	480450	831	+	PGF_00054988	276	Sulfate transport system permease protein CysW	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4557	PATRIC.2.9855.2.9855.con.0001.CDS.4796389.4797126.rev	PATRIC	CDS	4796389	4797126	738	-	PGF_00054034	245	Stage II sporulation protein required for processing of pro-sigma-E (SpoIIR)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4558	PATRIC.2.9855.2.9855.con.0001.CDS.4797190.4798032.rev	PATRIC	CDS	4797190	4798032	843	-	PGF_00423533	280	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	GO:0050515|4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4559	PATRIC.2.9855.2.9855.con.0001.CDS.4798181.4800823.rev	PATRIC	CDS	4798181	4800823	2643	-	PGF_00419870	880	Cyanophycin synthase (EC 6.3.2.29)(EC 6.3.2.30)	GO:0071160|cyanophycin synthetase activity (L-aspartate-adding);GO:0071161|cyanophycin synthetase activity (L-arginine-adding)
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4560	PATRIC.2.9855.2.9855.con.0001.CDS.4800795.4801640.rev	PATRIC	CDS	4800795	4801640	846	-	PGF_00419875	281	Cyanophycinase (EC 3.4.15.6)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4562	PATRIC.2.9855.2.9855.con.0001.CDS.4801970.4803532.rev	PATRIC	CDS	4801970	4803532	1563	-	PGF_00017761	520	LysM domain-containing membrane protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4563	PATRIC.2.9855.2.9855.con.0001.CDS.4803996.4804238.rev	PATRIC	CDS	4803996	4804238	243	-	PGF_04481164	80	Veg protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.422	PATRIC.2.9855.2.9855.con.0001.CDS.480456.481520.fwd	PATRIC	CDS	480456	481520	1065	+	PGF_05696702	354	Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)	GO:0015419|sulfate transmembrane-transporting ATPase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4564	PATRIC.2.9855.2.9855.con.0001.CDS.4804854.4805393.rev	PATRIC	CDS	4804854	4805393	540	-	PGF_08363070	179	Glutathione peroxidase (EC 1.11.1.9) @ Thioredoxin peroxidase (EC 1.11.1.15)	GO:0004602|glutathione peroxidase activity;GO:0051920|peroxiredoxin activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4565	PATRIC.2.9855.2.9855.con.0001.CDS.4805632.4806492.rev	PATRIC	CDS	4805632	4806492	861	-	PGF_00042913	286	Sporulation-specific protease YabG	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4566	PATRIC.2.9855.2.9855.con.0001.CDS.4806655.4807653.rev	PATRIC	CDS	4806655	4807653	999	-	PGF_00053850	332	Spore coat protein S	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4567	PATRIC.2.9855.2.9855.con.0001.CDS.4807762.4808883.fwd	PATRIC	CDS	4807762	4808883	1122	+	PGF_04305571	373	Glycosyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4568	PATRIC.2.9855.2.9855.con.0001.CDS.4809207.4810262.rev	PATRIC	CDS	4809207	4810262	1056	-	PGF_00053850	351	Spore coat protein S	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4569	PATRIC.2.9855.2.9855.con.0001.CDS.4810318.4811124.rev	PATRIC	CDS	4810318	4811124	807	-	PGF_01268353	268	Spore coat protein cotS related	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4570	PATRIC.2.9855.2.9855.con.0001.CDS.4811126.4812142.rev	PATRIC	CDS	4811126	4812142	1017	-	PGF_00053850	338	Spore coat protein S	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4571	PATRIC.2.9855.2.9855.con.0001.CDS.4812272.4813390.fwd	PATRIC	CDS	4812272	4813390	1119	+	PGF_04305571	372	Glycosyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4573	PATRIC.2.9855.2.9855.con.0001.CDS.4814715.4815023.rev	PATRIC	CDS	4814715	4815023	309	-	PGF_01629422	102	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4574	PATRIC.2.9855.2.9855.con.0001.CDS.4815223.4816452.rev	PATRIC	CDS	4815223	4816452	1230	-	PGF_01162199	409	Serine protease, DegP/HtrA, do-like (EC 3.4.21.-)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4575	PATRIC.2.9855.2.9855.con.0001.CDS.4816718.4817719.rev	PATRIC	CDS	4816718	4817719	1002	-	PGF_06574151	333	Hydrolase, alpha/beta fold family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4576	PATRIC.2.9855.2.9855.con.0001.CDS.4817729.4818748.rev	PATRIC	CDS	4817729	4818748	1020	-	PGF_07915158	339	N(6)-L-threonylcarbamoyladenine synthase (EC 2.3.1.234)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.423	PATRIC.2.9855.2.9855.con.0001.CDS.481817.483523.fwd	PATRIC	CDS	481817	483523	1707	+	PGF_00035871	568	Adenylylsulfate reductase alpha-subunit (EC 1.8.99.2)	GO:0009973|adenylyl-sulfate reductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4577	PATRIC.2.9855.2.9855.con.0001.CDS.4819225.4819923.fwd	PATRIC	CDS	4819225	4819923	699	+	PGF_00035083	232	Possible Zn-finger containing protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4578	PATRIC.2.9855.2.9855.con.0001.CDS.4819945.4820508.fwd	PATRIC	CDS	4819945	4820508	564	+	PGF_00644981	187	Arylesterase precursor (EC 3.1.1.2)	GO:0004064|arylesterase activity

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4579	PATRIC.2.9855.2.9855.con.0001.CDS.4820586.4821542.rev	PATRIC	CDS	4820586	4821542	957	-	PGF_02681495	318	Sarcosine oxidase alpha subunit (EC 1.5.3.1)	GO:0008115|sarcosine oxidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4581	PATRIC.2.9855.2.9855.con.0001.CDS.4822439.4824322.fwd	PATRIC	CDS	4822439	4824322	1884	+	PGF_00017475	627	Lipoteichoic acid synthase LtaS Type IVb	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4582	PATRIC.2.9855.2.9855.con.0001.CDS.4824379.4825188.rev	PATRIC	CDS	4824379	4825188	810	-	PGF_06535427	269	Uncharacterized DUF1113 membrane protein family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4583	PATRIC.2.9855.2.9855.con.0001.CDS.4825234.4826577.rev	PATRIC	CDS	4825234	4826577	1344	-	PGF_02960239	447	TldE protein, part of TldE/TldD proteolytic complex	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4584	PATRIC.2.9855.2.9855.con.0001.CDS.4826580.4827965.rev	PATRIC	CDS	4826580	4827965	1386	-	PGF_06707410	461	TldD protein, part of TldE/TldD proteolytic complex	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4585	PATRIC.2.9855.2.9855.con.0001.CDS.4828254.4829360.rev	PATRIC	CDS	4828254	4829360	1107	-	PGF_00406657	368	putative deacetylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4586	PATRIC.2.9855.2.9855.con.0001.CDS.4830146.4830724.fwd	PATRIC	CDS	4830146	4830724	579	+	PGF_03495000	192	Mobile element protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4588	PATRIC.2.9855.2.9855.con.0001.CDS.4834773.4836833.rev	PATRIC	CDS	4834773	4836833	2061	-	PGF_05695878	686	Peptidase, M13 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.424	PATRIC.2.9855.2.9855.con.0001.CDS.483507.483824.fwd	PATRIC	CDS	483507	483824	318	+	PGF_00035913	105	Adenylylsulfate reductase beta-subunit (EC 1.8.99.2)	GO:0009973|adenylyl-sulfate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4590	PATRIC.2.9855.2.9855.con.0001.CDS.4837351.4839813.rev	PATRIC	CDS	4837351	4839813	2463	-	PGF_01288419	820	Similarity with glutathionylspermidine synthase (EC 6.3.1.8), group 2	GO:0008885|glutathionylspermidine synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.425	PATRIC.2.9855.2.9855.con.0001.CDS.483957.484856.fwd	PATRIC	CDS	483957	484856	900	+	PGF_00054961	299	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	GO:0004781|sulfate adenylyltransferase (ATP) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4594	PATRIC.2.9855.2.9855.con.0001.CDS.4841331.4843379.rev	PATRIC	CDS	4841331	4843379	2049	-	PGF_02620852	682	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4597	PATRIC.2.9855.2.9855.con.0001.CDS.4845366.4846022.rev	PATRIC	CDS	4845366	4846022	657	-	PGF_00049467	218	SAM-dependent methyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.426	PATRIC.2.9855.2.9855.con.0001.CDS.484858.486546.fwd	PATRIC	CDS	484858	486546	1689	+	PGF_00054959	562	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)	GO:0004781|sulfate adenylyltransferase (ATP) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4600	PATRIC.2.9855.2.9855.con.0001.CDS.4849161.4849640.rev	PATRIC	CDS	4849161	4849640	480	-	PGF_09654405	159	FIG009886: phosphoesterase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4601	PATRIC.2.9855.2.9855.con.0001.CDS.4849717.4850331.rev	PATRIC	CDS	4849717	4850331	615	-	PGF_00026362	204	Nucleoside 5-triphosphatase RdgB (dHAPTP, dITP, XTP-specific) (EC 3.6.1.66)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4602	PATRIC.2.9855.2.9855.con.0001.CDS.4850545.4851522.rev	PATRIC	CDS	4850545	4851522	978	-	PGF_00013741	325	AIR Synthase, TMP kinase, hydrogenase maturation protein HypE superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4604	PATRIC.2.9855.2.9855.con.0001.CDS.4853499.4854995.rev	PATRIC	CDS	4853499	4854995	1497	-	PGF_02147779	498	Oligopeptide ABC transporter, substrate-binding protein OppA (TC 3.A.1.5.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4606	PATRIC.2.9855.2.9855.con.0001.CDS.4855437.4857428.rev	PATRIC	CDS	4855437	4857428	1992	-	PGF_04333086	663	DNA ligase (NAD(+)) (EC 6.5.1.2)	GO:0003911|DNA ligase (NAD+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4607	PATRIC.2.9855.2.9855.con.0001.CDS.4857448.4859715.rev	PATRIC	CDS	4857448	4859715	2268	-	PGF_10471233	755	ATP-dependent DNA helicase UvrD/PcrA (EC 3.6.4.12)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4608	PATRIC.2.9855.2.9855.con.0001.CDS.4859987.4861624.rev	PATRIC	CDS	4859987	4861624	1638	-	PGF_07849456	545	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4609	PATRIC.2.9855.2.9855.con.0001.CDS.4861804.4862025.rev	PATRIC	CDS	4861804	4862025	222	-	PGF_10323639	73	NifU-like domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4610	PATRIC.2.9855.2.9855.con.0001.CDS.4862090.4862524.rev	PATRIC	CDS	4862090	4862524	435	-	PGF_01259297	144	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4611	PATRIC.2.9855.2.9855.con.0001.CDS.4862667.4863011.rev	PATRIC	CDS	4862667	4863011	345	-	PGF_03320197	114	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4612	PATRIC.2.9855.2.9855.con.0001.CDS.4863146.4863811.fwd	PATRIC	CDS	4863146	4863811	666	+	PGF_00028947	221	Oxygen-insensitive NAD(P)H nitroreductase (EC 1.-.-.-) / Dihydropteridine reductase (EC 1.5.1.34)	GO:0008748|N-ethylmaleimide reductase activity;GO:0008748|reduced coenzyme F420 dehydrogenase activity;GO:0008748|sulfur oxygenase reductase activity;GO:0008748|malolactic enzyme activity;GO:0008748|NADPH:sulfur oxidoreductase activity;GO:0008748|epoxyqueuosine reductase activity;GO:0004155|6,7-dihydropteridine reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4613	PATRIC.2.9855.2.9855.con.0001.CDS.4864028.4864744.fwd	PATRIC	CDS	4864028	4864744	717	+	PGF_09626318	238	SSU rRNA pseudouridine(516) synthase (EC 5.4.99.19)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4614	PATRIC.2.9855.2.9855.con.0001.CDS.4865156.4865962.rev	PATRIC	CDS	4865156	4865962	807	-	PGF_00865282	268	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4615	PATRIC.2.9855.2.9855.con.0001.CDS.4866009.4868414.rev	PATRIC	CDS	4866009	4868414	2406	-	PGF_00412805	801	spoIID-like domain containing protein, peptidoglycan-binding domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.427	PATRIC.2.9855.2.9855.con.0001.CDS.486813.487859.fwd	PATRIC	CDS	486813	487859	1047	+	PGF_10540748	348	HD domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4616	PATRIC.2.9855.2.9855.con.0001.CDS.4868666.4869097.rev	PATRIC	CDS	4868666	4869097	432	-	PGF_00064228	143	UPF0178 protein CA_C2825	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4617	PATRIC.2.9855.2.9855.con.0001.CDS.4869105.4870454.rev	PATRIC	CDS	4869105	4870454	1350	-	PGF_10505717	449	Glucose-6-phosphate isomerase (EC 5.3.1.9)	GO:0004347|glucose-6-phosphate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4618	PATRIC.2.9855.2.9855.con.0001.CDS.4870869.4871684.rev	PATRIC	CDS	4870869	4871684	816	-	PGF_00053591	271	Sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140)	GO:0009010|sorbitol-6-phosphate 2-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4619	PATRIC.2.9855.2.9855.con.0001.CDS.4871767.4872135.rev	PATRIC	CDS	4871767	4872135	369	-	PGF_02077043	122	PTS system, glucitol/sorbitol-specific IIA component (EC 2.7.1.198)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4620	PATRIC.2.9855.2.9855.con.0001.CDS.4872200.4872880.rev	PATRIC	CDS	4872200	4872880	681	-	PGF_00057399	226	Transaldolase (EC 2.2.1.2)	GO:0004801|sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4621	PATRIC.2.9855.2.9855.con.0001.CDS.4872997.4874007.rev	PATRIC	CDS	4872997	4874007	1011	-	PGF_00029698	336	PTS system, glucitol/sorbitol-specific IIB component (EC 2.7.1.198) / PTS system, glucitol/sorbitol-specific IIC component 2	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4622	PATRIC.2.9855.2.9855.con.0001.CDS.4874025.4874573.rev	PATRIC	CDS	4874025	4874573	549	-	PGF_00029701	182	PTS system, glucitol/sorbitol-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4623	PATRIC.2.9855.2.9855.con.0001.CDS.4874589.4875041.rev	PATRIC	CDS	4874589	4875041	453	-	PGF_00007831	150	Glucitol operon activator protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4624	PATRIC.2.9855.2.9855.con.0001.CDS.4875056.4876981.rev	PATRIC	CDS	4875056	4876981	1926	-	PGF_10612161	641	Sorbitol operon transcription regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4626	PATRIC.2.9855.2.9855.con.0001.CDS.4878165.4879697.rev	PATRIC	CDS	4878165	4879697	1533	-	PGF_00006935	510	GMP synthase [glutamine-hydrolyzing], amidotransferase subunit (EC 6.3.5.2) / GMP synthase [glutamine-hydrolyzing], ATP pyrophosphatase subunit (EC 6.3.5.2)	GO:0003922|GMP synthase (glutamine-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4627	PATRIC.2.9855.2.9855.con.0001.CDS.4879885.4881342.rev	PATRIC	CDS	4879885	4881342	1458	-	PGF_10048015	485	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) / CBS domain	GO:0003938|IMP dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.428	PATRIC.2.9855.2.9855.con.0001.CDS.488036.488236.fwd	PATRIC	CDS	488036	488236	201	+	PGF_00417580	66	Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)	GO:0008984|protein-glutamate methylesterase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4628	PATRIC.2.9855.2.9855.con.0001.CDS.4881700.4882176.rev	PATRIC	CDS	4881700	4882176	477	-	PGF_01281745	158	Type II secretion envelope pseudopilin protein (PulG,guides folded protein to PulD in outer membrane)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4629	PATRIC.2.9855.2.9855.con.0001.CDS.4882500.4884125.rev	PATRIC	CDS	4882500	4884125	1626	-	PGF_01212739	541	Heat shock protein 60 kDa family chaperone GroEL	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4630	PATRIC.2.9855.2.9855.con.0001.CDS.4884217.4884501.rev	PATRIC	CDS	4884217	4884501	285	-	PGF_09581668	94	Heat shock protein 10 kDa family chaperone GroES	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.429	PATRIC.2.9855.2.9855.con.0001.CDS.488451.489365.fwd	PATRIC	CDS	488451	489365	915	+	PGF_02081147	304	Auxin efflux carrier family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4631	PATRIC.2.9855.2.9855.con.0001.CDS.4884909.4886399.rev	PATRIC	CDS	4884909	4886399	1491	-	PGF_00030905	496	[FeFe] hydrogenase (EC 1.12.7.2)	GO:0008901|ferredoxin hydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4632	PATRIC.2.9855.2.9855.con.0001.CDS.4886776.4887705.rev	PATRIC	CDS	4886776	4887705	930	-	PGF_00000278	309	8-oxoguanine DNA glycosylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4633	PATRIC.2.9855.2.9855.con.0001.CDS.4888228.4889076.rev	PATRIC	CDS	4888228	4889076	849	-	PGF_01456294	282	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	GO:0008691|3-hydroxybutyryl-CoA dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4634	PATRIC.2.9855.2.9855.con.0001.CDS.4889268.4890275.rev	PATRIC	CDS	4889268	4890275	1008	-	PGF_01308514	335	Electron bifurcating butyryl-CoA dehydrogenase, electron transfer flavoprotein alpha	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4635	PATRIC.2.9855.2.9855.con.0001.CDS.4890298.4891077.rev	PATRIC	CDS	4890298	4891077	780	-	PGF_00424111	259	Electron bifurcating butyryl-CoA dehydrogenase, electron transfer flavoprotein beta	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4636	PATRIC.2.9855.2.9855.con.0001.CDS.4891091.4892230.rev	PATRIC	CDS	4891091	4892230	1140	-	PGF_00424109	379	Electron bifurcating butyryl-CoA dehydrogenase (NAD+, ferredoxin)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4637	PATRIC.2.9855.2.9855.con.0001.CDS.4892315.4893100.rev	PATRIC	CDS	4892315	4893100	786	-	PGF_12694858	261	3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55)	GO:0003859|3-hydroxybutyryl-CoA dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4638	PATRIC.2.9855.2.9855.con.0001.CDS.4893478.4894113.rev	PATRIC	CDS	4893478	4894113	636	-	PGF_00047155	211	Redox-sensing transcriptional repressor Rex	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.430	PATRIC.2.9855.2.9855.con.0001.CDS.489375.489926.rev	PATRIC	CDS	489375	489926	552	-	PGF_00668486	183	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4640	PATRIC.2.9855.2.9855.con.0001.CDS.4895559.4896626.rev	PATRIC	CDS	4895559	4896626	1068	-	PGF_00019279	355	Mannose-1-phosphate guanylyltransferase (EC 2.7.7.13)	GO:0004475|mannose-1-phosphate guanylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4641	PATRIC.2.9855.2.9855.con.0001.CDS.4896742.4897419.rev	PATRIC	CDS	4896742	4897419	678	-	PGF_00057399	225	Transaldolase (EC 2.2.1.2)	GO:0004801|sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4642	PATRIC.2.9855.2.9855.con.0001.CDS.4897637.4898572.rev	PATRIC	CDS	4897637	4898572	936	-	PGF_08333365	311	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	GO:0043365|[formate-C-acetyltransferase]-activating enzyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4643	PATRIC.2.9855.2.9855.con.0001.CDS.4898576.4900930.rev	PATRIC	CDS	4898576	4900930	2355	-	PGF_06513690	784	Pyruvate formate-lyase (EC 2.3.1.54)	GO:0008861|formate C-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4645	PATRIC.2.9855.2.9855.con.0001.CDS.4902139.4902711.rev	PATRIC	CDS	4902139	4902711	573	-	PGF_01320713	190	RNA polymerase sigma factor SigV	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4646	PATRIC.2.9855.2.9855.con.0001.CDS.4903049.4904452.rev	PATRIC	CDS	4903049	4904452	1404	-	PGF_02917897	467	FAD/FMN-containing dehydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4647	PATRIC.2.9855.2.9855.con.0001.CDS.4904456.4905646.rev	PATRIC	CDS	4904456	4905646	1191	-	PGF_07072294	396	Electron transfer flavoprotein, alpha subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4648	PATRIC.2.9855.2.9855.con.0001.CDS.4905702.4906490.rev	PATRIC	CDS	4905702	4906490	789	-	PGF_05318435	262	Electron transfer flavoprotein, beta subunit	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4649	PATRIC.2.9855.2.9855.con.0001.CDS.4907015.4907716.rev	PATRIC	CDS	4907015	4907716	702	-	PGF_00016505	233	Lactate-responsive regulator LutR, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4650	PATRIC.2.9855.2.9855.con.0001.CDS.4907900.4908742.rev	PATRIC	CDS	4907900	4908742	843	-	PGF_00030083	280	Patatin-like phospholipase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4651	PATRIC.2.9855.2.9855.con.0001.CDS.4908977.4910686.rev	PATRIC	CDS	4908977	4910686	1710	-	PGF_07849456	569	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4652	PATRIC.2.9855.2.9855.con.0001.CDS.4911274.4913937.fwd	PATRIC	CDS	4911274	4913937	2664	+	PGF_00790788	887	Cation-transporting ATPase, E1-E2 family?	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.433	PATRIC.2.9855.2.9855.con.0001.CDS.491205.492467.fwd	PATRIC	CDS	491205	492467	1263	+	PGF_01269281	420	Two-component sensor histidine kinase, controlling glutamine utilization	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4653	PATRIC.2.9855.2.9855.con.0001.CDS.4914040.4916634.rev	PATRIC	CDS	4914040	4916634	2595	-	PGF_09084129	864	Acetaldehyde dehydrogenase (EC 1.2.1.10) / Alcohol dehydrogenase (EC 1.1.1.1)	GO:0008774|acetaldehyde dehydrogenase (acetylating) activity;GO:0004022|alcohol dehydrogenase (NAD) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4654	PATRIC.2.9855.2.9855.con.0001.CDS.4916933.4917259.rev	PATRIC	CDS	4916933	4917259	327	-	PGF_00064806	108	Uncharacterized membrane protein YvaE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4655	PATRIC.2.9855.2.9855.con.0001.CDS.4917268.4917657.rev	PATRIC	CDS	4917268	4917657	390	-	PGF_00106596	129	Uncharacterized protein YvaD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4656	PATRIC.2.9855.2.9855.con.0001.CDS.4917778.4918212.rev	PATRIC	CDS	4917778	4918212	435	-	PGF_10423881	144	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4657	PATRIC.2.9855.2.9855.con.0001.CDS.4918425.4919471.fwd	PATRIC	CDS	4918425	4919471	1047	+	PGF_02745651	348	[FeFe]-hydrogenase maturation protein HydE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4659	PATRIC.2.9855.2.9855.con.0001.CDS.4920874.4921833.fwd	PATRIC	CDS	4920874	4921833	960	+	PGF_10390435	319	Polysaccharide deacetylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4660	PATRIC.2.9855.2.9855.con.0001.CDS.4921849.4922880.rev	PATRIC	CDS	4921849	4922880	1032	-	PGF_01261860	343	no significant homology 1 putative transmembrane region was found by PSORT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4662	PATRIC.2.9855.2.9855.con.0001.CDS.4923262.4923738.fwd	PATRIC	CDS	4923262	4923738	477	+	PGF_06626131	158	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)	GO:0008685|2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.434	PATRIC.2.9855.2.9855.con.0001.CDS.492495.493385.fwd	PATRIC	CDS	492495	493385	891	+	PGF_00062556	296	Two-component response regulator, controlling glutamine utilization	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4665	PATRIC.2.9855.2.9855.con.0001.CDS.4925647.4928124.rev	PATRIC	CDS	4925647	4928124	2478	-	PGF_07849456	825	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.11	PATRIC.2.9855.2.9855.con.0001.CDS.4926.5042.fwd	PATRIC	CDS	4926	5042	117	+	PGF_00070550	38	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	GO:0003849|3-deoxy-7-phosphoheptulonate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4666	PATRIC.2.9855.2.9855.con.0001.CDS.4928722.4930653.fwd	PATRIC	CDS	4928722	4930653	1932	+	PGF_01175575	643	Threonyl-tRNA synthetase (EC 6.1.1.3)	GO:0004829|threonine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4668	PATRIC.2.9855.2.9855.con.0001.CDS.4933448.4934038.rev	PATRIC	CDS	4933448	4934038	591	-	PGF_04457297	196	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	GO:0030272|5-formyltetrahydrofolate cyclo-ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4669	PATRIC.2.9855.2.9855.con.0001.CDS.4934320.4934937.fwd	PATRIC	CDS	4934320	4934937	618	+	PGF_08203979	205	Stresses-induced protein Ves (HutD)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4671	PATRIC.2.9855.2.9855.con.0001.CDS.4935597.4936184.rev	PATRIC	CDS	4935597	4936184	588	-	PGF_01284176	195	Rubrerythrin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4672	PATRIC.2.9855.2.9855.con.0001.CDS.4936337.4938340.rev	PATRIC	CDS	4936337	4938340	2004	-	PGF_07849456	667	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.435	PATRIC.2.9855.2.9855.con.0001.CDS.493660.494382.fwd	PATRIC	CDS	493660	494382	723	+	PGF_07987137	240	ABC transporter, ATP-binding protein PebC (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4673	PATRIC.2.9855.2.9855.con.0001.CDS.4938677.4939348.fwd	PATRIC	CDS	4938677	4939348	672	+	PGF_10347208	223	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4674	PATRIC.2.9855.2.9855.con.0001.CDS.4939482.4941743.rev	PATRIC	CDS	4939482	4941743	2262	-	PGF_00019063	753	Maltodextrin phosphorylase (EC 2.4.1.1)	GO:0004645|phosphorylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4676	PATRIC.2.9855.2.9855.con.0001.CDS.4942729.4943364.rev	PATRIC	CDS	4942729	4943364	636	-	PGF_00884706	211	Efflux ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.436	PATRIC.2.9855.2.9855.con.0001.CDS.494466.495278.fwd	PATRIC	CDS	494466	495278	813	+	PGF_00018588	270	ABC transporter, substrate-binding protein PebA (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4680	PATRIC.2.9855.2.9855.con.0001.CDS.4945877.4946407.rev	PATRIC	CDS	4945877	4946407	531	-	PGF_07849456	176	Methyl-accepting chemotaxis protein	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4681	PATRIC.2.9855.2.9855.con.0001.CDS.4946424.4946912.rev	PATRIC	CDS	4946424	4946912	489	-	PGF_10423881	162	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4682	PATRIC.2.9855.2.9855.con.0001.CDS.4947080.4947658.fwd	PATRIC	CDS	4947080	4947658	579	+	PGF_00050217	192	Amidase/cyclase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4683	PATRIC.2.9855.2.9855.con.0001.CDS.4947888.4948361.fwd	PATRIC	CDS	4947888	4948361	474	+	PGF_10423881	157	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4685	PATRIC.2.9855.2.9855.con.0001.CDS.4949086.4949481.fwd	PATRIC	CDS	4949086	4949481	396	+	PGF_00015463	131	Iron-dependent repressor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4686	PATRIC.2.9855.2.9855.con.0001.CDS.4949514.4950833.fwd	PATRIC	CDS	4949514	4950833	1320	+	PGF_00828182	439	Uncharacterized MFS-type transporter YycB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4687	PATRIC.2.9855.2.9855.con.0001.CDS.4951049.4951597.rev	PATRIC	CDS	4951049	4951597	549	-	PGF_02278882	182	Iron-sulfur flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4688	PATRIC.2.9855.2.9855.con.0001.CDS.4951640.4952845.rev	PATRIC	CDS	4951640	4952845	1206	-	PGF_10527283	401	OrfZ protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.437	PATRIC.2.9855.2.9855.con.0001.CDS.495278.496006.fwd	PATRIC	CDS	495278	496006	729	+	PGF_00119238	242	ABC transporter, permease protein PebE (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4689	PATRIC.2.9855.2.9855.con.0001.CDS.4952975.4953586.fwd	PATRIC	CDS	4952975	4953586	612	+	PGF_07182652	203	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4692	PATRIC.2.9855.2.9855.con.0001.CDS.4954538.4955029.rev	PATRIC	CDS	4954538	4955029	492	-		163	Tn7-like transposition protein D	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4694	PATRIC.2.9855.2.9855.con.0001.CDS.4955320.4955922.fwd	PATRIC	CDS	4955320	4955922	603	+	PGF_01285243	200	Accessory gene regulator protein B (EC 3.4.-.-)	GO:0008234|cysteine-type peptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4695	PATRIC.2.9855.2.9855.con.0001.CDS.4955977.4957224.rev	PATRIC	CDS	4955977	4957224	1248	-	PGF_01284111	415	Accessory gene regulator C (sensor histidine kinase)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4696	PATRIC.2.9855.2.9855.con.0001.CDS.4957214.4958041.rev	PATRIC	CDS	4957214	4958041	828	-	PGF_01304223	275	Autolysis response regulater LytR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4700	PATRIC.2.9855.2.9855.con.0001.CDS.4959437.4961647.rev	PATRIC	CDS	4959437	4961647	2211	-	PGF_02745742	736	ABC transporter, fused permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.438	PATRIC.2.9855.2.9855.con.0001.CDS.496009.496641.fwd	PATRIC	CDS	496009	496641	633	+	PGF_05095111	210	ABC transporter, permease protein PebF (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4701	PATRIC.2.9855.2.9855.con.0001.CDS.4961688.4962386.rev	PATRIC	CDS	4961688	4962386	699	-	PGF_10425579	232	ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4702	PATRIC.2.9855.2.9855.con.0001.CDS.4962398.4963837.rev	PATRIC	CDS	4962398	4963837	1440	-	PGF_01283050	479	ABC transporter, RND-adapter-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4703	PATRIC.2.9855.2.9855.con.0001.CDS.4964219.4965670.rev	PATRIC	CDS	4964219	4965670	1452	-	PGF_09996723	483	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4704	PATRIC.2.9855.2.9855.con.0001.CDS.4965824.4966438.fwd	PATRIC	CDS	4965824	4966438	615	+	PGF_07182652	204	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4705	PATRIC.2.9855.2.9855.con.0001.CDS.4967400.4968668.rev	PATRIC	CDS	4967400	4968668	1269	-	PGF_02943429	422	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) in polyketide synthesis	GO:0004314|[acyl-carrier-protein] S-malonyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4706	PATRIC.2.9855.2.9855.con.0001.CDS.4968846.4969544.rev	PATRIC	CDS	4968846	4969544	699	-	PGF_10369163	232	4'-phosphopantetheinyl transferase (EC 2.7.8.-)	GO:0008808|cardiolipin synthase activity;GO:0008808|UDP-N-acetylglucosamine:serine-protein N-acetylglucosamine-1-phosphotransferase activity;GO:0008808|GDP-mannose:serine-protein mannose-1-phosphotransferase activity;GO:0008808|archaetidylserine synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4707	PATRIC.2.9855.2.9855.con.0001.CDS.4969769.4970524.rev	PATRIC	CDS	4969769	4970524	756	-	PGF_00033396	251	Acyl-CoA thioesterase 1	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.439	PATRIC.2.9855.2.9855.con.0001.CDS.497003.497674.fwd	PATRIC	CDS	497003	497674	672	+	PGF_10538053	223	ABC transporter-like sensor linked response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4708	PATRIC.2.9855.2.9855.con.0001.CDS.4970822.4972282.rev	PATRIC	CDS	4970822	4972282	1461	-	PGF_00978480	486	Non-ribosomal peptide synthetase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4710	PATRIC.2.9855.2.9855.con.0001.CDS.4973562.4975739.rev	PATRIC	CDS	4973562	4975739	2178	-	PGF_07514479	725	Non-ribosomal peptide synthetase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4711	PATRIC.2.9855.2.9855.con.0001.CDS.4975874.4979551.rev	PATRIC	CDS	4975874	4979551	3678	-	PGF_00978480	1225	Non-ribosomal peptide synthetase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.440	PATRIC.2.9855.2.9855.con.0001.CDS.497671.498684.fwd	PATRIC	CDS	497671	498684	1014	+	PGF_10458023	337	ABC transporter-like sensor linked histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4712	PATRIC.2.9855.2.9855.con.0001.CDS.4979812.4991916.rev	PATRIC	CDS	4979812	4991916	12105	-	PGF_00708729	4034	Gramicidin S synthetase 2 (Gramicidin S synthetase II) [Includes: ATP-dependent proline adenylase (ProA) (Proline activase); ATP-dependent valine adenylase (ValA) (Valine activase); ATP-dependent ornithine adenylase (OrnA) (Ornithine activase); ATP-dependent leucine adenylase (LeuA) (Leucine activase)]	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.441	PATRIC.2.9855.2.9855.con.0001.CDS.499064.499831.fwd	PATRIC	CDS	499064	499831	768	+	PGF_00998115	255	ABC transporter-like sensor ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4713	PATRIC.2.9855.2.9855.con.0001.CDS.4991967.4992980.rev	PATRIC	CDS	4991967	4992980	1014	-	PGF_00400378	337	iron aquisition yersiniabactin synthesis enzyme (Irp2)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4714	PATRIC.2.9855.2.9855.con.0001.CDS.4993057.4993770.rev	PATRIC	CDS	4993057	4993770	714	-	PGF_03278250	237	Thioesterase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4715	PATRIC.2.9855.2.9855.con.0001.CDS.4994197.4994850.rev	PATRIC	CDS	4994197	4994850	654	-	PGF_04695681	217	Serine acetyltransferase (EC 2.3.1.30)	GO:0009001|serine O-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4717	PATRIC.2.9855.2.9855.con.0001.CDS.4996179.4998005.rev	PATRIC	CDS	4996179	4998005	1827	-	PGF_01960322	608	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)	GO:0004360|glutamine-fructose-6-phosphate transaminase (isomerizing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.442	PATRIC.2.9855.2.9855.con.0001.CDS.499821.501854.fwd	PATRIC	CDS	499821	501854	2034	+	PGF_01674977	677	ABC transporter-like sensor and permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4718	PATRIC.2.9855.2.9855.con.0001.CDS.4998671.4999816.rev	PATRIC	CDS	4998671	4999816	1146	-	PGF_05200824	381	Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	GO:0008926|mannitol-1-phosphate 5-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4719	PATRIC.2.9855.2.9855.con.0001.CDS.4999818.5000258.rev	PATRIC	CDS	4999818	5000258	441	-	PGF_01253289	146	PTS system, mannitol-specific IIA component (EC 2.7.1.197)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4720	PATRIC.2.9855.2.9855.con.0001.CDS.5000258.5002309.rev	PATRIC	CDS	5000258	5002309	2052	-	PGF_07097065	683	Mannitol operon activator, BglG family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4721	PATRIC.2.9855.2.9855.con.0001.CDS.5002848.5004254.rev	PATRIC	CDS	5002848	5004254	1407	-	PGF_00029770	468	PTS system, mannitol-specific IIC component / PTS system, mannitol-specific IIB component (EC 2.7.1.197)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4722	PATRIC.2.9855.2.9855.con.0001.CDS.5004604.5005089.fwd	PATRIC	CDS	5004604	5005089	486	+	PGF_10423881	161	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4723	PATRIC.2.9855.2.9855.con.0001.CDS.5005275.5006411.rev	PATRIC	CDS	5005275	5006411	1137	-	PGF_03788463	378	Cystathionine beta-lyase (EC 4.4.1.8)	GO:0004121|cystathionine beta-lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4724	PATRIC.2.9855.2.9855.con.0001.CDS.5006446.5007594.rev	PATRIC	CDS	5006446	5007594	1149	-	PGF_01745391	382	Cystathionine gamma-synthase (EC 2.5.1.48)	GO:0003962|cystathionine gamma-synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4726	PATRIC.2.9855.2.9855.con.0001.CDS.5008210.5009481.rev	PATRIC	CDS	5008210	5009481	1272	-	PGF_01889881	423	ABC-type antimicrobial peptide transport system, permease component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4727	PATRIC.2.9855.2.9855.con.0001.CDS.5009472.5010218.rev	PATRIC	CDS	5009472	5010218	747	-	PGF_10347576	248	ABC-type antimicrobial peptide transport system, ATPase component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4728	PATRIC.2.9855.2.9855.con.0001.CDS.5010215.5011651.rev	PATRIC	CDS	5010215	5011651	1437	-	PGF_01283050	478	ABC transporter, RND-adapter-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4729	PATRIC.2.9855.2.9855.con.0001.CDS.5012081.5013286.rev	PATRIC	CDS	5012081	5013286	1206	-	PGF_06641194	401	Capsule biosynthesis protein capA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4730	PATRIC.2.9855.2.9855.con.0001.CDS.5013535.5014536.rev	PATRIC	CDS	5013535	5014536	1002	-	PGF_07008246	333	Maltose operon transcriptional repressor MalR, LacI family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4731	PATRIC.2.9855.2.9855.con.0001.CDS.5014922.5016412.rev	PATRIC	CDS	5014922	5016412	1491	-	PGF_03060077	496	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	GO:0004134|4-alpha-glucanotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4732	PATRIC.2.9855.2.9855.con.0001.CDS.5016567.5017466.rev	PATRIC	CDS	5016567	5017466	900	-	PGF_10466077	299	Maltodextrin ABC transporter, permease protein MdxG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4733	PATRIC.2.9855.2.9855.con.0001.CDS.5017466.5018332.rev	PATRIC	CDS	5017466	5018332	867	-	PGF_10365342	288	Maltodextrin ABC transporter, permease protein MdxF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4734	PATRIC.2.9855.2.9855.con.0001.CDS.5018441.5019754.rev	PATRIC	CDS	5018441	5019754	1314	-	PGF_07870324	437	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.443	PATRIC.2.9855.2.9855.con.0001.CDS.501994.503763.fwd	PATRIC	CDS	501994	503763	1770	+	PGF_00006821	589	GGDEF domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4735	PATRIC.2.9855.2.9855.con.0001.CDS.5020124.5020387.rev	PATRIC	CDS	5020124	5020387	264	-	PGF_09316422	87	UPF0213 protein YazA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4736	PATRIC.2.9855.2.9855.con.0001.CDS.5020598.5022127.rev	PATRIC	CDS	5020598	5022127	1530	-	PGF_00033474	509	Phosphoglucomutase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4737	PATRIC.2.9855.2.9855.con.0001.CDS.5022235.5022675.rev	PATRIC	CDS	5022235	5022675	441	-	PGF_01724713	146	Ribose-5-phosphate isomerase B (EC 5.3.1.6)	GO:0004751|ribose-5-phosphate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4738	PATRIC.2.9855.2.9855.con.0001.CDS.5022798.5023469.rev	PATRIC	CDS	5022798	5023469	672	-	PGF_10245672	223	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	GO:0004750|ribulose-phosphate 3-epimerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4739	PATRIC.2.9855.2.9855.con.0001.CDS.5023513.5024433.rev	PATRIC	CDS	5023513	5024433	921	-	PGF_00060399	306	Transketolase, C-terminal section (EC 2.2.1.1)	GO:0004802|transketolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4740	PATRIC.2.9855.2.9855.con.0001.CDS.5024433.5025251.rev	PATRIC	CDS	5024433	5025251	819	-	PGF_03267589	272	Transketolase, N-terminal section (EC 2.2.1.1)	GO:0004802|transketolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4741	PATRIC.2.9855.2.9855.con.0001.CDS.5025275.5026306.rev	PATRIC	CDS	5025275	5026306	1032	-	PGF_00007078	343	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)	GO:0008868|galactitol-1-phosphate 5-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4742	PATRIC.2.9855.2.9855.con.0001.CDS.5026376.5027650.rev	PATRIC	CDS	5026376	5027650	1275	-	PGF_00029677	424	PTS system, galactitol-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4743	PATRIC.2.9855.2.9855.con.0001.CDS.5027726.5028004.rev	PATRIC	CDS	5027726	5028004	279	-	PGF_00029672	92	PTS system, galactitol-specific IIB component (EC 2.7.1.200)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4744	PATRIC.2.9855.2.9855.con.0001.CDS.5028020.5028487.rev	PATRIC	CDS	5028020	5028487	468	-	PGF_04724541	155	PTS system, galactitol-specific IIA component (EC 2.7.1.200)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4745	PATRIC.2.9855.2.9855.con.0001.CDS.5028581.5029531.rev	PATRIC	CDS	5028581	5029531	951	-	PGF_00026324	316	NtrC family Transcriptional regulator, ATPase domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4746	PATRIC.2.9855.2.9855.con.0001.CDS.5029571.5031505.rev	PATRIC	CDS	5029571	5031505	1935	-	PGF_00026324	644	NtrC family Transcriptional regulator, ATPase domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4747	PATRIC.2.9855.2.9855.con.0001.CDS.5032050.5033054.rev	PATRIC	CDS	5032050	5033054	1005	-	PGF_00015855	334	Ketol-acid reductoisomerase (NADP(+)) (EC 1.1.1.86)	GO:0004455|ketol-acid reductoisomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4748	PATRIC.2.9855.2.9855.con.0001.CDS.5033067.5034470.rev	PATRIC	CDS	5033067	5034470	1404	-	PGF_00025090	467	Acetolactate synthase large subunit (EC 2.2.1.6)	GO:0003984|acetolactate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4749	PATRIC.2.9855.2.9855.con.0001.CDS.5034516.5034740.rev	PATRIC	CDS	5034516	5034740	225	-	PGF_00025090	74	Acetolactate synthase large subunit (EC 2.2.1.6)	GO:0003984|acetolactate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4750	PATRIC.2.9855.2.9855.con.0001.CDS.5034810.5035892.rev	PATRIC	CDS	5034810	5035892	1083	-	PGF_07191648	360	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	GO:0003862|3-isopropylmalate dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4751	PATRIC.2.9855.2.9855.con.0001.CDS.5036032.5036517.rev	PATRIC	CDS	5036032	5036517	486	-	PGF_06660812	161	3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	GO:0003861|3-isopropylmalate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4752	PATRIC.2.9855.2.9855.con.0001.CDS.5036531.5037790.rev	PATRIC	CDS	5036531	5037790	1260	-	PGF_00419420	419	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)	GO:0003861|3-isopropylmalate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4753	PATRIC.2.9855.2.9855.con.0001.CDS.5037804.5039399.rev	PATRIC	CDS	5037804	5039399	1596	-	PGF_00067382	531	(R)-citramalate synthase (EC 2.3.1.182)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4754	PATRIC.2.9855.2.9855.con.0001.CDS.5039465.5039974.rev	PATRIC	CDS	5039465	5039974	510	-	PGF_00025215	169	Acetolactate synthase small subunit (EC 2.2.1.6)	GO:0003984|acetolactate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4756	PATRIC.2.9855.2.9855.con.0001.CDS.5041246.5042592.rev	PATRIC	CDS	5041246	5042592	1347	-	PGF_01137124	448	Phosphoglucosamine mutase (EC 5.4.2.10)	GO:0008966|phosphoglucosamine mutase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4757	PATRIC.2.9855.2.9855.con.0001.CDS.5042808.5043161.rev	PATRIC	CDS	5042808	5043161	354	-	PGF_00011792	117	His repressor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4758	PATRIC.2.9855.2.9855.con.0001.CDS.5043315.5044151.rev	PATRIC	CDS	5043315	5044151	837	-	PGF_00010707	278	HTH DNA-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4759	PATRIC.2.9855.2.9855.con.0001.CDS.5044190.5045014.rev	PATRIC	CDS	5044190	5045014	825	-	PGF_00723222	274	Dihydroneopterin aldolase (EC 4.1.2.25) / 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3)	GO:0004150|dihydroneopterin aldolase activity;GO:0003848|2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4760	PATRIC.2.9855.2.9855.con.0001.CDS.5045027.5045836.rev	PATRIC	CDS	5045027	5045836	810	-	PGF_01853493	269	Dihydropteroate synthase (EC 2.5.1.15)	GO:0004156|dihydropteroate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4761	PATRIC.2.9855.2.9855.con.0001.CDS.5045853.5046326.rev	PATRIC	CDS	5045853	5046326	474	-	PGF_00039187	157	Putative DHNTP pyrophosphatase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4762	PATRIC.2.9855.2.9855.con.0001.CDS.5046471.5047538.rev	PATRIC	CDS	5046471	5047538	1068	-	PGF_03087931	355	Butyrate kinase (EC 2.7.2.7)	GO:0047761|butyrate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4763	PATRIC.2.9855.2.9855.con.0001.CDS.5047683.5048591.rev	PATRIC	CDS	5047683	5048591	909	-	PGF_02916109	302	Phosphate butyryltransferase (EC 2.3.1.19)	GO:0050182|phosphate butyryltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4764	PATRIC.2.9855.2.9855.con.0001.CDS.5048864.5050465.rev	PATRIC	CDS	5048864	5050465	1602	-	PGF_00024314	533	NAD(FAD)-utilizing dehydrogenase, sll0175 homolog	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4765	PATRIC.2.9855.2.9855.con.0001.CDS.5050637.5051857.rev	PATRIC	CDS	5050637	5051857	1221	-	PGF_05461869	406	Uncharacterized secreted protein associated with spyDAC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4766	PATRIC.2.9855.2.9855.con.0001.CDS.5051830.5052690.rev	PATRIC	CDS	5051830	5052690	861	-	PGF_01212500	286	Diadenylate cyclase spyDAC; Bacterial checkpoint controller DisA with nucleotide-binding domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.446	PATRIC.2.9855.2.9855.con.0001.CDS.505239.506981.fwd	PATRIC	CDS	505239	506981	1743	+	PGF_00006821	580	GGDEF domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4767	PATRIC.2.9855.2.9855.con.0001.CDS.5052923.5053528.fwd	PATRIC	CDS	5052923	5053528	606	+	PGF_00053912	201	Spore-cortex-lytic enzyme, SLEB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4768	PATRIC.2.9855.2.9855.con.0001.CDS.5053599.5054774.rev	PATRIC	CDS	5053599	5054774	1176	-	PGF_00015629	391	Isoaspartyl aminopeptidase (EC 3.4.19.5) @ Asp-X dipeptidase	GO:0008798|beta-aspartyl-peptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4769	PATRIC.2.9855.2.9855.con.0001.CDS.5054936.5056201.rev	PATRIC	CDS	5054936	5056201	1266	-	PGF_04749795	421	TPR-repeat-containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4770	PATRIC.2.9855.2.9855.con.0001.CDS.5056346.5057965.rev	PATRIC	CDS	5056346	5057965	1620	-	PGF_00033423	539	Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)	GO:0008965|phosphoenolpyruvate-protein phosphotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4771	PATRIC.2.9855.2.9855.con.0001.CDS.5058196.5059230.rev	PATRIC	CDS	5058196	5059230	1035	-	PGF_00048636	344	Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1)	GO:0004748|ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4772	PATRIC.2.9855.2.9855.con.0001.CDS.5059484.5061715.rev	PATRIC	CDS	5059484	5061715	2232	-	PGF_00048630	743	Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1)	GO:0004748|ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4773	PATRIC.2.9855.2.9855.con.0001.CDS.5061912.5063267.rev	PATRIC	CDS	5061912	5063267	1356	-	PGF_02620852	451	Two-component system sensor histidine kinase			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4774	PATRIC.2.9855.2.9855.con.0001.CDS.5063239.5063931.rev	PATRIC	CDS	5063239	5063931	693	-	PGF_07420062	230	Two-component transcriptional response regulator, OmpR family			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4775	PATRIC.2.9855.2.9855.con.0001.CDS.5063997.5064758.rev	PATRIC	CDS	5063997	5064758	762	-	PGF_00779224	253	TPR repeat			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4776	PATRIC.2.9855.2.9855.con.0001.CDS.5064799.5065356.rev	PATRIC	CDS	5064799	5065356	558	-	PGF_00947647	185	Fumarate hydratase class I, beta region (EC 4.2.1.2); L(+)-tartrate dehydratase beta subunit (EC 4.2.1.32)	GO:0004333|fumarate hydratase activity;GO:0008730|L(+)-tartrate dehydratase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4777	PATRIC.2.9855.2.9855.con.0001.CDS.5065561.5066403.rev	PATRIC	CDS	5065561	5066403	843	-	PGF_00006457	280	Fumarate hydratase class I, alpha region (EC 4.2.1.2); L(+)-tartrate dehydratase alpha subunit (EC 4.2.1.32)	GO:0004333|fumarate hydratase activity;GO:0008730|L(+)-tartrate dehydratase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4779	PATRIC.2.9855.2.9855.con.0001.CDS.5066982.5067644.rev	PATRIC	CDS	5066982	5067644	663	-	PGF_01466819	220	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	GO:0008745|N-acetylmuramoyl-L-alanine amidase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4780	PATRIC.2.9855.2.9855.con.0001.CDS.5068163.5068555.rev	PATRIC	CDS	5068163	5068555	393	-	PGF_00049909	130	SSU ribosomal protein S9p (S16e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4781	PATRIC.2.9855.2.9855.con.0001.CDS.5068582.5069016.rev	PATRIC	CDS	5068582	5069016	435	-	PGF_06180597	144	LSU ribosomal protein L13p (L13Ae)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4782	PATRIC.2.9855.2.9855.con.0001.CDS.5069177.5069911.rev	PATRIC	CDS	5069177	5069911	735	-	PGF_00413290	244	tRNA pseudouridine(38-40) synthase (EC 5.4.99.12)	GO:0009982|pseudouridine synthase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4783	PATRIC.2.9855.2.9855.con.0001.CDS.5069928.5070734.rev	PATRIC	CDS	5069928	5070734	807	-	PGF_02366581	268	Transmembrane component of general energizing module of ECF transporters			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4784	PATRIC.2.9855.2.9855.con.0001.CDS.5070743.5071612.rev	PATRIC	CDS	5070743	5071612	870	-	PGF_00843068	289	ATPase component of general energizing module of ECF transporters			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.447	PATRIC.2.9855.2.9855.con.0001.CDS.507146.507910.rev	PATRIC	CDS	507146	507910	765	-	PGF_00057506	254	Transcriptional regulator, MerR family			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4785	PATRIC.2.9855.2.9855.con.0001.CDS.5071597.5072448.rev	PATRIC	CDS	5071597	5072448	852	-	PGF_00843068	283	ATPase component of general energizing module of ECF transporters			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4786	PATRIC.2.9855.2.9855.con.0001.CDS.5072682.5073023.rev	PATRIC	CDS	5072682	5073023	342	-	PGF_00016346	113	LSU ribosomal protein L17p			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4787	PATRIC.2.9855.2.9855.con.0001.CDS.5073036.5073983.rev	PATRIC	CDS	5073036	5073983	948	-	PGF_00422271	315	DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)	GO:0003899|DNA-directed RNA polymerase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4788	PATRIC.2.9855.2.9855.con.0001.CDS.5074086.5074706.rev	PATRIC	CDS	5074086	5074706	621	-	PGF_01421572	206	SSU ribosomal protein S4p (S9e) @ SSU ribosomal protein S4p (S9e), zinc-dependent			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4789	PATRIC.2.9855.2.9855.con.0001.CDS.5074737.5075132.rev	PATRIC	CDS	5074737	5075132	396	-	PGF_00049837	131	SSU ribosomal protein S11p (S14e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4790	PATRIC.2.9855.2.9855.con.0001.CDS.5075148.5075516.rev	PATRIC	CDS	5075148	5075516	369	-	PGF_00049840	122	SSU ribosomal protein S13p (S18e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4791	PATRIC.2.9855.2.9855.con.0001.CDS.5075740.5075853.rev	PATRIC	CDS	5075740	5075853	114	-	PGF_00016424	37	LSU ribosomal protein L36p @ LSU ribosomal protein L36p, zinc-dependent			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4792	PATRIC.2.9855.2.9855.con.0001.CDS.5075908.5076126.rev	PATRIC	CDS	5075908	5076126	219	-	PGF_00060431	72	Translation initiation factor 1			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4793	PATRIC.2.9855.2.9855.con.0001.CDS.5076134.5076415.rev	PATRIC	CDS	5076134	5076415	282	-	PGF_01030652	93	L14e-like protein			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4794	PATRIC.2.9855.2.9855.con.0001.CDS.5076503.5077252.rev	PATRIC	CDS	5076503	5077252	750	-	PGF_06629251	249	Methionine aminopeptidase (EC 3.4.11.18)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4795	PATRIC.2.9855.2.9855.con.0001.CDS.5077252.5077902.rev	PATRIC	CDS	5077252	5077902	651	-	PGF_04244475	216	Adenylate kinase (EC 2.7.4.3)	GO:0004017|adenylate kinase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4796	PATRIC.2.9855.2.9855.con.0001.CDS.5077928.5079226.rev	PATRIC	CDS	5077928	5079226	1299	-	PGF_05581732	432	Protein translocase subunit SecY			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.52	PATRIC.2.9855.2.9855.con.0001.CDS.50788.51570.rev	PATRIC	CDS	50788	51570	783	-	PGF_10317708	260	Transcriptional regulator, AraC family			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4797	PATRIC.2.9855.2.9855.con.0001.CDS.5079228.5079668.rev	PATRIC	CDS	5079228	5079668	441	-	PGF_00016342	146	LSU ribosomal protein L15p (L27Ae)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4798	PATRIC.2.9855.2.9855.con.0001.CDS.5079690.5079869.rev	PATRIC	CDS	5079690	5079869	180	-	PGF_00016395	59	LSU ribosomal protein L30p (L7e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4799	PATRIC.2.9855.2.9855.con.0001.CDS.5079882.5080379.rev	PATRIC	CDS	5079882	5080379	498	-	PGF_00049896	165	SSU ribosomal protein S5p (S2e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4800	PATRIC.2.9855.2.9855.con.0001.CDS.5080400.5080759.rev	PATRIC	CDS	5080400	5080759	360	-	PGF_00016353	119	LSU ribosomal protein L18p (L5e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4801	PATRIC.2.9855.2.9855.con.0001.CDS.5080778.5081320.rev	PATRIC	CDS	5080778	5081320	543	-	PGF_00016444	180	LSU ribosomal protein L6p (L9e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.448	PATRIC.2.9855.2.9855.con.0001.CDS.508128.509840.fwd	PATRIC	CDS	508128	509840	1713	+	PGF_06337078	570	Methyl-accepting chemotaxis sensor/transducer protein			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4802	PATRIC.2.9855.2.9855.con.0001.CDS.5081389.5081787.rev	PATRIC	CDS	5081389	5081787	399	-	PGF_00049906	132	SSU ribosomal protein S8p (S15Ae)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4803	PATRIC.2.9855.2.9855.con.0001.CDS.5081820.5082005.rev	PATRIC	CDS	5081820	5082005	186	-	PGF_00049842	61	SSU ribosomal protein S14p (S29e) @ SSU ribosomal protein S14p (S29e), zinc-dependent			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4804	PATRIC.2.9855.2.9855.con.0001.CDS.5082022.5082561.rev	PATRIC	CDS	5082022	5082561	540	-	PGF_00016443	179	LSU ribosomal protein L5p (L11e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4805	PATRIC.2.9855.2.9855.con.0001.CDS.5082584.5082898.rev	PATRIC	CDS	5082584	5082898	315	-	PGF_00016377	104	LSU ribosomal protein L24p (L26e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4806	PATRIC.2.9855.2.9855.con.0001.CDS.5082914.5083282.rev	PATRIC	CDS	5082914	5083282	369	-	PGF_00016340	122	LSU ribosomal protein L14p (L23e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4807	PATRIC.2.9855.2.9855.con.0001.CDS.5083311.5083565.rev	PATRIC	CDS	5083311	5083565	255	-	PGF_00049854	84	SSU ribosomal protein S17p (S11e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4808	PATRIC.2.9855.2.9855.con.0001.CDS.5083589.5083801.rev	PATRIC	CDS	5083589	5083801	213	-	PGF_02899131	70	LSU ribosomal protein L29p (L35e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4809	PATRIC.2.9855.2.9855.con.0001.CDS.5083801.5084235.rev	PATRIC	CDS	5083801	5084235	435	-	PGF_00016343	144	LSU ribosomal protein L16p (L10e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4810	PATRIC.2.9855.2.9855.con.0001.CDS.5084253.5084918.rev	PATRIC	CDS	5084253	5084918	666	-	PGF_00049889	221	SSU ribosomal protein S3p (S3e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4811	PATRIC.2.9855.2.9855.con.0001.CDS.5084943.5085278.rev	PATRIC	CDS	5084943	5085278	336	-	PGF_00016368	111	LSU ribosomal protein L22p (L17e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4812	PATRIC.2.9855.2.9855.con.0001.CDS.5085299.5085571.rev	PATRIC	CDS	5085299	5085571	273	-	PGF_00049860	90	SSU ribosomal protein S19p (S15e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4813	PATRIC.2.9855.2.9855.con.0001.CDS.5085637.5086470.rev	PATRIC	CDS	5085637	5086470	834	-	PGF_00016393	277	LSU ribosomal protein L2p (L8e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.12	PATRIC.2.9855.2.9855.con.0001.CDS.5086.5604.fwd	PATRIC	CDS	5086	5604	519	+	PGF_00070550	172	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	GO:0003849|3-deoxy-7-phosphoheptulonate synthase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4814	PATRIC.2.9855.2.9855.con.0001.CDS.5086535.5086831.rev	PATRIC	CDS	5086535	5086831	297	-	PGF_03990071	98	LSU ribosomal protein L23p (L23Ae)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4815	PATRIC.2.9855.2.9855.con.0001.CDS.5086831.5087451.rev	PATRIC	CDS	5086831	5087451	621	-	PGF_04512522	206	LSU ribosomal protein L4p (L1e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4816	PATRIC.2.9855.2.9855.con.0001.CDS.5087478.5088107.rev	PATRIC	CDS	5087478	5088107	630	-	PGF_00016431	209	LSU ribosomal protein L3p (L3e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4817	PATRIC.2.9855.2.9855.con.0001.CDS.5088180.5088488.rev	PATRIC	CDS	5088180	5088488	309	-	PGF_00049828	102	SSU ribosomal protein S10p (S20e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4818	PATRIC.2.9855.2.9855.con.0001.CDS.5088943.5090136.rev	PATRIC	CDS	5088943	5090136	1194	-	PGF_00060428	397	Translation elongation factor Tu			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4819	PATRIC.2.9855.2.9855.con.0001.CDS.5090324.5092390.rev	PATRIC	CDS	5090324	5092390	2067	-	PGF_00060409	688	Translation elongation factor G			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4820	PATRIC.2.9855.2.9855.con.0001.CDS.5092474.5092944.rev	PATRIC	CDS	5092474	5092944	471	-	PGF_00049904	156	SSU ribosomal protein S7p (S5e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4821	PATRIC.2.9855.2.9855.con.0001.CDS.5093094.5093471.rev	PATRIC	CDS	5093094	5093471	378	-	PGF_06941403	125	SSU ribosomal protein S12p (S23e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4822	PATRIC.2.9855.2.9855.con.0001.CDS.5093728.5097264.rev	PATRIC	CDS	5093728	5097264	3537	-	PGF_02704551	1178	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	GO:0003899|DNA-directed RNA polymerase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4823	PATRIC.2.9855.2.9855.con.0001.CDS.5097286.5100996.rev	PATRIC	CDS	5097286	5100996	3711	-	PGF_02797402	1236	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	GO:0003899|DNA-directed RNA polymerase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.449	PATRIC.2.9855.2.9855.con.0001.CDS.510054.511988.fwd	PATRIC	CDS	510054	511988	1935	+	PGF_05421852	644	Chaperone protein HtpG			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4824	PATRIC.2.9855.2.9855.con.0001.CDS.5101327.5101692.rev	PATRIC	CDS	5101327	5101692	366	-	PGF_00016445	121	LSU ribosomal protein L7p/L12p (P1/P2)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4825	PATRIC.2.9855.2.9855.con.0001.CDS.5101743.5102246.rev	PATRIC	CDS	5101743	5102246	504	-	PGF_01213071	167	LSU ribosomal protein L10p (P0)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4826	PATRIC.2.9855.2.9855.con.0001.CDS.5102449.5103138.rev	PATRIC	CDS	5102449	5103138	690	-	PGF_00016357	229	LSU ribosomal protein L1p (L10Ae)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4827	PATRIC.2.9855.2.9855.con.0001.CDS.5103193.5103618.rev	PATRIC	CDS	5103193	5103618	426	-	PGF_07695531	141	LSU ribosomal protein L11p (L12e)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4828	PATRIC.2.9855.2.9855.con.0001.CDS.5103697.5104242.rev	PATRIC	CDS	5103697	5104242	546	-	PGF_03174068	181	Transcription antitermination protein NusG			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4829	PATRIC.2.9855.2.9855.con.0001.CDS.5104256.5104486.rev	PATRIC	CDS	5104256	5104486	231	-	PGF_09669766	76	Protein translocase subunit SecE			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4830	PATRIC.2.9855.2.9855.con.0001.CDS.5104535.5104684.rev	PATRIC	CDS	5104535	5104684	150	-	PGF_06609275	49	LSU ribosomal protein L33p @ LSU ribosomal protein L33p, zinc-dependent			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4831	PATRIC.2.9855.2.9855.con.0001.CDS.5104862.5106055.rev	PATRIC	CDS	5104862	5106055	1194	-	PGF_00060428	397	Translation elongation factor Tu			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4832	PATRIC.2.9855.2.9855.con.0001.CDS.5106273.5106920.rev	PATRIC	CDS	5106273	5106920	648	-	PGF_00046555	215	RNA polymerase sporulation specific sigma factor SigH			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4833	PATRIC.2.9855.2.9855.con.0001.CDS.5106980.5107492.rev	PATRIC	CDS	5106980	5107492	513	-	PGF_01752285	170	Uncharacterized protein YacP, similar to C-terminal domain of ribosome protection-type Tc-resistance proteins			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4834	PATRIC.2.9855.2.9855.con.0001.CDS.5107506.5108408.rev	PATRIC	CDS	5107506	5108408	903	-	PGF_08582746	300	23S rRNA (guanosine(2251)-2'-O)-methyltransferase (EC 2.1.1.185)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4835	PATRIC.2.9855.2.9855.con.0001.CDS.5108439.5108852.rev	PATRIC	CDS	5108439	5108852	414	-	PGF_00598888	137	Mini-ribonuclease III			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4836	PATRIC.2.9855.2.9855.con.0001.CDS.5108902.5110302.rev	PATRIC	CDS	5108902	5110302	1401	-	PGF_02797400	466	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	GO:0004817|cysteine-tRNA ligase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4837	PATRIC.2.9855.2.9855.con.0001.CDS.5110320.5112032.rev	PATRIC	CDS	5110320	5112032	1713	-	PGF_00037588	570	Prolyl-tRNA synthetase (EC 6.1.1.15), bacterial type	GO:0004827|proline-tRNA ligase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4838	PATRIC.2.9855.2.9855.con.0001.CDS.5112425.5113105.rev	PATRIC	CDS	5112425	5113105	681	-	PGF_08122432	226	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)	GO:0050518|2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4839	PATRIC.2.9855.2.9855.con.0001.CDS.5113127.5114227.rev	PATRIC	CDS	5113127	5114227	1101	-	PGF_00020147	366	Membrane-associated protein containing RNA-binding TRAM domain and ribonuclease PIN-domain, YacL B.subtilis ortholog			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4840	PATRIC.2.9855.2.9855.con.0001.CDS.5114470.5115546.rev	PATRIC	CDS	5114470	5115546	1077	-	PGF_00421347	358	DNA integrity scanning protein DisA			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4841	PATRIC.2.9855.2.9855.con.0001.CDS.5115773.5117149.rev	PATRIC	CDS	5115773	5117149	1377	-	PGF_00421792	458	DNA repair protein RadA			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4842	PATRIC.2.9855.2.9855.con.0001.CDS.5117635.5117862.fwd	PATRIC	CDS	5117635	5117862	228	+	PGF_00008366	75	Glutaredoxin and related proteins			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4843	PATRIC.2.9855.2.9855.con.0001.CDS.5117938.5118873.rev	PATRIC	CDS	5117938	5118873	936	-	PGF_01625234	311	Thioredoxin reductase (EC 1.8.1.9)	GO:0004791|thioredoxin-disulfide reductase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4844	PATRIC.2.9855.2.9855.con.0001.CDS.5119004.5121478.rev	PATRIC	CDS	5119004	5121478	2475	-	PGF_03999196	824	ATP-dependent Clp protease, ATP-binding subunit ClpC			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4845	PATRIC.2.9855.2.9855.con.0001.CDS.5121504.5122517.rev	PATRIC	CDS	5121504	5122517	1014	-	PGF_04146410	337	Protein-arginine kinase McsB (EC 2.7.14.1)			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4846	PATRIC.2.9855.2.9855.con.0001.CDS.5122510.5123088.rev	PATRIC	CDS	5122510	5123088	579	-	PGF_03789030	192	Protein-arginine kinase activator protein McsA			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4847	PATRIC.2.9855.2.9855.con.0001.CDS.5123103.5123558.rev	PATRIC	CDS	5123103	5123558	456	-	PGF_03889881	151	Transcriptional regulator CtsR			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4848	PATRIC.2.9855.2.9855.con.0001.CDS.5123728.5124378.fwd	PATRIC	CDS	5123728	5124378	651	+	PGF_03214662	216	Zn-dependent hydrolases of the metallo-beta-lactamase superfamily			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4849	PATRIC.2.9855.2.9855.con.0001.CDS.5124435.5124605.rev	PATRIC	CDS	5124435	5124605	171	-	PGF_08546938	56	Ferredoxin			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4851	PATRIC.2.9855.2.9855.con.0001.CDS.5124943.5125848.rev	PATRIC	CDS	5124943	5125848	906	-	PGF_00053991	301	Stage 0 sporulation protein YaaT			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4852	PATRIC.2.9855.2.9855.con.0001.CDS.5125852.5126784.rev	PATRIC	CDS	5125852	5126784	933	-	PGF_06755829	310	DNA polymerase III delta prime subunit (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4853	PATRIC.2.9855.2.9855.con.0001.CDS.5126804.5127136.rev	PATRIC	CDS	5126804	5127136	333	-	PGF_00404866	110	protein from nitrogen regulatory protein P-II (GLNB) family, ortholog YAAQ B. subtilis			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4854	PATRIC.2.9855.2.9855.con.0001.CDS.5127210.5127851.rev	PATRIC	CDS	5127210	5127851	642	-	PGF_06111020	213	Thymidylate kinase (EC 2.7.4.9)	GO:0004798|thymidylate kinase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4856	PATRIC.2.9855.2.9855.con.0001.CDS.5128490.5129650.fwd	PATRIC	CDS	5128490	5129650	1161	+	PGF_00050655	386	Amidohydrolase domain protein			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4857	PATRIC.2.9855.2.9855.con.0001.CDS.5129928.5130875.fwd	PATRIC	CDS	5129928	5130875	948	+	PGF_04846590	315	Magnesium and cobalt transport protein CorA			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4858	PATRIC.2.9855.2.9855.con.0001.CDS.5130915.5132312.rev	PATRIC	CDS	5130915	5132312	1398	-	PGF_00421077	465	D-xylose proton-symporter XylT			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4859	PATRIC.2.9855.2.9855.con.0001.CDS.5133722.5134168.fwd	PATRIC	CDS	5133722	5134168	447	+	PGF_03495000	148	Mobile element protein			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4861	PATRIC.2.9855.2.9855.con.0001.CDS.5138708.5139730.fwd	PATRIC	CDS	5138708	5139730	1023	+	PGF_01297906	340	Protein kinase			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4862	PATRIC.2.9855.2.9855.con.0001.CDS.5139793.5141169.rev	PATRIC	CDS	5139793	5141169	1377	-	PGF_06162930	458	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase (EC 6.3.2.9)	GO:0008764|UDP-N-acetylmuramoylalanine-D-glutamate ligase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4863	PATRIC.2.9855.2.9855.con.0001.CDS.5141318.5142709.rev	PATRIC	CDS	5141318	5142709	1392	-	PGF_00009966	463	Glycyl-tRNA synthetase (EC 6.1.1.14)	GO:0004820|glycine-tRNA ligase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4866	PATRIC.2.9855.2.9855.con.0001.CDS.5144214.5145719.rev	PATRIC	CDS	5144214	5145719	1506	-	PGF_00710545	501	Lysyl-tRNA synthetase (class II) (EC 6.1.1.6)	GO:0004824|lysine-tRNA ligase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4867	PATRIC.2.9855.2.9855.con.0001.CDS.5145734.5146216.rev	PATRIC	CDS	5145734	5146216	483	-	PGF_01043799	160	Transcription elongation factor GreA			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4868	PATRIC.2.9855.2.9855.con.0001.CDS.5146698.5147663.rev	PATRIC	CDS	5146698	5147663	966	-	PGF_00912265	321	tRNA-dihydrouridine synthase DusB			
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4869	PATRIC.2.9855.2.9855.con.0001.CDS.5147713.5148513.rev	PATRIC	CDS	5147713	5148513	801	-	PGF_04213876	266	Pantothenate kinase type III, CoaX-like (EC 2.7.1.33)	GO:0004594|pantothenate kinase activity		
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4870	PATRIC.2.9855.2.9855.con.0001.CDS.5148705.5150375.rev	PATRIC	CDS	5148705	5150375	1671	-	PGF_00006245	556	Formate--tetrahydrofolate ligase (EC 6.3.4.3)	GO:0004329|formate-tetrahydrofolate ligase activity		

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.451	PATRIC.2.9855.2.9855.con.0001.CDS.514906.515169.fwd	PATRIC	CDS	514906	515169	264	+	PGF_01283344	87	Phosphotransferase system EIIB, cysteine phosphorylation domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4871	PATRIC.2.9855.2.9855.con.0001.CDS.5150579.5152387.rev	PATRIC	CDS	5150579	5152387	1809	-	PGF_06275407	602	Cell division-associated, ATP-dependent zinc metalloprotease FtsH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4872	PATRIC.2.9855.2.9855.con.0001.CDS.5152462.5153001.rev	PATRIC	CDS	5152462	5153001	540	-	PGF_00013490	179	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	GO:0004422|hypoxanthine phosphoribosyltransferase activity;GO:0004422|guanine phosphoribosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4873	PATRIC.2.9855.2.9855.con.0001.CDS.5153004.5154410.rev	PATRIC	CDS	5153004	5154410	1407	-	PGF_09087715	468	tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.452	PATRIC.2.9855.2.9855.con.0001.CDS.515378.515515.fwd	PATRIC	CDS	515378	515515	138	+	PGF_03253752	45	Six-cysteine peptide SCIFF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4874	PATRIC.2.9855.2.9855.con.0001.CDS.5154677.5157073.rev	PATRIC	CDS	5154677	5157073	2397	-	PGF_02901183	798	Stage II sporulation serine phosphatase for sigma-F activation (SpoIIE)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.453	PATRIC.2.9855.2.9855.con.0001.CDS.515577.516938.fwd	PATRIC	CDS	515577	516938	1362	+	PGF_00060120	453	SCIFF radical SAM maturase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4875	PATRIC.2.9855.2.9855.con.0001.CDS.5159021.5159431.rev	PATRIC	CDS	5159021	5159431	411	-	PGF_00046199	136	RNA binding protein, contains ribosomal protein S1 domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4876	PATRIC.2.9855.2.9855.con.0001.CDS.5159581.5159868.rev	PATRIC	CDS	5159581	5159868	288	-	PGF_00416927	95	Cell division protein DivIC (FtsB), stabilizes FtsL against RasP cleavage	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4877	PATRIC.2.9855.2.9855.con.0001.CDS.5159946.5160338.rev	PATRIC	CDS	5159946	5160338	393	-	PGF_00053867	130	Spore cortex biosynthesis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4878	PATRIC.2.9855.2.9855.con.0001.CDS.5160348.5160641.rev	PATRIC	CDS	5160348	5160641	294	-	PGF_00000287	97	FIG007421: forespore shell protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4879	PATRIC.2.9855.2.9855.con.0001.CDS.5160845.5161105.rev	PATRIC	CDS	5160845	5161105	261	-	PGF_00048932	86	Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4880	PATRIC.2.9855.2.9855.con.0001.CDS.5161176.5161451.rev	PATRIC	CDS	5161176	5161451	276	-	PGF_01175502	91	DNA-binding protein HBsu	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4881	PATRIC.2.9855.2.9855.con.0001.CDS.5161672.5163123.rev	PATRIC	CDS	5161672	5163123	1452	-	PGF_00403691	483	possible tetrapyrrole methyltransferase domain / Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)	GO:0047693|ATP diphosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4882	PATRIC.2.9855.2.9855.con.0001.CDS.5163141.5164676.rev	PATRIC	CDS	5163141	5164676	1536	-	PGF_10409443	511	FIG006789: Stage V sporulation protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4883	PATRIC.2.9855.2.9855.con.0001.CDS.5164772.5165320.rev	PATRIC	CDS	5164772	5165320	549	-	PGF_00054116	182	Stage V sporulation protein T, AbrB family transcriptional regulator (SpoVT)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4884	PATRIC.2.9855.2.9855.con.0001.CDS.5165576.5166610.rev	PATRIC	CDS	5165576	5166610	1035	-	PGF_00342037	344	Foldase protein PrsA precursor (EC 5.2.1.8)	GO:0003755|peptidyl-prolyl cis-trans isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4885	PATRIC.2.9855.2.9855.con.0001.CDS.5166898.5170398.rev	PATRIC	CDS	5166898	5170398	3501	-	PGF_08675943	1166	Transcription-repair coupling factor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4886	PATRIC.2.9855.2.9855.con.0001.CDS.5170413.5170988.rev	PATRIC	CDS	5170413	5170988	576	-	PGF_04788810	191	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	GO:0004045|aminoacyl-tRNA hydrolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4887	PATRIC.2.9855.2.9855.con.0001.CDS.5171011.5172432.rev	PATRIC	CDS	5171011	5172432	1422	-	PGF_02620852	473	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4888	PATRIC.2.9855.2.9855.con.0001.CDS.5172433.5173119.rev	PATRIC	CDS	5172433	5173119	687	-	PGF_07420062	228	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.454	PATRIC.2.9855.2.9855.con.0001.CDS.517305.518549.fwd	PATRIC	CDS	517305	518549	1245	+	PGF_00067514	414	Zinc protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4889	PATRIC.2.9855.2.9855.con.0001.CDS.5173438.5174403.rev	PATRIC	CDS	5173438	5174403	966	-	PGF_00048782	321	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	GO:0004749|ribose phosphate diphosphokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4890	PATRIC.2.9855.2.9855.con.0001.CDS.5174451.5175818.rev	PATRIC	CDS	5174451	5175818	1368	-	PGF_08454293	455	N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23) / Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)	GO:0003977|UDP-N-acetylglucosamine diphosphorylase activity;GO:0019134|glucosamine-1-phosphate N-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4891	PATRIC.2.9855.2.9855.con.0001.CDS.5176014.5176289.rev	PATRIC	CDS	5176014	5176289	276	-	PGF_00422085	91	DNA-binding protein SpoVG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4893	PATRIC.2.9855.2.9855.con.0001.CDS.5176620.5177435.rev	PATRIC	CDS	5176620	5177435	816	-	PGF_00038971	271	Pur operon repressor PurR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4894	PATRIC.2.9855.2.9855.con.0001.CDS.5177723.5179102.fwd	PATRIC	CDS	5177723	5179102	1380	+	PGF_00063999	459	UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)	GO:0008763|UDP-N-acetylmuramate-L-alanine ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4896	PATRIC.2.9855.2.9855.con.0001.CDS.5180170.5181564.fwd	PATRIC	CDS	5180170	5181564	1395	+	PGF_00066502	464	Asparaginyl-tRNA synthetase (EC 6.1.1.22)	GO:0004816|asparagine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4897	PATRIC.2.9855.2.9855.con.0001.CDS.5182072.5183154.rev	PATRIC	CDS	5182072	5183154	1083	-	PGF_04477253	360	Phosphoserine aminotransferase (EC 2.6.1.52)	GO:0004648|O-phospho-L-serine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4898	PATRIC.2.9855.2.9855.con.0001.CDS.5183536.5184621.fwd	PATRIC	CDS	5183536	5184621	1086	+	PGF_01137083	361	HD-GYP hydrolase domain containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4899	PATRIC.2.9855.2.9855.con.0001.CDS.5184697.5185662.fwd	PATRIC	CDS	5184697	5185662	966	+	PGF_02622010	321	Uncharacterized glycosyltransferase YkoT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.455	PATRIC.2.9855.2.9855.con.0001.CDS.518564.519583.fwd	PATRIC	CDS	518564	519583	1020	+	PGF_12946886	339	Low-specificity L-threonine aldolase (EC 4.1.2.48)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4901	PATRIC.2.9855.2.9855.con.0001.CDS.5186042.5186653.rev	PATRIC	CDS	5186042	5186653	612	-	PGF_04198961	203	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)	GO:0003905|alkylbase DNA N-glycosylase activity;GO:0003905|DNA-3-methyladenine glycosylase activity;GO:0003905|DNA-7-methylguanine glycosylase activity;GO:0003905|DNA-7-methyladenine glycosylase activity;GO:0003905|DNA-3-methylguanine glycosylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4902	PATRIC.2.9855.2.9855.con.0001.CDS.5186819.5187328.rev	PATRIC	CDS	5186819	5187328	510	-	PGF_01641254	169	Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)	GO:0043365|[formate-C-acetyltransferase]-activating enzyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4903	PATRIC.2.9855.2.9855.con.0001.CDS.5187534.5189456.rev	PATRIC	CDS	5187534	5189456	1923	-	PGF_04243787	640	Aconitate hydratase (EC 4.2.1.3)	GO:0003994|aconitate hydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4904	PATRIC.2.9855.2.9855.con.0001.CDS.5189471.5190640.rev	PATRIC	CDS	5189471	5190640	1170	-	PGF_02965779	389	Re face-specific citrate synthase (EC 2.3.3.3)	GO:0050450|citrate (Re)-synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4905	PATRIC.2.9855.2.9855.con.0001.CDS.5191245.5193353.rev	PATRIC	CDS	5191245	5193353	2109	-	PGF_00048627	702	Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)	GO:0008998|ribonucleoside-triphosphate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4906	PATRIC.2.9855.2.9855.con.0001.CDS.5193814.5194662.fwd	PATRIC	CDS	5193814	5194662	849	+	PGF_00845945	282	DegV family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4908	PATRIC.2.9855.2.9855.con.0001.CDS.5195222.5195794.fwd	PATRIC	CDS	5195222	5195794	573	+	PGF_08815069	190	Substrate-specific component ThiT of thiamin ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4909	PATRIC.2.9855.2.9855.con.0001.CDS.5195763.5195900.fwd	PATRIC	CDS	5195763	5195900	138	+	PGF_08815069	45	Substrate-specific component ThiT of thiamin ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4910	PATRIC.2.9855.2.9855.con.0001.CDS.5196135.5196326.rev	PATRIC	CDS	5196135	5196326	192	-	PGF_08546938	63	Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4911	PATRIC.2.9855.2.9855.con.0001.CDS.5196456.5197295.rev	PATRIC	CDS	5196456	5197295	840	-	PGF_00401868	279	Iron-sulfur cluster carrier protein, CA_C2982 type	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.456	PATRIC.2.9855.2.9855.con.0001.CDS.519784.521211.fwd	PATRIC	CDS	519784	521211	1428	+	PGF_00065380	475	Uncharacterized protein YaaO	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4913	PATRIC.2.9855.2.9855.con.0001.CDS.5198140.5198910.rev	PATRIC	CDS	5198140	5198910	771	-	PGF_05621995	256	Prolipoprotein diacylglyceryl transferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4914	PATRIC.2.9855.2.9855.con.0001.CDS.5199130.5199702.rev	PATRIC	CDS	5199130	5199702	573	-	PGF_01281264	190	Membrane associated protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4916	PATRIC.2.9855.2.9855.con.0001.CDS.5201980.5202825.rev	PATRIC	CDS	5201980	5202825	846	-	PGF_00049827	281	SSU rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase (EC 2.1.1.182)	GO:0052908|16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4917	PATRIC.2.9855.2.9855.con.0001.CDS.5202826.5203383.rev	PATRIC	CDS	5202826	5203383	558	-	PGF_00048566	185	Ribonuclease M5 (EC 3.1.26.8)	GO:0043822|ribonuclease M5 activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4919	PATRIC.2.9855.2.9855.con.0001.CDS.5203546.5204598.rev	PATRIC	CDS	5203546	5204598	1053	-	PGF_00417313	350	Cell wall-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4920	PATRIC.2.9855.2.9855.con.0001.CDS.5204894.5205706.rev	PATRIC	CDS	5204894	5205706	813	-	PGF_02472178	270	Uncharacterized metal-dependent hydrolase YcfH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4921	PATRIC.2.9855.2.9855.con.0001.CDS.5206038.5207975.rev	PATRIC	CDS	5206038	5207975	1938	-	PGF_03609651	645	Methionyl-tRNA synthetase (EC 6.1.1.10)	GO:0004825|methionine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4922	PATRIC.2.9855.2.9855.con.0001.CDS.5208625.5210400.rev	PATRIC	CDS	5208625	5210400	1776	-	PGF_00066867	591	Xaa-Pro aminopeptidase (EC 3.4.11.9)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4923	PATRIC.2.9855.2.9855.con.0001.CDS.5210508.5211752.rev	PATRIC	CDS	5210508	5211752	1245	-	PGF_00066867	414	Xaa-Pro aminopeptidase (EC 3.4.11.9)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4924	PATRIC.2.9855.2.9855.con.0001.CDS.5211869.5212390.rev	PATRIC	CDS	5211869	5212390	522	-	PGF_00053897	173	Spore maturation protein B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4925	PATRIC.2.9855.2.9855.con.0001.CDS.5212444.5213019.rev	PATRIC	CDS	5212444	5213019	576	-	PGF_00053894	191	Spore maturation protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.457	PATRIC.2.9855.2.9855.con.0001.CDS.521336.521635.fwd	PATRIC	CDS	521336	521635	300	+	PGF_10480676	99	ATP-dependent Clp protease adaptor protein ClpS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4927	PATRIC.2.9855.2.9855.con.0001.CDS.5213373.5214746.rev	PATRIC	CDS	5213373	5214746	1374	-	PGF_08913741	457	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4928	PATRIC.2.9855.2.9855.con.0001.CDS.5214739.5215182.rev	PATRIC	CDS	5214739	5215182	444	-	PGF_10423881	147	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4929	PATRIC.2.9855.2.9855.con.0001.CDS.5215421.5216419.rev	PATRIC	CDS	5215421	5216419	999	-	PGF_00416683	332	Catabolite control protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.458	PATRIC.2.9855.2.9855.con.0001.CDS.521639.523915.fwd	PATRIC	CDS	521639	523915	2277	+	PGF_00016323	758	ATP-dependent Clp protease ATP-binding subunit ClpA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4930	PATRIC.2.9855.2.9855.con.0001.CDS.5216681.5219794.rev	PATRIC	CDS	5216681	5219794	3114	-	PGF_05171623	1037	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	GO:0004822|isoleucine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4932	PATRIC.2.9855.2.9855.con.0001.CDS.5220933.5221070.fwd	PATRIC	CDS	5220933	5221070	138	+	PGF_02275874	45	Uncharacterized protein MJ1492	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4933	PATRIC.2.9855.2.9855.con.0001.CDS.5221224.5222573.rev	PATRIC	CDS	5221224	5222573	1350	-	PGF_12866414	449	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4934	PATRIC.2.9855.2.9855.con.0001.CDS.5222577.5223260.rev	PATRIC	CDS	5222577	5223260	684	-	PGF_07420062	227	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4936	PATRIC.2.9855.2.9855.con.0001.CDS.5223854.5224570.rev	PATRIC	CDS	5223854	5224570	717	-	PGF_07762243	238	Probable 2-phosphosulfolactate phosphatase (EC 3.1.3.71)	GO:0050532|2-phosphosulfolactate phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4937	PATRIC.2.9855.2.9855.con.0001.CDS.5224611.5225540.rev	PATRIC	CDS	5224611	5225540	930	-	PGF_06874967	309	[4Fe-4S]-AdoMet protein YtqA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4938	PATRIC.2.9855.2.9855.con.0001.CDS.5225659.5226735.fwd	PATRIC	CDS	5225659	5226735	1077	+	PGF_01298361	358	Uncharacterized membrane protein CAC3241	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4939	PATRIC.2.9855.2.9855.con.0001.CDS.5226793.5227761.fwd	PATRIC	CDS	5226793	5227761	969	+	PGF_00411484	322	radical activating enzyme	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4940	PATRIC.2.9855.2.9855.con.0001.CDS.5227894.5230821.rev	PATRIC	CDS	5227894	5230821	2928	-	PGF_00053873	975	Spore cortex-lytic enzyme pre-pro-form	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4941	PATRIC.2.9855.2.9855.con.0001.CDS.5230882.5231079.rev	PATRIC	CDS	5230882	5231079	198	-	PGF_00053873	65	Spore cortex-lytic enzyme pre-pro-form	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4944	PATRIC.2.9855.2.9855.con.0001.CDS.5232326.5232850.rev	PATRIC	CDS	5232326	5232850	525	-	PGF_09954313	174	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	GO:0003755|peptidyl-prolyl cis-trans isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4945	PATRIC.2.9855.2.9855.con.0001.CDS.5232956.5233735.rev	PATRIC	CDS	5232956	5233735	780	-	PGF_00008106	259	Glutamate racemase (EC 5.1.1.3)	GO:0008881|glutamate racemase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4946	PATRIC.2.9855.2.9855.con.0001.CDS.5234212.5235321.fwd	PATRIC	CDS	5234212	5235321	1110	+	PGF_01137083	369	HD-GYP hydrolase domain containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4948	PATRIC.2.9855.2.9855.con.0001.CDS.5235871.5239080.rev	PATRIC	CDS	5235871	5239080	3210	-	PGF_00416410	1069	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	GO:0004088|carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4949	PATRIC.2.9855.2.9855.con.0001.CDS.5239095.5240144.rev	PATRIC	CDS	5239095	5240144	1050	-	PGF_07015581	349	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	GO:0004088|carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4950	PATRIC.2.9855.2.9855.con.0001.CDS.5240784.5241563.rev	PATRIC	CDS	5240784	5241563	780	-	PGF_10477124	259	Short-chain dehydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.459	PATRIC.2.9855.2.9855.con.0001.CDS.524158.524313.fwd	PATRIC	CDS	524158	524313	156	+	PGF_00067473	51	Zinc-ribbon domain Caur_1000.N	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4951	PATRIC.2.9855.2.9855.con.0001.CDS.5241857.5242216.rev	PATRIC	CDS	5241857	5242216	360	-	PGF_00020996	119	Methylglyoxal synthase (EC 4.2.3.3)	GO:0008929|methylglyoxal synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4952	PATRIC.2.9855.2.9855.con.0001.CDS.5242491.5243735.rev	PATRIC	CDS	5242491	5243735	1245	-	PGF_05387084	414	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	GO:0004350|glutamate-5-semialdehyde dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4953	PATRIC.2.9855.2.9855.con.0001.CDS.5243761.5244564.rev	PATRIC	CDS	5243761	5244564	804	-	PGF_00008059	267	Glutamate 5-kinase (EC 2.7.2.11)	GO:0004349|glutamate 5-kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4954	PATRIC.2.9855.2.9855.con.0001.CDS.5244794.5245441.rev	PATRIC	CDS	5244794	5245441	648	-	PGF_00002592	215	FIG01964566: Predicted membrane protein, hemolysin III homolog	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4956	PATRIC.2.9855.2.9855.con.0001.CDS.5246489.5248084.fwd	PATRIC	CDS	5246489	5248084	1596	+	PGF_00766022	531	Bis-ABC ATPase YbiT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4957	PATRIC.2.9855.2.9855.con.0001.CDS.5248232.5249020.rev	PATRIC	CDS	5248232	5249020	789	-	PGF_10455049	262	Cof-like hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4958	PATRIC.2.9855.2.9855.con.0001.CDS.5249182.5249766.rev	PATRIC	CDS	5249182	5249766	585	-	PGF_07182652	194	Transcriptional regulator, AcrR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.460	PATRIC.2.9855.2.9855.con.0001.CDS.524923.525402.fwd	PATRIC	CDS	524923	525402	480	+	PGF_01424767	159	Transcriptional regulator, AsnC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4959	PATRIC.2.9855.2.9855.con.0001.CDS.5250148.5251038.fwd	PATRIC	CDS	5250148	5251038	891	+	PGF_03938996	296	Phosphatidylserine decarboxylase (EC 4.1.1.65)	GO:0004609|phosphatidylserine decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4960	PATRIC.2.9855.2.9855.con.0001.CDS.5251335.5252282.rev	PATRIC	CDS	5251335	5252282	948	-	PGF_02620852	315	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4962	PATRIC.2.9855.2.9855.con.0001.CDS.5253153.5254334.fwd	PATRIC	CDS	5253153	5254334	1182	+	PGF_00969415	393	cell surface protein, ErfK family	

Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.461	PATRIC.2.9855.2.9855.con.0001.CDS.525399.526571.fwd	PATRIC	CDS	525399	526571	1173	+	PGF_04544396	390	Aspartate aminotransferase (EC 2.6.1.1)	GO:0004069|L-aspartate:2-oxoglutarate aminotransferase activity;GO:0004069|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4963	PATRIC.2.9855.2.9855.con.0001.CDS.5254412.5258149.rev	PATRIC	CDS	5254412	5258149	3738	-	PGF_00019221	1245	ATP-dependent helicase/nuclease AddAB, subunit A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4964	PATRIC.2.9855.2.9855.con.0001.CDS.5258242.5261721.rev	PATRIC	CDS	5258242	5261721	3480	-	PGF_06122323	1159	ATP-dependent helicase/nuclease AddAB, subunit B	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4965	PATRIC.2.9855.2.9855.con.0001.CDS.5261718.5262233.rev	PATRIC	CDS	5261718	5262233	516	-	PGF_10519603	171	Acetyltransferase, GNAT family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4967	PATRIC.2.9855.2.9855.con.0001.CDS.5263333.5264718.rev	PATRIC	CDS	5263333	5264718	1386	-	PGF_00008605	461	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	GO:0004368|glycerol-3-phosphate dehydrogenase activity;GO:0004368|sn-glycerol-3-phosphate:ubiquinone oxidoreductase activity;GO:0004368|sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4968	PATRIC.2.9855.2.9855.con.0001.CDS.5264721.5265242.rev	PATRIC	CDS	5264721	5265242	522	-	PGF_00060261	173	Transcriptional repressor for NAD biosynthesis in gram-positives	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4969	PATRIC.2.9855.2.9855.con.0001.CDS.5265257.5265772.rev	PATRIC	CDS	5265257	5265772	516	-	PGF_00010526	171	HD protein (lojap analog?)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4970	PATRIC.2.9855.2.9855.con.0001.CDS.5266663.5267046.fwd	PATRIC	CDS	5266663	5267046	384	+	PGF_03495000	127	Mobile element protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.463	PATRIC.2.9855.2.9855.con.0001.CDS.526993.528009.fwd	PATRIC	CDS	526993	528009	1017	+	PGF_09774558	338	Transcriptional regulator, LacI family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4972	PATRIC.2.9855.2.9855.con.0001.CDS.5271410.5273890.rev	PATRIC	CDS	5271410	5273890	2481	-	PGF_03272313	826	DNA gyrase subunit A (EC 5.99.1.3)	GO:0003918|DNA topoisomerase type II (ATP-hydrolyzing) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4973	PATRIC.2.9855.2.9855.con.0001.CDS.5273914.5275821.rev	PATRIC	CDS	5273914	5275821	1908	-	PGF_06703483	635	DNA gyrase subunit B (EC 5.99.1.3)	GO:0003918|DNA topoisomerase type II (ATP-hydrolyzing) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4974	PATRIC.2.9855.2.9855.con.0001.CDS.5275876.5276136.rev	PATRIC	CDS	5275876	5276136	261	-	PGF_00027460	86	OrfX	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4975	PATRIC.2.9855.2.9855.con.0001.CDS.5276136.5277239.rev	PATRIC	CDS	5276136	5277239	1104	-	PGF_10387199	367	DNA recombination and repair protein RecF	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4976	PATRIC.2.9855.2.9855.con.0001.CDS.5277288.5277500.rev	PATRIC	CDS	5277288	5277500	213	-	PGF_06916058	70	Uncharacterized S4 RNA-binding-domain protein YbcJ	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4977	PATRIC.2.9855.2.9855.con.0001.CDS.5277531.5278631.rev	PATRIC	CDS	5277531	5278631	1101	-	PGF_06473395	366	DNA polymerase III beta subunit (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4978	PATRIC.2.9855.2.9855.con.0001.CDS.5278893.5280242.rev	PATRIC	CDS	5278893	5280242	1350	-	PGF_00876106	449	Chromosomal replication initiator protein DnaA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4979	PATRIC.2.9855.2.9855.con.0001.CDS.5280741.5280875.fwd	PATRIC	CDS	5280741	5280875	135	+	PGF_00016418	44	LSU ribosomal protein L34p	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4980	PATRIC.2.9855.2.9855.con.0001.CDS.5280935.5281312.fwd	PATRIC	CDS	5280935	5281312	378	+	PGF_08424570	125	Ribonuclease P protein component (EC 3.1.26.5)	GO:0004526|ribonuclease P activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4981	PATRIC.2.9855.2.9855.con.0001.CDS.5281284.5281493.fwd	PATRIC	CDS	5281284	5281493	210	+	PGF_03751658	69	Membrane protein insertion efficiency factor YidD	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4982	PATRIC.2.9855.2.9855.con.0001.CDS.5281517.5282281.fwd	PATRIC	CDS	5281517	5282281	765	+	PGF_00014264	254	Inner membrane protein translocase and chaperone YidC, short form Oxal-like	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4983	PATRIC.2.9855.2.9855.con.0001.CDS.5282327.5282953.fwd	PATRIC	CDS	5282327	5282953	627	+	PGF_06701488	208	RNA-binding protein Jag	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.464	PATRIC.2.9855.2.9855.con.0001.CDS.528268.529326.fwd	PATRIC	CDS	528268	529326	1059	+	PGF_10314822	352	ABC transporter, substrate-binding protein (cluster 11, riboflavin/purine nucleoside/unknown)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4984	PATRIC.2.9855.2.9855.con.0001.CDS.5283134.5284522.fwd	PATRIC	CDS	5283134	5284522	1389	+	PGF_00007057	462	tRNA-5-carboxymethylaminomethyl-2-thiouridine(34) synthesis protein MnmE	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4985	PATRIC.2.9855.2.9855.con.0001.CDS.5284532.5286412.fwd	PATRIC	CDS	5284532	5286412	1881	+	PGF_00413300	626	tRNA-5-carboxymethylaminomethyl-2-thiouridine(34) synthesis protein MnmG	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4986	PATRIC.2.9855.2.9855.con.0001.CDS.5286436.5287155.fwd	PATRIC	CDS	5286436	5287155	720	+	PGF_00008838	239	16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4987	PATRIC.2.9855.2.9855.con.0001.CDS.5287293.5288075.fwd	PATRIC	CDS	5287293	5288075	783	+	PGF_04872827	260	Chromosome (plasmid) partitioning protein ParB-2	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4988	PATRIC.2.9855.2.9855.con.0001.CDS.5288420.5289181.fwd	PATRIC	CDS	5288420	5289181	762	+	PGF_04370656	253	Chromosome (plasmid) partitioning protein ParA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4989	PATRIC.2.9855.2.9855.con.0001.CDS.5289190.5290050.fwd	PATRIC	CDS	5289190	5290050	861	+	PGF_03475877	286	Chromosome (plasmid) partitioning protein ParB	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4994	PATRIC.2.9855.2.9855.con.0001.CDS.5292324.5292911.rev	PATRIC	CDS	5292324	5292911	588	-	PGF_02713816	195	Uncharacterized protein YyaC	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4995	PATRIC.2.9855.2.9855.con.0001.CDS.5293078.5294229.rev	PATRIC	CDS	5293078	5294229	1152	-	PGF_10025016	383	Cysteine desulfurase (EC 2.8.1.7)	GO:0031071|cysteine desulfurase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.465	PATRIC.2.9855.2.9855.con.0001.CDS.529520.531070.fwd	PATRIC	CDS	529520	531070	1551	+	PGF_01899917	516	ABC transporter, ATP-binding protein (cluster 11, riboflavin/purine nucleoside/unknown) / ABC transporter, ATP-binding protein (cluster 11, riboflavin/purine nucleoside/unknown)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4998	PATRIC.2.9855.2.9855.con.0001.CDS.5295319.5296242.fwd	PATRIC	CDS	5295319	5296242	924	+	PGF_10340618	307	Potassium efflux system KefA protein / Small-conductance mechanosensitive channel	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4999	PATRIC.2.9855.2.9855.con.0001.CDS.5296242.5296436.fwd	PATRIC	CDS	5296242	5296436	195	+	PGF_06429692	64	Uncharacterized protein CAC3725	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5000	PATRIC.2.9855.2.9855.con.0001.CDS.5296538.5296825.fwd	PATRIC	CDS	5296538	5296825	288	+	PGF_00049901	95	SSU ribosomal protein S6p	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5001	PATRIC.2.9855.2.9855.con.0001.CDS.5296839.5297288.fwd	PATRIC	CDS	5296839	5297288	450	+	PGF_02142873	149	Single-stranded DNA-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5002	PATRIC.2.9855.2.9855.con.0001.CDS.5297313.5297573.fwd	PATRIC	CDS	5297313	5297573	261	+	PGF_06948903	86	SSU ribosomal protein S18p @ SSU ribosomal protein S18p, zinc-dependent	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5004	PATRIC.2.9855.2.9855.con.0001.CDS.5298092.5300032.fwd	PATRIC	CDS	5298092	5300032	1941	+	PGF_00033444	646	Cyclic-di-AMP phosphodiesterase GdpP	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5005	PATRIC.2.9855.2.9855.con.0001.CDS.5300036.5300482.fwd	PATRIC	CDS	5300036	5300482	447	+	PGF_00016452	148	LSU ribosomal protein L9p	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5006	PATRIC.2.9855.2.9855.con.0001.CDS.5300495.5302390.fwd	PATRIC	CDS	5300495	5302390	1896	+	PGF_00020025	631	ATP-dependent protease LonB-like Type I	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5007	PATRIC.2.9855.2.9855.con.0001.CDS.5302526.5303863.fwd	PATRIC	CDS	5302526	5303863	1338	+	PGF_10518765	445	Replicative DNA helicase (DnaB) (EC 3.6.4.12)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5009	PATRIC.2.9855.2.9855.con.0001.CDS.5304454.5305254.fwd	PATRIC	CDS	5304454	5305254	801	+	PGF_07609122	266	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	GO:0004735|pyrroline-5-carboxylate reductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5011	PATRIC.2.9855.2.9855.con.0001.CDS.5306203.5307378.rev	PATRIC	CDS	5306203	5307378	1176	-	PGF_06447349	391	NADP-dependent malic enzyme (EC 1.1.1.40)	GO:0004473|malate dehydrogenase (decarboxylating) (NADP+) activity;GO:0004473|oxaloacetate decarboxylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5012	PATRIC.2.9855.2.9855.con.0001.CDS.5307629.5308915.fwd	PATRIC	CDS	5307629	5308915	1287	+	PGF_06935032	428	Adenylosuccinate synthetase (EC 6.3.4.4)	GO:0004019|adenylosuccinate synthase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5013	PATRIC.2.9855.2.9855.con.0001.CDS.5309014.5309196.fwd	PATRIC	CDS	5309014	5309196	183	+	PGF_00158423	60	Uncharacterized protein CPF_2956	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5014	PATRIC.2.9855.2.9855.con.0001.CDS.5309498.5310244.fwd	PATRIC	CDS	5309498	5310244	747	+	PGF_00033822	248	Acyl-acyl carrier protein thioesterase (EC 3.1.2.14)	GO:0004320|oleoyl-[acyl-carrier-protein] hydrolase activity;GO:0004320|myristoyl-[acyl-carrier-protein] hydrolase activity;GO:0004320|palmitoyl-[acyl-carrier-protein] hydrolase activity;GO:0004320|acyl-[acyl-carrier-protein] hydrolase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5015	PATRIC.2.9855.2.9855.con.0001.CDS.5310348.5311592.rev	PATRIC	CDS	5310348	5311592	1245	-	PGF_10444879	414	NAD(FAD)-utilizing dehydrogenases	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.466	PATRIC.2.9855.2.9855.con.0001.CDS.531045.532172.fwd	PATRIC	CDS	531045	532172	1128	+	PGF_04065085	375	ABC transporter, permease protein 1 (cluster 11, riboflavin/purine nucleoside/unknown)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5017	PATRIC.2.9855.2.9855.con.0001.CDS.5313811.5314791.rev	PATRIC	CDS	5313811	5314791	981	-	PGF_03673574	326	DNA replication helicase loader DnaC/DnaI	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5018	PATRIC.2.9855.2.9855.con.0001.CDS.5314784.5315770.rev	PATRIC	CDS	5314784	5315770	987	-	PGF_00421828	328	DNA replication protein DnaD	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5019	PATRIC.2.9855.2.9855.con.0001.CDS.5316091.5317290.rev	PATRIC	CDS	5316091	5317290	1200	-	PGF_00068103	399	alkaline serine protease	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5020	PATRIC.2.9855.2.9855.con.0001.CDS.5317495.5318310.rev	PATRIC	CDS	5317495	5318310	816	-	PGF_01067597	271	Outer membrane protein romA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5021	PATRIC.2.9855.2.9855.con.0001.CDS.5318328.5318759.rev	PATRIC	CDS	5318328	5318759	432	-	PGF_03037518	143	Membrane protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5022	PATRIC.2.9855.2.9855.con.0001.CDS.5318849.5319325.rev	PATRIC	CDS	5318849	5319325	477	-	PGF_00423433	158	Dimeric dUTPase (EC 3.6.1.23)	GO:0004170|dUTP diphosphatase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5024	PATRIC.2.9855.2.9855.con.0001.CDS.5320536.5321801.fwd	PATRIC	CDS	5320536	5321801	1266	+	PGF_00900122	421	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	GO:0008760|UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.467	PATRIC.2.9855.2.9855.con.0001.CDS.532162.532446.fwd	PATRIC	CDS	532162	532446	285	+	PGF_04055837	94	ABC transporter, permease protein 2 (cluster 11, riboflavin/purine nucleoside/unknown)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5025	PATRIC.2.9855.2.9855.con.0001.CDS.5321828.5322619.fwd	PATRIC	CDS	5321828	5322619	792	+	PGF_01127158	263	Zn-dependent hydrolase YycI/WalJ, required for cell wall metabolism and coordination of cell division with DNA replication	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5026	PATRIC.2.9855.2.9855.con.0001.CDS.5322690.5323193.fwd	PATRIC	CDS	5322690	5323193	504	+	PGF_00038707	167	Protein with domain similar to SecA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5027	PATRIC.2.9855.2.9855.con.0001.CDS.5323471.5325645.fwd	PATRIC	CDS	5323471	5325645	2175	+	PGF_07849456	724	Methyl-accepting chemotaxis protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.468	PATRIC.2.9855.2.9855.con.0001.CDS.532506.532889.fwd	PATRIC	CDS	532506	532889	384	+	PGF_04055837	127	ABC transporter, permease protein 2 (cluster 11, riboflavin/purine nucleoside/unknown)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5028	PATRIC.2.9855.2.9855.con.0001.CDS.5326138.5327565.fwd	PATRIC	CDS	5326138	5327565	1428	+	PGF_09996723	475	Uncharacterized MFS-type transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5029	PATRIC.2.9855.2.9855.con.0001.CDS.5327725.5328204.fwd	PATRIC	CDS	5327725	5328204	480	+	PGF_07480521	159	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase (EC 2.1.1.177)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5030	PATRIC.2.9855.2.9855.con.0001.CDS.5328653.5330557.fwd	PATRIC	CDS	5328653	5330557	1905	+	PGF_07194500	634	Acyl-CoA dehydrogenase-like protein Cbei_5056	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5031	PATRIC.2.9855.2.9855.con.0001.CDS.5330600.5331799.fwd	PATRIC	CDS	5330600	5331799	1200	+	PGF_08126536	399	Flavoprotein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5032	PATRIC.2.9855.2.9855.con.0001.CDS.5332059.5333933.rev	PATRIC	CDS	5332059	5333933	1875	-	PGF_00052554	624	Similar to carbon monoxide dehydrogenase CooS subunit	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.469	PATRIC.2.9855.2.9855.con.0001.CDS.533252.533902.fwd	PATRIC	CDS	533252	533902	651	+	PGF_05026985	216	Deoxyribose-phosphate aldolase (EC 4.1.2.4)	GO:0004139|deoxyribose-phosphate aldolase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5033	PATRIC.2.9855.2.9855.con.0001.CDS.5334046.5334459.rev	PATRIC	CDS	5334046	5334459	414	-	PGF_00049228	137	Rrf2 family transcriptional regulator	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5036	PATRIC.2.9855.2.9855.con.0001.CDS.5336260.5338395.rev	PATRIC	CDS	5336260	5338395	2136	-	PGF_00045941	711	Pyrophosphate-energized proton pump (EC 3.6.1.1)	GO:0004427|inorganic diphosphatase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5040	PATRIC.2.9855.2.9855.con.0001.CDS.5339767.5340471.rev	PATRIC	CDS	5339767	5340471	705	-	PGF_00700305	234	Branched-chain amino acid ABC transporter, ATP-binding protein LivF (TC 3.A.1.4.1)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.470	PATRIC.2.9855.2.9855.con.0001.CDS.533977.534690.fwd	PATRIC	CDS	533977	534690	714	+	PGF_00038987	237	Purine nucleoside phosphorylase (EC 2.4.2.1)	GO:0004731|purine-nucleoside phosphorylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5041	PATRIC.2.9855.2.9855.con.0001.CDS.5340474.5341232.rev	PATRIC	CDS	5340474	5341232	759	-	PGF_01726878	252	Branched-chain amino acid ABC transporter, ATP-binding protein LivG (TC 3.A.1.4.1)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5042	PATRIC.2.9855.2.9855.con.0001.CDS.5341237.5342202.rev	PATRIC	CDS	5341237	5342202	966	-	PGF_03231750	321	Branched-chain amino acid ABC transporter, permease protein LivM (TC 3.A.1.4.1)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5043	PATRIC.2.9855.2.9855.con.0001.CDS.5342212.5343087.rev	PATRIC	CDS	5342212	5343087	876	-	PGF_06868199	291	Branched-chain amino acid ABC transporter, permease protein LivH (TC 3.A.1.4.1)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5044	PATRIC.2.9855.2.9855.con.0001.CDS.5343113.5344267.rev	PATRIC	CDS	5343113	5344267	1155	-	PGF_10343884	384	Branched-chain amino acid ABC transporter, substrate-binding protein LivJ (TC 3.A.1.4.1)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5046	PATRIC.2.9855.2.9855.con.0001.CDS.5345932.5346801.fwd	PATRIC	CDS	5345932	5346801	870	+	PGF_00045788	289	Pyridoxal 5'-phosphate synthase (glutamine hydrolyzing), synthase subunit (EC 4.3.3.6)	GO:0036381|pyridoxal 5'-phosphate synthase (glutamine hydrolysing) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5047	PATRIC.2.9855.2.9855.con.0001.CDS.5346803.5347375.rev	PATRIC	CDS	5346803	5347375	573	+	PGF_00045787	190	Pyridoxal 5'-phosphate synthase (glutamine hydrolyzing), glutaminase subunit (EC 4.3.3.6)	GO:0036381|pyridoxal 5'-phosphate synthase (glutamine hydrolysing) activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.471	PATRIC.2.9855.2.9855.con.0001.CDS.535087.535434.fwd	PATRIC	CDS	535087	535434	348	+	PGF_00068769	115	FIG138056: a glutathione-dependent thiol reductase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5048	PATRIC.2.9855.2.9855.con.0001.CDS.5358942.5359718.fwd	PATRIC	CDS	5358942	5359718	777	+	PGF_10546386	258	Transmembrane protein YfcA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5050	PATRIC.2.9855.2.9855.con.0001.CDS.5360066.5360935.fwd	PATRIC	CDS	5360066	5360935	870	+	PGF_02982546	289	Dihydrodipicolinate synthase family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.473	PATRIC.2.9855.2.9855.con.0001.CDS.536032.537117.fwd	PATRIC	CDS	536032	537117	1086	+	PGF_01137083	361	HD-GYP hydrolase domain containing protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5051	PATRIC.2.9855.2.9855.con.0001.CDS.5361127.5362782.fwd	PATRIC	CDS	5361127	5362782	1656	+	PGF_08030327	551	Sulfate permease	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5053	PATRIC.2.9855.2.9855.con.0001.CDS.5364198.5365442.fwd	PATRIC	CDS	5364198	5365442	1245	+	PGF_06614457	414	Ammonium transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5054	PATRIC.2.9855.2.9855.con.0001.CDS.5365591.5365929.fwd	PATRIC	CDS	5365591	5365929	339	+	PGF_02518459	112	Nitrogen regulatory protein P-II	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5055	PATRIC.2.9855.2.9855.con.0001.CDS.5366184.5366816.fwd	PATRIC	CDS	5366184	5366816	633	+	PGF_00010528	210	HD superfamily hydrolase CA_C3562	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5056	PATRIC.2.9855.2.9855.con.0001.CDS.5367310.5369436.rev	PATRIC	CDS	5367310	5369436	2127	-	PGF_00026324	708	NtrC family Transcriptional regulator, ATPase domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5058	PATRIC.2.9855.2.9855.con.0001.CDS.5370366.5371943.rev	PATRIC	CDS	5370366	5371943	1578	-	PGF_00421098	525	DEAD-box ATP-dependent RNA helicase DeaD (= CshA) (EC 3.6.4.13)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5059	PATRIC.2.9855.2.9855.con.0001.CDS.5372166.5372888.rev	PATRIC	CDS	5372166	5372888	723	-	PGF_04252606	240	Acyl-CoA:1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	GO:0003841|1-acylglycerol-3-phosphate O-acyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5060	PATRIC.2.9855.2.9855.con.0001.CDS.5373119.5375509.fwd	PATRIC	CDS	5373119	5375509	2391	+	PGF_02952136	796	Cation-transporting ATPase, E1-E2 family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.474	PATRIC.2.9855.2.9855.con.0001.CDS.537417.538445.fwd	PATRIC	CDS	537417	538445	1029	+	PGF_05863337	342	Lysophospholipase L2 (EC 3.1.1.5)	GO:0004622|lysophospholipase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5061	PATRIC.2.9855.2.9855.con.0001.CDS.5376875.5377567.fwd	PATRIC	CDS	5376875	5377567	693	+	PGF_07420062	230	Two-component transcriptional response regulator, OmpR family	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5062	PATRIC.2.9855.2.9855.con.0001.CDS.5377572.5378624.fwd	PATRIC	CDS	5377572	5378624	1053	+	PGF_02637676	350	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5064	PATRIC.2.9855.2.9855.con.0001.CDS.5378952.5380118.fwd	PATRIC	CDS	5378952	5380118	1167	+	PGF_00004254	388	Fermentation/respiration switch protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5068	PATRIC.2.9855.2.9855.con.0001.CDS.5383279.5383674.fwd	PATRIC	CDS	5383279	5383674	396	+	PGF_09655255	131	Transcriptional regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5069	PATRIC.2.9855.2.9855.con.0001.CDS.5383762.5384037.fwd	PATRIC	CDS	5383762	5384037	276	+	PGF_09655255	91	Transcriptional regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5070	PATRIC.2.9855.2.9855.con.0001.CDS.5384166.5385761.fwd	PATRIC	CDS	5384166	5385761	1596	+	PGF_03352446	531	PTS system, maltose and glucose-specific IIC component / PTS system, maltose and glucose-specific IIB component (EC 2.7.1.208)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5071	PATRIC.2.9855.2.9855.con.0001.CDS.5385822.5387147.fwd	PATRIC	CDS	5385822	5387147	1326	+	PGF_00019116	441	Maltose-6'-phosphate glucosidase (EC 3.2.1.122)	GO:0050081|maltose-6'-phosphate glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5072	PATRIC.2.9855.2.9855.con.0001.CDS.5387156.5387641.fwd	PATRIC	CDS	5387156	5387641	486	+	PGF_01309240	161	PTS system, glucose-specific IIA component (EC 2.7.1.199)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5078	PATRIC.2.9855.2.9855.con.0001.CDS.5390675.5392030.fwd	PATRIC	CDS	5390675	5392030	1356	+	PGF_04999141	451	PTS system, sucrose-specific IIB component (EC 2.7.1.211) / PTS system, sucrose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5079	PATRIC.2.9855.2.9855.con.0001.CDS.5392220.5393212.fwd	PATRIC	CDS	5392220	5393212	993	+	PGF_05752125	330	Sucrose operon repressor ScrR, LacI family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.476	PATRIC.2.9855.2.9855.con.0001.CDS.539249.540592.fwd	PATRIC	CDS	539249	540592	1344	+	PGF_02633300	447	Neopullulanase (EC 3.2.1.135)	GO:0031216|neopullulanase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5080	PATRIC.2.9855.2.9855.con.0001.CDS.5393234.5394691.fwd	PATRIC	CDS	5393234	5394691	1458	+	PGF_08147841	485	Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	GO:0004564|beta-fructofuranosidase activity;GO:0004564|sucrose alpha-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5081	PATRIC.2.9855.2.9855.con.0001.CDS.5394684.5395622.fwd	PATRIC	CDS	5394684	5395622	939	+	PGF_07085092	312	Fructokinase (EC 2.7.1.4)	GO:0008865|fructokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5083	PATRIC.2.9855.2.9855.con.0001.CDS.5395837.5396286.fwd	PATRIC	CDS	5395837	5396286	450	+	PGF_07596127	149	tRNA-specific adenosine-34 deaminase (EC 3.5.4.33)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5084	PATRIC.2.9855.2.9855.con.0001.CDS.5396575.5396925.fwd	PATRIC	CDS	5396575	5396925	351	+	PGF_01151115	116	Antiholin-like protein LrgA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5085	PATRIC.2.9855.2.9855.con.0001.CDS.5396922.5397626.fwd	PATRIC	CDS	5396922	5397626	705	+	PGF_00017655	234	LrgA-associated membrane protein LrgB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5087	PATRIC.2.9855.2.9855.con.0001.CDS.5398252.5398923.fwd	PATRIC	CDS	5398252	5398923	672	+	PGF_06916656	223	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5088	PATRIC.2.9855.2.9855.con.0001.CDS.5399006.5400181.fwd	PATRIC	CDS	5399006	5400181	1176	+	PGF_00821117	391	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	GO:0008825|cyclopropane-fatty-acyl-phospholipid synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5089	PATRIC.2.9855.2.9855.con.0001.CDS.5401314.5402102.fwd	PATRIC	CDS	5401314	5402102	789	+	PGF_00411988	262	salicylate esterase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5090	PATRIC.2.9855.2.9855.con.0001.CDS.5402364.5402795.fwd	PATRIC	CDS	5402364	5402795	432	+	PGF_10423881	143	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5091	PATRIC.2.9855.2.9855.con.0001.CDS.5402844.5404292.fwd	PATRIC	CDS	5402844	5404292	1449	+	PGF_09996723	482	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5092	PATRIC.2.9855.2.9855.con.0001.CDS.5404691.5405134.fwd	PATRIC	CDS	5404691	5405134	444	+	PGF_10423881	147	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5093	PATRIC.2.9855.2.9855.con.0001.CDS.5405188.5406636.fwd	PATRIC	CDS	5405188	5406636	1449	+	PGF_09996723	482	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.477	PATRIC.2.9855.2.9855.con.0001.CDS.540692.542665.fwd	PATRIC	CDS	540692	542665	1974	+	PGF_02875184	657	Pullulanase (EC 3.2.1.41)	GO:0051060|pullulanase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5096	PATRIC.2.9855.2.9855.con.0001.CDS.5408117.5408887.rev	PATRIC	CDS	5408117	5408887	771	-	PGF_01280824	256	Xylose activator XylR (AraC family)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5097	PATRIC.2.9855.2.9855.con.0001.CDS.5409038.5411167.fwd	PATRIC	CDS	5409038	5411167	2130	+	PGF_00007805	709	Glucan 1,4-beta-glucosidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5098	PATRIC.2.9855.2.9855.con.0001.CDS.5411263.5412240.fwd	PATRIC	CDS	5411263	5412240	978	+	PGF_00067114	325	Xylosidase/arabinosidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5099	PATRIC.2.9855.2.9855.con.0001.CDS.5412443.5414050.fwd	PATRIC	CDS	5412443	5414050	1608	+	PGF_00917167	535	Xylan 1,4-beta-xylosidase (EC 3.2.1.37)	GO:0009044|xylan 1,4-beta-xylosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5100	PATRIC.2.9855.2.9855.con.0001.CDS.5414172.5414528.rev	PATRIC	CDS	5414172	5414528	357	-	PGF_03320197	118	Transcriptional regulator, HxlR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5101	PATRIC.2.9855.2.9855.con.0001.CDS.5414663.5415316.fwd	PATRIC	CDS	5414663	5415316	654	+	PGF_02278882	217	Iron-sulfur flavoprotein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5102	PATRIC.2.9855.2.9855.con.0001.CDS.5415404.5415922.fwd	PATRIC	CDS	5415404	5415922	519	+	PGF_06672158	172	Nitroreductase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5104	PATRIC.2.9855.2.9855.con.0001.CDS.5416530.5418041.fwd	PATRIC	CDS	5416530	5418041	1512	+	PGF_01343909	503	ABC transporter, ATP-binding protein (cluster 2, ribose/xylose/arabinose/galactose) / ABC transporter, ATP-binding protein (cluster 2, ribose/xylose/arabinose/galactose)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5105	PATRIC.2.9855.2.9855.con.0001.CDS.5418025.5419041.fwd	PATRIC	CDS	5418025	5419041	1017	+	PGF_10234027	338	ABC transporter, permease protein (cluster 2, ribose/xylose/arabinose/galactose)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5106	PATRIC.2.9855.2.9855.con.0001.CDS.5419160.5420185.fwd	PATRIC	CDS	5419160	5420185	1026	+	PGF_10487056	341	ABC transporter, substrate-binding protein (cluster 2, ribose/xylose/arabinose/galactose)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5107	PATRIC.2.9855.2.9855.con.0001.CDS.5420398.5422110.fwd	PATRIC	CDS	5420398	5422110	1713	+	PGF_02910829	570	Membrane assosiated methyl-accepting chemotaxis protein with HAMP domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5108	PATRIC.2.9855.2.9855.con.0001.CDS.5422235.5423551.fwd	PATRIC	CDS	5422235	5423551	1317	+	PGF_07870324	438	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5109	PATRIC.2.9855.2.9855.con.0001.CDS.5423567.5425327.fwd	PATRIC	CDS	5423567	5425327	1761	+	PGF_00050455	586	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5110	PATRIC.2.9855.2.9855.con.0001.CDS.5425372.5426175.fwd	PATRIC	CDS	5425372	5426175	804	+	PGF_00062533	267	Two-component response regulator yesN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5111	PATRIC.2.9855.2.9855.con.0001.CDS.5426488.5426928.fwd	PATRIC	CDS	5426488	5426928	441	+	PGF_01171887	146	Large-conductance mechanosensitive channel	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.478	PATRIC.2.9855.2.9855.con.0001.CDS.542694.543464.fwd	PATRIC	CDS	542694	543464	771	+	PGF_00797092	256	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	GO:0017103|UTP:galactose-1-phosphate uridylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5112	PATRIC.2.9855.2.9855.con.0001.CDS.5427238.5428518.fwd	PATRIC	CDS	5427238	5428518	1281	+	PGF_00045963	426	Pyruvate carboxylase (EC 6.4.1.1)	GO:0004736|pyruvate carboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5113	PATRIC.2.9855.2.9855.con.0001.CDS.5428544.5430679.fwd	PATRIC	CDS	5428544	5430679	2136	+	PGF_00045963	711	Pyruvate carboxylase (EC 6.4.1.1)	GO:0004736|pyruvate carboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5114	PATRIC.2.9855.2.9855.con.0001.CDS.5430972.5431907.fwd	PATRIC	CDS	5430972	5431907	936	+	PGF_00417537	311	Response regulator receiver domain / CheX-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5115	PATRIC.2.9855.2.9855.con.0001.CDS.5431889.5432356.fwd	PATRIC	CDS	5431889	5432356	468	+	PGF_08907828	155	Chemotaxis protein CheX	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5116	PATRIC.2.9855.2.9855.con.0001.CDS.5432491.5433126.fwd	PATRIC	CDS	5432491	5433126	636	+	PGF_10401875	211	Integral membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5117	PATRIC.2.9855.2.9855.con.0001.CDS.5433275.5433652.fwd	PATRIC	CDS	5433275	5433652	378	+	PGF_06545170	125	Fluoride ion transporter CrcB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5119	PATRIC.2.9855.2.9855.con.0001.CDS.5435059.5435943.rev	PATRIC	CDS	5435059	5435943	885	-	PGF_00400052	294	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5120	PATRIC.2.9855.2.9855.con.0001.CDS.5436070.5436561.rev	PATRIC	CDS	5436070	5436561	492	-	PGF_09348764	163	Dihydrofolate reductase (EC 1.5.1.3)	GO:0004146|dihydrofolate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5121	PATRIC.2.9855.2.9855.con.0001.CDS.5436630.5437421.rev	PATRIC	CDS	5436630	5437421	792	-	PGF_00056897	263	Thymidylate synthase (EC 2.1.1.45)	GO:0004799|thymidylate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.479	PATRIC.2.9855.2.9855.con.0001.CDS.543698.545413.fwd	PATRIC	CDS	543698	545413	1716	+	PGF_10447617	571	Ribonuclease J (endonuclease and 5' exonuclease)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5122	PATRIC.2.9855.2.9855.con.0001.CDS.5437720.5439366.fwd	PATRIC	CDS	5437720	5439366	1647	+	PGF_10365126	548	DNA polymerase III subunits gamma and tau (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5123	PATRIC.2.9855.2.9855.con.0001.CDS.5439452.5439793.fwd	PATRIC	CDS	5439452	5439793	342	+	PGF_02141223	113	Nucleoid-associated protein YaaK	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5124	PATRIC.2.9855.2.9855.con.0001.CDS.5439902.5440501.fwd	PATRIC	CDS	5439902	5440501	600	+	PGF_02463284	199	Recombination protein RecR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5126	PATRIC.2.9855.2.9855.con.0001.CDS.5441015.5441146.fwd	PATRIC	CDS	5441015	5441146	132	+	PGF_03240628	43	Inhibitor of pro-sigmaK processing BofA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5127	PATRIC.2.9855.2.9855.con.0001.CDS.5441629.5442903.fwd	PATRIC	CDS	5441629	5442903	1275	+	PGF_00417743	424	Choline binding protein PcpA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5128	PATRIC.2.9855.2.9855.con.0001.CDS.5443047.5445077.fwd	PATRIC	CDS	5443047	5445077	2031	+	PGF_05695878	676	Peptidase, M13 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.54	PATRIC.2.9855.2.9855.con.0001.CDS.54437.55756.fwd	PATRIC	CDS	54437	55756	1320	+	PGF_03173405	439	D-galactonate transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5130	PATRIC.2.9855.2.9855.con.0001.CDS.5445224.5445400.fwd	PATRIC	CDS	5445224	5445400	177	+	PGF_01294288	58	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5131	PATRIC.2.9855.2.9855.con.0001.CDS.5445620.5446381.fwd	PATRIC	CDS	5445620	5446381	762	+	PGF_00058683	253	Transcriptional regulator VpsT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5132	PATRIC.2.9855.2.9855.con.0001.CDS.5446548.5446895.fwd	PATRIC	CDS	5446548	5446895	348	+	PGF_02518459	115	Nitrogen regulatory protein P-II	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5133	PATRIC.2.9855.2.9855.con.0001.CDS.5447026.5448108.fwd	PATRIC	CDS	5447026	5448108	1083	+	PGF_10327309	360	Spermidine/putrescine import ABC transporter substrate-binding protein PotD (TC 3.A.1.11.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5134	PATRIC.2.9855.2.9855.con.0001.CDS.5448140.5449267.fwd	PATRIC	CDS	5448140	5449267	1128	+	PGF_08196377	375	Spermidine/putrescine import ABC transporter ATP-binding protein PotA (TC 3.A.1.11.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5135	PATRIC.2.9855.2.9855.con.0001.CDS.5449280.5450143.fwd	PATRIC	CDS	5449280	5450143	864	+	PGF_00053700	287	Spermidine/putrescine import ABC transporter permease protein PotB (TC 3.A.1.11.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5136	PATRIC.2.9855.2.9855.con.0001.CDS.5450145.5450945.fwd	PATRIC	CDS	5450145	5450945	801	+	PGF_05048110	266	Spermidine/putrescine import ABC transporter permease protein PotC (TC 3.A.1.11.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5137	PATRIC.2.9855.2.9855.con.0001.CDS.5451044.5452423.fwd	PATRIC	CDS	5451044	5452423	1380	+	PGF_07293934	459	N-acyl-D-amino-acid deacylase (EC 3.5.1.81)	GO:0047420|N-acyl-D-amino-acid deacylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5138	PATRIC.2.9855.2.9855.con.0001.CDS.5452702.5452878.fwd	PATRIC	CDS	5452702	5452878	177	+	PGF_07597988	58	Aldehyde dehydrogenase (EC 1.2.1.3)	GO:0004029|aldehyde dehydrogenase (NAD) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5139	PATRIC.2.9855.2.9855.con.0001.CDS.5452889.5453509.fwd	PATRIC	CDS	5452889	5453509	621	+	PGF_07597988	206	Aldehyde dehydrogenase (EC 1.2.1.3)	GO:0004029|aldehyde dehydrogenase (NAD) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5140	PATRIC.2.9855.2.9855.con.0001.CDS.5453463.5454185.fwd	PATRIC	CDS	5453463	5454185	723	+	PGF_07597988	240	Aldehyde dehydrogenase (EC 1.2.1.3)	GO:0004029|aldehyde dehydrogenase (NAD) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5142	PATRIC.2.9855.2.9855.con.0001.CDS.5455531.5456886.fwd	PATRIC	CDS	5455531	5456886	1356	+	PGF_00045727	451	Putrescine aminotransferase (EC 2.6.1.82)	GO:0033094|butane-1,4-diamine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.480	PATRIC.2.9855.2.9855.con.0001.CDS.545818.546993.fwd	PATRIC	CDS	545818	546993	1176	+	PGF_03753601	391	Aminotransferase, DegT/Dnr1/EryC1/StrS family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5144	PATRIC.2.9855.2.9855.con.0001.CDS.5458614.5459540.fwd	PATRIC	CDS	5458614	5459540	927	+	PGF_00977978	308	Oligopeptide ABC transporter, permease protein OppB (TC 3.A.1.5.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5145	PATRIC.2.9855.2.9855.con.0001.CDS.5459554.5460498.fwd	PATRIC	CDS	5459554	5460498	945	+	PGF_10569020	314	Oligopeptide ABC transporter, permease protein OppC (TC 3.A.1.5.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5146	PATRIC.2.9855.2.9855.con.0001.CDS.5460515.5461522.fwd	PATRIC	CDS	5460515	5461522	1008	+	PGF_09990804	335	Oligopeptide ABC transporter, ATP-binding protein OppD (TC 3.A.1.5.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5147	PATRIC.2.9855.2.9855.con.0001.CDS.5461522.5462505.fwd	PATRIC	CDS	5461522	5462505	984	+	PGF_07131324	327	Oligopeptide ABC transporter, ATP-binding protein OppF (TC 3.A.1.5.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5148	PATRIC.2.9855.2.9855.con.0001.CDS.5462654.5464309.fwd	PATRIC	CDS	5462654	5464309	1656	+	PGF_02147779	551	Oligopeptide ABC transporter, substrate-binding protein OppA (TC 3.A.1.5.1)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5149	PATRIC.2.9855.2.9855.con.0001.CDS.5464992.5465900.fwd	PATRIC	CDS	5464992	5465900	909	+	PGF_00012987	302	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	GO:0004617|phosphoglycerate dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5150	PATRIC.2.9855.2.9855.con.0001.CDS.5465918.5467174.fwd	PATRIC	CDS	5465918	5467174	1257	+	PGF_00047479	418	Related to HTH domain of SpoOJ/ParA/ParB/repB family, involved in chromosome partitioning	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5152	PATRIC.2.9855.2.9855.con.0001.CDS.5467887.5469632.fwd	PATRIC	CDS	5467887	5469632	1746	+	PGF_02620852	581	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5155	PATRIC.2.9855.2.9855.con.0001.CDS.5470559.5471764.rev	PATRIC	CDS	5470559	5471764	1206	-	PGF_00856931	401	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5156	PATRIC.2.9855.2.9855.con.0001.CDS.5471784.5472215.rev	PATRIC	CDS	5471784	5472215	432	-	PGF_10423881	143	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5158	PATRIC.2.9855.2.9855.con.0001.CDS.5473665.5475005.fwd	PATRIC	CDS	5473665	5475005	1341	+	PGF_00015830	446	Kef-type K+ transport system, predicted NAD-binding component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5160	PATRIC.2.9855.2.9855.con.0001.CDS.5475887.5476708.fwd	PATRIC	CDS	5475887	5476708	822	+	PGF_00004397	273	Ferredoxin-like domain fused to nitroreductase-like domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5161	PATRIC.2.9855.2.9855.con.0001.CDS.5477096.5479102.fwd	PATRIC	CDS	5477096	5479102	2007	+	PGF_07849456	668	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5162	PATRIC.2.9855.2.9855.con.0001.CDS.5479214.5479906.rev	PATRIC	CDS	5479214	5479906	693	-	PGF_00777996	230	5'-methylthioadenosine nucleosidase (EC 3.2.2.16) @ S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)	GO:0008930|methylthioadenosine nucleosidase activity;GO:0008782|adenosylhomocysteine nucleosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5163	PATRIC.2.9855.2.9855.con.0001.CDS.5480340.5481101.fwd	PATRIC	CDS	5480340	5481101	762	+	PGF_01767358	253	HesA/MoeB/ThiF family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.482	PATRIC.2.9855.2.9855.con.0001.CDS.548100.549260.fwd	PATRIC	CDS	548100	549260	1161	+	PGF_00057506	386	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5164	PATRIC.2.9855.2.9855.con.0001.CDS.5481281.5484079.fwd	PATRIC	CDS	5481281	5484079	2799	+	PGF_00026324	932	NtrC family Transcriptional regulator, ATPase domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5165	PATRIC.2.9855.2.9855.con.0001.CDS.5484231.5484716.fwd	PATRIC	CDS	5484231	5484716	486	+	PGF_06621789	161	PTS system, mannose-specific IIA component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5166	PATRIC.2.9855.2.9855.con.0001.CDS.5484791.5485282.fwd	PATRIC	CDS	5484791	5485282	492	+	PGF_08661804	163	PTS system, mannose-specific IIB component (EC 2.7.1.191)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5167	PATRIC.2.9855.2.9855.con.0001.CDS.5485431.5486222.fwd	PATRIC	CDS	5485431	5486222	792	+	PGF_01653368	263	PTS system, mannose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5168	PATRIC.2.9855.2.9855.con.0001.CDS.5486244.5487065.fwd	PATRIC	CDS	5486244	5487065	822	+	PGF_00644224	273	PTS system, mannose-specific IID component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5169	PATRIC.2.9855.2.9855.con.0001.CDS.5487680.5488627.fwd	PATRIC	CDS	5487680	5488627	948	+	PGF_01670799	315	Ribosomal-protein-S5p-alanine acetyltransferase (EC 2.3.1.128)	GO:0008999|ribosomal-protein-alanine N-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5171	PATRIC.2.9855.2.9855.con.0001.CDS.5492937.5493380.rev	PATRIC	CDS	5492937	5493380	444	-	PGF_03495000	147	Mobile element protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.483	PATRIC.2.9855.2.9855.con.0001.CDS.549420.550187.fwd	PATRIC	CDS	549420	550187	768	+	PGF_08238312	255	Transcriptional regulator, IclR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5173	PATRIC.2.9855.2.9855.con.0001.CDS.5498845.5499282.rev	PATRIC	CDS	5498845	5499282	438	-	PGF_03495000	145	Mobile element protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5174	PATRIC.2.9855.2.9855.con.0001.CDS.5500512.5503061.fwd	PATRIC	CDS	5500512	5503061	2550	+	PGF_09031534	849	1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)	GO:0003844|1,4-alpha-glucan branching enzyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.484	PATRIC.2.9855.2.9855.con.0001.CDS.550272.551159.fwd	PATRIC	CDS	550272	551159	888	+	PGF_07894470	295	Dihydrodipicolinate synthase family	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5175	PATRIC.2.9855.2.9855.con.0001.CDS.5503157.5504596.fwd	PATRIC	CDS	5503157	5504596	1440	+	PGF_00008876	479	Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21)	GO:0009011|starch synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5176	PATRIC.2.9855.2.9855.con.0001.CDS.5504630.5507065.fwd	PATRIC	CDS	5504630	5507065	2436	+	PGF_00008874	811	Glycogen phosphorylase (EC 2.4.1.1)	GO:0004645|phosphorylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5177	PATRIC.2.9855.2.9855.con.0001.CDS.5507079.5508905.fwd	PATRIC	CDS	5507079	5508905	1827	+	PGF_02633300	608	Neopullulanase (EC 3.2.1.135)	GO:0031216|neopullulanase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5178	PATRIC.2.9855.2.9855.con.0001.CDS.5509181.5509366.fwd	PATRIC	CDS	5509181	5509366	186	+	PGF_10149521	61	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)	GO:0008878|glucose-1-phosphate adenylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5179	PATRIC.2.9855.2.9855.con.0001.CDS.5509443.5510342.fwd	PATRIC	CDS	5509443	5510342	900	+	PGF_10149521	299	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)	GO:0008878|glucose-1-phosphate adenylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5180	PATRIC.2.9855.2.9855.con.0001.CDS.5510368.5511480.fwd	PATRIC	CDS	5510368	5511480	1113	+	PGF_00008864	370	Glycogen biosynthesis protein GlgD, glucose-1-phosphate adenylyltransferase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.485	PATRIC.2.9855.2.9855.con.0001.CDS.551225.552961.fwd	PATRIC	CDS	551225	552961	1737	+	PGF_05070366	578	Dihydroxy-acid dehydratase (EC 4.2.1.9)	GO:0004160|dihydroxy-acid dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5183	PATRIC.2.9855.2.9855.con.0001.CDS.5516112.5516495.rev	PATRIC	CDS	5516112	5516495	384	-	PGF_03495000	127	Mobile element protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5184	PATRIC.2.9855.2.9855.con.0001.CDS.5517444.5518391.fwd	PATRIC	CDS	5517444	5518391	948	+	PGF_03941737	315	L-lactate dehydrogenase (EC 1.1.1.27)	GO:0004459|L-lactate dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5186	PATRIC.2.9855.2.9855.con.0001.CDS.5519910.5520716.fwd	PATRIC	CDS	5519910	5520716	807	+	PGF_00033411	268	Phosphoenolpyruvate synthase regulatory protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5187	PATRIC.2.9855.2.9855.con.0001.CDS.5526555.5526992.fwd	PATRIC	CDS	5526555	5526992	438	+	PGF_01294267	145	no significant homology.	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5188	PATRIC.2.9855.2.9855.con.0001.CDS.5527038.5527490.fwd	PATRIC	CDS	5527038	5527490	453	+	PGF_00037266	150	Probable phosphotransbutyrylase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5189	PATRIC.2.9855.2.9855.con.0001.CDS.5527782.5529281.rev	PATRIC	CDS	5527782	5529281	1500	-	PGF_01159317	499	Membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5190	PATRIC.2.9855.2.9855.con.0001.CDS.5529554.5531635.fwd	PATRIC	CDS	5529554	5531635	2082	+	PGF_00060412	693	Elongation factor G-like protein TM_1651	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.486	PATRIC.2.9855.2.9855.con.0001.CDS.553123.554784.fwd	PATRIC	CDS	553123	554784	1662	+	PGF_00917167	553	Xylan 1,4-beta-xylosidase (EC 3.2.1.37)	GO:0009044|xylan 1,4-beta-xylosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5192	PATRIC.2.9855.2.9855.con.0001.CDS.5532224.5533177.fwd	PATRIC	CDS	5532224	5533177	954	+	PGF_00735927	317	Putative ROK-family transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5193	PATRIC.2.9855.2.9855.con.0001.CDS.5533662.5534894.fwd	PATRIC	CDS	5533662	5534894	1233	+	PGF_08110123	410	ADP-ribose pyrophosphatase of COG1058 family (EC 3.6.1.13) / Nicotinamide-nucleotide amidase (EC 3.5.1.42)	GO:0047631|ADP-ribose diphosphatase activity;GO:0019159|nicotinamide-nucleotide amidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5194	PATRIC.2.9855.2.9855.con.0001.CDS.5535066.5535797.rev	PATRIC	CDS	5535066	5535797	732	-	PGF_10024837	243	NAD-dependent protein deacetylase of SIR2 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5196	PATRIC.2.9855.2.9855.con.0001.CDS.5536957.5537634.rev	PATRIC	CDS	5536957	5537634	678	-	PGF_00066139	225	Uracil-DNA glycosylase, family 1 (EC 3.2.2.27)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5197	PATRIC.2.9855.2.9855.con.0001.CDS.5537815.5538561.fwd	PATRIC	CDS	5537815	5538561	747	+	PGF_00342037	248	Foldase protein PrsA precursor (EC 5.2.1.8)	GO:0003755|peptidyl-prolyl cis-trans isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5198	PATRIC.2.9855.2.9855.con.0001.CDS.5538852.5539496.rev	PATRIC	CDS	5538852	5539496	645	-	PGF_03247561	214	Hydrolase, haloacid dehalogenase-like family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5199	PATRIC.2.9855.2.9855.con.0001.CDS.5540174.5541388.fwd	PATRIC	CDS	5540174	5541388	1215	+	PGF_00025007	404	NLP/P60 family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5200	PATRIC.2.9855.2.9855.con.0001.CDS.5541580.5542329.fwd	PATRIC	CDS	5541580	5542329	750	+	PGF_05969969	249	tRNA(1)(Val) (adenine(37)-N(6))-methyltransferase (EC 2.1.1.223)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5201	PATRIC.2.9855.2.9855.con.0001.CDS.5542331.5543176.fwd	PATRIC	CDS	5542331	5543176	846	+	PGF_03215471	281	16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5202	PATRIC.2.9855.2.9855.con.0001.CDS.5543280.5543525.rev	PATRIC	CDS	5543280	5543525	246	-	PGF_05632115	81	Transition state regulatory protein AbrB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5204	PATRIC.2.9855.2.9855.con.0001.CDS.5544823.5547108.fwd	PATRIC	CDS	5544823	5547108	2286	+	PGF_00423471	761	DinG family ATP-dependent helicase CPE1197	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5205	PATRIC.2.9855.2.9855.con.0001.CDS.5547346.5548527.fwd	PATRIC	CDS	5547346	5548527	1182	+	PGF_03753601	393	Aminotransferase, DegT/Dnr1/EryC1/StrS family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5206	PATRIC.2.9855.2.9855.con.0001.CDS.5548613.5549188.fwd	PATRIC	CDS	5548613	5549188	576	+	PGF_00063943	191	UDP-2-acetamido-3-amino-2,3-dideoxy-D-glucuronic acid acetyltransferase (EC 2.3.1.201)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5207	PATRIC.2.9855.2.9855.con.0001.CDS.5549301.5550617.fwd	PATRIC	CDS	5549301	5550617	1317	+	PGF_07093307	438	UDP-N-acetyl-D-glucosamine 6-dehydrogenase (EC 1.1.1.136)	GO:0047004|UDP-N-acetylglucosamine 6-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.487	PATRIC.2.9855.2.9855.con.0001.CDS.555027.556400.fwd	PATRIC	CDS	555027	556400	1374	+	PGF_01350985	457	Xyloside transporter XynT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5208	PATRIC.2.9855.2.9855.con.0001.CDS.5550849.5551703.fwd	PATRIC	CDS	5550849	5551703	855	+	PGF_05930156	284	Inner membrane protein YihY, formerly thought to be RNase BN	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5209	PATRIC.2.9855.2.9855.con.0001.CDS.5551803.5552144.fwd	PATRIC	CDS	5551803	5552144	342	+	PGF_02142873	113	Single-stranded DNA-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5211	PATRIC.2.9855.2.9855.con.0001.CDS.5553316.5553687.fwd	PATRIC	CDS	5553316	5553687	372	+	PGF_10373331	123	Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7)	GO:0008897|holo-[acyl-carrier-protein] synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5212	PATRIC.2.9855.2.9855.con.0001.CDS.5553687.5555195.fwd	PATRIC	CDS	5553687	5555195	1509	+	PGF_06230969	502	NAD(P)H-hydrate epimerase (EC 5.1.99.6) / ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5213	PATRIC.2.9855.2.9855.con.0001.CDS.5555261.5555893.fwd	PATRIC	CDS	5555261	5555893	633	+	PGF_01281263	210	Membrane associated protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5214	PATRIC.2.9855.2.9855.con.0001.CDS.5556120.5556377.fwd	PATRIC	CDS	5556120	5556377	258	+	PGF_00037481	85	Programmed cell death antitoxin YdcD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5215	PATRIC.2.9855.2.9855.con.0001.CDS.5556387.5556740.fwd	PATRIC	CDS	5556387	5556740	354	+	PGF_10301671	117	Programmed cell death toxin YdcE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5216	PATRIC.2.9855.2.9855.con.0001.CDS.5556968.5557789.fwd	PATRIC	CDS	5556968	5557789	822	+	PGF_03267589	273	Transketolase, N-terminal section (EC 2.2.1.1)	GO:0004802|transketolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5217	PATRIC.2.9855.2.9855.con.0001.CDS.5557789.5558733.fwd	PATRIC	CDS	5557789	5558733	945	+	PGF_00060399	314	Transketolase, C-terminal section (EC 2.2.1.1)	GO:0004802|transketolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5218	PATRIC.2.9855.2.9855.con.0001.CDS.5558890.5559750.fwd	PATRIC	CDS	5558890	5559750	861	+	PGF_03087500	286	Uncharacterized UPF0750 membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5219	PATRIC.2.9855.2.9855.con.0001.CDS.5559877.5560563.fwd	PATRIC	CDS	5559877	5560563	687	+	PGF_06857975	228	Cell-division-associated, ABC-transporter-like signaling protein FtsE	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5220	PATRIC.2.9855.2.9855.con.0001.CDS.5560553.5561443.fwd	PATRIC	CDS	5560553	5561443	891	+	PGF_03701810	296	Cell-division-associated, ABC-transporter-like signaling protein FtsX	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5221	PATRIC.2.9855.2.9855.con.0001.CDS.5561605.5562867.fwd	PATRIC	CDS	5561605	5562867	1263	+	PGF_00030577	420	Peptidase, S41 family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5222	PATRIC.2.9855.2.9855.con.0001.CDS.5562879.5564237.fwd	PATRIC	CDS	5562879	5564237	1359	+	PGF_03742550	452	Cell division topological determinant MinJ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5223	PATRIC.2.9855.2.9855.con.0001.CDS.5564514.5566487.fwd	PATRIC	CDS	5564514	5566487	1974	+	PGF_00950554	657	Excinuclease ABC subunit B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5224	PATRIC.2.9855.2.9855.con.0001.CDS.5566564.5569389.fwd	PATRIC	CDS	5566564	5569389	2826	+	PGF_04041316	941	Excinuclease ABC subunit A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.488	PATRIC.2.9855.2.9855.con.0001.CDS.556833.558533.fwd	PATRIC	CDS	556833	558533	1701	+	PGF_06837078	566	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5225	PATRIC.2.9855.2.9855.con.0001.CDS.5569754.5570197.fwd	PATRIC	CDS	5569754	5570197	444	+	PGF_10397144	147	FHA-domain-containing protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5226	PATRIC.2.9855.2.9855.con.0001.CDS.5570350.5571570.fwd	PATRIC	CDS	5570350	5571570	1221	+	PGF_06377994	406	FtsW-like cell division membrane protein CA_C0505	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5227	PATRIC.2.9855.2.9855.con.0001.CDS.5571574.5573043.fwd	PATRIC	CDS	5571574	5573043	1470	+	PGF_10511254	489	FtsI-like cell elongation transpeptidase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5228	PATRIC.2.9855.2.9855.con.0001.CDS.5573187.5575052.fwd	PATRIC	CDS	5573187	5575052	1866	+	PGF_00424971	621	Excinuclease ABC subunit C	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5229	PATRIC.2.9855.2.9855.con.0001.CDS.5575290.5576204.fwd	PATRIC	CDS	5575290	5576204	915	+	PGF_00063974	304	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5230	PATRIC.2.9855.2.9855.con.0001.CDS.5576431.5577315.fwd	PATRIC	CDS	5576431	5577315	885	+	PGF_03788368	294	RNase adapter protein RapZ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5231	PATRIC.2.9855.2.9855.con.0001.CDS.5577312.5578664.fwd	PATRIC	CDS	5577312	5578664	1353	+	PGF_08005402	450	FIG002813: LPPG:FO 2-phospho-L-lactate transferase like, CofD-like	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5232	PATRIC.2.9855.2.9855.con.0001.CDS.5578707.5579654.fwd	PATRIC	CDS	5578707	5579654	948	+	PGF_00425738	315	Sporulation transcription regulator WhiA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5233	PATRIC.2.9855.2.9855.con.0001.CDS.5579678.5579962.fwd	PATRIC	CDS	5579678	5579962	285	+	PGF_01512040	94	Stress responsive alpha-beta barrel domain protein Dabb	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5234	PATRIC.2.9855.2.9855.con.0001.CDS.5580066.5583641.fwd	PATRIC	CDS	5580066	5583641	3576	+	PGF_10406880	1191	DNA polymerase III alpha subunit (EC 2.7.7.7)	GO:0003887|DNA-directed DNA polymerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5235	PATRIC.2.9855.2.9855.con.0001.CDS.5584098.5585054.fwd	PATRIC	CDS	5584098	5585054	957	+	PGF_07421229	318	6-phosphofructokinase (EC 2.7.1.11)	GO:0003872|6-phosphofructokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5236	PATRIC.2.9855.2.9855.con.0001.CDS.5585199.5586620.fwd	PATRIC	CDS	5585199	5586620	1422	+	PGF_07760799	473	Pyruvate kinase (EC 2.7.1.40)	GO:0004743|pyruvate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5237	PATRIC.2.9855.2.9855.con.0001.CDS.5587257.5588621.fwd	PATRIC	CDS	5587257	5588621	1365	+	PGF_07941512	454	23S rRNA (uracil(1939)-C(5))-methyltransferase (EC 2.1.1.190)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5238	PATRIC.2.9855.2.9855.con.0001.CDS.5589131.5590231.fwd	PATRIC	CDS	5589131	5590231	1101	+	PGF_00024643	366	NADH-dependent dehydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5239	PATRIC.2.9855.2.9855.con.0001.CDS.5590266.5591237.fwd	PATRIC	CDS	5590266	5591237	972	+	PGF_03085680	323	Inosose isomerase (EC 5.3.99.11)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5240	PATRIC.2.9855.2.9855.con.0001.CDS.5591269.5592318.fwd	PATRIC	CDS	5591269	5592318	1050	+	PGF_10517561	349	Oxidoreductase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5241	PATRIC.2.9855.2.9855.con.0001.CDS.5592365.5593216.fwd	PATRIC	CDS	5592365	5593216	852	+	PGF_10358654	283	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5242	PATRIC.2.9855.2.9855.con.0001.CDS.5593242.5594033.fwd	PATRIC	CDS	5593242	5594033	792	+	PGF_01984142	263	weak similarity to aminoglycoside N(3)-acetyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5243	PATRIC.2.9855.2.9855.con.0001.CDS.5594173.5596023.rev	PATRIC	CDS	5594173	5596023	1851	-	PGF_04512237	616	PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component / PTS system, beta-glucoside-specific IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.490	PATRIC.2.9855.2.9855.con.0001.CDS.559522.560709.fwd	PATRIC	CDS	559522	560709	1188	+	PGF_00043821	395	Putative ribosomal RNA large subunit methyltransferase YwbD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5244	PATRIC.2.9855.2.9855.con.0001.CDS.5596290.5597489.fwd	PATRIC	CDS	5596290	5597489	1200	+	PGF_00054157	399	Starvation sensing protein RspA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5245	PATRIC.2.9855.2.9855.con.0001.CDS.5597502.5598221.rev	PATRIC	CDS	5597502	5598221	720	-	PGF_00058812	239	Transcriptional regulator of succinyl CoA synthetase operon	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5246	PATRIC.2.9855.2.9855.con.0001.CDS.5598492.5599598.fwd	PATRIC	CDS	5598492	5599598	1107	+	PGF_03790089	368	Uncharacterized di-Fe4-S4 cluster-containing protein AF_1153	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5247	PATRIC.2.9855.2.9855.con.0001.CDS.5599920.5600615.fwd	PATRIC	CDS	5599920	5600615	696	+	PGF_00798173	231	Manganese catalase (EC 1.11.1.6)	GO:0004096|catalase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5248	PATRIC.2.9855.2.9855.con.0001.CDS.5601045.5602487.fwd	PATRIC	CDS	5601045	5602487	1443	+	PGF_08148954	480	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5249	PATRIC.2.9855.2.9855.con.0001.CDS.5602778.5604502.fwd	PATRIC	CDS	5602778	5604502	1725	+	PGF_01284138	574	Membrane assosiated methyl-accepting chemotaxis protein with HAMP domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.55	PATRIC.2.9855.2.9855.con.0001.CDS.56035.57510.fwd	PATRIC	CDS	56035	57510	1476	+	PGF_00421041	491	D-serine/D-alanine/glycine transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5250	PATRIC.2.9855.2.9855.con.0001.CDS.5605078.5605863.fwd	PATRIC	CDS	5605078	5605863	786	+	PGF_04321257	261	Flagellar motor rotation protein MotA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5251	PATRIC.2.9855.2.9855.con.0001.CDS.5605881.5606615.fwd	PATRIC	CDS	5605881	5606615	735	+	PGF_01899924	244	Flagellar motor rotation protein MotB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5252	PATRIC.2.9855.2.9855.con.0001.CDS.5606874.5608922.fwd	PATRIC	CDS	5606874	5608922	2049	+	PGF_08121553	682	Signal transduction histidine kinase CheA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5253	PATRIC.2.9855.2.9855.con.0001.CDS.5608975.5610696.fwd	PATRIC	CDS	5608975	5610696	1722	+	PGF_06837078	573	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.491	PATRIC.2.9855.2.9855.con.0001.CDS.560938.562119.fwd	PATRIC	CDS	560938	562119	1182	+	PGF_00821117	393	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	GO:0008825|cyclopropane-fatty-acyl-phospholipid synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5254	PATRIC.2.9855.2.9855.con.0001.CDS.5610712.5611527.fwd	PATRIC	CDS	5610712	5611527	816	+	PGF_08449066	271	Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)	GO:0008983|protein-glutamate O-methyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5255	PATRIC.2.9855.2.9855.con.0001.CDS.5611570.5612595.fwd	PATRIC	CDS	5611570	5612595	1026	+	PGF_00417580	341	Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)	GO:0008984|protein-glutamate methylesterase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5256	PATRIC.2.9855.2.9855.con.0001.CDS.5612607.5613263.rev	PATRIC	CDS	5612607	5613263	657	-	PGF_09666309	218	Two-component transcriptional response regulator, LuxR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5258	PATRIC.2.9855.2.9855.con.0001.CDS.5613706.5614077.fwd	PATRIC	CDS	5613706	5614077	372	+	PGF_10238627	123	Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5259	PATRIC.2.9855.2.9855.con.0001.CDS.5614176.5616800.fwd	PATRIC	CDS	5614176	5616800	2625	+	PGF_03149691	874	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5260	PATRIC.2.9855.2.9855.con.0001.CDS.5616835.5617332.fwd	PATRIC	CDS	5616835	5617332	498	+	PGF_07311230	165	Positive regulator of CheA protein activity (CheW)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5261	PATRIC.2.9855.2.9855.con.0001.CDS.5617348.5618952.fwd	PATRIC	CDS	5617348	5618952	1605	+	PGF_06837078	534	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5262	PATRIC.2.9855.2.9855.con.0001.CDS.5618994.5620466.fwd	PATRIC	CDS	5618994	5620466	1473	+	PGF_10416542	490	Sensory box histidine kinase/response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5263	PATRIC.2.9855.2.9855.con.0001.CDS.5620493.5620900.fwd	PATRIC	CDS	5620493	5620900	408	+	PGF_03682232	135	Response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5264	PATRIC.2.9855.2.9855.con.0001.CDS.5621019.5621426.fwd	PATRIC	CDS	5621019	5621426	408	+	PGF_03751069	135	Hemerythrin domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5266	PATRIC.2.9855.2.9855.con.0001.CDS.5621781.5622338.fwd	PATRIC	CDS	5621781	5622338	558	+	PGF_03751069	185	Hemerythrin domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5268	PATRIC.2.9855.2.9855.con.0001.CDS.5622870.5625809.rev	PATRIC	CDS	5622870	5625809	2940	-	PGF_04080807	979	PAS	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5270	PATRIC.2.9855.2.9855.con.0001.CDS.5626778.5627122.fwd	PATRIC	CDS	5626778	5627122	345	+	PGF_01657055	114	Domain of unknown function / Tautomerase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5271	PATRIC.2.9855.2.9855.con.0001.CDS.5627223.5628014.fwd	PATRIC	CDS	5627223	5628014	792	+	PGF_00847718	263	Aliphatic amidase AmiE (EC 3.5.1.4)	GO:0004040|amidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.492	PATRIC.2.9855.2.9855.con.0001.CDS.562776.565289.fwd	PATRIC	CDS	562776	565289	2514	+	PGF_00015722	837	Isoniazid inductible protein IniA, dynamin-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.13	PATRIC.2.9855.2.9855.con.0001.CDS.5628.6461.fwd	PATRIC	CDS	5628	6461	834	+	PGF_00036551	277	Prephenate and/or arogenate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43)	GO:0008977|prephenate dehydrogenase activity;GO:0047794|cyclohexadienyl dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5272	PATRIC.2.9855.2.9855.con.0001.CDS.5628044.5629072.fwd	PATRIC	CDS	5628044	5629072	1029	+	PGF_01315021	342	CAAX amino terminal protease family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5273	PATRIC.2.9855.2.9855.con.0001.CDS.5629123.5630310.fwd	PATRIC	CDS	5629123	5630310	1188	+	PGF_10543640	395	N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)	GO:0004046|aminoacylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5274	PATRIC.2.9855.2.9855.con.0001.CDS.5630611.5632374.fwd	PATRIC	CDS	5630611	5632374	1764	+	PGF_00006821	587	GGDEF domain protein	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5275	PATRIC.2.9855.2.9855.con.0001.CDS.5632560.5633285.fwd	PATRIC	CDS	5632560	5633285	726	+	PGF_09655255	241	Transcriptional regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5276	PATRIC.2.9855.2.9855.con.0001.CDS.5633527.5635122.fwd	PATRIC	CDS	5633527	5635122	1596	+	PGF_03352446	531	PTS system, maltose and glucose-specific IIC component / PTS system, maltose and glucose-specific IIB component (EC 2.7.1.208)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5277	PATRIC.2.9855.2.9855.con.0001.CDS.5635144.5636472.fwd	PATRIC	CDS	5635144	5636472	1329	+	PGF_00019116	442	Maltose-6'-phosphate glucosidase (EC 3.2.1.122)	GO:0050081|maltose-6'-phosphate glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5278	PATRIC.2.9855.2.9855.con.0001.CDS.5636481.5636822.fwd	PATRIC	CDS	5636481	5636822	342	+	PGF_01309240	113	PTS system, glucose-specific IIA component (EC 2.7.1.199)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5279	PATRIC.2.9855.2.9855.con.0001.CDS.5637237.5637503.fwd	PATRIC	CDS	5637237	5637503	267	+	PGF_00047642	88	Repressor CsoR of the copZA operon	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5280	PATRIC.2.9855.2.9855.con.0001.CDS.5637658.5640087.fwd	PATRIC	CDS	5637658	5640087	2430	+	PGF_07109475	809	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)	GO:0008551|cadmium-exporting ATPase activity;GO:0016463|zinc-exporting ATPase activity;GO:0004008|copper-exporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5281	PATRIC.2.9855.2.9855.con.0001.CDS.5640237.5640443.fwd	PATRIC	CDS	5640237	5640443	207	+	PGF_02705782	68	Copper(I) chaperone CopZ	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5282	PATRIC.2.9855.2.9855.con.0001.CDS.5640768.5641139.fwd	PATRIC	CDS	5640768	5641139	372	+	PGF_05873585	123	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5283	PATRIC.2.9855.2.9855.con.0001.CDS.5641126.5641602.fwd	PATRIC	CDS	5641126	5641602	477	+	PGF_05873585	158	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5284	PATRIC.2.9855.2.9855.con.0001.CDS.5642102.5643070.fwd	PATRIC	CDS	5642102	5643070	969	+	PGF_00043266	322	Putative phosphosugar isomerase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5285	PATRIC.2.9855.2.9855.con.0001.CDS.5643097.5643939.fwd	PATRIC	CDS	5643097	5643939	843	+	PGF_01971913	280	Uncharacterized sugar kinase, ribokinase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5286	PATRIC.2.9855.2.9855.con.0001.CDS.5644118.5644849.fwd	PATRIC	CDS	5644118	5644849	732	+	PGF_06916656	243	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5287	PATRIC.2.9855.2.9855.con.0001.CDS.5645310.5646521.rev	PATRIC	CDS	5645310	5646521	1212	-	PGF_10368922	403	Alanyl-tRNA synthetase family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5288	PATRIC.2.9855.2.9855.con.0001.CDS.5646821.5647345.fwd	PATRIC	CDS	5646821	5647345	525	+	PGF_00409287	174	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5289	PATRIC.2.9855.2.9855.con.0001.CDS.5647441.5648631.rev	PATRIC	CDS	5647441	5648631	1191	-	PGF_00403927	396	Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.57) @ Aspartate aminotransferase (EC 2.6.1.1)	GO:0008793|aromatic-amino-acid:2-oxoglutarate aminotransferase activity;GO:0008793|L-phenylalanine:2-oxoglutarate aminotransferase activity;GO:0004069|L-aspartate:2-oxoglutarate aminotransferase activity;GO:0004069|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5290	PATRIC.2.9855.2.9855.con.0001.CDS.5649316.5650578.fwd	PATRIC	CDS	5649316	5650578	1263	+	PGF_07849456	420	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.493	PATRIC.2.9855.2.9855.con.0001.CDS.565286.565987.fwd	PATRIC	CDS	565286	565987	702	+	PGF_08176248	233	Chromosome partition protein smc	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5293	PATRIC.2.9855.2.9855.con.0001.CDS.5653405.5654079.fwd	PATRIC	CDS	5653405	5654079	675	+	PGF_00404184	224	probable enzyme with TIM-barrel fold	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5294	PATRIC.2.9855.2.9855.con.0001.CDS.5654744.5656039.fwd	PATRIC	CDS	5654744	5656039	1296	+	PGF_10373476	431	Diaminopimelate decarboxylase (EC 4.1.1.20)	GO:0008836|diaminopimelate decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5295	PATRIC.2.9855.2.9855.con.0001.CDS.5656411.5656965.fwd	PATRIC	CDS	5656411	5656965	555	+	PGF_05785543	184	Signal peptidase I (EC 3.4.21.89)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5296	PATRIC.2.9855.2.9855.con.0001.CDS.5657050.5657715.fwd	PATRIC	CDS	5657050	5657715	666	+	PGF_05785543	221	Signal peptidase I (EC 3.4.21.89)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5298	PATRIC.2.9855.2.9855.con.0001.CDS.5658357.5660489.fwd	PATRIC	CDS	5658357	5660489	2133	+	PGF_06275407	710	Cell division-associated, ATP-dependent zinc metalloprotease FtsH	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.494	PATRIC.2.9855.2.9855.con.0001.CDS.565994.567766.fwd	PATRIC	CDS	565994	567766	1773	+	PGF_00015720	590	Isoniazid inductible protein IniA, dynamin-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5299	PATRIC.2.9855.2.9855.con.0001.CDS.5660847.5663021.fwd	PATRIC	CDS	5660847	5663021	2175	+	PGF_06513921	724	ATP-dependent DNA helicase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5301	PATRIC.2.9855.2.9855.con.0001.CDS.5663572.5664408.fwd	PATRIC	CDS	5663572	5664408	837	+	PGF_05873585	278	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5302	PATRIC.2.9855.2.9855.con.0001.CDS.5665169.5665828.fwd	PATRIC	CDS	5665169	5665828	660	+	PGF_07804709	219	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5303	PATRIC.2.9855.2.9855.con.0001.CDS.5665815.5666537.fwd	PATRIC	CDS	5665815	5666537	723	+	PGF_10106935	240	ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5305	PATRIC.2.9855.2.9855.con.0001.CDS.5668015.5669190.rev	PATRIC	CDS	5668015	5669190	1176	-	PGF_04493258	391	Cobalt-zinc-cadmium resistance protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5306	PATRIC.2.9855.2.9855.con.0001.CDS.5669397.5670281.fwd	PATRIC	CDS	5669397	5670281	885	+	PGF_00549380	294	4-hydroxy-tetrahydrodipicolinate synthase	GO:0008840|4-hydroxy-tetrahydrodipicolinate synthase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5307	PATRIC.2.9855.2.9855.con.0001.CDS.5670698.5671753.fwd	PATRIC	CDS	5670698	5671753	1056	+	PGF_01282273	351	Protein gp49, replication initiation [Bacteriophage A118]	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5308	PATRIC.2.9855.2.9855.con.0001.CDS.5671854.5673188.fwd	PATRIC	CDS	5671854	5673188	1335	+	PGF_01990221	444	Aspartyl aminopeptidase (EC 3.4.11.21)	[illegible] mannosyltransferase activity;GO:0000009|mannosyltransferase activity;GO:0000009|alpha-1,3-mannosyltransferase activity;GO:0000009|alpha-1,3-galactosyltransferase activity;GO:0000009|UDP-glucose:glycoprotein glucosyltransferase activity;GO:0000009|glycolipid mannosyltransferase activity;GO:0000009|oligosaccharyl transferase activity;GO:0000009|dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase activity;GO:0000009|acetylglucosaminyltransferase activity;GO:0000009|acetylgalactosaminyltransferase activity;GO:0000009|galactosyltransferase activity;GO:0000009|fucosyltransferase activity;GO:0000009|O antigen polymerase activity;GO:0000009|lipopolysaccharide-1,6-galactosyltransferase activity;GO:0000009|cellulose synthase activity;GO:0000009|9-phenanthrol UDP-glucuronosyltransferase activity;GO:0000009|1-phenanthrol glycosyltransferase activity;GO:0000009|9-phenanthrol glycosyltransferase activity;GO:0000009|1,2-dihydroxy-phenanthrene glycosyltransferase activity;GO:0000009|phenanthrol glycosyltransferase activity;GO:0000009|beta-1,4-mannosyltransferase activity;GO:0000009|alpha-1,2-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man7GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|lipopolysaccharide-1,5-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|inositol phosphoceramide synthase activity;GO:0000009|glucosyltransferase activity;GO:0000009|alpha-(1->3)-fucosyltransferase activity;GO:0000009|alpha-(1->6)-fucosyltransferase activity;GO:0000009|indole-3-butyrate beta-glucosyltransferase activity;GO:0000009|salicylic acid glucosyltransferase (ester-forming) activity;GO:0000009|salicylic acid glucosyltransferase (glucoside-forming) activity;GO:0000009|benzoic acid glucosyltransferase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5309	PATRIC.2.9855.2.9855.con.0001.CDS.5673614.5682859.fwd	PATRIC	CDS	5673614	5682859	9246	+	PGF_00419899	3081	Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.495	PATRIC.2.9855.2.9855.con.0001.CDS.567772.569577.fwd	PATRIC	CDS	567772	569577	1806	+	PGF_00020691	601	ATP/GTP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5310	PATRIC.2.9855.2.9855.con.0001.CDS.5683789.5685906.fwd	PATRIC	CDS	5683789	5685906	2118	+	PGF_07849456	705	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5311	PATRIC.2.9855.2.9855.con.0001.CDS.5686124.5686984.fwd	PATRIC	CDS	5686124	5686984	861	+	PGF_00409415	286	UPF0750 membrane protein YvjA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5316	PATRIC.2.9855.2.9855.con.0001.CDS.5688579.5690306.fwd	PATRIC	CDS	5688579	5690306	1728	+	PGF_00417736	575	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5317	PATRIC.2.9855.2.9855.con.0001.CDS.5690850.5692151.fwd	PATRIC	CDS	5690850	5692151	1302	+	PGF_03510298	433	Surface protein PspC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5318	PATRIC.2.9855.2.9855.con.0001.CDS.5692308.5693582.fwd	PATRIC	CDS	5692308	5693582	1275	+	PGF_00417736	424	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5320	PATRIC.2.9855.2.9855.con.0001.CDS.5693812.5695359.fwd	PATRIC	CDS	5693812	5695359	1548	+	PGF_00417736	515	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5321	PATRIC.2.9855.2.9855.con.0001.CDS.5695410.5696654.fwd	PATRIC	CDS	5695410	5696654	1245	+	PGF_00417736	414	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5322	PATRIC.2.9855.2.9855.con.0001.CDS.5696798.5698015.fwd	PATRIC	CDS	5696798	5698015	1218	+	PGF_00417736	405	Choline binding protein A	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5323	PATRIC.2.9855.2.9855.con.0001.CDS.5698957.5700756.fwd	PATRIC	CDS	5698957	5700756	1800	+	PGF_00417743	599	Choline binding protein PcpA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.496	PATRIC.2.9855.2.9855.con.0001.CDS.570016.571179.rev	PATRIC	CDS	570016	571179	1164	-	PGF_08932911	387	Alanine racemase (EC 5.1.1.1)	GO:0008784|alanine racemase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5326	PATRIC.2.9855.2.9855.con.0001.CDS.5705153.5706577.rev	PATRIC	CDS	5705153	5706577	1425	-	PGF_03803951	474	Capsular polysaccharide biosynthesis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5330	PATRIC.2.9855.2.9855.con.0001.CDS.5710274.5711533.fwd	PATRIC	CDS	5710274	5711533	1260	+	PGF_02896943	419	Teichoic acid export ATP-binding protein TagH (EC 3.6.3.40)	GO:0015438|teichoic-acid-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.497	PATRIC.2.9855.2.9855.con.0001.CDS.571597.572085.fwd	PATRIC	CDS	571597	572085	489	+	PGF_01351149	162	Bifurcating [FeFe] hydrogenase, gamma subunit (EC 1.12.1.4)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.498	PATRIC.2.9855.2.9855.con.0001.CDS.572075.573955.fwd	PATRIC	CDS	572075	573955	1881	+	PGF_04003286	626	Bifurcating [FeFe] hydrogenase, beta subunit (EC 1.12.1.4)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5344	PATRIC.2.9855.2.9855.con.0001.CDS.5730738.5731016.fwd	PATRIC	CDS	5730738	5731016	279	+	PGF_00029672	92	PTS system, galactitol-specific IIC component (EC 2.7.1.200)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5345	PATRIC.2.9855.2.9855.con.0001.CDS.5731055.5732437.fwd	PATRIC	CDS	5731055	5732437	1383	+	PGF_00029677	460	PTS system, galactitol-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5346	PATRIC.2.9855.2.9855.con.0001.CDS.5732409.5733449.fwd	PATRIC	CDS	5732409	5733449	1041	+	PGF_00007078	346	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)	GO:0008868|galactitol-1-phosphate 5-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5347	PATRIC.2.9855.2.9855.con.0001.CDS.5733466.5734323.fwd	PATRIC	CDS	5733466	5734323	858	+	PGF_00055986	285	Tagatose 1,6-bisphosphate aldolase (EC 4.1.2.40)	GO:0009025|tagatose-bisphosphate aldolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5348	PATRIC.2.9855.2.9855.con.0001.CDS.5734540.5735874.fwd	PATRIC	CDS	5734540	5735874	1335	+	PGF_03046602	444	Tagatose-6-phosphate kinase AgaZ (EC 2.7.1.144)	GO:0009024|tagatose-6-phosphate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5350	PATRIC.2.9855.2.9855.con.0001.CDS.5737321.5738325.rev	PATRIC	CDS	5737321	5738325	1005	-	PGF_00025007	334	NLP/P60 family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5351	PATRIC.2.9855.2.9855.con.0001.CDS.5738591.5739682.fwd	PATRIC	CDS	5738591	5739682	1092	+	PGF_03892353	363	UPF0118 membrane protein YdbI	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.499	PATRIC.2.9855.2.9855.con.0001.CDS.574035.575738.fwd	PATRIC	CDS	574035	575738	1704	+	PGF_00403274	567	Bifurcating [FeFe] hydrogenase, alpha subunit (EC 1.12.1.4)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5353	PATRIC.2.9855.2.9855.con.0001.CDS.5740403.5741368.fwd	PATRIC	CDS	5740403	5741368	966	+	PGF_00068866	321	avirulence protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5354	PATRIC.2.9855.2.9855.con.0001.CDS.5741518.5742210.fwd	PATRIC	CDS	5741518	5742210	693	+	PGF_03255161	230	Tyrosine-protein kinase transmembrane modulator EpsC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5355	PATRIC.2.9855.2.9855.con.0001.CDS.5742401.5743213.fwd	PATRIC	CDS	5742401	5743213	813	+	PGF_10450882	270	Tyrosine-protein kinase EpsD (EC 2.7.10.2)	GO:0004715|non-membrane spanning protein tyrosine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5356	PATRIC.2.9855.2.9855.con.0001.CDS.5743338.5744120.fwd	PATRIC	CDS	5743338	5744120	783	+	PGF_07751295	260	Tyrosine-protein phosphatase CpsB (EC 3.1.3.48)	GO:0004725|protein tyrosine phosphatase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5357	PATRIC.2.9855.2.9855.con.0001.CDS.5744465.5745127.fwd	PATRIC	CDS	5744465	5745127	663	+	PGF_08794816	220	Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)	GO:0047360|undecaprenyl-phosphate galactose phosphotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5359	PATRIC.2.9855.2.9855.con.0001.CDS.5745285.5746634.fwd	PATRIC	CDS	5745285	5746634	1350	+	PGF_10410292	449	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	GO:0003979|UDP-glucose 6-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5360	PATRIC.2.9855.2.9855.con.0001.CDS.5746751.5747200.fwd	PATRIC	CDS	5746751	5747200	450	+	PGF_00034844	149	Polysaccharide biosynthesis protein CpsF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5361	PATRIC.2.9855.2.9855.con.0001.CDS.5747197.5747685.fwd	PATRIC	CDS	5747197	5747685	489	+	PGF_00401330	162	Beta-1,4-galactosyltransferase CpsIVG	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5362	PATRIC.2.9855.2.9855.con.0001.CDS.5747716.5748804.fwd	PATRIC	CDS	5747716	5748804	1089	+	PGF_00034569	362	Poly(glycerol-phosphate) alpha-glucosyltransferase (EC 2.4.1.52)	GO:0047265|poly(glycerol-phosphate) alpha-glucosyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5363	PATRIC.2.9855.2.9855.con.0001.CDS.5749030.5749587.fwd	PATRIC	CDS	5749030	5749587	558	+	PGF_00660064	185	Galactoside O-acetyltransferase (EC 2.3.1.18)	GO:0008870|galactoside O-acetyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5365	PATRIC.2.9855.2.9855.con.0001.CDS.5749891.5751120.fwd	PATRIC	CDS	5749891	5751120	1230	+	PGF_00027115	409	Oligosaccharide repeat unit polymerase Wzy	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5366	PATRIC.2.9855.2.9855.con.0001.CDS.5751255.5752415.fwd	PATRIC	CDS	5751255	5752415	1161	+	PGF_00416253	386	Capsular polysaccharide biosynthesis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5367	PATRIC.2.9855.2.9855.con.0001.CDS.5752457.5753425.fwd	PATRIC	CDS	5752457	5753425	969	+	PGF_01308267	322	Beta-1,3-glucosyltransferase	

Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5368	PATRIC.2.9855.2.9855.con.0001.CDS.5753646.5754824.fwd	PATRIC	CDS	5753646	5754824	1179	+	PGF_05995165	392	Alpha-1,4-N-acetylgalactosamine transferase PglH (EC 2.4.1.-)	GO:0000035|alpha-1,6-mannosyltransferase activity;GO:0000035|alpha-1,2-mannosyltransferase activity;GO:0000009|mannosyltransferase activity;GO:0000009|alpha-1,3-mannosyltransferase activity;GO:0000009|alpha-1,3-galactosyltransferase activity;GO:0000009|UDP-glucose:glycoprotein glucosyltransferase activity;GO:0000009|glycolipid mannosyltransferase activity;GO:0000009|oligosaccharyl transferase activity;GO:0000009|dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase activity;GO:0000009|acetylglucosaminyltransferase activity;GO:0000009|acetylgalactosaminyltransferase activity;GO:0000009|galactosyltransferase activity;GO:0000009|fucosyltransferase activity;GO:0000009|O antigen polymerase activity;GO:0000009|lipopolysaccharide-1,6-galactosyltransferase activity;GO:0000009|cellulose synthase activity;GO:0000009|9-phenanthrol UDP-glucuronosyltransferase activity;GO:0000009|1-phenanthrol glycosyltransferase activity;GO:0000009|9-phenanthrol glycosyltransferase activity;GO:0000009|1,2-dihydroxy-phenanthrene glycosyltransferase activity;GO:0000009|phenanthrol glycosyltransferase activity;GO:0000009|beta-1,4-mannosyltransferase activity;GO:0000009|alpha-1,2-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man7GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|lipopolysaccharide-1,5-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|inositol phosphoceramide synthase activity;GO:0000009|glucosyltransferase activity;GO:0000009|alpha-(1->3)-fucosyltransferase activity;GO:0000009|alpha-(1->6)-fucosyltransferase activity;GO:0000009|indole-3-butyrate beta-glucosyltransferase activity;GO:0000009|salicylic acid glucosyltransferase (ester-forming) activity;GO:0000009|salicylic acid glucosyltransferase (glucoside-forming) activity;GO:0000009|benzoic acid glucosyltransferase
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5369	PATRIC.2.9855.2.9855.con.0001.CDS.5754862.5756292.fwd	PATRIC	CDS	5754862	5756292	1431	+	PGF_01321948	476	putative polysaccharide biosynthesis protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5370	PATRIC.2.9855.2.9855.con.0001.CDS.5756333.5758294.fwd	PATRIC	CDS	5756333	5758294	1962	+	PGF_00003251	653	Macrolide export ATP-binding/permease protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.500	PATRIC.2.9855.2.9855.con.0001.CDS.575895.576290.rev	PATRIC	CDS	575895	576290	396	-	PGF_00025678	131	NimC/NimA family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5371	PATRIC.2.9855.2.9855.con.0001.CDS.5759323.5761104.fwd	PATRIC	CDS	5759323	5761104	1782	+	PGF_00417743	593	Choline binding protein PcpA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5372	PATRIC.2.9855.2.9855.con.0001.CDS.5761537.5762958.fwd	PATRIC	CDS	5761537	5762958	1422	+	PGF_00417743	473	Choline binding protein PcpA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5373	PATRIC.2.9855.2.9855.con.0001.CDS.5763281.5765515.fwd	PATRIC	CDS	5763281	5765515	2235	+	PGF_00417743	744	Choline binding protein PcpA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.501	PATRIC.2.9855.2.9855.con.0001.CDS.576418.576768.fwd	PATRIC	CDS	576418	576768	351	+	PGF_03320197	116	Transcriptional regulator, HxlR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5374	PATRIC.2.9855.2.9855.con.0001.CDS.5765785.5767092.fwd	PATRIC	CDS	5765785	5767092	1308	+	PGF_02910829	435	Membrane assosiated methyl-accepting chemotaxis protein with HAMP domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5375	PATRIC.2.9855.2.9855.con.0001.CDS.5767365.5769467.fwd	PATRIC	CDS	5767365	5769467	2103	+	PGF_00417736	700	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5376	PATRIC.2.9855.2.9855.con.0001.CDS.5769783.5773100.fwd	PATRIC	CDS	5769783	5773100	3318	+	PGF_00035759	1105	Predicted cell-wall-anchored protein SasA (LPXTG motif)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.502	PATRIC.2.9855.2.9855.con.0001.CDS.577114.577587.fwd	PATRIC	CDS	577114	577587	474	+	PGF_07488148	157	Mn-dependent transcriptional regulator MntR	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5377	PATRIC.2.9855.2.9855.con.0001.CDS.5773192.5774259.fwd	PATRIC	CDS	5773192	5774259	1068	+	PGF_00417736	355	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.56	PATRIC.2.9855.2.9855.con.0001.CDS.57737.58426.rev	PATRIC	CDS	57737	58426	690	-	PGF_01281740	229	Transcriptional regulator of succinyl CoA synthetase operon	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5378	PATRIC.2.9855.2.9855.con.0001.CDS.5774551.5775423.fwd	PATRIC	CDS	5774551	5775423	873	+	PGF_04776928	290	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	GO:0008889|glycerophosphodiester phosphodiesterase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5379	PATRIC.2.9855.2.9855.con.0001.CDS.5775697.5777646.rev	PATRIC	CDS	5775697	5777646	1950	-	PGF_00417736	649	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.503	PATRIC.2.9855.2.9855.con.0001.CDS.577788.579173.fwd	PATRIC	CDS	577788	579173	1386	+	PGF_00930759	461	L,D-transpeptidase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5380	PATRIC.2.9855.2.9855.con.0001.CDS.5777962.5779752.rev	PATRIC	CDS	5777962	5779752	1791	-	PGF_00417736	596	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5381	PATRIC.2.9855.2.9855.con.0001.CDS.5780283.5782166.rev	PATRIC	CDS	5780283	5782166	1884	-	PGF_00417736	627	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5382	PATRIC.2.9855.2.9855.con.0001.CDS.5782695.5784290.fwd	PATRIC	CDS	5782695	5784290	1596	+	PGF_00030643	531	Peptide chain release factor 3	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5385	PATRIC.2.9855.2.9855.con.0001.CDS.5786464.5788974.fwd	PATRIC	CDS	5786464	5788974	2511	+	PGF_00009437	836	Glycosyl transferase, group 1 family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5386	PATRIC.2.9855.2.9855.con.0001.CDS.5788971.5789933.fwd	PATRIC	CDS	5788971	5789933	963	+	PGF_01033123	320	UDP-glucose 4-epimerase (EC 5.1.3.2)	GO:0003978|UDP-glucose 4-epimerase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5387	PATRIC.2.9855.2.9855.con.0001.CDS.5789926.5791029.fwd	PATRIC	CDS	5789926	5791029	1104	+	PGF_01494614	367	DegT/DnrJ/EryC1/StrS aminotransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5389	PATRIC.2.9855.2.9855.con.0001.CDS.5792078.5792914.fwd	PATRIC	CDS	5792078	5792914	837	+	PGF_00063948	278	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.191)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.504	PATRIC.2.9855.2.9855.con.0001.CDS.579309.581042.fwd	PATRIC	CDS	579309	581042	1734	+	PGF_09700850	577	Amine oxidase, flavin-containing	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5390	PATRIC.2.9855.2.9855.con.0001.CDS.5793300.5794616.fwd	PATRIC	CDS	5793300	5794616	1317	+	PGF_07093307	438	UDP-N-acetyl-D-glucosamine 6-dehydrogenase (EC 1.1.1.136)	GO:0047004|UDP-N-acetylglucosamine 6-dehydrogenase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5391	PATRIC.2.9855.2.9855.con.0001.CDS.5794672.5796459.fwd	PATRIC	CDS	5794672	5796459	1788	+	PGF_00009518	595	Glycosyl transferase, group 2 family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5392	PATRIC.2.9855.2.9855.con.0001.CDS.5796913.5797389.rev	PATRIC	CDS	5796913	5797389	477	-	PGF_01309240	158	PTS system, glucose-specific IIA component (EC 2.7.1.199)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5393	PATRIC.2.9855.2.9855.con.0001.CDS.5797823.5799385.fwd	PATRIC	CDS	5797823	5799385	1563	+	PGF_03294256	520	PTS system, maltose-specific IIC component / PTS system, maltose-specific IIB component (EC 2.7.1.208)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5394	PATRIC.2.9855.2.9855.con.0001.CDS.5799905.5801239.fwd	PATRIC	CDS	5799905	5801239	1335	+	PGF_00019116	444	Maltose-6'-phosphate glucosidase (EC 3.2.1.122)	GO:0050081|maltose-6'-phosphate glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5395	PATRIC.2.9855.2.9855.con.0001.CDS.5801493.5802284.fwd	PATRIC	CDS	5801493	5802284	792	+	PGF_12862080	263	Transcriptional regulator, RpiR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5396	PATRIC.2.9855.2.9855.con.0001.CDS.5802262.5803008.fwd	PATRIC	CDS	5802262	5803008	747	+	PGF_12862080	248	Transcriptional regulator, RpiR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5397	PATRIC.2.9855.2.9855.con.0001.CDS.5803095.5804165.rev	PATRIC	CDS	5803095	5804165	1071	-	PGF_00006821	356	GGDEF domain protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5399	PATRIC.2.9855.2.9855.con.0001.CDS.5805003.5807273.fwd	PATRIC	CDS	5805003	5807273	2271	+	PGF_00417736	756	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5400	PATRIC.2.9855.2.9855.con.0001.CDS.5807739.5809724.fwd	PATRIC	CDS	5807739	5809724	1986	+	PGF_00417736	661	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5402	PATRIC.2.9855.2.9855.con.0001.CDS.5810847.5814005.fwd	PATRIC	CDS	5810847	5814005	3159	+	PGF_03510298	1052	Surface protein PspC	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.505	PATRIC.2.9855.2.9855.con.0001.CDS.581161.582552.fwd	PATRIC	CDS	581161	582552	1392	+	PGF_00930759	463	L,D-transpeptidase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5403	PATRIC.2.9855.2.9855.con.0001.CDS.5814459.5816309.fwd	PATRIC	CDS	5814459	5816309	1851	+	PGF_00417795	616	Choline-phosphate cytidylyltransferase (EC 2.7.7.15) / Choline kinase (EC 2.7.1.32)	GO:0004105|choline-phosphate cytidylyltransferase activity;GO:0004103|choline kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5404	PATRIC.2.9855.2.9855.con.0001.CDS.5816433.5817128.fwd	PATRIC	CDS	5816433	5817128	696	+	PGF_04703276	231	Choline-phosphate cytidylyltransferase (EC 2.7.7.15)	GO:0004105|choline-phosphate cytidylyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5406	PATRIC.2.9855.2.9855.con.0001.CDS.5817950.5818558.rev	PATRIC	CDS	5817950	5818558	609	-	PGF_07182652	202	Transcriptional regulator, AcrR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5407	PATRIC.2.9855.2.9855.con.0001.CDS.5819058.5820518.fwd	PATRIC	CDS	5819058	5820518	1461	+	PGF_02933248	486	Membrane protein involved in the export of O-antigen, teichoic acid lipoteichoic acids	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5408	PATRIC.2.9855.2.9855.con.0001.CDS.5820931.5822028.fwd	PATRIC	CDS	5820931	5822028	1098	+	PGF_01148540	365	Choline permease LicB	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5410	PATRIC.2.9855.2.9855.con.0001.CDS.5822713.5825115.fwd	PATRIC	CDS	5822713	5825115	2403	+	PGF_00050889	800	Sensory box sensor/GGDEF/EAL domain protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5411	PATRIC.2.9855.2.9855.con.0001.CDS.5825325.5827490.fwd	PATRIC	CDS	5825325	5827490	2166	+	PGF_12779560	721	Phage infection protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.506	PATRIC.2.9855.2.9855.con.0001.CDS.582699.583385.fwd	PATRIC	CDS	582699	583385	687	+	PGF_08127950	228	Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5412	PATRIC.2.9855.2.9855.con.0001.CDS.5827762.5830449.fwd	PATRIC	CDS	5827762	5830449	2688	+	PGF_00026324	895	NtrC family Transcriptional regulator, ATPase domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5413	PATRIC.2.9855.2.9855.con.0001.CDS.5830881.5831204.fwd	PATRIC	CDS	5830881	5831204	324	+	PGF_01629422	107	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5414	PATRIC.2.9855.2.9855.con.0001.CDS.5831282.5831590.fwd	PATRIC	CDS	5831282	5831590	309	+	PGF_05148511	102	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5415	PATRIC.2.9855.2.9855.con.0001.CDS.5831779.5833089.fwd	PATRIC	CDS	5831779	5833089	1311	+	PGF_00029610	436	PTS system, cellobiose-specific IIC component	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5416	PATRIC.2.9855.2.9855.con.0001.CDS.5833244.5834992.rev	PATRIC	CDS	5833244	5834992	1749	-	PGF_07849456	582	Methyl-accepting chemotaxis protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5417	PATRIC.2.9855.2.9855.con.0001.CDS.5835442.5836914.fwd	PATRIC	CDS	5835442	5836914	1473	+	PGF_00403859	490	predicted xylose isomerase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5418	PATRIC.2.9855.2.9855.con.0001.CDS.5837270.5838583.fwd	PATRIC	CDS	5837270	5838583	1314	+	PGF_00067052	437	Xylose ABC transporter, substrate-binding component	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5419	PATRIC.2.9855.2.9855.con.0001.CDS.5838850.5839725.fwd	PATRIC	CDS	5838850	5839725	876	+	PGF_02876233	291	ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5420	PATRIC.2.9855.2.9855.con.0001.CDS.5839756.5840598.fwd	PATRIC	CDS	5839756	5840598	843	+	PGF_10552060	280	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5421	PATRIC.2.9855.2.9855.con.0001.CDS.5840656.5842425.fwd	PATRIC	CDS	5840656	5842425	1770	+	PGF_00850716	589	Two-component sensor kinase YesM (EC 2.7.3.-)	GO:0000155|phosphorelay sensor kinase activity;GO:0000155|histone arginine kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5422	PATRIC.2.9855.2.9855.con.0001.CDS.5842425.5844020.fwd	PATRIC	CDS	5842425	5844020	1596	+	PGF_00062533	531	Two-component response regulator yesN	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5423	PATRIC.2.9855.2.9855.con.0001.CDS.5843983.5845308.fwd	PATRIC	CDS	5843983	5845308	1326	+	PGF_00026616	441	O-Glycosyl hydrolase family 30	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5424	PATRIC.2.9855.2.9855.con.0001.CDS.5845365.5847494.fwd	PATRIC	CDS	5845365	5847494	2130	+	PGF_00007805	709	Glucan 1,4-beta-glucosidase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5425	PATRIC.2.9855.2.9855.con.0001.CDS.5847567.5848352.rev	PATRIC	CDS	5847567	5848352	786	-	PGF_00660535	261	Lipase/Acylhydrolase with GDSL-like motif	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5426	PATRIC.2.9855.2.9855.con.0001.CDS.5848369.5849373.rev	PATRIC	CDS	5848369	5849373	1005	-	PGF_10522988	334	ABC transporter, permease protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5427	PATRIC.2.9855.2.9855.con.0001.CDS.5849387.5850301.rev	PATRIC	CDS	5849387	5850301	915	-	PGF_00884706	304	Efflux ABC transporter, ATP-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.508	PATRIC.2.9855.2.9855.con.0001.CDS.585046.586029.fwd	PATRIC	CDS	585046	586029	984	+	PGF_10509026	327	RND efflux system, membrane fusion protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5428	PATRIC.2.9855.2.9855.con.0001.CDS.5850874.5852235.fwd	PATRIC	CDS	5850874	5852235	1362	+	PGF_02163575	453	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5429	PATRIC.2.9855.2.9855.con.0001.CDS.5852376.5853833.fwd	PATRIC	CDS	5852376	5853833	1458	+	PGF_08148954	485	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5430	PATRIC.2.9855.2.9855.con.0001.CDS.5854158.5855063.fwd	PATRIC	CDS	5854158	5855063	906	+	PGF_02486076	301	Zinc ABC transporter, substrate-binding protein ZnuA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5431	PATRIC.2.9855.2.9855.con.0001.CDS.5855599.5857425.fwd	PATRIC	CDS	5855599	5857425	1827	+	PGF_00033596	608	Phosphoglycerol transferase MdoB related protein, alkaline phosphatase superfamily	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5432	PATRIC.2.9855.2.9855.con.0001.CDS.5857566.5858888.fwd	PATRIC	CDS	5857566	5858888	1323	+	PGF_00417736	440	Choline binding protein A	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.57	PATRIC.2.9855.2.9855.con.0001.CDS.58585.59955.fwd	PATRIC	CDS	58585	59955	1371	+	PGF_08148954	456	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5433	PATRIC.2.9855.2.9855.con.0001.CDS.5858955.5860436.fwd	PATRIC	CDS	5858955	5860436	1482	+	PGF_03495584	493	Glucan-binding domain / Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (EC 3.2.1.17)	GO:0003796|lysozyme activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.509	PATRIC.2.9855.2.9855.con.0001.CDS.586049.586702.fwd	PATRIC	CDS	586049	586702	654	+	PGF_06780452	217	Multidrug resistance protein [function not yet clear]	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5434	PATRIC.2.9855.2.9855.con.0001.CDS.5860615.5861556.fwd	PATRIC	CDS	5860615	5861556	942	+	PGF_00037043	313	Probable endo-1,4-beta-xylanase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5436	PATRIC.2.9855.2.9855.con.0001.CDS.5862624.5864228.rev	PATRIC	CDS	5862624	5864228	1605	-	PGF_03342342	534	Uncharacterized membrane protein, YraQ family	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5437	PATRIC.2.9855.2.9855.con.0001.CDS.5864648.5865523.rev	PATRIC	CDS	5864648	5865523	876	-	PGF_00058797	291	Transcriptional regulator of rhamnose utilization, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5438	PATRIC.2.9855.2.9855.con.0001.CDS.5865862.5866536.fwd	PATRIC	CDS	5865862	5866536	675	+	PGF_06916656	224	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5439	PATRIC.2.9855.2.9855.con.0001.CDS.5866715.5867776.fwd	PATRIC	CDS	5866715	5867776	1062	+	PGF_06985891	353	Mannonate dehydratase (EC 4.2.1.8)	GO:0008927|mannonate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.510	PATRIC.2.9855.2.9855.con.0001.CDS.586715.588307.fwd	PATRIC	CDS	586715	588307	1593	+	PGF_09996723	530	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5440	PATRIC.2.9855.2.9855.con.0001.CDS.5867896.5869509.fwd	PATRIC	CDS	5867896	5869509	1614	+	PGF_05151036	537	D-mannonate oxidoreductase (EC 1.1.1.57)	GO:0008866|fructuronate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5441	PATRIC.2.9855.2.9855.con.0001.CDS.5869880.5871283.fwd	PATRIC	CDS	5869880	5871283	1404	+	PGF_00066263	467	Uronate isomerase (EC 5.3.1.12)	GO:0008880|glucuronate isomerase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5442	PATRIC.2.9855.2.9855.con.0001.CDS.5871333.5872862.fwd	PATRIC	CDS	5871333	5872862	1530	+	PGF_00026896	509	Oligogalacturonide transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5443	PATRIC.2.9855.2.9855.con.0001.CDS.5873045.5875555.fwd	PATRIC	CDS	5873045	5875555	2511	+	PGF_00047556	836	Alpha-glucosidase (EC 3.2.1.20)	GO:0004558|alpha-1,4-glucosidase activity;GO:0004558|maltose alpha-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5444	PATRIC.2.9855.2.9855.con.0001.CDS.5875905.5876846.fwd	PATRIC	CDS	5875905	5876846	942	+	PGF_10512761	313	Lysophospholipase (EC 3.1.1.5); Monoglyceride lipase (EC 3.1.1.23)	GO:0004622|lysophospholipase activity;GO:0047372|acylglycerol lipase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5445	PATRIC.2.9855.2.9855.con.0001.CDS.5876944.5879433.fwd	PATRIC	CDS	5876944	5879433	2490	+	PGF_00047556	829	Alpha-glucosidase (EC 3.2.1.20)	GO:0004558|alpha-1,4-glucosidase activity;GO:0004558|maltose alpha-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5446	PATRIC.2.9855.2.9855.con.0001.CDS.5879756.5880616.fwd	PATRIC	CDS	5879756	5880616	861	+	PGF_03318195	286	Cof-like hydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5447	PATRIC.2.9855.2.9855.con.0001.CDS.5881062.5882348.fwd	PATRIC	CDS	5881062	5882348	1287	+	PGF_00401234	428	2-ketogluconate transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.511	PATRIC.2.9855.2.9855.con.0001.CDS.588273.588752.fwd	PATRIC	CDS	588273	588752	480	+	PGF_10438382	159	Transcriptional regulator, MarR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5448	PATRIC.2.9855.2.9855.con.0001.CDS.5882730.5883779.fwd	PATRIC	CDS	5882730	5883779	1050	+	PGF_00058573	349	Transcriptional regulator KdgR, KDG operon repressor	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5449	PATRIC.2.9855.2.9855.con.0001.CDS.5883792.5884565.fwd	PATRIC	CDS	5883792	5884565	774	+	PGF_00054834	257	Sugar phosphate isomerases/epimerases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5450	PATRIC.2.9855.2.9855.con.0001.CDS.5884558.5885523.fwd	PATRIC	CDS	5884558	5885523	966	+	PGF_05097244	321	2-dehydro-3-deoxygluconokinase (EC 2.7.1.45)	GO:0008673|2-dehydro-3-deoxygluconokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5451	PATRIC.2.9855.2.9855.con.0001.CDS.5885542.5886165.fwd	PATRIC	CDS	5885542	5886165	624	+	PGF_00420894	207	D-arabino-3-hexulose 6-phosphate formaldehyde-lyase (EC 4.1.2.43)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5452	PATRIC.2.9855.2.9855.con.0001.CDS.5886162.5886704.fwd	PATRIC	CDS	5886162	5886704	543	+	PGF_02897110	180	6-phospho-3-hexuloisomerase (EC 5.3.1.27)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5453	PATRIC.2.9855.2.9855.con.0001.CDS.5886744.5887391.fwd	PATRIC	CDS	5886744	5887391	648	+	PGF_00057399	215	Transaldolase (EC 2.2.1.2)	GO:0004801|sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5454	PATRIC.2.9855.2.9855.con.0001.CDS.5887868.5889859.fwd	PATRIC	CDS	5887868	5889859	1992	+	PGF_01136362	663	Transketolase (EC 2.2.1.1)	GO:0004802|transketolase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5455	PATRIC.2.9855.2.9855.con.0001.CDS.5890194.5891606.fwd	PATRIC	CDS	5890194	5891606	1413	+	PGF_08148954	470	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.512	PATRIC.2.9855.2.9855.con.0001.CDS.589165.590568.fwd	PATRIC	CDS	589165	590568	1404	+	PGF_00014114	467	Inner membrane permease YcaM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5456	PATRIC.2.9855.2.9855.con.0001.CDS.5891950.5892699.fwd	PATRIC	CDS	5891950	5892699	750	+	PGF_09655255	249	Transcriptional regulator, RpiR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5457	PATRIC.2.9855.2.9855.con.0001.CDS.5892756.5895443.rev	PATRIC	CDS	5892756	5895443	2688	-	PGF_00026324	895	NtrC family Transcriptional regulator, ATPase domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5458	PATRIC.2.9855.2.9855.con.0001.CDS.5896009.5896329.fwd	PATRIC	CDS	5896009	5896329	321	+	PGF_01629422	106	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5459	PATRIC.2.9855.2.9855.con.0001.CDS.5896483.5896794.fwd	PATRIC	CDS	5896483	5896794	312	+	PGF_05148511	103	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5460	PATRIC.2.9855.2.9855.con.0001.CDS.5897076.5898416.fwd	PATRIC	CDS	5897076	5898416	1341	+	PGF_00029610	446	PTS system, cellobiose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5462	PATRIC.2.9855.2.9855.con.0001.CDS.5899374.5899694.fwd	PATRIC	CDS	5899374	5899694	321	+	PGF_01629422	106	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5463	PATRIC.2.9855.2.9855.con.0001.CDS.5899775.5900083.fwd	PATRIC	CDS	5899775	5900083	309	+	PGF_05148511	102	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5464	PATRIC.2.9855.2.9855.con.0001.CDS.5900171.5901499.fwd	PATRIC	CDS	5900171	5901499	1329	+	PGF_00029610	442	PTS system, cellobiose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5465	PATRIC.2.9855.2.9855.con.0001.CDS.5901617.5903461.rev	PATRIC	CDS	5901617	5903461	1845	-	PGF_01283015	614	Choline-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5466	PATRIC.2.9855.2.9855.con.0001.CDS.5903777.5904745.rev	PATRIC	CDS	5903777	5904745	969	-	PGF_01281722	322	Polysaccharide biosynthesis glycosyl transferase CpsJ	GO:0008808|cardiolipin synthase activity;GO:0008808|UDP-N-acetylglucosamine:serine-protein N-acetylglucosamine-1-phosphotransferase activity;GO:0008808|GDP-mannose:serine-protein mannose-1-phosphotransferase activity;GO:0008808|archaetidylserine synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5467	PATRIC.2.9855.2.9855.con.0001.CDS.5904957.5905805.fwd	PATRIC	CDS	5904957	5905805	849	+	PGF_06489838	282	Lipopolysaccharide cholinephosphotransferase LicD1 (EC 2.7.8.-)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5468	PATRIC.2.9855.2.9855.con.0001.CDS.5906256.5907239.fwd	PATRIC	CDS	5906256	5907239	984	+	PGF_01308267	327	Beta-1,3-glucosyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5469	PATRIC.2.9855.2.9855.con.0001.CDS.5907294.5909156.fwd	PATRIC	CDS	5907294	5909156	1863	+	PGF_03556786	620	UDP-N-acetylglucosamine 4,6-dehydratase (EC 4.2.1.135)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5470	PATRIC.2.9855.2.9855.con.0001.CDS.5909159.5910664.fwd	PATRIC	CDS	5909159	5910664	1506	+	PGF_01290988	501	Teichuronic acid biosynthesis protein TuaE, putative secreted polysaccharide polymerase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5471	PATRIC.2.9855.2.9855.con.0001.CDS.5910819.5911883.rev	PATRIC	CDS	5910819	5911883	1065	-	PGF_01545194	354	UDP-2,3-diacetamido-2,3-dideoxy-D-glucuronic acid 2-epimerase (EC 5.1.3.23)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.513	PATRIC.2.9855.2.9855.con.0001.CDS.591125.591853.fwd	PATRIC	CDS	591125	591853	729	+	PGF_06916656	242	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5472	PATRIC.2.9855.2.9855.con.0001.CDS.5912422.5913678.fwd	PATRIC	CDS	5912422	5913678	1257	+	PGF_04305571	418	Glycosyltransferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5473	PATRIC.2.9855.2.9855.con.0001.CDS.5914241.5914969.fwd	PATRIC	CDS	5914241	5914969	729	+	PGF_00040366	242	Alkaline phosphatase synthesis transcriptional regulatory protein phoP	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5474	PATRIC.2.9855.2.9855.con.0001.CDS.5914996.5916390.fwd	PATRIC	CDS	5914996	5916390	1395	+	PGF_01323686	464	ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine kinase A, N-terminal	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5475	PATRIC.2.9855.2.9855.con.0001.CDS.5916620.5917654.fwd	PATRIC	CDS	5916620	5917654	1035	+	PGF_00417743	344	Choline binding protein PcpA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5477	PATRIC.2.9855.2.9855.con.0001.CDS.5919971.5921188.fwd	PATRIC	CDS	5919971	5921188	1218	+	PGF_00040983	405	Putative glycosyl transferase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.514	PATRIC.2.9855.2.9855.con.0001.CDS.592084.593799.fwd	PATRIC	CDS	592084	593799	1716	+	PGF_05070366	571	Dihydroxy-acid dehydratase (EC 4.2.1.9)	GO:0004160|dihydroxy-acid dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5478	PATRIC.2.9855.2.9855.con.0001.CDS.5921299.5921904.fwd	PATRIC	CDS	5921299	5921904	606	+	PGF_03207284	201	Lipid carrier : UDP-N-acetylgalactosaminyltransferase (EC 2.4.1.-)	mannosyltransferase activity;GO:0000009|mannosyltransferase activity;GO:0000009|alpha-1,3-mannosyltransferase activity;GO:0000009|alpha-1,3-galactosyltransferase activity;GO:0000009|UDP-glucose:glycoprotein glucosyltransferase activity;GO:0000009|glycolipid mannosyltransferase activity;GO:0000009|oligosaccharyl transferase activity;GO:0000009|dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase activity;GO:0000009|acetylglucosaminyltransferase activity;GO:0000009|acetylgalactosaminyltransferase activity;GO:0000009|galactosyltransferase activity;GO:0000009|fucosyltransferase activity;GO:0000009|O antigen polymerase activity;GO:0000009|lipopolysaccharide-1,6-galactosyltransferase activity;GO:0000009|cellulose synthase activity;GO:0000009|9-phenanthrol UDP-glucuronosyltransferase activity;GO:0000009|1-phenanthrol glycosyltransferase activity;GO:0000009|9-phenanthrol glycosyltransferase activity;GO:0000009|1,2-dihydroxy-phenanthrene glycosyltransferase activity;GO:0000009|phenanthrol glycosyltransferase activity;GO:0000009|beta-1,4-mannosyltransferase activity;GO:0000009|alpha-1,2-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man7GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|lipopolysaccharide-1,5-galactosyltransferase activity;GO:0000009|dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;GO:0000009|inositol phosphoceramide synthase activity;GO:0000009|glucosyltransferase activity;GO:0000009|alpha-(1->3)-fucosyltransferase activity;GO:0000009|alpha-(1->6)-fucosyltransferase activity;GO:0000009|indole-3-butyrate beta-glucosyltransferase activity;GO:0000009|salicylic acid glucosyltransferase (ester-forming) activity;GO:0000009|salicylic acid glucosyltransferase (glucoside-forming) activity;GO:0000009|benzoic acid glucosyltransferase
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5479	PATRIC.2.9855.2.9855.con.0001.CDS.5922145.5923233.fwd	PATRIC	CDS	5922145	5923233	1089	+	PGF_03031015	362	Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	GO:0050112|inositol 2-dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5480	PATRIC.2.9855.2.9855.con.0001.CDS.5923417.5924292.fwd	PATRIC	CDS	5923417	5924292	876	+	PGF_00064393	291	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	GO:0003983|UTP:glucose-1-phosphate uridylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5482	PATRIC.2.9855.2.9855.con.0001.CDS.5924925.5926007.fwd	PATRIC	CDS	5924925	5926007	1083	+	PGF_00006821	360	GGDEF domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5483	PATRIC.2.9855.2.9855.con.0001.CDS.5926214.5927362.fwd	PATRIC	CDS	5926214	5927362	1149	+	PGF_03124559	382	ATP-dependent DNA helicase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5484	PATRIC.2.9855.2.9855.con.0001.CDS.5927660.5928880.fwd	PATRIC	CDS	5927660	5928880	1221	+	PGF_00063916	406	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	GO:0004831|tyrosine-tRNA ligase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5485	PATRIC.2.9855.2.9855.con.0001.CDS.5929142.5929432.rev	PATRIC	CDS	5929142	5929432	291	-	PGF_01284186	96	Spore coat protein F	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5489	PATRIC.2.9855.2.9855.con.0001.CDS.5930432.5930659.fwd	PATRIC	CDS	5930432	5930659	228	+	PGF_02708531	75	Small, acid-soluble spore protein Tlp	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5491	PATRIC.2.9855.2.9855.con.0001.CDS.5931092.5932162.fwd	PATRIC	CDS	5931092	5932162	1071	+	PGF_04858171	356	Branched-chain acyl kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5493	PATRIC.2.9855.2.9855.con.0001.CDS.5934469.5934729.fwd	PATRIC	CDS	5934469	5934729	261	+	PGF_00960894	86	Uncharacterized homolog of the cytoplasmic domain of flagellar protein FhlB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5494	PATRIC.2.9855.2.9855.con.0001.CDS.5934757.5935446.fwd	PATRIC	CDS	5934757	5935446	690	+	PGF_00033658	229	Phosphohydrolase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5495	PATRIC.2.9855.2.9855.con.0001.CDS.5935628.5936506.fwd	PATRIC	CDS	5935628	5936506	879	+	PGF_00016470	292	LacX protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5496	PATRIC.2.9855.2.9855.con.0001.CDS.5936596.5937549.rev	PATRIC	CDS	5936596	5937549	954	-	PGF_07849456	317	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5498	PATRIC.2.9855.2.9855.con.0001.CDS.5938437.5939264.fwd	PATRIC	CDS	5938437	5939264	828	+	PGF_00007007	275	GTP pyrophosphokinase (EC 2.7.6.5)	GO:0008728|GTP diphosphokinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5500	PATRIC.2.9855.2.9855.con.0001.CDS.5940594.5941682.fwd	PATRIC	CDS	5940594	5941682	1089	+	PGF_00022687	362	MoxR-like ATPases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.515	PATRIC.2.9855.2.9855.con.0001.CDS.594204.594395.fwd	PATRIC	CDS	594204	594395	192	+	PGF_09580746	63	Uncharacterized protein CA_C2659	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5503	PATRIC.2.9855.2.9855.con.0001.CDS.5943950.5944279.rev	PATRIC	CDS	5943950	5944279	330	-	PGF_08058864	109	probable iron binding protein from the HesB_IscA_SufA family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5505	PATRIC.2.9855.2.9855.con.0001.CDS.5945391.5945912.fwd	PATRIC	CDS	5945391	5945912	522	+	PGF_00422918	173	Deoxycytidine triphosphate deaminase (EC 3.5.4.13)	GO:0008829|dCTP deaminase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5506	PATRIC.2.9855.2.9855.con.0001.CDS.5946435.5947379.fwd	PATRIC	CDS	5946435	5947379	945	+	PGF_00012987	314	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	GO:0004617|phosphoglycerate dehydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5509	PATRIC.2.9855.2.9855.con.0001.CDS.5948712.5949947.fwd	PATRIC	CDS	5948712	5949947	1236	+	PGF_00062925	411	Two-component system sensor histidine kinase DSY3867	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.517	PATRIC.2.9855.2.9855.con.0001.CDS.594886.595947.fwd	PATRIC	CDS	594886	595947	1062	+	PGF_00008548	353	Glycerol-1-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.261)	GO:0050492|glycerol-1-phosphate dehydrogenase [NAD(P)+] activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5510	PATRIC.2.9855.2.9855.con.0001.CDS.5950104.5950790.fwd	PATRIC	CDS	5950104	5950790	687	+	PGF_00062495	228	Two-component response regulator DSY3866	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5511	PATRIC.2.9855.2.9855.con.0001.CDS.5951008.5953458.rev	PATRIC	CDS	5951008	5953458	2451	-	PGF_06812369	816	Leucyl-tRNA synthetase (EC 6.1.1.4)	GO:0004823|leucine-tRNA ligase activity

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5512	PATRIC.2.9855.2.9855.con.0001.CDS.5954111.5955544.fwd	PATRIC	CDS	5954111	5955544	1434	+	PGF_10482116	477	Cardiolipin synthase, bacterial type ClsA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5513	PATRIC.2.9855.2.9855.con.0001.CDS.5955809.5956969.fwd	PATRIC	CDS	5955809	5956969	1161	+	PGF_00787618	386	Uncharacterized MFS-type transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5515	PATRIC.2.9855.2.9855.con.0001.CDS.5957531.5960500.fwd	PATRIC	CDS	5957531	5960500	2970	+	PGF_12943678	989	Lanthionine biosynthesis protein LanM	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5517	PATRIC.2.9855.2.9855.con.0001.CDS.5961273.5962019.fwd	PATRIC	CDS	5961273	5962019	747	+	PGF_00884706	248	Efflux ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5518	PATRIC.2.9855.2.9855.con.0001.CDS.5961988.5963565.fwd	PATRIC	CDS	5961988	5963565	1578	+	PGF_08234189	525	ABC transporter, permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5519	PATRIC.2.9855.2.9855.con.0001.CDS.5963577.5965199.fwd	PATRIC	CDS	5963577	5965199	1623	+	PGF_01297233	540	ABC-type multidrug/protein/lipid transport system, ATPase component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.519	PATRIC.2.9855.2.9855.con.0001.CDS.596543.596986.fwd	PATRIC	CDS	596543	596986	444	+	PGF_12823045	147	Acetyltransferase, GNAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5521	PATRIC.2.9855.2.9855.con.0001.CDS.5967132.5967857.rev	PATRIC	CDS	5967132	5967857	726	-	PGF_02034105	241	Response regulator FasA or ComE or BlpR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5522	PATRIC.2.9855.2.9855.con.0001.CDS.5967873.5969192.rev	PATRIC	CDS	5967873	5969192	1320	-	PGF_02007986	439	Accessory gene regulator protein C	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5523	PATRIC.2.9855.2.9855.con.0001.CDS.5969893.5970513.rev	PATRIC	CDS	5969893	5970513	621	-	PGF_01304759	206	Accessory gene regulator protein B (EC 3.4.-.-)	GO:0008234|cysteine-type peptidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5524	PATRIC.2.9855.2.9855.con.0001.CDS.5971552.5972565.fwd	PATRIC	CDS	5971552	5972565	1014	+	PGF_00070550	337	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	GO:0003849|3-deoxy-7-phosphoheptulonate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5525	PATRIC.2.9855.2.9855.con.0001.CDS.5972693.5973745.fwd	PATRIC	CDS	5972693	5973745	1053	+	PGF_00417658	350	3-dehydroquinate synthase (EC 4.2.3.4)	GO:0003856|3-dehydroquinate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5526	PATRIC.2.9855.2.9855.con.0001.CDS.5973832.5975139.fwd	PATRIC	CDS	5973832	5975139	1308	+	PGF_07844318	435	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	GO:0003866|3-phosphoshikimate 1-carboxyvinyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5527	PATRIC.2.9855.2.9855.con.0001.CDS.5975117.5976190.fwd	PATRIC	CDS	5975117	5976190	1074	+	PGF_00417840	357	Chorismate synthase (EC 4.2.3.5)	GO:0004107|chorismate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5528	PATRIC.2.9855.2.9855.con.0001.CDS.5976565.5977476.fwd	PATRIC	CDS	5976565	5977476	912	+	PGF_02877184	303	Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51)	GO:0004106|chorismate mutase activity;GO:0004664|prephenate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5529	PATRIC.2.9855.2.9855.con.0001.CDS.5977491.5978303.fwd	PATRIC	CDS	5977491	5978303	813	+	PGF_08181546	270	Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)	GO:0004764|shikimate 3-dehydrogenase (NADP+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5530	PATRIC.2.9855.2.9855.con.0001.CDS.5978313.5978573.fwd	PATRIC	CDS	5978313	5978573	261	+	PGF_02838109	86	Shikimate kinase I (EC 2.7.1.71)	GO:0004765|shikimate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5531	PATRIC.2.9855.2.9855.con.0001.CDS.5978540.5978686.fwd	PATRIC	CDS	5978540	5978686	147	+	PGF_02838109	48	Shikimate kinase I (EC 2.7.1.71)	GO:0004765|shikimate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5532	PATRIC.2.9855.2.9855.con.0001.CDS.5978688.5978813.fwd	PATRIC	CDS	5978688	5978813	126	+	PGF_02838109	41	Shikimate kinase I (EC 2.7.1.71)	GO:0004765|shikimate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5533	PATRIC.2.9855.2.9855.con.0001.CDS.5979061.5979501.fwd	PATRIC	CDS	5979061	5979501	441	+	PGF_00417577	146	3-dehydroquinate dehydratase II (EC 4.2.1.10)	GO:0003855|3-dehydroquinate dehydratase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5534	PATRIC.2.9855.2.9855.con.0001.CDS.5979653.5980666.fwd	PATRIC	CDS	5979653	5980666	1014	+	PGF_00070550	337	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	GO:0003849|3-deoxy-7-phosphoheptulonate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.521	PATRIC.2.9855.2.9855.con.0001.CDS.597992.599854.fwd	PATRIC	CDS	597992	599854	1863	+	PGF_00778630	620	Uncharacterized amino acid permease, GabP family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5535	PATRIC.2.9855.2.9855.con.0001.CDS.5980690.5981523.fwd	PATRIC	CDS	5980690	5981523	834	+	PGF_00036551	277	Prephenate and/or arogenate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43)	GO:0008977|prephenate dehydrogenase activity;GO:0047794|cyclohexadienyl dehydrogenase activity [illegible] regulator activity;GO:0008443|cobinamide kinase activity;GO:0008443|phytol kinase activity;GO:0008443|phosphatidylinositol phosphate kinase activity;GO:0008443|cyclin-dependent protein serine/threonine kinase regulator activity;GO:0008443|phenol kinase activity;GO:0008443|cyclin-dependent protein kinase activating kinase regulator activity;GO:0008443|inositol tetrakisphosphate 2-kinase activity;GO:0008443|heptose 7-phosphate kinase activity;GO:0008443|aminoglycoside phosphotransferase activity;GO:0008443|phosphatidylinositol 3-kinase activity;GO:0008443|eukaryotic elongation factor-2 kinase regulator activity;GO:0008443|eukaryotic elongation factor-2 kinase activator activity;GO:0008443|LPPG:FO 2-phospho-L-lactate transferase activity;GO:0008443|cytidine kinase activity;GO:0008443|glycerate 2-kinase activity;GO:0008443|(S)-lactate 2-kinase activity;GO:0008443|phosphoserine:homoserine phosphotransferase activity;GO:0008443|L-seryl-tRNA(Sec) kinase activity;GO:0008443|phosphocholine transferase activity;GO:0008443|polynucleotide 5'-hydroxyl-kinase activity;GO:0008443|ATP-dependent polynucleotide kinase activity;GO:0008443|GTP-dependent polynucleotide kinase activity;GO:0008443|farnesol kinase activity;GO:0008443|CTP:2-trans,-6-trans-farnesol kinase activity;GO:0008443|geraniol kinase activity;GO:0008443|geranylgeraniol kinase activity;GO:0008443|CTP:geranylgeraniol kinase activity;GO:0008443|prenol kinase activity;GO:0008443|1-phosphatidylinositol-5-kinase activity;GO:0008443|1-phosphatidylinositol-3-phosphate 4-kinase activity;GO:0008443|phosphatidylinositol-3,4-bisphosphate 5-kinase activity;GO:0008443|phosphatidylinositol bisphosphate kinase activity;GO:0008443|inositol-3,4,6-trisphosphate 1-kinase activity;GO:0008443|inositol 5-diphosphate pentakisphosphate 5-kinase activity;GO:0008443|inositol diphosphate tetrakisphosphate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5536	PATRIC.2.9855.2.9855.con.0001.CDS.5981737.5982081.fwd	PATRIC	CDS	5981737	5982081	345	+	PGF_00054802	114	Sugar kinase and transcription regulator (EC 2.7.1.-)	[illegible] regulator activity;GO:0008443|cobinamide kinase activity;GO:0008443|phytol kinase activity;GO:0008443|phosphatidylinositol phosphate kinase activity;GO:0008443|cyclin-dependent protein serine/threonine kinase regulator activity;GO:0008443|phenol kinase activity;GO:0008443|cyclin-dependent protein kinase activating kinase regulator activity;GO:0008443|inositol tetrakisphosphate 2-kinase activity;GO:0008443|heptose 7-phosphate kinase activity;GO:0008443|aminoglycoside phosphotransferase activity;GO:0008443|phosphatidylinositol 3-kinase activity;GO:0008443|eukaryotic elongation factor-2 kinase regulator activity;GO:0008443|eukaryotic elongation factor-2 kinase activator activity;GO:0008443|LPPG:FO 2-phospho-L-lactate transferase activity;GO:0008443|cytidine kinase activity;GO:0008443|glycerate 2-kinase activity;GO:0008443|(S)-lactate 2-kinase activity;GO:0008443|phosphoserine:homoserine phosphotransferase activity;GO:0008443|L-seryl-tRNA(Sec) kinase activity;GO:0008443|phosphocholine transferase activity;GO:0008443|polynucleotide 5'-hydroxyl-kinase activity;GO:0008443|ATP-dependent polynucleotide kinase activity;GO:0008443|GTP-dependent polynucleotide kinase activity;GO:0008443|farnesol kinase activity;GO:0008443|CTP:2-trans,-6-trans-farnesol kinase activity;GO:0008443|geraniol kinase activity;GO:0008443|geranylgeraniol kinase activity;GO:0008443|CTP:geranylgeraniol kinase activity;GO:0008443|prenol kinase activity;GO:0008443|1-phosphatidylinositol-5-kinase activity;GO:0008443|1-phosphatidylinositol-3-phosphate 4-kinase activity;GO:0008443|phosphatidylinositol-3,4-bisphosphate 5-kinase activity;GO:0008443|phosphatidylinositol bisphosphate kinase activity;GO:0008443|inositol-3,4,6-trisphosphate 1-kinase activity;GO:0008443|inositol 5-diphosphate pentakisphosphate 5-kinase activity;GO:0008443|inositol diphosphate tetrakisphosphate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5537	PATRIC.2.9855.2.9855.con.0001.CDS.5982050.5982451.fwd	PATRIC	CDS	5982050	5982451	402	+	PGF_00054802	133	Sugar kinase and transcription regulator (EC 2.7.1.-)	

															regulator activity;GO:0008443|cobinamide kinase activity;GO:0008443|phytol kinase activity;GO:0008443|phosphatidylinositol phosphate kinase activity;GO:0008443|cyclin-dependent protein serine/threonine kinase regulator activity;GO:0008443|phenol kinase activity;GO:0008443|cyclin-dependent protein kinase activating kinase regulator activity;GO:0008443|inositol tetrakisphosphate 2-kinase activity;GO:0008443|heptose 7-phosphate kinase activity;GO:0008443|aminoglycoside phosphotransferase activity;GO:0008443|phosphatidylinositol 3-kinase activity;GO:0008443|eukaryotic elongation factor-2 kinase regulator activity;GO:0008443|eukaryotic elongation factor-2 kinase activator activity;GO:0008443|LPPG:FO 2-phospho-L-lactate transferase activity;GO:0008443|cytidine kinase activity;GO:0008443|glycerate 2-kinase activity;GO:0008443|(S)-lactate 2-kinase activity;GO:0008443|phosphoserine:homoserine phosphotransferase activity;GO:0008443|L-seryl-tRNA(Sec) kinase activity;GO:0008443|phosphocholine transferase activity;GO:0008443|polynucleotide 5'-hydroxyl-kinase activity;GO:0008443|ATP-dependent polynucleotide kinase activity;GO:0008443|GTP-dependent polynucleotide kinase activity;GO:0008443|farnesol kinase activity;GO:0008443|CTP:2-trans,-6-trans-farnesol kinase activity;GO:0008443|geraniol kinase activity;GO:0008443|geranylgeraniol kinase activity;GO:0008443|CTP:geranylgeraniol kinase activity;GO:0008443|prenol kinase activity;GO:0008443|1-phosphatidylinositol-5-kinase activity;GO:0008443|1-phosphatidylinositol-3-phosphate 4-kinase activity;GO:0008443|phosphatidylinositol-3,4-bisphosphate 5-kinase activity;GO:0008443|phosphatidylinositol bisphosphate kinase activity;GO:0008443|inositol-3,4,6-trisphosphate 1-kinase activity;GO:0008443|inositol 5-diphosphate pentakisphosphate 5-kinase activity;GO:0008443|inositol diphosphate tetrakisphosphate kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5538	PATRIC.2.9855.2.9855.con.0001.CDS.5982457.5982639.fwd	PATRIC	CDS	5982457	5982639	183	+	PGF_00054802	60	Sugar kinase and transcription regulator (EC 2.7.1.-)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5539	PATRIC.2.9855.2.9855.con.0001.CDS.5982723.5982839.fwd	PATRIC	CDS	5982723	5982839	117	+	PGF_08148954	38	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5540	PATRIC.2.9855.2.9855.con.0001.CDS.5983067.5983855.fwd	PATRIC	CDS	5983067	5983855	789	+	PGF_08148954	262	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5541	PATRIC.2.9855.2.9855.con.0001.CDS.5983825.5983995.fwd	PATRIC	CDS	5983825	5983995	171	+	PGF_08148954	56	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5542	PATRIC.2.9855.2.9855.con.0001.CDS.5983952.5984092.fwd	PATRIC	CDS	5983952	5984092	141	+	PGF_08148954	46	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5543	PATRIC.2.9855.2.9855.con.0001.CDS.5984210.5984362.fwd	PATRIC	CDS	5984210	5984362	153	+	PGF_00827664	50	Transcriptional regulator	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.522	PATRIC.2.9855.2.9855.con.0001.CDS.599934.601109.rev	PATRIC	CDS	599934	601109	1176	-	PGF_07870324	391	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.523	PATRIC.2.9855.2.9855.con.0001.CDS.601191.602870.rev	PATRIC	CDS	601191	602870	1680	-	PGF_07849456	559	Methyl-accepting chemotaxis protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.58	PATRIC.2.9855.2.9855.con.0001.CDS.60178.60804.rev	PATRIC	CDS	60178	60804	627	-	PGF_00023289	208	Multimeric flavodoxin WrbA family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.524	PATRIC.2.9855.2.9855.con.0001.CDS.603217.603888.fwd	PATRIC	CDS	603217	603888	672	+	PGF_06916656	223	Transcriptional regulator, GntR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.525	PATRIC.2.9855.2.9855.con.0001.CDS.604079.605140.fwd	PATRIC	CDS	604079	605140	1062	+	PGF_06985891	353	Mannonate dehydratase (EC 4.2.1.8)	GO:0008927|mannonate dehydratase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.526	PATRIC.2.9855.2.9855.con.0001.CDS.605254.606867.fwd	PATRIC	CDS	605254	606867	1614	+	PGF_05151036	537	D-mannonate oxidoreductase (EC 1.1.1.57)	GO:0008866|fructuronate reductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.527	PATRIC.2.9855.2.9855.con.0001.CDS.607280.608692.fwd	PATRIC	CDS	607280	608692	1413	+	PGF_00066263	470	Uronate isomerase (EC 5.3.1.12)	GO:0008880|glucuronate isomerase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.528	PATRIC.2.9855.2.9855.con.0001.CDS.608731.610236.fwd	PATRIC	CDS	608731	610236	1506	+	PGF_00026896	501	Oligogalacturonide transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.59	PATRIC.2.9855.2.9855.con.0001.CDS.60893.61423.rev	PATRIC	CDS	60893	61423	531	-	PGF_10153092	176	Nitroreductase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.529	PATRIC.2.9855.2.9855.con.0001.CDS.610521.610943.fwd	PATRIC	CDS	610521	610943	423	+	PGF_04001818	140	HIT family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.530	PATRIC.2.9855.2.9855.con.0001.CDS.611831.612388.fwd	PATRIC	CDS	611831	612388	558	+	PGF_08585032	185	Ribosomal RNA adenine dimethylase domain protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.531	PATRIC.2.9855.2.9855.con.0001.CDS.612963.614426.fwd	PATRIC	CDS	612963	614426	1464	+	PGF_01283127	487	Two-component system sensor histidine kinase/response regulator hybrid	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.532	PATRIC.2.9855.2.9855.con.0001.CDS.614509.616206.fwd	PATRIC	CDS	614509	616206	1698	+	PGF_07849456	565	Methyl-accepting chemotaxis protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.60	PATRIC.2.9855.2.9855.con.0001.CDS.61527.62627.rev	PATRIC	CDS	61527	62627	1101	-	PGF_07939795	366	Nuclease subunit of the excinuclease complex	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.533	PATRIC.2.9855.2.9855.con.0001.CDS.616372.617289.fwd	PATRIC	CDS	616372	617289	918	+	PGF_02382389	305	Ribokinase (EC 2.7.1.15)	GO:0004747|ribokinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.536	PATRIC.2.9855.2.9855.con.0001.CDS.619297.620067.fwd	PATRIC	CDS	619297	620067	771	+	PGF_00038766	256	Protein, containing LuxR family transcriptional regulator HTH domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.537	PATRIC.2.9855.2.9855.con.0001.CDS.620158.621108.fwd	PATRIC	CDS	620158	621108	951	+	PGF_03941737	316	L-lactate dehydrogenase (EC 1.1.1.27)	GO:0004459|L-lactate dehydrogenase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.538	PATRIC.2.9855.2.9855.con.0001.CDS.621312.621881.rev	PATRIC	CDS	621312	621881	570	-	PGF_00042029	189	Putative membrane-spanning protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.539	PATRIC.2.9855.2.9855.con.0001.CDS.622162.623460.rev	PATRIC	CDS	622162	623460	1299	-	PGF_00905234	432	Manganese transport protein MntH	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.540	PATRIC.2.9855.2.9855.con.0001.CDS.623681.624151.fwd	PATRIC	CDS	623681	624151	471	+	PGF_07488148	156	Mn-dependent transcriptional regulator MntR	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.541	PATRIC.2.9855.2.9855.con.0001.CDS.624526.625281.fwd	PATRIC	CDS	624526	625281	756	+	PGF_00010707	251	HTH DNA-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.542	PATRIC.2.9855.2.9855.con.0001.CDS.626021.627361.fwd	PATRIC	CDS	626021	627361	1341	+	PGF_00066964	446	Xanthine/uracil/thiamine/ascorbate permease family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.543	PATRIC.2.9855.2.9855.con.0001.CDS.627539.628162.rev	PATRIC	CDS	627539	628162	624	-	PGF_01667671	207	Cytidylate kinase (EC 2.7.4.25)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.545	PATRIC.2.9855.2.9855.con.0001.CDS.628919.629299.fwd	PATRIC	CDS	628919	629299	381	+	PGF_00304652	126	Ethanolamine utilization protein similar to PduU	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.546	PATRIC.2.9855.2.9855.con.0001.CDS.629308.629760.fwd	PATRIC	CDS	629308	629760	453	+	PGF_00122822	150	Propanediol utilization protein PduV	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.61	PATRIC.2.9855.2.9855.con.0001.CDS.62970.63890.rev	PATRIC	CDS	62970	63890	921	-	PGF_02346669	306	Ornithine carbamoyltransferase (EC 2.1.3.3)	GO:0004585|ornithine carbamoyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.547	PATRIC.2.9855.2.9855.con.0001.CDS.629834.630409.fwd	PATRIC	CDS	629834	630409	576	+	PGF_00723627	191	Intracellular protease	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.548	PATRIC.2.9855.2.9855.con.0001.CDS.630524.633058.fwd	PATRIC	CDS	630524	633058	2535	+	PGF_06513690	844	Pyruvate formate-lyase (EC 2.3.1.54)	GO:0008861|formate C-acetyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.549	PATRIC.2.9855.2.9855.con.0001.CDS.633153.634070.fwd	PATRIC	CDS	633153	634070	918	+	PGF_08333365	305	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	GO:0043365|[formate-C-acetyltransferase]-activating enzyme activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.550	PATRIC.2.9855.2.9855.con.0001.CDS.634100.634897.fwd	PATRIC	CDS	634100	634897	798	+	PGF_00037637	265	Propanediol utilization polyhedral body protein PduB	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.551	PATRIC.2.9855.2.9855.con.0001.CDS.635058.635336.fwd	PATRIC	CDS	635058	635336	279	+	PGF_00037636	92	Propanediol utilization polyhedral body protein PduA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.553	PATRIC.2.9855.2.9855.con.0001.CDS.636311.636934.fwd	PATRIC	CDS	636311	636934	624	+	PGF_02930502	207	Propanediol utilization polyhedral body protein PduK	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.554	PATRIC.2.9855.2.9855.con.0001.CDS.636980.637237.fwd	PATRIC	CDS	636980	637237	258	+	PGF_00037661	85	Propanediol utilization polyhedral body protein PduN	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.555	PATRIC.2.9855.2.9855.con.0001.CDS.637275.638624.fwd	PATRIC	CDS	637275	638624	1350	+	PGF_00418181	449	CoA-acylating propionaldehyde dehydrogenase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.556	PATRIC.2.9855.2.9855.con.0001.CDS.638641.639756.fwd	PATRIC	CDS	638641	639756	1116	+	PGF_00041783	371	Propanol dehydrogenase [NAD+]	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.557	PATRIC.2.9855.2.9855.con.0001.CDS.639825.641138.fwd	PATRIC	CDS	639825	641138	1314	+	PGF_12713759	437	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.62	PATRIC.2.9855.2.9855.con.0001.CDS.63986.65167.rev	PATRIC	CDS	63986	65167	1182	-	PGF_00027514	393	N-acetylornithine aminotransferase (EC 2.6.1.11)	GO:0003992|N2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.558	PATRIC.2.9855.2.9855.con.0001.CDS.641141.642151.fwd	PATRIC	CDS	641141	642151	1011	+	PGF_10378356	336	Transcriptional regulator, AraC family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.559	PATRIC.2.9855.2.9855.con.0001.CDS.642181.643380.fwd	PATRIC	CDS	642181	643380	1200	+	PGF_03202156	399	S-adenosylmethionine synthetase (EC 2.5.1.6)	GO:0004478|methionine adenosyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.560	PATRIC.2.9855.2.9855.con.0001.CDS.643401.644270.fwd	PATRIC	CDS	643401	644270	870	+	PGF_00415241	289	COG0531: Amino acid transporters	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.561	PATRIC.2.9855.2.9855.con.0001.CDS.644304.644582.fwd	PATRIC	CDS	644304	644582	279	+	PGF_00037636	92	Propanediol utilization polyhedral body protein PduA	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.562	PATRIC.2.9855.2.9855.con.0001.CDS.644619.645257.fwd	PATRIC	CDS	644619	645257	639	+	PGF_03374020	212	Ethanolamine utilization protein similar to PduL	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.563	PATRIC.2.9855.2.9855.con.0001.CDS.645297.646115.fwd	PATRIC	CDS	645297	646115	819	+	PGF_06927367	272	Ethanolamine utilization protein EutJ	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.564	PATRIC.2.9855.2.9855.con.0001.CDS.646141.647559.fwd	PATRIC	CDS	646141	647559	1419	+	PGF_00418181	472	CoA-acylating propionaldehyde dehydrogenase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.565	PATRIC.2.9855.2.9855.con.0001.CDS.647778.649103.fwd	PATRIC	CDS	647778	649103	1326	+	PGF_00418250	441	Cob(III)alamin reductase @ Cob(II)alamin reductase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.566	PATRIC.2.9855.2.9855.con.0001.CDS.649123.649692.fwd	PATRIC	CDS	649123	649692	570	+	PGF_00037663	189	Propanediol utilization polyhedral body protein PduT	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.567	PATRIC.2.9855.2.9855.con.0001.CDS.650677.652362.fwd	PATRIC	CDS	650677	652362	1686	+	PGF_00410279	561	2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase, gamma subunit (EC 1.2.7.-) / 2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.-)	GO:0043873|pyruvate-flavodoxin oxidoreductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.568	PATRIC.2.9855.2.9855.con.0001.CDS.652362.653213.fwd	PATRIC	CDS	652362	653213	852	+	PGF_03977347	283	2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase, beta subunit (EC 1.2.7.-)	GO:0043873|pyruvate-flavodoxin oxidoreductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.63	PATRIC.2.9855.2.9855.con.0001.CDS.65282.66136.rev	PATRIC	CDS	65282	66136	855	-	PGF_00026615	284	N-acetylglutamate kinase (EC 2.7.2.8)	GO:0003991|acetylglutamate kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.569	PATRIC.2.9855.2.9855.con.0001.CDS.653516.654742.fwd	PATRIC	CDS	653516	654742	1227	+	PGF_00053966	408	Aminopeptidase S (Leu, Val, Phe, Tyr preference) (EC 3.4.11.24)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.573	PATRIC.2.9855.2.9855.con.0001.CDS.657169.657906.fwd	PATRIC	CDS	657169	657906	738	+	PGF_01677570	245	Cellobiose phosphotransferase system YdjC-like protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.574	PATRIC.2.9855.2.9855.con.0001.CDS.658325.659638.fwd	PATRIC	CDS	658325	659638	1314	+	PGF_02163575	437	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.575	PATRIC.2.9855.2.9855.con.0001.CDS.659685.661037.rev	PATRIC	CDS	659685	661037	1353	-	PGF_09985786	450	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	GO:0004069|L-aspartate:2-oxoglutarate aminotransferase activity;GO:0004069|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.64	PATRIC.2.9855.2.9855.con.0001.CDS.66236.67480.rev	PATRIC	CDS	66236	67480	1245	-	PGF_00008075	414	Glutamate N-acetyltransferase (EC 2.3.1.35) @ N-acetylglutamate synthase (EC 2.3.1.1)	GO:0004358|glutamate N-acetyltransferase activity;GO:0004042|acetyl-CoA:L-glutamate N-acetyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.579	PATRIC.2.9855.2.9855.con.0001.CDS.663638.664624.fwd	PATRIC	CDS	663638	664624	987	+	PGF_00421061	328	3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.180)	GO:0033818|beta-ketoacyl-acyl-carrier-protein synthase III activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.580	PATRIC.2.9855.2.9855.con.0001.CDS.664872.665738.fwd	PATRIC	CDS	664872	665738	867	+	PGF_05366249	288	Radical SAM domain protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.583	PATRIC.2.9855.2.9855.con.0001.CDS.666290.667750.fwd	PATRIC	CDS	666290	667750	1461	+	PGF_12920079	486	dolichyl-phosphate-mannose-protein mannosyltransferase family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.585	PATRIC.2.9855.2.9855.con.0001.CDS.667861.669216.fwd	PATRIC	CDS	667861	669216	1356	+	PGF_00051368	451	Serine/threonine exchanger SteT	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.586	PATRIC.2.9855.2.9855.con.0001.CDS.669311.670285.rev	PATRIC	CDS	669311	670285	975	-	PGF_00029894	324	Activator of 2-hydroxyglutaryl-CoA dehydratase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.587	PATRIC.2.9855.2.9855.con.0001.CDS.670273.671364.rev	PATRIC	CDS	670273	671364	1092	-	PGF_01333294	363	Activator of (R)-2-hydroxyglutaryl-CoA dehydratase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.588	PATRIC.2.9855.2.9855.con.0001.CDS.671369.672256.rev	PATRIC	CDS	671369	672256	888	-	PGF_01333294	295	Activator of (R)-2-hydroxyglutaryl-CoA dehydratase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.589	PATRIC.2.9855.2.9855.con.0001.CDS.672572.673525.fwd	PATRIC	CDS	672572	673525	954	+	PGF_07201805	317	Permease of the drug/metabolite transporter (DMT) superfamily	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.590	PATRIC.2.9855.2.9855.con.0001.CDS.673640.674395.fwd	PATRIC	CDS	673640	674395	756	+	PGF_05143949	251	N-acetylmuramoyl-L-alanine amidase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.591	PATRIC.2.9855.2.9855.con.0001.CDS.674547.676811.rev	PATRIC	CDS	674547	676811	2265	-	PGF_00069013	754	beta-glucosidase (EC 3.2.1.21)	GO:0008422|beta-glucosidase activity

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.65	PATRIC.2.9855.2.9855.con.0001.CDS.67557.68591.rev	PATRIC	CDS	67557	68591	1035	-	PGF_07889681	344	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)	GO:0003942|N-acetyl-gamma-glutamyl-phosphate reductase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.592	PATRIC.2.9855.2.9855.con.0001.CDS.677000.677785.fwd	PATRIC	CDS	677000	677785	786	+	PGF_00010468	261	Hydrolase (HAD superfamily) in cluster with DUF1447	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.593	PATRIC.2.9855.2.9855.con.0001.CDS.678358.678711.fwd	PATRIC	CDS	678358	678711	354	+	PGF_10238627	117	Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.594	PATRIC.2.9855.2.9855.con.0001.CDS.678736.680799.fwd	PATRIC	CDS	678736	680799	2064	+	PGF_08121553	687	Signal transduction histidine kinase CheA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.595	PATRIC.2.9855.2.9855.con.0001.CDS.680823.681326.fwd	PATRIC	CDS	680823	681326	504	+	PGF_07311230	167	Positive regulator of CheA protein activity (CheW)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.14	PATRIC.2.9855.2.9855.con.0001.CDS.6812.7588.fwd	PATRIC	CDS	6812	7588	777	+	PGF_00054802	258	Sugar kinase and transcription regulator (EC 2.7.1.-)	[illegible] regulator activity;GO:0008443|cobinamide kinase activity;GO:0008443|phytol kinase activity;GO:0008443|phosphatidylinositol phosphate kinase activity;GO:0008443|cyclin-dependent protein serine/threonine kinase regulator activity;GO:0008443|phenol kinase activity;GO:0008443|cyclin-dependent protein kinase activating kinase regulator activity;GO:0008443|inositol tetrakisphosphate 2-kinase activity;GO:0008443|heptose 7-phosphate kinase activity;GO:0008443|aminoglycoside phosphotransferase activity;GO:0008443|phosphatidylinositol 3-kinase activity;GO:0008443|eukaryotic elongation factor-2 kinase regulator activity;GO:0008443|eukaryotic elongation factor-2 kinase activator activity;GO:0008443|LPPG:FO 2-phospho-L-lactate transferase activity;GO:0008443|cytidine kinase activity;GO:0008443|glycerate 2-kinase activity;GO:0008443|(S)-lactate 2-kinase activity;GO:0008443|phosphoserine:homoserine phosphotransferase activity;GO:0008443|L-seryl-tRNA(Sec) kinase activity;GO:0008443|phosphocholine transferase activity;GO:0008443|polynucleotide 5'-hydroxyl-kinase activity;GO:0008443|ATP-dependent polynucleotide kinase activity;GO:0008443|GTP-dependent polynucleotide kinase activity;GO:0008443|farnesol kinase activity;GO:0008443|CTP:2-trans,-6-trans-farnesol kinase activity;GO:0008443|geraniol kinase activity;GO:0008443|geranylgeraniol kinase activity;GO:0008443|CTP:geranylgeraniol kinase activity;GO:0008443|prenol kinase activity;GO:0008443|1-phosphatidylinositol-5-kinase activity;GO:0008443|1-phosphatidylinositol-3-phosphate 4-kinase activity;GO:0008443|phosphatidylinositol-3,4-bisphosphate 5-kinase activity;GO:0008443|phosphatidylinositol bisphosphate kinase activity;GO:0008443|inositol-3,4,6-trisphosphate 1-kinase activity;GO:0008443|inositol 5-diphosphate pentakisphosphate 5-kinase activity;GO:0008443|inositol diphosphate tetrakisphosphate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.596	PATRIC.2.9855.2.9855.con.0001.CDS.681405.684299.fwd	PATRIC	CDS	681405	684299	2895	+	PGF_07849456	964	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.597	PATRIC.2.9855.2.9855.con.0001.CDS.684460.685989.fwd	PATRIC	CDS	684460	685989	1530	+	PGF_10416542	509	Sensory box histidine kinase/response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.598	PATRIC.2.9855.2.9855.con.0001.CDS.686025.686426.fwd	PATRIC	CDS	686025	686426	402	+	PGF_03682232	133	Response regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.599	PATRIC.2.9855.2.9855.con.0001.CDS.686721.688061.fwd	PATRIC	CDS	686721	688061	1341	+	PGF_10388619	446	NADH peroxidase Npx (EC 1.11.1.1)	GO:0016692|NADH peroxidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.600	PATRIC.2.9855.2.9855.con.0001.CDS.688144.689661.rev	PATRIC	CDS	688144	689661	1518	-	PGF_09985786	505	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	GO:0004069|L-aspartate:2-oxoglutarate aminotransferase activity;GO:0004069|L-phenylalanine:2-oxoglutarate aminotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.66	PATRIC.2.9855.2.9855.con.0001.CDS.68917.70302.rev	PATRIC	CDS	68917	70302	1386	-	PGF_02620298	461	Argininosuccinate lyase (EC 4.3.2.1)	GO:0004056|argininosuccinate lyase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.601	PATRIC.2.9855.2.9855.con.0001.CDS.690021.691820.fwd	PATRIC	CDS	690021	691820	1800	+	PGF_07849456	599	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.603	PATRIC.2.9855.2.9855.con.0001.CDS.692438.692890.fwd	PATRIC	CDS	692438	692890	453	+	PGF_03518291	150	Transcriptional regulator LrpC, AsnC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.604	PATRIC.2.9855.2.9855.con.0001.CDS.692959.693774.fwd	PATRIC	CDS	692959	693774	816	+	PGF_01330610	271	Membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.605	PATRIC.2.9855.2.9855.con.0001.CDS.694117.695289.fwd	PATRIC	CDS	694117	695289	1173	+	PGF_06447349	390	NADP-dependent malic enzyme (EC 1.1.1.40)	GO:0004473|malate dehydrogenase (decarboxylating) (NADP+) activity;GO:0004473|oxaloacetate decarboxylase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.606	PATRIC.2.9855.2.9855.con.0001.CDS.695492.696466.fwd	PATRIC	CDS	695492	696466	975	+	PGF_00071934	324	2-keto-3-deoxygluconate permease (KDG permease)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.607	PATRIC.2.9855.2.9855.con.0001.CDS.696649.697719.fwd	PATRIC	CDS	696649	697719	1071	+	PGF_04858171	356	Branched-chain acyl kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.608	PATRIC.2.9855.2.9855.con.0001.CDS.697984.699558.fwd	PATRIC	CDS	697984	699558	1575	+	PGF_03694968	524	Two-component sensor histidine kinase, malate (EC 2.7.3.-)	GO:0000155|phosphorelay sensor kinase activity;GO:0000155|histone arginine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.609	PATRIC.2.9855.2.9855.con.0001.CDS.699563.700258.fwd	PATRIC	CDS	699563	700258	696	+	PGF_00062557	231	Two-component response regulator, malate (EC 2.7.3.-)	GO:0000155|phosphorelay sensor kinase activity;GO:0000155|histone arginine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.610	PATRIC.2.9855.2.9855.con.0001.CDS.700351.701118.rev	PATRIC	CDS	700351	701118	768	-	PGF_00036787	255	Probable DNA polymerase III epsilon chain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.611	PATRIC.2.9855.2.9855.con.0001.CDS.701259.701837.rev	PATRIC	CDS	701259	701837	579	-	PGF_00285620	192	ATP-dependent Clp protease proteolytic subunit ClpP (EC 3.4.21.92)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.612	PATRIC.2.9855.2.9855.con.0001.CDS.701874.702257.rev	PATRIC	CDS	701874	702257	384	-	PGF_01671660	127	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.613	PATRIC.2.9855.2.9855.con.0001.CDS.702499.704079.fwd	PATRIC	CDS	702499	704079	1581	+	PGF_02316562	526	Periplasmic [FeFe] hydrogenase large subunit (EC 1.12.7.2)	GO:0008901|ferredoxin hydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.67	PATRIC.2.9855.2.9855.con.0001.CDS.70302.71525.rev	PATRIC	CDS	70302	71525	1224	-	PGF_02862285	407	Argininosuccinate synthase (EC 6.3.4.5)	GO:0004055|argininosuccinate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.614	PATRIC.2.9855.2.9855.con.0001.CDS.704548.705336.fwd	PATRIC	CDS	704548	705336	789	+	PGF_06180612	262	Uncharacterized SAM-binding protein YdcF	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.615	PATRIC.2.9855.2.9855.con.0001.CDS.705389.706249.fwd	PATRIC	CDS	705389	706249	861	+	PGF_07026465	286	23S rRNA (guanine(745)-N(1))-methyltransferase (EC 2.1.1.187)	GO:0052911|23S rRNA (guanine(745)-N(1))-methyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.616	PATRIC.2.9855.2.9855.con.0001.CDS.706479.707294.fwd	PATRIC	CDS	706479	707294	816	+	PGF_00067362	271	AB hydrolase superfamily protein YisY	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.617	PATRIC.2.9855.2.9855.con.0001.CDS.707576.708118.fwd	PATRIC	CDS	707576	708118	543	+	PGF_05785543	180	Signal peptidase I (EC 3.4.21.89)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.620	PATRIC.2.9855.2.9855.con.0001.CDS.709483.710529.rev	PATRIC	CDS	709483	710529	1047	-	PGF_05728830	348	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.623	PATRIC.2.9855.2.9855.con.0001.CDS.711421.712713.fwd	PATRIC	CDS	711421	712713	1293	+	PGF_02818638	430	Hemolysins and related proteins containing CBS domains	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.625	PATRIC.2.9855.2.9855.con.0001.CDS.714003.714896.rev	PATRIC	CDS	714003	714896	894	-	PGF_10554973	297	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.626	PATRIC.2.9855.2.9855.con.0001.CDS.715200.716435.fwd	PATRIC	CDS	715200	716435	1236	+	PGF_06652053	411	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	GO:0033817|beta-ketoacyl-acyl-carrier-protein synthase II activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.627	PATRIC.2.9855.2.9855.con.0001.CDS.716822.717625.rev	PATRIC	CDS	716822	717625	804	-	PGF_02679108	267	CAAX amino terminal protease family protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4	PATRIC.2.9855.2.9855.con.0001.CDS.718.1125.fwd	PATRIC	CDS	718	1125	408	+	PGF_00417840	135	Chorismate synthase (EC 4.2.3.5)	GO:0004107|chorismate synthase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.630	PATRIC.2.9855.2.9855.con.0001.CDS.719020.720054.fwd	PATRIC	CDS	719020	720054	1035	+	PGF_03087097	344	Uncharacterized protein, YkwD family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.631	PATRIC.2.9855.2.9855.con.0001.CDS.720612.722045.fwd	PATRIC	CDS	720612	722045	1434	+	PGF_08148954	477	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.632	PATRIC.2.9855.2.9855.con.0001.CDS.722430.724781.fwd	PATRIC	CDS	722430	724781	2352	+	PGF_02620852	783	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.633	PATRIC.2.9855.2.9855.con.0001.CDS.724822.725250.fwd	PATRIC	CDS	724822	725250	429	+	PGF_02920407	142	Membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.634	PATRIC.2.9855.2.9855.con.0001.CDS.725546.727222.fwd	PATRIC	CDS	725546	727222	1677	+	PGF_09108724	558	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.635	PATRIC.2.9855.2.9855.con.0001.CDS.727325.728296.fwd	PATRIC	CDS	727325	728296	972	+	PGF_07935890	323	ABC transporter, permease protein 1 (cluster 5, nickel/peptides/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.636	PATRIC.2.9855.2.9855.con.0001.CDS.728309.729151.fwd	PATRIC	CDS	728309	729151	843	+	PGF_10565701	280	ABC transporter, permease protein 2 (cluster 5, nickel/peptides/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.637	PATRIC.2.9855.2.9855.con.0001.CDS.729163.730152.fwd	PATRIC	CDS	729163	730152	990	+	PGF_08284191	329	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.638	PATRIC.2.9855.2.9855.con.0001.CDS.730145.731131.fwd	PATRIC	CDS	730145	731131	987	+	PGF_08284191	328	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.640	PATRIC.2.9855.2.9855.con.0001.CDS.732101.733051.fwd	PATRIC	CDS	732101	733051	951	+	PGF_00043387	316	Putative protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.70	PATRIC.2.9855.2.9855.con.0001.CDS.73295.74950.fwd	PATRIC	CDS	73295	74950	1656	+	PGF_00066245	551	Uridine kinase, type 2 (EC 2.7.1.48)	GO:0004849|uridine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.641	PATRIC.2.9855.2.9855.con.0001.CDS.733238.734233.fwd	PATRIC	CDS	733238	734233	996	+	PGF_00041767	331	Putative ion-channel protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.642	PATRIC.2.9855.2.9855.con.0001.CDS.734347.734772.fwd	PATRIC	CDS	734347	734772	426	+	PGF_00057506	141	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.643	PATRIC.2.9855.2.9855.con.0001.CDS.735601.736995.fwd	PATRIC	CDS	735601	736995	1395	+	PGF_03106082	464	Amino-acid permease AapA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.645	PATRIC.2.9855.2.9855.con.0001.CDS.737695.738615.fwd	PATRIC	CDS	737695	738615	921	+	PGF_00041544	306	Putative inner membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.647	PATRIC.2.9855.2.9855.con.0001.CDS.739857.741230.fwd	PATRIC	CDS	739857	741230	1374	+	PGF_03587816	457	FAD-linked oxidoreductase family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.649	PATRIC.2.9855.2.9855.con.0001.CDS.743030.743797.fwd	PATRIC	CDS	743030	743797	768	+	PGF_01304223	255	Autolysis response regulater LytR	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.650	PATRIC.2.9855.2.9855.con.0001.CDS.743791.745041.fwd	PATRIC	CDS	743791	745041	1251	+	PGF_01281288	416	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.651	PATRIC.2.9855.2.9855.con.0001.CDS.745096.745698.rev	PATRIC	CDS	745096	745698	603	-	PGF_01283003	200	Accessory gene regulator B	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.652	PATRIC.2.9855.2.9855.con.0001.CDS.745995.746930.fwd	PATRIC	CDS	745995	746930	936	+	PGF_01283102	311	Secretory antigen precursor SsaA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.654	PATRIC.2.9855.2.9855.con.0001.CDS.753943.755466.fwd	PATRIC	CDS	753943	755466	1524	+	PGF_02889260	507	serine alkaline protease (subtilisin E)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.655	PATRIC.2.9855.2.9855.con.0001.CDS.755731.757701.fwd	PATRIC	CDS	755731	757701	1971	+	PGF_07849456	656	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.71	PATRIC.2.9855.2.9855.con.0001.CDS.75598.76311.fwd	PATRIC	CDS	75598	76311	714	+	PGF_00008542	237	Glycerol uptake facilitator protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.657	PATRIC.2.9855.2.9855.con.0001.CDS.758588.758941.rev	PATRIC	CDS	758588	758941	354	-	PGF_06335969	117	Transcriptional regulator, Xre family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.662	PATRIC.2.9855.2.9855.con.0001.CDS.761727.762173.fwd	PATRIC	CDS	761727	762173	447	+	PGF_07311230	148	Positive regulator of CheA protein activity (CheW)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.663	PATRIC.2.9855.2.9855.con.0001.CDS.762151.763866.fwd	PATRIC	CDS	762151	763866	1716	+	PGF_06837078	571	Methyl-accepting chemotaxis sensor/transducer protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.72	PATRIC.2.9855.2.9855.con.0001.CDS.76397.76954.fwd	PATRIC	CDS	76397	76954	558	+	PGF_03077457	185	Glycerol-3-phosphate responsive antiterminator (mRNA-binding)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.664	PATRIC.2.9855.2.9855.con.0001.CDS.764026.764757.fwd	PATRIC	CDS	764026	764757	732	+	PGF_12850510	243	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.665	PATRIC.2.9855.2.9855.con.0001.CDS.764942.765799.fwd	PATRIC	CDS	764942	765799	858	+	PGF_03087500	285	Uncharacterized UPF0750 membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.666	PATRIC.2.9855.2.9855.con.0001.CDS.766059.766271.fwd	PATRIC	CDS	766059	766271	213	+	PGF_03810679	70	SOS-response repressor and protease LexA (EC 3.4.21.88)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.15	PATRIC.2.9855.2.9855.con.0001.CDS.7672.9069.fwd	PATRIC	CDS	7672	9069	1398	+	PGF_08148954	465	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.668	PATRIC.2.9855.2.9855.con.0001.CDS.767375.768190.rev	PATRIC	CDS	767375	768190	816	-	PGF_08546938	271	Ferredoxin	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.669	PATRIC.2.9855.2.9855.con.0001.CDS.768351.768707.fwd	PATRIC	CDS	768351	768707	357	+	PGF_03320197	118	Transcriptional regulator, HxlR family	

															GO:0004147|diacylglycerol O-acyltransferase activity;GO:0004147|sterol O-acyltransferase activity;GO:0004147|N-acetyltransferase activity;GO:0004147|O-acyltransferase activity;GO:0004147|palmitoleoyl|acyl-carrier-protein]-dependent acyltransferase activity;GO:0004147|carnitine O-acyltransferase activity;GO:0004147|acetyltransferase activity;GO:0004147|C-acyltransferase activity;GO:0004147|palmitoyltransferase activity;GO:0004147|N-acyltransferase activity;GO:0004147|acylglycerol O-acyltransferase activity;GO:0004147|serine O-acyltransferase activity;GO:0004147|O-acetyltransferase activity;GO:0004147|O-octanoyltransferase activity;GO:0004147|octanoyltransferase activity;GO:0004147|O-palmitoyltransferase activity;GO:0004147|S-acyltransferase activity;GO:0004147|S-acetyltransferase activity;GO:0004147|S-malonyltransferase activity;GO:0004147|malonyltransferase activity;GO:0004147|C-palmitoyltransferase activity;GO:0004147|succinyltransferase activity;GO:0004147|N-succinyltransferase activity;GO:0004147|O-succinyltransferase activity;GO:0004147|S-succinyltransferase activity;GO:0004147|sinapoyltransferase activity;GO:0004147|O-sinapoyltransferase activity;GO:0004147|peptidyl-lysine N6-myristoyltransferase activity;GO:0004147|peptidyl-lysine N6-palmitoyltransferase activity;GO:0004147|benzoyl acetate-CoA thiolase activity;GO:0004147|3-hydroxybutyryl-CoA thiolase activity;GO:0004147|3-ketopimelyl-CoA thiolase activity;GO:0004147|N-palmitoyltransferase activity;GO:0004147|myristoyltransferase activity;GO:0004147|acyl-CoA N-acyltransferase activity;GO:0004147|protein-cysteine S-myristoyltransferase activity;GO:0004147|protein-cysteine S-acyltransferase activity;GO:0004147|dihydrolipoamide S-acyltransferase activity;GO:0004147|glucosaminyl-phosphotidylinositol O-acyltransferase activity;GO:0004147|ergosterol O-acyltransferase activity;GO:0004147|lanosterol O-
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.673	PATRIC.2.9855.2.9855.con.0001.CDS.771319.771762.fwd	PATRIC	CDS	771319	771762	444	+	PGF_00013502	147	IAA acetyltransferase (EC 2.3.1.-)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.674	PATRIC.2.9855.2.9855.con.0001.CDS.771875.772429.fwd	PATRIC	CDS	771875	772429	555	+	PGF_00989632	184	Acetyltransferase TM0577	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.73	PATRIC.2.9855.2.9855.con.0001.CDS.77247.78746.fwd	PATRIC	CDS	77247	78746	1500	+	PGF_00008537	499	Glycerol kinase (EC 2.7.1.30)	GO:0004370|glycerol kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.676	PATRIC.2.9855.2.9855.con.0001.CDS.773025.773474.fwd	PATRIC	CDS	773025	773474	450	+	PGF_00071980	149	gnl|WGS:AAAB|ebiP470|gb|EAA02729	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.677	PATRIC.2.9855.2.9855.con.0001.CDS.773638.774684.fwd	PATRIC	CDS	773638	774684	1047	+	PGF_05728830	348	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.680	PATRIC.2.9855.2.9855.con.0001.CDS.775973.776401.fwd	PATRIC	CDS	775973	776401	429	+	PGF_10420503	142	Acetyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.681	PATRIC.2.9855.2.9855.con.0001.CDS.776700.777482.fwd	PATRIC	CDS	776700	777482	783	+	PGF_03510298	260	Surface protein PspC	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.682	PATRIC.2.9855.2.9855.con.0001.CDS.778041.778316.rev	PATRIC	CDS	778041	778316	276	-	PGF_05728830	91	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.685	PATRIC.2.9855.2.9855.con.0001.CDS.779613.780425.fwd	PATRIC	CDS	779613	780425	813	+	PGF_00067362	270	AB hydrolase superfamily protein YisY	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.686	PATRIC.2.9855.2.9855.con.0001.CDS.780821.783583.fwd	PATRIC	CDS	780821	783583	2763	+	PGF_02620852	920	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.689	PATRIC.2.9855.2.9855.con.0001.CDS.785054.785554.fwd	PATRIC	CDS	785054	785554	501	+	PGF_10519603	166	Acetyltransferase, GNAT family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.690	PATRIC.2.9855.2.9855.con.0001.CDS.785746.786288.fwd	PATRIC	CDS	785746	786288	543	+	PGF_05785543	180	Signal peptidase I (EC 3.4.21.89)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.691	PATRIC.2.9855.2.9855.con.0001.CDS.786566.787087.fwd	PATRIC	CDS	786566	787087	522	+	PGF_10420503	173	Acetyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.693	PATRIC.2.9855.2.9855.con.0001.CDS.787577.788224.fwd	PATRIC	CDS	787577	788224	648	+	PGF_09583846	215	Metal-dependent hydrolase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.694	PATRIC.2.9855.2.9855.con.0001.CDS.788251.788604.fwd	PATRIC	CDS	788251	788604	354	+	PGF_00016556	117	Lactoylglutathione lyase (LGUL) family protein, diverged	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.696	PATRIC.2.9855.2.9855.con.0001.CDS.789069.790334.fwd	PATRIC	CDS	789069	790334	1266	+	PGF_12805602	421	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.74	PATRIC.2.9855.2.9855.con.0001.CDS.79078.80505.fwd	PATRIC	CDS	79078	80505	1428	+	PGF_00008605	475	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	GO:0004368|glycerol-3-phosphate dehydrogenase activity;GO:0004368|sn-glycerol-3-phosphate:ubiquinone oxidoreductase activity;GO:0004368|sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.697	PATRIC.2.9855.2.9855.con.0001.CDS.790846.791559.fwd	PATRIC	CDS	790846	791559	714	+	PGF_02921701	237	Phosphoglycerate mutase family 1	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.699	PATRIC.2.9855.2.9855.con.0001.CDS.793145.794197.fwd	PATRIC	CDS	793145	794197	1053	+	PGF_05728830	350	Galactose/methyl galactoside ABC transporter, substrate-binding protein MglB (EC 3.6.3.17)	GO:0015407|monosaccharide-transporting ATPase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.701	PATRIC.2.9855.2.9855.con.0001.CDS.795213.795896.fwd	PATRIC	CDS	795213	795896	684	+	PGF_00411862	227	rhamnogalacturonan acetylesterase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.703	PATRIC.2.9855.2.9855.con.0001.CDS.796584.797786.rev	PATRIC	CDS	796584	797786	1203	-	PGF_09996723	400	Uncharacterized MFS-type transporter	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.704	PATRIC.2.9855.2.9855.con.0001.CDS.797790.798212.rev	PATRIC	CDS	797790	798212	423	-	PGF_10423881	140	Transcriptional regulator, MarR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.705	PATRIC.2.9855.2.9855.con.0001.CDS.798692.799021.fwd	PATRIC	CDS	798692	799021	330	+	PGF_01662006	109	Transcriptional regulator, PadR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.706	PATRIC.2.9855.2.9855.con.0001.CDS.799036.799752.fwd	PATRIC	CDS	799036	799752	717	+	PGF_10538468	238	Pentapeptide repeat family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.707	PATRIC.2.9855.2.9855.con.0001.CDS.800182.800700.fwd	PATRIC	CDS	800182	800700	519	+	PGF_01304795	172	Uncharacterized membrane spanning protein, contains VanZ-like domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.709	PATRIC.2.9855.2.9855.con.0001.CDS.801610.802320.fwd	PATRIC	CDS	801610	802320	711	+	PGF_09655255	236	Transcriptional regulator, RpiR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.710	PATRIC.2.9855.2.9855.con.0001.CDS.802408.802785.fwd	PATRIC	CDS	802408	802785	378	+	PGF_00660064	125	Galactoside O-acetyltransferase (EC 2.3.1.18)	GO:0008870|galactoside O-acetyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.712	PATRIC.2.9855.2.9855.con.0001.CDS.803264.803758.fwd	PATRIC	CDS	803264	803758	495	+	PGF_01284185	164	Spermidine N1-acetyltransferase (EC 2.3.1.57)	GO:0004145|diamine N-acetyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.713	PATRIC.2.9855.2.9855.con.0001.CDS.803866.804405.fwd	PATRIC	CDS	803866	804405	540	+	PGF_10153092	179	Nitroreductase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.714	PATRIC.2.9855.2.9855.con.0001.CDS.804560.805300.rev	PATRIC	CDS	804560	805300	741	-	PGF_10532194	246	Oxidoreductase, short-chain dehydrogenase/reductase family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.75	PATRIC.2.9855.2.9855.con.0001.CDS.80523.81776.fwd	PATRIC	CDS	80523	81776	1254	+	PGF_02681495	417	Sarcosine oxidase alpha subunit (EC 1.5.3.1)	GO:0008115|sarcosine oxidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.715	PATRIC.2.9855.2.9855.con.0001.CDS.805506.806441.fwd	PATRIC	CDS	805506	806441	936	+	PGF_01671660	311	Transcriptional regulator, AraC family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.719	PATRIC.2.9855.2.9855.con.0001.CDS.809065.809598.fwd	PATRIC	CDS	809065	809598	534	+	PGF_01653535	177	RNA polymerase sigma factor SigZ	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.720	PATRIC.2.9855.2.9855.con.0001.CDS.809612.810703.fwd	PATRIC	CDS	809612	810703	1092	+	PGF_01284126	363	ECF-type sigma factor negative effector	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.721	PATRIC.2.9855.2.9855.con.0001.CDS.811206.811514.fwd	PATRIC	CDS	811206	811514	309	+	PGF_01662006	102	Transcriptional regulator, PadR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.723	PATRIC.2.9855.2.9855.con.0001.CDS.812648.813484.fwd	PATRIC	CDS	812648	813484	837	+	PGF_01671660	278	Transcriptional regulator, AraC family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.725	PATRIC.2.9855.2.9855.con.0001.CDS.814288.814842.fwd	PATRIC	CDS	814288	814842	555	+	PGF_10420503	184	Acetyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.726	PATRIC.2.9855.2.9855.con.0001.CDS.815074.815517.rev	PATRIC	CDS	815074	815517	444	-	PGF_10423881	147	Transcriptional regulator, MarR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.729	PATRIC.2.9855.2.9855.con.0001.CDS.817699.818256.rev	PATRIC	CDS	817699	818256	558	-	PGF_07182652	185	Transcriptional regulator, AcrR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.730	PATRIC.2.9855.2.9855.con.0001.CDS.818506.819555.fwd	PATRIC	CDS	818506	819555	1050	+	PGF_02366792	349	HlyD family secretion protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.731	PATRIC.2.9855.2.9855.con.0001.CDS.819583.820758.fwd	PATRIC	CDS	819583	820758	1176	+	PGF_01269065	391	Domain of unknown function / Efflux ABC transporter, permease protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.732	PATRIC.2.9855.2.9855.con.0001.CDS.820733.821947.fwd	PATRIC	CDS	820733	821947	1215	+	PGF_01304417	404	Domain of unknown function / Efflux ABC transporter, permease protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.77	PATRIC.2.9855.2.9855.con.0001.CDS.82413.83093.fwd	PATRIC	CDS	82413	83093	681	+	PGF_00016224	226	L-serine dehydratase, beta subunit (EC 4.3.1.17)	GO:0003941|L-serine ammonia-lyase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.737	PATRIC.2.9855.2.9855.con.0001.CDS.827409.828299.fwd	PATRIC	CDS	827409	828299	891	+	PGF_01074106	296	Multiple sugar ABC transporter, permease protein MsmF	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.739	PATRIC.2.9855.2.9855.con.0001.CDS.829266.830681.fwd	PATRIC	CDS	829266	830681	1416	+	PGF_00054577	471	Sucrose phosphorylase (EC 2.4.1.7)	GO:0009018|sucrose phosphorylase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.740	PATRIC.2.9855.2.9855.con.0001.CDS.830724.832211.fwd	PATRIC	CDS	830724	832211	1488	+	PGF_09125277	495	beta-fructofuranosidase (EC 3.2.1.26)	GO:0004564|beta-fructofuranosidase activity;GO:0004564|sucrose alpha-glucosidase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.78	PATRIC.2.9855.2.9855.con.0001.CDS.83095.83973.fwd	PATRIC	CDS	83095	83973	879	+	PGF_00016223	292	L-serine dehydratase, alpha subunit (EC 4.3.1.17)	GO:0003941|L-serine ammonia-lyase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.741	PATRIC.2.9855.2.9855.con.0001.CDS.832371.833318.fwd	PATRIC	CDS	832371	833318	948	+	PGF_07085092	315	Fructokinase (EC 2.7.1.4)	GO:0008865|fructokinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.744	PATRIC.2.9855.2.9855.con.0001.CDS.834640.835227.fwd	PATRIC	CDS	834640	835227	588	+	PGF_03950680	195	Transporter, LysE family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.745	PATRIC.2.9855.2.9855.con.0001.CDS.835233.835628.fwd	PATRIC	CDS	835233	835628	396	+	PGF_03320197	131	Transcriptional regulator, HxlR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.746	PATRIC.2.9855.2.9855.con.0001.CDS.835628.836038.fwd	PATRIC	CDS	835628	836038	411	+	PGF_01283064	136	NH2-acetyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.747	PATRIC.2.9855.2.9855.con.0001.CDS.836105.838462.rev	PATRIC	CDS	836105	838462	2358	-	PGF_05965846	785	Pyruvate-utilizing enzyme, similar to phosphoenolpyruvate synthase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.748	PATRIC.2.9855.2.9855.con.0001.CDS.838492.839115.rev	PATRIC	CDS	838492	839115	624	-	PGF_07182652	207	Transcriptional regulator, AcrR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.749	PATRIC.2.9855.2.9855.con.0001.CDS.839587.840039.fwd	PATRIC	CDS	839587	840039	453	+	PGF_10423881	150	Transcriptional regulator, MarR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.750	PATRIC.2.9855.2.9855.con.0001.CDS.840328.842871.fwd	PATRIC	CDS	840328	842871	2544	+	PGF_05965846	847	Pyruvate-utilizing enzyme, similar to phosphoenolpyruvate synthase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.751	PATRIC.2.9855.2.9855.con.0001.CDS.843389.844123.fwd	PATRIC	CDS	843389	844123	735	+	PGF_10420457	244	MBL-fold metallo-hydrolase superfamily	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.752	PATRIC.2.9855.2.9855.con.0001.CDS.844460.845056.rev	PATRIC	CDS	844460	845056	597	-	PGF_07182652	198	Transcriptional regulator, AcrR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.753	PATRIC.2.9855.2.9855.con.0001.CDS.845464.846441.fwd	PATRIC	CDS	845464	846441	978	+	PGF_01003946	325	Epoxide hydrolase (EC 3.3.2.9)	GO:0033961|cis-stilbene-oxide hydrolase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.754	PATRIC.2.9855.2.9855.con.0001.CDS.846874.847641.fwd	PATRIC	CDS	846874	847641	768	+	PGF_00998115	255	ABC transporter-like sensor ATP-binding protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.755	PATRIC.2.9855.2.9855.con.0001.CDS.847628.849622.fwd	PATRIC	CDS	847628	849622	1995	+	PGF_01674977	664	ABC transporter-like sensor and permease protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.756	PATRIC.2.9855.2.9855.con.0001.CDS.849954.850628.fwd	PATRIC	CDS	849954	850628	675	+	PGF_10538053	224	ABC transporter-like sensor linked response regulator	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.757	PATRIC.2.9855.2.9855.con.0001.CDS.850625.851644.fwd	PATRIC	CDS	850625	851644	1020	+	PGF_10458023	339	ABC transporter-like sensor linked histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.81	PATRIC.2.9855.2.9855.con.0001.CDS.85131.85820.fwd	PATRIC	CDS	85131	85820	690	+	PGF_07420062	229	Two-component transcriptional response regulator, OmpR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.759	PATRIC.2.9855.2.9855.con.0001.CDS.852272.852895.fwd	PATRIC	CDS	852272	852895	624	+	PGF_00010904	207	Haloacid dehalogenase-like hydrolase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.761	PATRIC.2.9855.2.9855.con.0001.CDS.854021.854878.fwd	PATRIC	CDS	854021	854878	858	+	PGF_01671660	285	Transcriptional regulator, AraC family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.765	PATRIC.2.9855.2.9855.con.0001.CDS.856506.856817.fwd	PATRIC	CDS	856506	856817	312	+	PGF_10519603	103	Acetyltransferase, GNAT family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.766	PATRIC.2.9855.2.9855.con.0001.CDS.857059.857658.fwd	PATRIC	CDS	857059	857658	600	+	PGF_00660064	199	Galactoside O-acetyltransferase (EC 2.3.1.18)	GO:0008870|galactoside O-acetyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.82	PATRIC.2.9855.2.9855.con.0001.CDS.85817.87373.fwd	PATRIC	CDS	85817	87373	1557	+	PGF_12874602	518	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.769	PATRIC.2.9855.2.9855.con.0001.CDS.859062.859655.fwd	PATRIC	CDS	859062	859655	594	+	PGF_01323228	197	Acyl-phosphate:glycerol-3-phosphate O-acyltransferase PlsY (EC 2.3.1.n3)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.770	PATRIC.2.9855.2.9855.con.0001.CDS.859774.860229.fwd	PATRIC	CDS	859774	860229	456	+	PGF_05300095	151	Acetyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.772	PATRIC.2.9855.2.9855.con.0001.CDS.861272.862012.rev	PATRIC	CDS	861272	862012	741	-	PGF_00024681	246	Acetoacetate decarboxylase (EC 4.1.1.4)	GO:0047602|acetoacetate decarboxylase activity

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.773	PATRIC.2.9855.2.9855.con.0001.CDS.862085.862750.rev	PATRIC	CDS	862085	862750	666	-	PGF_08079989	221	Butyrate--acetoacetate CoA-transferase subunit B (EC 2.8.3.9)	GO:0047371|butyrate-acetoacetate CoA-transferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.774	PATRIC.2.9855.2.9855.con.0001.CDS.862751.863404.rev	PATRIC	CDS	862751	863404	654	-	PGF_00959691	217	Butyrate--acetoacetate CoA-transferase subunit A (EC 2.8.3.9)	GO:0047371|butyrate-acetoacetate CoA-transferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.775	PATRIC.2.9855.2.9855.con.0001.CDS.863496.864902.rev	PATRIC	CDS	863496	864902	1407	-	PGF_00418181	468	CoA-acylating propionaldehyde dehydrogenase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.776	PATRIC.2.9855.2.9855.con.0001.CDS.865469.866113.fwd	PATRIC	CDS	865469	866113	645	+	PGF_05748227	214	Uncharacterized conserved protein YfiP, contains DTW domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.779	PATRIC.2.9855.2.9855.con.0001.CDS.867706.868284.fwd	PATRIC	CDS	867706	868284	579	+	PGF_06906103	192	Intracellular protease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.781	PATRIC.2.9855.2.9855.con.0001.CDS.868809.869060.fwd	PATRIC	CDS	868809	869060	252	+	PGF_00071453	83	fragment of DAK2 domain	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.782	PATRIC.2.9855.2.9855.con.0001.CDS.869592.870707.fwd	PATRIC	CDS	869592	870707	1116	+	PGF_06335969	371	Transcriptional regulator, Xre family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.783	PATRIC.2.9855.2.9855.con.0001.CDS.870709.871626.fwd	PATRIC	CDS	870709	871626	918	+	PGF_00884706	305	Efflux ABC transporter, ATP-binding protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.784	PATRIC.2.9855.2.9855.con.0001.CDS.871645.872439.fwd	PATRIC	CDS	871645	872439	795	+	PGF_10490507	264	ABC transporter, permease protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.785	PATRIC.2.9855.2.9855.con.0001.CDS.872770.873318.fwd	PATRIC	CDS	872770	873318	549	+	PGF_10519603	182	Acetyltransferase, GNAT family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.786	PATRIC.2.9855.2.9855.con.0001.CDS.873727.874572.fwd	PATRIC	CDS	873727	874572	846	+	PGF_07849456	281	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.83	PATRIC.2.9855.2.9855.con.0001.CDS.87456.88460.fwd	PATRIC	CDS	87456	88460	1005	+	PGF_06690407	334	FAD:protein FMN transferase (EC 2.7.1.180)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.790	PATRIC.2.9855.2.9855.con.0001.CDS.878591.879301.rev	PATRIC	CDS	878591	879301	711	-	PGF_06916656	236	Transcriptional regulator, GntR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.791	PATRIC.2.9855.2.9855.con.0001.CDS.879512.880900.fwd	PATRIC	CDS	879512	880900	1389	+	PGF_08148954	462	6-phospho-beta-glucosidase (EC 3.2.1.86)	GO:0008706|6-phospho-beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.792	PATRIC.2.9855.2.9855.con.0001.CDS.880917.882218.fwd	PATRIC	CDS	880917	882218	1302	+	PGF_00029599	433	PTS system, beta-glucoside-specific, IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.793	PATRIC.2.9855.2.9855.con.0001.CDS.882257.882559.fwd	PATRIC	CDS	882257	882559	303	+	PGF_05148511	100	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.794	PATRIC.2.9855.2.9855.con.0001.CDS.882571.882894.fwd	PATRIC	CDS	882571	882894	324	+	PGF_01629422	107	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.795	PATRIC.2.9855.2.9855.con.0001.CDS.883053.883946.fwd	PATRIC	CDS	883053	883946	894	+	PGF_00054802	297	Sugar kinase and transcription regulator (EC 2.7.1.-)	GO:0008443|phosphoribulokinase activity;GO:0008443|phosphofructokinase activity;GO:0008443|phosphofructokinase activity;GO:0008443|cobinamide kinase activity;GO:0008443|phytol kinase activity;GO:0008443|phosphatidylinositol phosphate kinase activity;GO:0008443|cyclin-dependent protein serine/threonine kinase regulator activity;GO:0008443|phenol kinase activity;GO:0008443|cyclin-dependent protein kinase activating kinase regulator activity;GO:0008443|inositol tetrakisphosphate 2-kinase activity;GO:0008443|heptose 7-phosphate kinase activity;GO:0008443|aminoglycoside phosphotransferase activity;GO:0008443|phosphatidylinositol 3-kinase activity;GO:0008443|eukaryotic elongation factor-2 kinase regulator activity;GO:0008443|eukaryotic elongation factor-2 kinase activator activity;GO:0008443|LPPG:FO 2-phospho-L-lactate transferase activity;GO:0008443|cytidine kinase activity;GO:0008443|glycerate 2-kinase activity;GO:0008443|(S)-lactate 2-kinase activity;GO:0008443|phosphoserine:homoserine phosphotransferase activity;GO:0008443|L-seryl-tRNA(Sec) kinase activity;GO:0008443|phosphocholine transferase activity;GO:0008443|polynucleotide 5'-hydroxyl-kinase activity;GO:0008443|ATP-dependent polynucleotide kinase activity;GO:0008443|GTP-dependent polynucleotide kinase activity;GO:0008443|farnesol kinase activity;GO:0008443|CTP:2-trans,-6-trans-farnesol kinase activity;GO:0008443|geraniol kinase activity;GO:0008443|geranylgeraniol kinase activity;GO:0008443|CTP:geranylgeraniol kinase activity;GO:0008443|prenol kinase activity;GO:0008443|1-phosphatidylinositol-5-kinase activity;GO:0008443|1-phosphatidylinositol-3-phosphate 4-kinase activity;GO:0008443|phosphatidylinositol-3,4-bisphosphate 5-kinase activity;GO:0008443|phosphatidylinositol bisphosphate kinase activity;GO:0008443|inositol-3,4,6-trisphosphate 1-kinase activity;GO:0008443|inositol 5-diphosphate pentakisphosphate 5-kinase activity;GO:0008443|inositol diphosphate tetrakisphosphate kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.798	PATRIC.2.9855.2.9855.con.0001.CDS.885882.886505.fwd	PATRIC	CDS	885882	886505	624	+	PGF_01641254	207	Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)	GO:0043365|[formate-C-acetyltransferase]-activating enzyme activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.801	PATRIC.2.9855.2.9855.con.0001.CDS.889477.891168.fwd	PATRIC	CDS	889477	891168	1692	+	PGF_07849456	563	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.802	PATRIC.2.9855.2.9855.con.0001.CDS.891346.891834.rev	PATRIC	CDS	891346	891834	489	-	PGF_00022507	162	Molybdopterin adenylyltransferase (EC 2.7.7.75)	GO:0061598|molybdopterin adenylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.804	PATRIC.2.9855.2.9855.con.0001.CDS.892681.894822.fwd	PATRIC	CDS	892681	894822	2142	+	PGF_00006129	713	Formate dehydrogenase H (EC 1.2.1.2)	GO:0008863|formate dehydrogenase (NAD+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.805	PATRIC.2.9855.2.9855.con.0001.CDS.894957.896168.fwd	PATRIC	CDS	894957	896168	1212	+	PGF_09188652	403	Molybdopterin molybdenumtransferase (EC 2.10.1.1)	GO:0061599|molybdopterin molybdotransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.806	PATRIC.2.9855.2.9855.con.0001.CDS.896146.896724.fwd	PATRIC	CDS	896146	896724	579	+	PGF_10499347	192	Molybdopterin-guanine dinucleotide biosynthesis protein MobB	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.807	PATRIC.2.9855.2.9855.con.0001.CDS.896702.897493.fwd	PATRIC	CDS	896702	897493	792	+	PGF_01668012	263	Sulfur carrier protein FdhD	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.808	PATRIC.2.9855.2.9855.con.0001.CDS.897913.898467.fwd	PATRIC	CDS	897913	898467	555	+	PGF_10492441	184	Quad-[4Fe-4S] ferredoxin, HycB/HydN/HyfA family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.809	PATRIC.2.9855.2.9855.con.0001.CDS.898486.899871.fwd	PATRIC	CDS	898486	899871	1386	+	PGF_02316562	461	Periplasmic [FeFe] hydrogenase large subunit (EC 1.12.7.2)	GO:0008901|ferredoxin hydrogenase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.810	PATRIC.2.9855.2.9855.con.0001.CDS.899872.900441.fwd	PATRIC	CDS	899872	900441	570	+	PGF_10492441	189	Quad-[4Fe-4S] ferredoxin, HycB/HydN/HyfA family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.811	PATRIC.2.9855.2.9855.con.0001.CDS.900446.901072.fwd	PATRIC	CDS	900446	901072	627	+	PGF_02230794	208	Molybdenum cofactor guanylyltransferase (EC 2.7.7.77)	GO:0061603|molybdenum cofactor guanylyltransferase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.812	PATRIC.2.9855.2.9855.con.0001.CDS.901065.902021.fwd	PATRIC	CDS	901065	902021	957	+	PGF_10244701	318	GTP 3',8-cyclase (EC 4.1.99.22)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.813	PATRIC.2.9855.2.9855.con.0001.CDS.902026.902496.fwd	PATRIC	CDS	902026	902496	471	+	PGF_00419913	156	Cyclic pyranopterin monophosphate synthase (EC 4.6.1.17)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.814	PATRIC.2.9855.2.9855.con.0001.CDS.902505.902936.fwd	PATRIC	CDS	902505	902936	432	+	PGF_00003238	143	FIG060329: MOSC domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.815	PATRIC.2.9855.2.9855.con.0001.CDS.903282.904997.fwd	PATRIC	CDS	903282	904997	1716	+	PGF_06932478	571	Methyl-accepting chemotaxis protein tlpA	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.816	PATRIC.2.9855.2.9855.con.0001.CDS.905248.905751.rev	PATRIC	CDS	905248	905751	504	-	PGF_00408675	167	putative membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.818	PATRIC.2.9855.2.9855.con.0001.CDS.906042.906578.rev	PATRIC	CDS	906042	906578	537	-	PGF_01281282	178	RNA polymerase sigma factor SigW	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.820	PATRIC.2.9855.2.9855.con.0001.CDS.907878.909158.fwd	PATRIC	CDS	907878	909158	1281	+	PGF_10493211	426	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.85	PATRIC.2.9855.2.9855.con.0001.CDS.90829.91368.fwd	PATRIC	CDS	90829	91368	540	+	PGF_00054415	179	Substrate-specific component ThiW of predicted thiazole ECF transporter	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.821	PATRIC.2.9855.2.9855.con.0001.CDS.909151.909813.fwd	PATRIC	CDS	909151	909813	663	+	PGF_09666309	220	Two-component transcriptional response regulator, LuxR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.823	PATRIC.2.9855.2.9855.con.0001.CDS.911253.912074.rev	PATRIC	CDS	911253	912074	822	-	PGF_07849456	273	Methyl-accepting chemotaxis protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.824	PATRIC.2.9855.2.9855.con.0001.CDS.912354.913172.rev	PATRIC	CDS	912354	913172	819	-	PGF_00057506	272	Transcriptional regulator, MerR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.825	PATRIC.2.9855.2.9855.con.0001.CDS.913272.915380.fwd	PATRIC	CDS	913272	915380	2109	+	PGF_01474349	702	Formate dehydrogenase-O, major subunit (EC 1.2.1.2)	GO:0008863|formate dehydrogenase (NAD+) activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.86	PATRIC.2.9855.2.9855.con.0001.CDS.91399.92205.fwd	PATRIC	CDS	91399	92205	807	+	PGF_05520131	268	Hydroxymethylpyrimidine phosphate kinase ThiD (EC 2.7.4.7)	GO:0008972|phosphomethylpyrimidine kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.826	PATRIC.2.9855.2.9855.con.0001.CDS.915394.916638.fwd	PATRIC	CDS	915394	916638	1245	+	PGF_01283062	414	HoxF-like protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.827	PATRIC.2.9855.2.9855.con.0001.CDS.916699.917952.fwd	PATRIC	CDS	916699	917952	1254	+	PGF_00006497	417	redox proteins related to the succinate dehydrogenases and fumarate reductases	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.16	PATRIC.2.9855.2.9855.con.0001.CDS.9177.10085.fwd	PATRIC	CDS	9177	10085	909	+	PGF_00827664	302	Transcriptional regulator	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.828	PATRIC.2.9855.2.9855.con.0001.CDS.918513.918743.fwd	PATRIC	CDS	918513	918743	231	+	PGF_00009894	76	Glycosyltransferase involved in cell wall biogenesis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.829	PATRIC.2.9855.2.9855.con.0001.CDS.918700.919209.fwd	PATRIC	CDS	918700	919209	510	+	PGF_00009894	169	Glycosyltransferase involved in cell wall biogenesis	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.831	PATRIC.2.9855.2.9855.con.0001.CDS.919380.919724.fwd	PATRIC	CDS	919380	919724	345	+	PGF_12829436	114	Permease of the drug/metabolite transporter (DMT) superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.832	PATRIC.2.9855.2.9855.con.0001.CDS.919736.921001.fwd	PATRIC	CDS	919736	921001	1266	+	PGF_00019913	421	Membrane protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.833	PATRIC.2.9855.2.9855.con.0001.CDS.921003.921701.fwd	PATRIC	CDS	921003	921701	699	+	PGF_07420062	232	Two-component transcriptional response regulator, OmpR family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.834	PATRIC.2.9855.2.9855.con.0001.CDS.921714.923087.fwd	PATRIC	CDS	921714	923087	1374	+	PGF_02620852	457	Two-component system sensor histidine kinase	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.87	PATRIC.2.9855.2.9855.con.0001.CDS.92276.93586.fwd	PATRIC	CDS	92276	93586	1311	+	PGF_00012969	436	Phosphomethylpyrimidine synthase ThiC (EC 4.1.99.17)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.835	PATRIC.2.9855.2.9855.con.0001.CDS.923466.924839.fwd	PATRIC	CDS	923466	924839	1374	+	PGF_08147841	457	Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	GO:0004564|beta-fructofuranosidase activity;GO:0004564|sucrose alpha-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.836	PATRIC.2.9855.2.9855.con.0001.CDS.924832.926226.fwd	PATRIC	CDS	924832	926226	1395	+	PGF_04999141	464	PTS system, sucrose-specific IIB component (EC 2.7.1.211) / PTS system, sucrose-specific IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.837	PATRIC.2.9855.2.9855.con.0001.CDS.926239.928386.fwd	PATRIC	CDS	926239	928386	2148	+	PGF_00069013	715	beta-glucosidase (EC 3.2.1.21)	GO:0008422|beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.838	PATRIC.2.9855.2.9855.con.0001.CDS.928606.930084.fwd	PATRIC	CDS	928606	930084	1479	+	PGF_01285273	492	PRD/PTS system IIA 2 domain protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.839	PATRIC.2.9855.2.9855.con.0001.CDS.930074.930931.fwd	PATRIC	CDS	930074	930931	858	+	PGF_02899915	285	Hydrolase, HAD superfamily	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.840	PATRIC.2.9855.2.9855.con.0001.CDS.931042.931515.fwd	PATRIC	CDS	931042	931515	474	+	PGF_01579531	157	PTS system, glucose-specific IIA component (EC 2.7.1.199)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.842	PATRIC.2.9855.2.9855.con.0001.CDS.932481.933413.fwd	PATRIC	CDS	932481	933413	933	+	PGF_10564020	310	Transcriptional regulator, AraC family	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.843	PATRIC.2.9855.2.9855.con.0001.CDS.933416.935485.fwd	PATRIC	CDS	933416	935485	2070	+	PGF_00979709	689	Thermostable beta-glucosidase B (EC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucoside glucohydrolase)	GO:0008422|beta-glucosidase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.844	PATRIC.2.9855.2.9855.con.0001.CDS.935802.937142.fwd	PATRIC	CDS	935802	937142	1341	+	PGF_01350985	446	Xyloside transporter XynT	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.845	PATRIC.2.9855.2.9855.con.0001.CDS.937693.938718.fwd	PATRIC	CDS	937693	938718	1026	+	PGF_05612489	341	ABC-type Fe3+-hydroxamate transport system, periplasmic component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.88	PATRIC.2.9855.2.9855.con.0001.CDS.93792.94622.fwd	PATRIC	CDS	93792	94622	831	+	PGF_02787474	276	Hydroxyethylthiazole kinase (EC 2.7.1.50)	GO:0004417|hydroxyethylthiazole kinase activity
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.846	PATRIC.2.9855.2.9855.con.0001.CDS.938718.939716.fwd	PATRIC	CDS	938718	939716	999	+	PGF_01325005	332	Iron ABC transporter permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.847	PATRIC.2.9855.2.9855.con.0001.CDS.939713.940744.fwd	PATRIC	CDS	939713	940744	1032	+	PGF_00015248	343	Iron ABC transporter permease	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.848	PATRIC.2.9855.2.9855.con.0001.CDS.940744.941550.fwd	PATRIC	CDS	940744	941550	807	+	PGF_10567400	268	Ferrichrome transport ATP-binding protein FhuC	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.850	PATRIC.2.9855.2.9855.con.0001.CDS.944064.944513.fwd	PATRIC	CDS	944064	944513	450	+	PGF_02777111	149	PTS system, IIA component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.851	PATRIC.2.9855.2.9855.con.0001.CDS.944516.944827.fwd	PATRIC	CDS	944516	944827	312	+	PGF_02754640	103	PTS system, IIB component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.852	PATRIC.2.9855.2.9855.con.0001.CDS.944984.946096.fwd	PATRIC	CDS	944984	946096	1113	+	PGF_02770427	370	PTS system, IIC component	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.853	PATRIC.2.9855.2.9855.con.0001.CDS.946181.948853.fwd	PATRIC	CDS	946181	948853	2673	+	PGF_07867148	890	Mannosylglycerate hydrolase (EC 3.2.1.170)	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.89	PATRIC.2.9855.2.9855.con.0001.CDS.94715.95344.fwd	PATRIC	CDS	94715	95344	630	+	PGF_01291823	209	Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)	GO:0004789|thiamine-phosphate diphosphorylase activity

Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.854	PATRIC.2.9855.2.9855.con.0001.CDS.948997.949875.fwd	PATRIC	CDS	948997	949875	879	+	PGF_00054802	292	Sugar kinase and transcription regulator (EC 2.7.1.-)	GO:0008443|phosphinothricin acetyltransferase activity;GO:0008443|phosphinothricin kinase regulator activity;GO:0008443|cobinamide kinase activity;GO:0008443|phytol kinase activity;GO:0008443|phosphatidylinositol phosphate kinase activity;GO:0008443|cyclin-dependent protein serine/threonine kinase regulator activity;GO:0008443|phenol kinase activity;GO:0008443|cyclin-dependent protein kinase activating kinase regulator activity;GO:0008443|inositol tetrakisphosphate 2-kinase activity;GO:0008443|heptose 7-phosphate kinase activity;GO:0008443|aminoglycoside phosphotransferase activity;GO:0008443|phosphatidylinositol 3-kinase activity;GO:0008443|eukaryotic elongation factor-2 kinase regulator activity;GO:0008443|eukaryotic elongation factor-2 kinase activator activity;GO:0008443|LPPG:FO 2-phospho-L-lactate transferase activity;GO:0008443|cytidine kinase activity;GO:0008443|glycerate 2-kinase activity;GO:0008443|(S)-lactate 2-kinase activity;GO:0008443|phosphoserine:homoserine phosphotransferase activity;GO:0008443|L-seryl-tRNA(Sec) kinase activity;GO:0008443|phosphocholine transferase activity;GO:0008443|polynucleotide 5'-hydroxyl-kinase activity;GO:0008443|ATP-dependent polynucleotide kinase activity;GO:0008443|GTP-dependent polynucleotide kinase activity;GO:0008443|farnesol kinase activity;GO:0008443|CTP:2-trans,-6-trans-farnesol kinase activity;GO:0008443|geraniol kinase activity;GO:0008443|geranylgeraniol kinase activity;GO:0008443|CTP:geranylgeraniol kinase activity;GO:0008443|prenol kinase activity;GO:0008443|1-phosphatidylinositol-5-kinase activity;GO:0008443|1-phosphatidylinositol-3-phosphate 4-kinase activity;GO:0008443|phosphatidylinositol-3,4-bisphosphate 5-kinase activity;GO:0008443|phosphatidylinositol bisphosphate kinase activity;GO:0008443|inositol-3,4,6-trisphosphate 1-kinase activity;GO:0008443|inositol 5-diphosphate pentakisphosphate 5-kinase activity;GO:0008443|inositol diphosphate tetrakisphosphate kinase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.856	PATRIC.2.9855.2.9855.con.0001.CDS.950633.952006.fwd	PATRIC	CDS	950633	952006	1374	+	PGF_00425528	457	Uncharacterized FAD-linked oxidoreductase YvdP (CotQ)	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.857	PATRIC.2.9855.2.9855.con.0001.CDS.952434.956351.fwd	PATRIC	CDS	952434	956351	3918	+	PGF_01333294	1305	Activator of (R)-2-hydroxyglutaryl-CoA dehydratase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.90	PATRIC.2.9855.2.9855.con.0001.CDS.95599.96876.fwd	PATRIC	CDS	95599	96876	1278	+	PGF_01283071	425	Similar to periplasmic protein TorT	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.859	PATRIC.2.9855.2.9855.con.0001.CDS.956717.957052.fwd	PATRIC	CDS	956717	957052	336	+	PGF_00064652	111	Uncharacterized conserved protein, contains double-stranded beta-helix domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.860	PATRIC.2.9855.2.9855.con.0001.CDS.957461.957877.rev	PATRIC	CDS	957461	957877	417	-	PGF_00072164	138	Hemerythrin domain protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.861	PATRIC.2.9855.2.9855.con.0001.CDS.958508.958918.fwd	PATRIC	CDS	958508	958918	411	+	PGF_00049337	136	S-adenosylmethionine-dependent methyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.863	PATRIC.2.9855.2.9855.con.0001.CDS.959437.959904.fwd	PATRIC	CDS	959437	959904	468	+	PGF_00016612	155	Lactoylglutation lyase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.865	PATRIC.2.9855.2.9855.con.0001.CDS.960941.962020.fwd	PATRIC	CDS	960941	962020	1080	+	PGF_06335969	359	Transcriptional regulator, Xre family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.873	PATRIC.2.9855.2.9855.con.0001.CDS.965448.966110.fwd	PATRIC	CDS	965448	966110	663	+	PGF_10460277	220	Phosphoglycolate phosphatase (EC 3.1.3.18)	GO:0008967|phosphoglycolate phosphatase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.875	PATRIC.2.9855.2.9855.con.0001.CDS.966626.967108.fwd	PATRIC	CDS	966626	967108	483	+	PGF_10423881	160	Transcriptional regulator, MarR family	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.91	PATRIC.2.9855.2.9855.con.0001.CDS.96887.98836.fwd	PATRIC	CDS	96887	98836	1950	+	PGF_01283107	649	Serine/threonine kinase with two-component sensor domain	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.879	PATRIC.2.9855.2.9855.con.0001.CDS.971560.972780.fwd	PATRIC	CDS	971560	972780	1221	+	PGF_00242238	406	YibE/F family protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.880	PATRIC.2.9855.2.9855.con.0001.CDS.973473.974114.fwd	PATRIC	CDS	973473	974114	642	+	PGF_02278882	213	Iron-sulfur flavoprotein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.881	PATRIC.2.9855.2.9855.con.0001.CDS.974304.975539.fwd	PATRIC	CDS	974304	975539	1236	+	PGF_02873213	411	Multidrug-efflux transporter, major facilitator superfamily (MFS); Efflux pump Lde	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.884	PATRIC.2.9855.2.9855.con.0001.CDS.976861.977649.fwd	PATRIC	CDS	976861	977649	789	+	PGF_12753546	262	Protein gp49, replication initiation [Bacteriophage A118]	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.885	PATRIC.2.9855.2.9855.con.0001.CDS.977711.978322.fwd	PATRIC	CDS	977711	978322	612	+	PGF_00421821	203	DNA replication helicase loader DnaC/DnaI	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.891	PATRIC.2.9855.2.9855.con.0001.CDS.982397.983182.fwd	PATRIC	CDS	982397	983182	786	+	PGF_05179218	261	Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (EC 3.2.1.17)	GO:0003796|lysozyme activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.896	PATRIC.2.9855.2.9855.con.0001.CDS.985204.987348.rev	PATRIC	CDS	985204	987348	2145	-	PGF_00663189	714	putative peptidoglycan binding domain protein	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.897	PATRIC.2.9855.2.9855.con.0001.CDS.987648.988490.fwd	PATRIC	CDS	987648	988490	843	+	PGF_00739388	280	2,5-didehydrogluconate reductase (2-dehydro-D-gluconate-forming) (EC 1.1.1.274)	GO:0050580|2,5-didehydrogluconate reductase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.92	PATRIC.2.9855.2.9855.con.0001.CDS.98909.100615.fwd	PATRIC	CDS	98909	100615	1707	+	PGF_02620852	568	Two-component system sensor histidine kinase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.901	PATRIC.2.9855.2.9855.con.0001.CDS.990635.991363.fwd	PATRIC	CDS	990635	991363	729	+	PGF_00043435	242	Putative reductase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.902	PATRIC.2.9855.2.9855.con.0001.CDS.991403.991993.fwd	PATRIC	CDS	991403	991993	591	+	PGF_00660064	196	Galactoside O-acetyltransferase (EC 2.3.1.18)	GO:0008870|galactoside O-acetyltransferase activity
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.906	PATRIC.2.9855.2.9855.con.0001.CDS.994175.994678.rev	PATRIC	CDS	994175	994678	504	-	PGF_00049610	167	SAM-dependent methyltransferase	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.911	PATRIC.2.9855.2.9855.con.0001.CDS.997644.997802.rev	PATRIC	CDS	997644	997802	159	-	PGF_01310631	52	Uncharacterized protein CA_C3540	
Bacteria	DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.912	PATRIC.2.9855.2.9855.con.0001.CDS.999014.999922.fwd	PATRIC	CDS	999014	999922	909	+	PGF_00060510	302	Cobalt ECF transporter, transmembrane component of energizing module CbiQ	

PATRIC Hypothetical Proteins

Genome	Genome ID	Accession	PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	Feature ID	Annotation	Feature Type	Start	End	Length	Strand	FIGfam ID	PATRIC genus-specific families (PLfams)	PATRIC cross-genus families (PGfams)	Protein ID	AA Length	Gene Symbol	Product	GO
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.927			PATRIC.2.9855.2.9855.con.0001.CDS.1017854.1018012.fwd	PATRIC	CDS	1017854	1018012	159	+			PGF_01290843		52		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.928			PATRIC.2.9855.2.9855.con.0001.CDS.1018096.1018518.rev	PATRIC	CDS	1018096	1018518	423	-			PGF_08225224		140		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.936			PATRIC.2.9855.2.9855.con.0001.CDS.1026247.1026588.fwd	PATRIC	CDS	1026247	1026588	342	+			PGF_07639480		113		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.937			PATRIC.2.9855.2.9855.con.0001.CDS.1026805.1027128.rev	PATRIC	CDS	1026805	1027128	324	-			PGF_01283162		107		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.938			PATRIC.2.9855.2.9855.con.0001.CDS.1027180.1027494.rev	PATRIC	CDS	1027180	1027494	315	-			PGF_01291920		104		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.939			PATRIC.2.9855.2.9855.con.0001.CDS.1027843.1028061.rev	PATRIC	CDS	1027843	1028061	219	-			PGF_00915583		72		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.940			PATRIC.2.9855.2.9855.con.0001.CDS.1028180.1028404.rev	PATRIC	CDS	1028180	1028404	225	-			PGF_01282349		74		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.942			PATRIC.2.9855.2.9855.con.0001.CDS.1029445.1030563.fwd	PATRIC	CDS	1029445	1030563	1119	+			PGF_08225224		372		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.945			PATRIC.2.9855.2.9855.con.0001.CDS.1035123.1036136.fwd	PATRIC	CDS	1035123	1036136	1014	+			PGF_01284600		337		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.950			PATRIC.2.9855.2.9855.con.0001.CDS.1040565.1041497.fwd	PATRIC	CDS	1040565	1041497	933	+			PGF_00788525		310		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.951			PATRIC.2.9855.2.9855.con.0001.CDS.1041630.1043138.fwd	PATRIC	CDS	1041630	1043138	1509	+			PGF_08225224		502		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.953			PATRIC.2.9855.2.9855.con.0001.CDS.1044325.1045323.fwd	PATRIC	CDS	1044325	1045323	999	+			PGF_01285521		332		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.954			PATRIC.2.9855.2.9855.con.0001.CDS.1045649.1047343.fwd	PATRIC	CDS	1045649	1047343	1695	+			PGF_00110155		564		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.958			PATRIC.2.9855.2.9855.con.0001.CDS.1050722.1051483.rev	PATRIC	CDS	1050722	1051483	762	-			PGF_12800061		253		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.959			PATRIC.2.9855.2.9855.con.0001.CDS.1051480.1053297.rev	PATRIC	CDS	1051480	1053297	1818	-			PGF_08225224		605		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.960			PATRIC.2.9855.2.9855.con.0001.CDS.1053444.1054757.fwd	PATRIC	CDS	1053444	1054757	1314	+			PGF_06208022		437		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.961			PATRIC.2.9855.2.9855.con.0001.CDS.1054825.1055703.fwd	PATRIC	CDS	1054825	1055703	879	+			PGF_12797539		292		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.962			PATRIC.2.9855.2.9855.con.0001.CDS.1055703.1056530.fwd	PATRIC	CDS	1055703	1056530	828	+			PGF_04961500		275		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.965			PATRIC.2.9855.2.9855.con.0001.CDS.1061622.1062161.rev	PATRIC	CDS	1061622	1062161	540	-			PGF_10457918		179		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.966			PATRIC.2.9855.2.9855.con.0001.CDS.1062466.1063011.fwd	PATRIC	CDS	1062466	1063011	546	+			PGF_07171868		181		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.967			PATRIC.2.9855.2.9855.con.0001.CDS.1063164.1063391.fwd	PATRIC	CDS	1063164	1063391	228	+			PGF_07319340		75		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.968			PATRIC.2.9855.2.9855.con.0001.CDS.1063480.1063929.fwd	PATRIC	CDS	1063480	1063929	450	+			PGF_07035928		149		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.976			PATRIC.2.9855.2.9855.con.0001.CDS.1070735.1070962.fwd	PATRIC	CDS	1070735	1070962	228	+			PGF_07056945		75		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.979			PATRIC.2.9855.2.9855.con.0001.CDS.1073024.1073611.fwd	PATRIC	CDS	1073024	1073611	588	+			PGF_01746686		195		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.980			PATRIC.2.9855.2.9855.con.0001.CDS.1073761.1074594.rev	PATRIC	CDS	1073761	1074594	834	-			PGF_08184525		277		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.988			PATRIC.2.9855.2.9855.con.0001.CDS.1083737.1084267.fwd	PATRIC	CDS	1083737	1084267	531	+			PGF_01286913		176		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.989			PATRIC.2.9855.2.9855.con.0001.CDS.1084542.1085090.fwd	PATRIC	CDS	1084542	1085090	549	+			PGF_08225224		182		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.990			PATRIC.2.9855.2.9855.con.0001.CDS.1085103.1085537.fwd	PATRIC	CDS	1085103	1085537	435	+			PGF_01312098		144		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.997			PATRIC.2.9855.2.9855.con.0001.CDS.1090548.1090661.fwd	PATRIC	CDS	1090548	1090661	114	+					37		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.998			PATRIC.2.9855.2.9855.con.0001.CDS.1090738.1091193.fwd	PATRIC	CDS	1090738	1091193	456	+			PGF_01292515		151		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1002			PATRIC.2.9855.2.9855.con.0001.CDS.1092945.1093073.fwd	PATRIC	CDS	1092945	1093073	129	+			PGF_12874033		42		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1007			PATRIC.2.9855.2.9855.con.0001.CDS.1097935.1098060.fwd	PATRIC	CDS	1097935	1098060	126	+					41		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1008			PATRIC.2.9855.2.9855.con.0001.CDS.1098106.1098246.fwd	PATRIC	CDS	1098106	1098246	141	+					46		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1012			PATRIC.2.9855.2.9855.con.0001.CDS.1103438.1103827.fwd	PATRIC	CDS	1103438	1103827	390	+					129		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1013			PATRIC.2.9855.2.9855.con.0001.CDS.1104030.1104851.fwd	PATRIC	CDS	1104030	1104851	822	+					273		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1014			PATRIC.2.9855.2.9855.con.0001.CDS.1104971.1105084.fwd	PATRIC	CDS	1104971	1105084	114	+					37		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1015			PATRIC.2.9855.2.9855.con.0001.CDS.1105213.1105968.fwd	PATRIC	CDS	1105213	1105968	756	+			PGF_07212382		251		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1016			PATRIC.2.9855.2.9855.con.0001.CDS.1105961.1106098.fwd	PATRIC	CDS	1105961	1106098	138	+					45		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1017			PATRIC.2.9855.2.9855.con.0001.CDS.1106353.1106961.fwd	PATRIC	CDS	1106353	1106961	609	+			PGF_12694225		202		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1018			PATRIC.2.9855.2.9855.con.0001.CDS.1107013.1107378.fwd	PATRIC	CDS	1107013	1107378	366	+					121		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1019			PATRIC.2.9855.2.9855.con.0001.CDS.1107656.1108438.fwd	PATRIC	CDS	1107656	1108438	783	+			PGF_08225224		260		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1020			PATRIC.2.9855.2.9855.con.0001.CDS.1108586.1108705.fwd	PATRIC	CDS	1108586	1108705	120	+					39		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1021			PATRIC.2.9855.2.9855.con.0001.CDS.1108822.1109424.fwd	PATRIC	CDS	1108822	1109424	603	+					200		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1022			PATRIC.2.9855.2.9855.con.0001.CDS.1109488.1109733.fwd	PATRIC	CDS	1109488	1109733	246	+			PGF_08225224		81		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1023			PATRIC.2.9855.2.9855.con.0001.CDS.1109855.1110193.rev	PATRIC	CDS	1109855	1110193	339	-			PGF_01307360		112		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1024			PATRIC.2.9855.2.9855.con.0001.CDS.1110229.1110393.rev	PATRIC	CDS	1110229	1110393	165	-					54		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1025			PATRIC.2.9855.2.9855.con.0001.CDS.1110579.1111955.fwd	PATRIC	CDS	1110579	1111955	1377	+					458		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1028			PATRIC.2.9855.2.9855.con.0001.CDS.1113797.1115362.rev	PATRIC	CDS	1113797	1115362	1566	-			PGF_12773173		521		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1029			PATRIC.2.9855.2.9855.con.0001.CDS.1115709.1115861.fwd	PATRIC	CDS	1115709	1115861	153	+					50		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1033			PATRIC.2.9855.2.9855.con.0001.CDS.1119570.1120781.fwd	PATRIC	CDS	1119570	1120781	1212	+			PGF_03152613		403		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1036			PATRIC.2.9855.2.9855.con.0001.CDS.1123353.1123709.fwd	PATRIC	CDS	1123353	1123709	357	+			PGF_01284224		118		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1040			PATRIC.2.9855.2.9855.con.0001.CDS.1128216.1128704.fwd	PATRIC	CDS	1128216	1128704	489	+			PGF_01984375		162		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1041			PATRIC.2.9855.2.9855.con.0001.CDS.1128720.1129082.fwd	PATRIC	CDS	1128720	1129082	363	+			PGF_00256877		120		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1044			PATRIC.2.9855.2.9855.con.0001.CDS.1132712.1133770.rev	PATRIC	CDS	1132712	1133770	1059	-			PGF_12906558		352		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1045			PATRIC.2.9855.2.9855.con.0001.CDS.1133748.1133957.rev	PATRIC	CDS	1133748	1133957	210	-			PGF_12906558		69		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1046			PATRIC.2.9855.2.9855.con.0001.CDS.1134023.1135312.rev	PATRIC	CDS	1134023	1135312	1290	-			PGF_12906558		429		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1048			PATRIC.2.9855.2.9855.con.0001.CDS.1136199.1137017.fwd	PATRIC	CDS	1136199	1137017	819	+			PGF_01311957		272		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1056			PATRIC.2.9855.2.9855.con.0001.CDS.1142224.1142394.fwd	PATRIC	CDS	1142224	1142394	171	+			PGF_08225224		56		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1057			PATRIC.2.9855.2.9855.con.0001.CDS.1142460.1142588.rev	PATRIC	CDS	1142460	1142588	129	-			PGF_00677272		42		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1061			PATRIC.2.9855.2.9855.con.0001.CDS.1145242.1145502.fwd	PATRIC	CDS	1145242	1145502	261	+			PGF_01286930		86		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1062			PATRIC.2.9855.2.9855.con.0001.CDS.1145591.1145941.fwd	PATRIC	CDS	1145591	1145941	351	+			PGF_08225224		116		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1063			PATRIC.2.9855.2.9855.con.0001.CDS.1146117.1146803.rev	PATRIC	CDS	1146117	1146803	687	-			PGF_08225224		228		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1072			PATRIC.2.9855.2.9855.con.0001.CDS.1154136.1154276.fwd	PATRIC	CDS	1154136	1154276	141	+			PGF_01272418		46		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1075			PATRIC.2.9855.2.9855.con.0001.CDS.1156207.1156362.fwd	PATRIC	CDS	1156207	1156362	156	+					51		hypothetical protein	
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1080			PATRIC.2.9855.2.9855.con.0001.CDS.1161359.1161520.fwd	PATRIC	CDS	1161359	1161520	162	+			PGF_01294658		53		hypothetical protein	

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1083	PATRIC.2.9855.2.9855.con.0001.CDS.1163698.1163811.fwd	PATRIC	CDS	1163698	1163811	114	+	PGF_01281800	37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1084	PATRIC.2.9855.2.9855.con.0001.CDS.1163976.1164353.fwd	PATRIC	CDS	1163976	1164353	378	+	PGF_06890106	125	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1085	PATRIC.2.9855.2.9855.con.0001.CDS.1164588.1164902.fwd	PATRIC	CDS	1164588	1164902	315	+	PGF_01281800	104	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1089	PATRIC.2.9855.2.9855.con.0001.CDS.1167206.1167349.fwd	PATRIC	CDS	1167206	1167349	144	+		47	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1091	PATRIC.2.9855.2.9855.con.0001.CDS.1168591.1168977.fwd	PATRIC	CDS	1168591	1168977	387	+	PGF_01282565	128	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1093	PATRIC.2.9855.2.9855.con.0001.CDS.1170118.1170243.rev	PATRIC	CDS	1170118	1170243	126	-	PGF_01297094	41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1095	PATRIC.2.9855.2.9855.con.0001.CDS.1171481.1172260.rev	PATRIC	CDS	1171481	1172260	780	-	PGF_01283509	259	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1097	PATRIC.2.9855.2.9855.con.0001.CDS.1172834.1173343.rev	PATRIC	CDS	1172834	1173343	510	-	PGF_00223692	169	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1099	PATRIC.2.9855.2.9855.con.0001.CDS.1174411.1174548.fwd	PATRIC	CDS	1174411	1174548	138	+		45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1100	PATRIC.2.9855.2.9855.con.0001.CDS.1174573.1175274.fwd	PATRIC	CDS	1174573	1175274	702	+	PGF_08225224	233	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1102	PATRIC.2.9855.2.9855.con.0001.CDS.1176062.1176532.fwd	PATRIC	CDS	1176062	1176532	471	+	PGF_08225224	156	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1103	PATRIC.2.9855.2.9855.con.0001.CDS.1176585.1176746.fwd	PATRIC	CDS	1176585	1176746	162	+	PGF_01268900	53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1104	PATRIC.2.9855.2.9855.con.0001.CDS.1176835.1177089.fwd	PATRIC	CDS	1176835	1177089	255	+	PGF_10511651	84	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1105	PATRIC.2.9855.2.9855.con.0001.CDS.1177091.1177378.fwd	PATRIC	CDS	1177091	1177378	288	+	PGF_10511651	95	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1106	PATRIC.2.9855.2.9855.con.0001.CDS.1177766.1178197.fwd	PATRIC	CDS	1177766	1178197	432	+	PGF_08225224	143	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.103	PATRIC.2.9855.2.9855.con.0001.CDS.117958.118215.fwd	PATRIC	CDS	117958	118215	258	+	PGF_01283338	85	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1112	PATRIC.2.9855.2.9855.con.0001.CDS.1182904.1184208.fwd	PATRIC	CDS	1182904	1184208	1305	+	PGF_08225224	434	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1113	PATRIC.2.9855.2.9855.con.0001.CDS.1184192.1185205.fwd	PATRIC	CDS	1184192	1185205	1014	+	PGF_01321636	337	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1116	PATRIC.2.9855.2.9855.con.0001.CDS.1188952.1189278.fwd	PATRIC	CDS	1188952	1189278	327	+	PGF_01283214	108	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1118	PATRIC.2.9855.2.9855.con.0001.CDS.1190181.1191200.fwd	PATRIC	CDS	1190181	1191200	1020	+	PGF_04851492	339	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1119	PATRIC.2.9855.2.9855.con.0001.CDS.1191224.1191598.fwd	PATRIC	CDS	1191224	1191598	375	+	PGF_00094591	124	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1120	PATRIC.2.9855.2.9855.con.0001.CDS.1191767.1192912.fwd	PATRIC	CDS	1191767	1192912	1146	+	PGF_08225224	381	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.105	PATRIC.2.9855.2.9855.con.0001.CDS.119439.120383.fwd	PATRIC	CDS	119439	120383	945	+	PGF_08225224	314	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1123	PATRIC.2.9855.2.9855.con.0001.CDS.1195680.1195814.fwd	PATRIC	CDS	1195680	1195814	135	+	PGF_01284012	44	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1124	PATRIC.2.9855.2.9855.con.0001.CDS.1196018.1196878.fwd	PATRIC	CDS	1196018	1196878	861	+	PGF_00013059	286	Hypothetical domain / Uncharacterized protein COG3236
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1132	PATRIC.2.9855.2.9855.con.0001.CDS.1204069.1205130.fwd	PATRIC	CDS	1204069	1205130	1062	+	PGF_08225224	353	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.106	PATRIC.2.9855.2.9855.con.0001.CDS.120791.120916.fwd	PATRIC	CDS	120791	120916	126	+		41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1146	PATRIC.2.9855.2.9855.con.0001.CDS.1216820.1216987.fwd	PATRIC	CDS	1216820	1216987	168	+	PGF_07320946	55	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1149	PATRIC.2.9855.2.9855.con.0001.CDS.1219742.1220413.fwd	PATRIC	CDS	1219742	1220413	672	+	PGF_00128694	223	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1153	PATRIC.2.9855.2.9855.con.0001.CDS.1225030.1225146.fwd	PATRIC	CDS	1225030	1225146	117	+	PGF_04045828	38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1157	PATRIC.2.9855.2.9855.con.0001.CDS.1230757.1231350.rev	PATRIC	CDS	1230757	1231350	594	-	PGF_08187303	197	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1161	PATRIC.2.9855.2.9855.con.0001.CDS.1234209.1234322.fwd	PATRIC	CDS	1234209	1234322	114	+		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1162	PATRIC.2.9855.2.9855.con.0001.CDS.1234343.1234876.fwd	PATRIC	CDS	1234343	1234876	534	+	PGF_01260638	177	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1163	PATRIC.2.9855.2.9855.con.0001.CDS.1234947.1235060.fwd	PATRIC	CDS	1234947	1235060	114	+		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1168	PATRIC.2.9855.2.9855.con.0001.CDS.1239715.1240230.rev	PATRIC	CDS	1239715	1240230	516	-	PGF_02621288	171	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1169	PATRIC.2.9855.2.9855.con.0001.CDS.1240370.1240780.rev	PATRIC	CDS	1240370	1240780	411	-	PGF_01285707	136	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1170	PATRIC.2.9855.2.9855.con.0001.CDS.1240777.1241235.rev	PATRIC	CDS	1240777	1241235	459	-	PGF_00817199	152	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1171	PATRIC.2.9855.2.9855.con.0001.CDS.1241684.1242109.fwd	PATRIC	CDS	1241684	1242109	426	+	PGF_01293926	141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1172	PATRIC.2.9855.2.9855.con.0001.CDS.1242291.1243520.fwd	PATRIC	CDS	1242291	1243520	1230	+	PGF_00770942	409	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1177	PATRIC.2.9855.2.9855.con.0001.CDS.1248274.1248393.fwd	PATRIC	CDS	1248274	1248393	120	+		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1178	PATRIC.2.9855.2.9855.con.0001.CDS.1248398.1248760.rev	PATRIC	CDS	1248398	1248760	363	-		120	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1179	PATRIC.2.9855.2.9855.con.0001.CDS.1248979.1249179.fwd	PATRIC	CDS	1248979	1249179	201	+		66	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1180	PATRIC.2.9855.2.9855.con.0001.CDS.1249273.1249434.fwd	PATRIC	CDS	1249273	1249434	162	+		53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1182	PATRIC.2.9855.2.9855.con.0001.CDS.1250162.1250278.fwd	PATRIC	CDS	1250162	1250278	117	+		38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1183	PATRIC.2.9855.2.9855.con.0001.CDS.1250328.1250522.fwd	PATRIC	CDS	1250328	1250522	195	+		64	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1184	PATRIC.2.9855.2.9855.con.0001.CDS.1250534.1250950.fwd	PATRIC	CDS	1250534	1250950	417	+		138	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1185	PATRIC.2.9855.2.9855.con.0001.CDS.1251039.1251206.fwd	PATRIC	CDS	1251039	1251206	168	+		55	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1186	PATRIC.2.9855.2.9855.con.0001.CDS.1251211.1251894.fwd	PATRIC	CDS	1251211	1251894	684	+	PGF_08225224	227	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1187	PATRIC.2.9855.2.9855.con.0001.CDS.1252139.1252588.fwd	PATRIC	CDS	1252139	1252588	450	+	PGF_00877238	149	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1188	PATRIC.2.9855.2.9855.con.0001.CDS.1252602.1253015.fwd	PATRIC	CDS	1252602	1253015	414	+		137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1189	PATRIC.2.9855.2.9855.con.0001.CDS.1253029.1253490.fwd	PATRIC	CDS	1253029	1253490	462	+		153	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1190	PATRIC.2.9855.2.9855.con.0001.CDS.1253501.1254304.fwd	PATRIC	CDS	1253501	1254304	804	+		267	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1191	PATRIC.2.9855.2.9855.con.0001.CDS.1254316.1254822.fwd	PATRIC	CDS	1254316	1254822	507	+		168	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1192	PATRIC.2.9855.2.9855.con.0001.CDS.1254837.1254953.fwd	PATRIC	CDS	1254837	1254953	117	+		38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1193	PATRIC.2.9855.2.9855.con.0001.CDS.1254955.1255827.fwd	PATRIC	CDS	1254955	1255827	873	+		290	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1194	PATRIC.2.9855.2.9855.con.0001.CDS.1255925.1256335.fwd	PATRIC	CDS	1255925	1256335	411	+		136	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1195	PATRIC.2.9855.2.9855.con.0001.CDS.1256342.1256680.fwd	PATRIC	CDS	1256342	1256680	339	+		112	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1196	PATRIC.2.9855.2.9855.con.0001.CDS.1256733.1256894.rev	PATRIC	CDS	1256733	1256894	162	-		53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1197	PATRIC.2.9855.2.9855.con.0001.CDS.1257136.1257309.fwd	PATRIC	CDS	1257136	1257309	174	+		57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1198	PATRIC.2.9855.2.9855.con.0001.CDS.1257453.1258163.fwd	PATRIC	CDS	1257453	1258163	711	+	PGF_08167161	236	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1199	PATRIC.2.9855.2.9855.con.0001.CDS.1258240.1258443.rev	PATRIC	CDS	1258240	1258443	204	-		67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1200	PATRIC.2.9855.2.9855.con.0001.CDS.1258622.1258909.fwd	PATRIC	CDS	1258622	1258909	288	+		95	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1201	PATRIC.2.9855.2.9855.con.0001.CDS.1258914.1259063.fwd	PATRIC	CDS	1258914	1259063	150	+		49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1202	PATRIC.2.9855.2.9855.con.0001.CDS.1259131.1259295.fwd	PATRIC	CDS	1259131	1259295	165	+		54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1203	PATRIC.2.9855.2.9855.con.0001.CDS.1259298.1259576.fwd	PATRIC	CDS	1259298	1259576	279	+		92	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1204	PATRIC.2.9855.2.9855.con.0001.CDS.1259589.1259768.fwd	PATRIC	CDS	1259589	1259768	180	+		59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1205	PATRIC.2.9855.2.9855.con.0001.CDS.1259773.1260276.fwd	PATRIC	CDS	1259773	1260276	504	+	PGF_07524966	167	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1206	PATRIC.2.9855.2.9855.con.0001.CDS.1260326.1260484.fwd	PATRIC	CDS	1260326	1260484	159	+		52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1208	PATRIC.2.9855.2.9855.con.0001.CDS.1261031.1261150.fwd	PATRIC	CDS	1261031	1261150	120	+		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1209	PATRIC.2.9855.2.9855.con.0001.CDS.1261234.1261323.fwd	PATRIC	CDS	1261234	1261323	90	+		29	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1210	PATRIC.2.9855.2.9855.con.0001.CDS.1261338.1261523.fwd	PATRIC	CDS	1261338	1261523	186	+		61	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1211	PATRIC.2.9855.2.9855.con.0001.CDS.1261665.1261841.fwd	PATRIC	CDS	1261665	1261841	177	+		58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1212	PATRIC.2.9855.2.9855.con.0001.CDS.1261842.1262150.fwd	PATRIC	CDS	1261842	1262150	309	+		102	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1213	PATRIC.2.9855.2.9855.con.0001.CDS.1262291.1262668.fwd	PATRIC	CDS	1262291	1262668	378	+		125	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1214	PATRIC.2.9855.2.9855.con.0001.CDS.1262796.1263698.fwd	PATRIC	CDS	1262796	1263698	903	+		300	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1215	PATRIC.2.9855.2.9855.con.0001.CDS.1263714.1264370.fwd	PATRIC	CDS	1263714	1264370	657	+		218	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1216	PATRIC.2.9855.2.9855.con.0001.CDS.1264373.1264678.fwd	PATRIC	CDS	1264373	1264678	306	+		101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1217	PATRIC.2.9855.2.9855.con.0001.CDS.1264678.1264869.fwd	PATRIC	CDS	1264678	1264869	192	+		63	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1220	PATRIC.2.9855.2.9855.con.0001.CDS.1267578.1267730.fwd	PATRIC	CDS	1267578	1267730	153	+		50	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1221	PATRIC.2.9855.2.9855.con.0001.CDS.1267884.1269335.fwd	PATRIC	CDS	1267884	1269335	1452	+		483	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1222	PATRIC.2.9855.2.9855.con.0001.CDS.1269611.1270216.fwd	PATRIC	CDS	1269611	1270216	606	+		201	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1223	PATRIC.2.9855.2.9855.con.0001.CDS.1270420.1271106.fwd	PATRIC	CDS	1270420	1271106	687	+		228	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1224	PATRIC.2.9855.2.9855.con.0001.CDS.1271167.1272327.fwd	PATRIC	CDS	1271167	1272327	1161	+		386	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1225	PATRIC.2.9855.2.9855.con.0001.CDS.1272395.1273555.fwd	PATRIC	CDS	1272395	1273555	1161	+		386	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1226	PATRIC.2.9855.2.9855.con.0001.CDS.1273729.1273998.fwd	PATRIC	CDS	1273729	1273998	270	+		89	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1227	PATRIC.2.9855.2.9855.con.0001.CDS.1274203.1274844.fwd	PATRIC	CDS	1274203	1274844	642	+		213	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1229	PATRIC.2.9855.2.9855.con.0001.CDS.1275780.1276061.fwd	PATRIC	CDS	1275780	1276061	282	+		93	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1230	PATRIC.2.9855.2.9855.con.0001.CDS.1276074.1276475.fwd	PATRIC	CDS	1276074	1276475	402	+		133	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1231	PATRIC.2.9855.2.9855.con.0001.CDS.1276475.1276918.fwd	PATRIC	CDS	1276475	1276918	444	+		147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1232	PATRIC.2.9855.2.9855.con.0001.CDS.1276920.1277300.fwd	PATRIC	CDS	1276920	1277300	381	+		126	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1233	PATRIC.2.9855.2.9855.con.0001.CDS.1277300.1277740.fwd	PATRIC	CDS	1277300	1277740	441	+		146	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1234	PATRIC.2.9855.2.9855.con.0001.CDS.1277763.1278578.fwd	PATRIC	CDS	1277763	1278578	816	+		271	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1235	PATRIC.2.9855.2.9855.con.0001.CDS.1278600.1279259.fwd	PATRIC	CDS	1278600	1279259	660	+	PGF_08225224	219	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1236	PATRIC.2.9855.2.9855.con.0001.CDS.1279320.1284785.fwd	PATRIC	CDS	1279320	1284785	5466	+	PGF_08225224	1821	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1237	PATRIC.2.9855.2.9855.con.0001.CDS.1284799.1285485.fwd	PATRIC	CDS	1284799	1285485	687	+		228	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1238	PATRIC.2.9855.2.9855.con.0001.CDS.1285485.1287266.fwd	PATRIC	CDS	1285485	1287266	1782	+	PGF_00760094	593	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1239	PATRIC.2.9855.2.9855.con.0001.CDS.1287336.1287737.fwd	PATRIC	CDS	1287336	1287737	402	+		133	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1241	PATRIC.2.9855.2.9855.con.0001.CDS.1288797.1289633.fwd	PATRIC	CDS	1288797	1289633	837	+		278	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1242	PATRIC.2.9855.2.9855.con.0001.CDS.1289651.1291132.fwd	PATRIC	CDS	1289651	1291132	1482	+		493	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1243	PATRIC.2.9855.2.9855.con.0001.CDS.1291145.1291555.fwd	PATRIC	CDS	1291145	1291555	411	+	PGF_07008306	136	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1244	PATRIC.2.9855.2.9855.con.0001.CDS.1291555.1291710.fwd	PATRIC	CDS	1291555	1291710	156	+	PGF_08036572	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1245	PATRIC.2.9855.2.9855.con.0001.CDS.1291832.1292071.fwd	PATRIC	CDS	1291832	1292071	240	+		79	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1246	PATRIC.2.9855.2.9855.con.0001.CDS.1292090.1292599.fwd	PATRIC	CDS	1292090	1292599	510	+	PGF_01270000	169	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1247	PATRIC.2.9855.2.9855.con.0001.CDS.1292659.1293420.fwd	PATRIC	CDS	1292659	1293420	762	+	PGF_01312648	253	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1248	PATRIC.2.9855.2.9855.con.0001.CDS.1293733.1293837.rev	PATRIC	CDS	1293733	1293837	105	-		34	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1249	PATRIC.2.9855.2.9855.con.0001.CDS.1294079.1294204.fwd	PATRIC	CDS	1294079	1294204	126	+		41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1250	PATRIC.2.9855.2.9855.con.0001.CDS.1294225.1294488.rev	PATRIC	CDS	1294225	1294488	264	-		87	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1251	PATRIC.2.9855.2.9855.con.0001.CDS.1294530.1294865.fwd	PATRIC	CDS	1294530	1294865	336	+		111	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1252	PATRIC.2.9855.2.9855.con.0001.CDS.1294881.1295096.fwd	PATRIC	CDS	1294881	1295096	216	+		71	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1253	PATRIC.2.9855.2.9855.con.0001.CDS.1295086.1297065.fwd	PATRIC	CDS	1295086	1297065	1980	+		659	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1256	PATRIC.2.9855.2.9855.con.0001.CDS.1298798.1299025.fwd	PATRIC	CDS	1298798	1299025	228	+		75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1257	PATRIC.2.9855.2.9855.con.0001.CDS.1299169.1299657.fwd	PATRIC	CDS	1299169	1299657	489	+		162	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1258	PATRIC.2.9855.2.9855.con.0001.CDS.1299932.1300309.rev	PATRIC	CDS	1299932	1300309	378	-		125	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1259	PATRIC.2.9855.2.9855.con.0001.CDS.1300314.1300796.rev	PATRIC	CDS	1300314	1300796	483	-		160	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1260	PATRIC.2.9855.2.9855.con.0001.CDS.1300979.1301398.fwd	PATRIC	CDS	1300979	1301398	420	+		139	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1264	PATRIC.2.9855.2.9855.con.0001.CDS.1305328.1305537.fwd	PATRIC	CDS	1305328	1305537	210	+		69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1267	PATRIC.2.9855.2.9855.con.0001.CDS.1307161.1307667.fwd	PATRIC	CDS	1307161	1307667	507	+	PGF_10560490	168	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1268	PATRIC.2.9855.2.9855.con.0001.CDS.1307737.1307856.fwd	PATRIC	CDS	1307737	1307856	120	+	PGF_07246530	39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1272	PATRIC.2.9855.2.9855.con.0001.CDS.1310301.1310618.rev	PATRIC	CDS	1310301	1310618	318	-	PGF_01005459	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1280	PATRIC.2.9855.2.9855.con.0001.CDS.1315585.1315890.fwd	PATRIC	CDS	1315585	1315890	306	+	PGF_01254208	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1282	PATRIC.2.9855.2.9855.con.0001.CDS.1316438.1316893.fwd	PATRIC	CDS	1316438	1316893	456	+	PGF_07475370	151	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1283	PATRIC.2.9855.2.9855.con.0001.CDS.1316978.1317322.fwd	PATRIC	CDS	1316978	1317322	345	+	PGF_08225224	114	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1284	PATRIC.2.9855.2.9855.con.0001.CDS.1317347.1317703.fwd	PATRIC	CDS	1317347	1317703	357	+	PGF_01289709	118	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1289	PATRIC.2.9855.2.9855.con.0001.CDS.1322346.1322903.fwd	PATRIC	CDS	1322346	1322903	558	+	PGF_08225224	185	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1293	PATRIC.2.9855.2.9855.con.0001.CDS.1325908.1326456.fwd	PATRIC	CDS	1325908	1326456	549	+	PGF_02783859	182	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1294	PATRIC.2.9855.2.9855.con.0001.CDS.1326783.1327943.fwd	PATRIC	CDS	1326783	1327943	1161	+	PGF_01282238	386	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1295	PATRIC.2.9855.2.9855.con.0001.CDS.1328066.1328179.fwd	PATRIC	CDS	1328066	1328179	114	+		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1298	PATRIC.2.9855.2.9855.con.0001.CDS.1330237.1330668.fwd	PATRIC	CDS	1330237	1330668	432	+	PGF_01282398	143	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1302	PATRIC.2.9855.2.9855.con.0001.CDS.1333798.1334907.fwd	PATRIC	CDS	1333798	1334907	1110	+	PGF_08225224	369	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1304	PATRIC.2.9855.2.9855.con.0001.CDS.1336258.1336446.fwd	PATRIC	CDS	1336258	1336446	189	+	PGF_07405275	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1305	PATRIC.2.9855.2.9855.con.0001.CDS.1336561.1336839.fwd	PATRIC	CDS	1336561	1336839	279	+	PGF_01289711	92	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1306	PATRIC.2.9855.2.9855.con.0001.CDS.1336998.1337414.fwd	PATRIC	CDS	1336998	1337414	417	+	PGF_02970543	138	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1310	PATRIC.2.9855.2.9855.con.0001.CDS.1341017.1341478.fwd	PATRIC	CDS	1341017	1341478	462	+	PGF_03969001	153	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1311	PATRIC.2.9855.2.9855.con.0001.CDS.1341599.1341916.rev	PATRIC	CDS	1341599	1341916	318	-	PGF_01296568	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1314	PATRIC.2.9855.2.9855.con.0001.CDS.1344033.1344872.rev	PATRIC	CDS	1344033	1344872	840	-	PGF_08549140	279	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1315	PATRIC.2.9855.2.9855.con.0001.CDS.1345291.1346313.fwd	PATRIC	CDS	1345291	1346313	1023	+	PGF_08225224	340	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1317	PATRIC.2.9855.2.9855.con.0001.CDS.1347517.1347990.fwd	PATRIC	CDS	1347517	1347990	474	+	PGF_00675550	157	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1327	PATRIC.2.9855.2.9855.con.0001.CDS.1356934.1357470.fwd	PATRIC	CDS	1356934	1357470	537	+	PGF_12700102	178	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1328	PATRIC.2.9855.2.9855.con.0001.CDS.1357544.1358029.fwd	PATRIC	CDS	1357544	1358029	486	+	PGF_10308155	161	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1329	PATRIC.2.9855.2.9855.con.0001.CDS.1358192.1358950.fwd	PATRIC	CDS	1358192	1358950	759	+	PGF_08187303	252	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1334	PATRIC.2.9855.2.9855.con.0001.CDS.1361437.1361646.fwd	PATRIC	CDS	1361437	1361646	210	+	PGF_01283379	69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1338	PATRIC.2.9855.2.9855.con.0001.CDS.1364864.1364989.fwd	PATRIC	CDS	1364864	1364989	126	+	PGF_01276065	41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1341	PATRIC.2.9855.2.9855.con.0001.CDS.1366790.1366909.fwd	PATRIC	CDS	1366790	1366909	120	+	PGF_08225224	39	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1342	PATRIC.2.9855.2.9855.con.0001.CDS.1366903.1367316.fwd	PATRIC	CDS	1366903	1367316	414	+	PGF_08225224	137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1344	PATRIC.2.9855.2.9855.con.0001.CDS.1368085.1368384.fwd	PATRIC	CDS	1368085	1368384	300	+	PGF_01284226	99	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1346	PATRIC.2.9855.2.9855.con.0001.CDS.1369553.1369807.fwd	PATRIC	CDS	1369553	1369807	255	+		84	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1350	PATRIC.2.9855.2.9855.con.0001.CDS.1372492.1373058.rev	PATRIC	CDS	1372492	1373058	567	-	PGF_08225224	188	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1353	PATRIC.2.9855.2.9855.con.0001.CDS.1375417.1375731.rev	PATRIC	CDS	1375417	1375731	315	-	PGF_01280860	104	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1354	PATRIC.2.9855.2.9855.con.0001.CDS.1375978.1376517.rev	PATRIC	CDS	1375978	1376517	540	-	PGF_01322673	179	hypothetical protein formerly called flagellar hook-length control protein FliK
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1355	PATRIC.2.9855.2.9855.con.0001.CDS.1376975.1377166.fwd	PATRIC	CDS	1376975	1377166	192	+	PGF_07202428	63	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1361	PATRIC.2.9855.2.9855.con.0001.CDS.1386830.1387336.fwd	PATRIC	CDS	1386830	1387336	507	+	PGF_01283165	168	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1362	PATRIC.2.9855.2.9855.con.0001.CDS.1387411.1388076.rev	PATRIC	CDS	1387411	1388076	666	-	PGF_00135552	221	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1363	PATRIC.2.9855.2.9855.con.0001.CDS.1388277.1388399.fwd	PATRIC	CDS	1388277	1388399	123	+	PGF_10486504	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1364	PATRIC.2.9855.2.9855.con.0001.CDS.1388568.1389002.fwd	PATRIC	CDS	1388568	1389002	435	+	PGF_01281383	144	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1367	PATRIC.2.9855.2.9855.con.0001.CDS.1390984.1391388.fwd	PATRIC	CDS	1390984	1391388	405	+	PGF_01281346	134	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1371	PATRIC.2.9855.2.9855.con.0001.CDS.1395478.1395801.fwd	PATRIC	CDS	1395478	1395801	324	+	PGF_01282435	107	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1375	PATRIC.2.9855.2.9855.con.0001.CDS.1398032.1398685.fwd	PATRIC	CDS	1398032	1398685	654	+	PGF_08225224	217	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1376	PATRIC.2.9855.2.9855.con.0001.CDS.1398859.1399020.fwd	PATRIC	CDS	1398859	1399020	162	+	PGF_08225224	53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1378	PATRIC.2.9855.2.9855.con.0001.CDS.1399654.1401324.fwd	PATRIC	CDS	1399654	1401324	1671	+	PGF_08225224	556	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1379	PATRIC.2.9855.2.9855.con.0001.CDS.1401342.1401653.fwd	PATRIC	CDS	1401342	1401653	312	+	PGF_01284291	103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1380	PATRIC.2.9855.2.9855.con.0001.CDS.1401688.1401861.fwd	PATRIC	CDS	1401688	1401861	174	+	PGF_01253927	57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1381	PATRIC.2.9855.2.9855.con.0001.CDS.1402023.1402256.fwd	PATRIC	CDS	1402023	1402256	234	+	PGF_00013376	77	Hypothetical protein, CF-8 family
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1382	PATRIC.2.9855.2.9855.con.0001.CDS.1402260.1402658.fwd	PATRIC	CDS	1402260	1402658	399	+	PGF_01270000	132	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1385	PATRIC.2.9855.2.9855.con.0001.CDS.1404578.1404928.fwd	PATRIC	CDS	1404578	1404928	351	+	PGF_00813290	116	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1389	PATRIC.2.9855.2.9855.con.0001.CDS.1410396.1411079.fwd	PATRIC	CDS	1410396	1411079	684	+	PGF_01456236	227	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1394	PATRIC.2.9855.2.9855.con.0001.CDS.1414959.1415294.fwd	PATRIC	CDS	1414959	1415294	336	+	PGF_01293823	111	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1403	PATRIC.2.9855.2.9855.con.0001.CDS.1425367.1426212.fwd	PATRIC	CDS	1425367	1426212	846	+	PGF_01305219	281	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1418	PATRIC.2.9855.2.9855.con.0001.CDS.1443492.1443725.fwd	PATRIC	CDS	1443492	1443725	234	+	PGF_08225224	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1420	PATRIC.2.9855.2.9855.con.0001.CDS.1444378.1444830.fwd	PATRIC	CDS	1444378	1444830	453	+	PGF_00364435	150	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1425	PATRIC.2.9855.2.9855.con.0001.CDS.1448900.1449244.fwd	PATRIC	CDS	1448900	1449244	345	+	PGF_01283345	114	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1429	PATRIC.2.9855.2.9855.con.0001.CDS.1452875.1454923.fwd	PATRIC	CDS	1452875	1454923	2049	+	PGF_08225224	682	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1430	PATRIC.2.9855.2.9855.con.0001.CDS.1455166.1455492.fwd	PATRIC	CDS	1455166	1455492	327	+	PGF_00426789	108	FIG00590374: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.124	PATRIC.2.9855.2.9855.con.0001.CDS.146051.146164.fwd	PATRIC	CDS	146051	146164	114	+		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.125	PATRIC.2.9855.2.9855.con.0001.CDS.146182.146454.fwd	PATRIC	CDS	146182	146454	273	+	PGF_01283384	90	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1440	PATRIC.2.9855.2.9855.con.0001.CDS.1466669.1467199.rev	PATRIC	CDS	1466669	1467199	531	-	PGF_00113841	176	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1447	PATRIC.2.9855.2.9855.con.0001.CDS.1473388.1474521.fwd	PATRIC	CDS	1473388	1474521	1134	+	PGF_00988851	377	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1448	PATRIC.2.9855.2.9855.con.0001.CDS.1474607.1474891.rev	PATRIC	CDS	1474607	1474891	285	-	PGF_01282321	94	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1463	PATRIC.2.9855.2.9855.con.0001.CDS.1493578.1493802.fwd	PATRIC	CDS	1493578	1493802	225	+	PGF_01282399	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1471	PATRIC.2.9855.2.9855.con.0001.CDS.1498496.1498780.fwd	PATRIC	CDS	1498496	1498780	285	+	PGF_01283647	94	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1472	PATRIC.2.9855.2.9855.con.0001.CDS.1499292.1499429.rev	PATRIC	CDS	1499292	1499429	138	-	PGF_10308203	45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1473	PATRIC.2.9855.2.9855.con.0001.CDS.1499706.1500689.fwd	PATRIC	CDS	1499706	1500689	984	+	PGF_08225224	327	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1474	PATRIC.2.9855.2.9855.con.0001.CDS.1500778.1500918.fwd	PATRIC	CDS	1500778	1500918	141	+	PGF_01047791	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1475	PATRIC.2.9855.2.9855.con.0001.CDS.1501196.1501366.fwd	PATRIC	CDS	1501196	1501366	171	+	PGF_01282732	56	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1476	PATRIC.2.9855.2.9855.con.0001.CDS.1501533.1501790.fwd	PATRIC	CDS	1501533	1501790	258	+	PGF_00973617	85	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1477	PATRIC.2.9855.2.9855.con.0001.CDS.1502016.1502186.fwd	PATRIC	CDS	1502016	1502186	171	+	PGF_01286330	56	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1478	PATRIC.2.9855.2.9855.con.0001.CDS.1502836.1503273.fwd	PATRIC	CDS	1502836	1503273	438	+	PGF_08225224	145	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1482	PATRIC.2.9855.2.9855.con.0001.CDS.1507584.1508072.fwd	PATRIC	CDS	1507584	1508072	489	+	PGF_01282322	162	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1486	PATRIC.2.9855.2.9855.con.0001.CDS.1512505.1512636.fwd	PATRIC	CDS	1512505	1512636	132	+	PGF_01263250	43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.130	PATRIC.2.9855.2.9855.con.0001.CDS.152130.152579.rev	PATRIC	CDS	152130	152579	450	-	PGF_01254052	149	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1494	PATRIC.2.9855.2.9855.con.0001.CDS.1521631.1521786.fwd	PATRIC	CDS	1521631	1521786	156	+	PGF_01284287	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1495	PATRIC.2.9855.2.9855.con.0001.CDS.1522091.1522351.fwd	PATRIC	CDS	1522091	1522351	261	+	PGF_01283337	86	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1496	PATRIC.2.9855.2.9855.con.0001.CDS.1522695.1522952.fwd	PATRIC	CDS	1522695	1522952	258	+	PGF_01281537	85	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1498	PATRIC.2.9855.2.9855.con.0001.CDS.1525004.1525174.fwd	PATRIC	CDS	1525004	1525174	171	+		56	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1499	PATRIC.2.9855.2.9855.con.0001.CDS.1525436.1526074.fwd	PATRIC	CDS	1525436	1526074	639	+	PGF_01281381	212	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1500	PATRIC.2.9855.2.9855.con.0001.CDS.1526510.1526899.fwd	PATRIC	CDS	1526510	1526899	390	+	PGF_08225224	129	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1507	PATRIC.2.9855.2.9855.con.0001.CDS.1534042.1534485.rev	PATRIC	CDS	1534042	1534485	444	-	PGF_01289928	147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1508	PATRIC.2.9855.2.9855.con.0001.CDS.1534764.1535555.fwd	PATRIC	CDS	1534764	1535555	792	+	PGF_08225224	263	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1509	PATRIC.2.9855.2.9855.con.0001.CDS.1535682.1536059.fwd	PATRIC	CDS	1535682	1536059	378	+	PGF_01283167	125	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1510	PATRIC.2.9855.2.9855.con.0001.CDS.1536587.1537132.fwd	PATRIC	CDS	1536587	1537132	546	+	PGF_03031932	181	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1513	PATRIC.2.9855.2.9855.con.0001.CDS.1538973.1539368.fwd	PATRIC	CDS	1538973	1539368	396	+	PGF_01269351	131	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1517	PATRIC.2.9855.2.9855.con.0001.CDS.1541698.1541862.rev	PATRIC	CDS	1541698	1541862	165	-	PGF_00936056	54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1518	PATRIC.2.9855.2.9855.con.0001.CDS.1542447.1542611.fwd	PATRIC	CDS	1542447	1542611	165	+	PGF_01280942	54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1523	PATRIC.2.9855.2.9855.con.0001.CDS.1549371.1549802.fwd	PATRIC	CDS	1549371	1549802	432	+	PGF_01280900	143	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1524	PATRIC.2.9855.2.9855.con.0001.CDS.1549941.1550324.fwd	PATRIC	CDS	1549941	1550324	384	+		127	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1533	PATRIC.2.9855.2.9855.con.0001.CDS.1556168.1556743.fwd	PATRIC	CDS	1556168	1556743	576	+	PGF_01293936	191	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1535	PATRIC.2.9855.2.9855.con.0001.CDS.1557494.1557622.fwd	PATRIC	CDS	1557494	1557622	129	+	PGF_08251595	42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1536	PATRIC.2.9855.2.9855.con.0001.CDS.1557692.1557841.fwd	PATRIC	CDS	1557692	1557841	150	+		49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1537	PATRIC.2.9855.2.9855.con.0001.CDS.1557897.1558226.fwd	PATRIC	CDS	1557897	1558226	330	+	PGF_01317555	109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1539	PATRIC.2.9855.2.9855.con.0001.CDS.1558770.1559078.fwd	PATRIC	CDS	1558770	1559078	309	+	PGF_08225224	102	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1540	PATRIC.2.9855.2.9855.con.0001.CDS.1559262.1559603.fwd	PATRIC	CDS	1559262	1559603	342	+	PGF_00862695	113	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1541	PATRIC.2.9855.2.9855.con.0001.CDS.1559751.1560134.fwd	PATRIC	CDS	1559751	1560134	384	+	PGF_01285519	127	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1542	PATRIC.2.9855.2.9855.con.0001.CDS.1560229.1560462.fwd	PATRIC	CDS	1560229	1560462	234	+	PGF_02899668	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1546	PATRIC.2.9855.2.9855.con.0001.CDS.1566300.1566809.fwd	PATRIC	CDS	1566300	1566809	510	+	PGF_01286983	169	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1548	PATRIC.2.9855.2.9855.con.0001.CDS.1568402.1568719.rev	PATRIC	CDS	1568402	1568719	318	-		PGF_01283233	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1550	PATRIC.2.9855.2.9855.con.0001.CDS.1569786.1570118.rev	PATRIC	CDS	1569786	1570118	333	-		PGF_07764778	110	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1551	PATRIC.2.9855.2.9855.con.0001.CDS.1570155.1570472.rev	PATRIC	CDS	1570155	1570472	318	-		PGF_07124081	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1552	PATRIC.2.9855.2.9855.con.0001.CDS.1570858.1571724.fwd	PATRIC	CDS	1570858	1571724	867	+		PGF_08361742	288	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1555	PATRIC.2.9855.2.9855.con.0001.CDS.1572909.1573292.rev	PATRIC	CDS	1572909	1573292	384	-		PGF_01278792	127	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1556	PATRIC.2.9855.2.9855.con.0001.CDS.1573297.1574145.rev	PATRIC	CDS	1573297	1574145	849	-		PGF_01289569	282	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1557	PATRIC.2.9855.2.9855.con.0001.CDS.1574494.1575168.fwd	PATRIC	CDS	1574494	1575168	675	+		PGF_00109561	224	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1558	PATRIC.2.9855.2.9855.con.0001.CDS.1575350.1576108.fwd	PATRIC	CDS	1575350	1576108	759	+		PGF_06963150	252	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1559	PATRIC.2.9855.2.9855.con.0001.CDS.1576398.1577027.fwd	PATRIC	CDS	1576398	1577027	630	+		PGF_01283192	209	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1561	PATRIC.2.9855.2.9855.con.0001.CDS.1578267.1578551.fwd	PATRIC	CDS	1578267	1578551	285	+		PGF_12955843	94	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1565	PATRIC.2.9855.2.9855.con.0001.CDS.1583987.1584604.fwd	PATRIC	CDS	1583987	1584604	618	+		PGF_00826940	205	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1567	PATRIC.2.9855.2.9855.con.0001.CDS.1590316.1590435.rev	PATRIC	CDS	1590316	1590435	120	-			39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1568	PATRIC.2.9855.2.9855.con.0001.CDS.1591101.1591955.fwd	PATRIC	CDS	1591101	1591955	855	+		PGF_08225224	284	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1569	PATRIC.2.9855.2.9855.con.0001.CDS.1591991.1592947.fwd	PATRIC	CDS	1591991	1592947	957	+		PGF_12845931	318	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1570	PATRIC.2.9855.2.9855.con.0001.CDS.1592994.1594625.fwd	PATRIC	CDS	1592994	1594625	1632	+		PGF_08225224	543	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1571	PATRIC.2.9855.2.9855.con.0001.CDS.1594626.1595465.fwd	PATRIC	CDS	1594626	1595465	840	+		PGF_08225224	279	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1572	PATRIC.2.9855.2.9855.con.0001.CDS.1595734.1595928.rev	PATRIC	CDS	1595734	1595928	195	-			64	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1573	PATRIC.2.9855.2.9855.con.0001.CDS.1595954.1596187.rev	PATRIC	CDS	1595954	1596187	234	-		PGF_01300704	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1574	PATRIC.2.9855.2.9855.con.0001.CDS.1596433.1596876.rev	PATRIC	CDS	1596433	1596876	444	-		PGF_01289997	147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1575	PATRIC.2.9855.2.9855.con.0001.CDS.1597053.1597523.rev	PATRIC	CDS	1597053	1597523	471	-		PGF_01286659	156	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1576	PATRIC.2.9855.2.9855.con.0001.CDS.1597741.1597953.fwd	PATRIC	CDS	1597741	1597953	213	+		PGF_01290437	70	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1577	PATRIC.2.9855.2.9855.con.0001.CDS.1598303.1599217.fwd	PATRIC	CDS	1598303	1599217	915	+		PGF_06659490	304	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1583	PATRIC.2.9855.2.9855.con.0001.CDS.1603113.1603280.fwd	PATRIC	CDS	1603113	1603280	168	+		PGF_01271251	55	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1585	PATRIC.2.9855.2.9855.con.0001.CDS.1604928.1605542.fwd	PATRIC	CDS	1604928	1605542	615	+		PGF_01283199	204	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1586	PATRIC.2.9855.2.9855.con.0001.CDS.1605672.1605890.rev	PATRIC	CDS	1605672	1605890	219	-		PGF_00915583	72	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1587	PATRIC.2.9855.2.9855.con.0001.CDS.1606059.1606283.rev	PATRIC	CDS	1606059	1606283	225	-		PGF_01282349	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1588	PATRIC.2.9855.2.9855.con.0001.CDS.1606723.1607088.fwd	PATRIC	CDS	1606723	1607088	366	+		PGF_01261338	121	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1589	PATRIC.2.9855.2.9855.con.0001.CDS.1607350.1607967.fwd	PATRIC	CDS	1607350	1607967	618	+		PGF_00212552	205	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1590	PATRIC.2.9855.2.9855.con.0001.CDS.1608057.1608578.fwd	PATRIC	CDS	1608057	1608578	522	+		PGF_00124964	173	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1591	PATRIC.2.9855.2.9855.con.0001.CDS.1608788.1609240.fwd	PATRIC	CDS	1608788	1609240	453	+		PGF_01299695	150	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1592	PATRIC.2.9855.2.9855.con.0001.CDS.1609645.1610307.fwd	PATRIC	CDS	1609645	1610307	663	+		PGF_01299694	220	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1593	PATRIC.2.9855.2.9855.con.0001.CDS.1610489.1610830.fwd	PATRIC	CDS	1610489	1610830	342	+		PGF_01299693	113	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.137	PATRIC.2.9855.2.9855.con.0001.CDS.161502.161753.fwd	PATRIC	CDS	161502	161753	252	+		PGF_08225224	83	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1596	PATRIC.2.9855.2.9855.con.0001.CDS.1615189.1615998.fwd	PATRIC	CDS	1615189	1615998	810	+		PGF_06968345	269	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1601	PATRIC.2.9855.2.9855.con.0001.CDS.1620755.1620919.rev	PATRIC	CDS	1620755	1620919	165	-		PGF_01295556	54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1606	PATRIC.2.9855.2.9855.con.0001.CDS.1623933.1624901.rev	PATRIC	CDS	1623933	1624901	969	-		PGF_08225224	322	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1608	PATRIC.2.9855.2.9855.con.0001.CDS.1626129.1626269.fwd	PATRIC	CDS	1626129	1626269	141	+			46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1609	PATRIC.2.9855.2.9855.con.0001.CDS.1626736.1627362.fwd	PATRIC	CDS	1626736	1627362	627	+			208	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1610	PATRIC.2.9855.2.9855.con.0001.CDS.1627502.1627741.fwd	PATRIC	CDS	1627502	1627741	240	+			79	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1611	PATRIC.2.9855.2.9855.con.0001.CDS.1627837.1628214.fwd	PATRIC	CDS	1627837	1628214	378	+			125	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1612	PATRIC.2.9855.2.9855.con.0001.CDS.1628300.1628764.fwd	PATRIC	CDS	1628300	1628764	465	+		PGF_01253531	154	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1613	PATRIC.2.9855.2.9855.con.0001.CDS.1628774.1628935.fwd	PATRIC	CDS	1628774	1628935	162	+			53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1614	PATRIC.2.9855.2.9855.con.0001.CDS.1629006.1629338.fwd	PATRIC	CDS	1629006	1629338	333	+		PGF_01291395	110	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1615	PATRIC.2.9855.2.9855.con.0001.CDS.1629402.1629650.fwd	PATRIC	CDS	1629402	1629650	249	+			82	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1616	PATRIC.2.9855.2.9855.con.0001.CDS.1629831.1630238.fwd	PATRIC	CDS	1629831	1630238	408	+		PGF_01255474	135	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1617	PATRIC.2.9855.2.9855.con.0001.CDS.1630397.1630663.fwd	PATRIC	CDS	1630397	1630663	267	+			88	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1618	PATRIC.2.9855.2.9855.con.0001.CDS.1630744.1631238.fwd	PATRIC	CDS	1630744	1631238	495	+		PGF_01326384	164	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1619	PATRIC.2.9855.2.9855.con.0001.CDS.1631451.1631786.fwd	PATRIC	CDS	1631451	1631786	336	+		PGF_01287553	111	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1620	PATRIC.2.9855.2.9855.con.0001.CDS.1631839.1632117.fwd	PATRIC	CDS	1631839	1632117	279	+		PGF_07072662	92	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1621	PATRIC.2.9855.2.9855.con.0001.CDS.1632438.1632839.fwd	PATRIC	CDS	1632438	1632839	402	+		PGF_01281805	133	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1622	PATRIC.2.9855.2.9855.con.0001.CDS.1632894.1633094.fwd	PATRIC	CDS	1632894	1633094	201	+		PGF_06403110	66	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1624	PATRIC.2.9855.2.9855.con.0001.CDS.1634242.1634712.fwd	PATRIC	CDS	1634242	1634712	471	+		PGF_10486504	156	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1625	PATRIC.2.9855.2.9855.con.0001.CDS.1634787.1634933.fwd	PATRIC	CDS	1634787	1634933	147	+			48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1628	PATRIC.2.9855.2.9855.con.0001.CDS.1637767.1637907.fwd	PATRIC	CDS	1637767	1637907	141	+		PGF_01284145	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1630	PATRIC.2.9855.2.9855.con.0001.CDS.1638627.1639622.fwd	PATRIC	CDS	1638627	1639622	996	+		PGF_01289596	331	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1631	PATRIC.2.9855.2.9855.con.0001.CDS.1639780.1640286.fwd	PATRIC	CDS	1639780	1640286	507	+		PGF_12718765	168	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1635	PATRIC.2.9855.2.9855.con.0001.CDS.1644493.1646199.fwd	PATRIC	CDS	1644493	1646199	1707	+		PGF_08225224	568	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1637	PATRIC.2.9855.2.9855.con.0001.CDS.1647439.1647630.fwd	PATRIC	CDS	1647439	1647630	192	+			63	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1639	PATRIC.2.9855.2.9855.con.0001.CDS.1649013.1649582.fwd	PATRIC	CDS	1649013	1649582	570	+		PGF_01284504	189	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1640	PATRIC.2.9855.2.9855.con.0001.CDS.1649718.1649852.fwd	PATRIC	CDS	1649718	1649852	135	+			44	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1641	PATRIC.2.9855.2.9855.con.0001.CDS.1649963.1650784.fwd	PATRIC	CDS	1649963	1650784	822	+		PGF_00865716	273	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1642	PATRIC.2.9855.2.9855.con.0001.CDS.1650774.1654139.fwd	PATRIC	CDS	1650774	1654139	3366	+		PGF_08225224	1121	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1643	PATRIC.2.9855.2.9855.con.0001.CDS.1654247.1654378.fwd	PATRIC	CDS	1654247	1654378	132	+			43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1644	PATRIC.2.9855.2.9855.con.0001.CDS.1654453.1655052.fwd	PATRIC	CDS	1654453	1655052	600	+			199	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1645	PATRIC.2.9855.2.9855.con.0001.CDS.1655347.1655886.fwd	PATRIC	CDS	1655347	1655886	540	+			179	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1646	PATRIC.2.9855.2.9855.con.0001.CDS.1655887.1659669.fwd	PATRIC	CDS	1655887	1659669	3783	+			1260	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1650	PATRIC.2.9855.2.9855.con.0001.CDS.1667415.1667693.fwd	PATRIC	CDS	1667415	1667693	279	+		PGF_01285518	92	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1653	PATRIC.2.9855.2.9855.con.0001.CDS.1669287.1669529.rev	PATRIC	CDS	1669287	1669529	243	-		PGF_00788155	80	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1655	PATRIC.2.9855.2.9855.con.0001.CDS.1670328.1671680.rev	PATRIC	CDS	1670328	1671680	1353	-		PGF_10514785	450	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1659	PATRIC.2.9855.2.9855.con.0001.CDS.1674569.1674751.fwd	PATRIC	CDS	1674569	1674751	183	+		PGF_04032346	60	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1666	PATRIC.2.9855.2.9855.con.0001.CDS.1679039.1679191.fwd	PATRIC	CDS	1679039	1679191	153	+		PGF_01269897	50	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1669	PATRIC.2.9855.2.9855.con.0001.CDS.1680673.1680789.rev	PATRIC	CDS	1680673	1680789	117	-			38	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1670	PATRIC.2.9855.2.9855.con.0001.CDS.1681128.1681574.fwd	PATRIC	CDS	1681128	1681574	447	+	PGF_02943552	148	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1672	PATRIC.2.9855.2.9855.con.0001.CDS.1682262.1682801.fwd	PATRIC	CDS	1682262	1682801	540	+	PGF_10547644	179	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1678	PATRIC.2.9855.2.9855.con.0001.CDS.1687557.1687934.rev	PATRIC	CDS	1687557	1687934	378	-	PGF_00308376	125	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1679	PATRIC.2.9855.2.9855.con.0001.CDS.1687985.1688308.rev	PATRIC	CDS	1687985	1688308	324	-	PGF_01282325	107	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1681	PATRIC.2.9855.2.9855.con.0001.CDS.1689805.1690653.rev	PATRIC	CDS	1689805	1690653	849	-	PGF_01289569	282	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1682	PATRIC.2.9855.2.9855.con.0001.CDS.1691490.1691870.fwd	PATRIC	CDS	1691490	1691870	381	+	PGF_07346538	126	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1697	PATRIC.2.9855.2.9855.con.0001.CDS.1709063.1709326.fwd	PATRIC	CDS	1709063	1709326	264	+	PGF_01284234	87	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1698	PATRIC.2.9855.2.9855.con.0001.CDS.1709574.1710092.rev	PATRIC	CDS	1709574	1710092	519	-	PGF_10409313	172	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1699	PATRIC.2.9855.2.9855.con.0001.CDS.1710387.1711157.fwd	PATRIC	CDS	1710387	1711157	771	+	PGF_08225224	256	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1700	PATRIC.2.9855.2.9855.con.0001.CDS.1711282.1711488.rev	PATRIC	CDS	1711282	1711488	207	-	PGF_01261178	68	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1702	PATRIC.2.9855.2.9855.con.0001.CDS.1712572.1712709.rev	PATRIC	CDS	1712572	1712709	138	-	PGF_01262262	45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1704	PATRIC.2.9855.2.9855.con.0001.CDS.1713576.1713818.rev	PATRIC	CDS	1713576	1713818	243	-	PGF_01286084	80	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1709	PATRIC.2.9855.2.9855.con.0001.CDS.1720862.1721617.fwd	PATRIC	CDS	1720862	1721617	756	+	PGF_10536983	251	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1714	PATRIC.2.9855.2.9855.con.0001.CDS.1726012.1727412.fwd	PATRIC	CDS	1726012	1727412	1401	+	PGF_08225224	466	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1717	PATRIC.2.9855.2.9855.con.0001.CDS.1733002.1733166.fwd	PATRIC	CDS	1733002	1733166	165	+	PGF_06491897	54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1725	PATRIC.2.9855.2.9855.con.0001.CDS.1743117.1743278.rev	PATRIC	CDS	1743117	1743278	162	-	PGF_01281978	53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1730	PATRIC.2.9855.2.9855.con.0001.CDS.1748943.1749242.fwd	PATRIC	CDS	1748943	1749242	300	+	PGF_02791623	99	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1731	PATRIC.2.9855.2.9855.con.0001.CDS.1749636.1749896.fwd	PATRIC	CDS	1749636	1749896	261	+	PGF_10392208	86	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1733	PATRIC.2.9855.2.9855.con.0001.CDS.1750480.1751049.fwd	PATRIC	CDS	1750480	1751049	570	+	PGF_08225224	189	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1747	PATRIC.2.9855.2.9855.con.0001.CDS.1769943.1770263.rev	PATRIC	CDS	1769943	1770263	321	-	PGF_08225224	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1748	PATRIC.2.9855.2.9855.con.0001.CDS.1770441.1771691.fwd	PATRIC	CDS	1770441	1771691	1251	+	PGF_03237127	416	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1751	PATRIC.2.9855.2.9855.con.0001.CDS.1774751.1775026.rev	PATRIC	CDS	1774751	1775026	276	-	PGF_08225224	91	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1753	PATRIC.2.9855.2.9855.con.0001.CDS.1776817.1777755.fwd	PATRIC	CDS	1776817	1777755	939	+	PGF_10491990	312	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.149	PATRIC.2.9855.2.9855.con.0001.CDS.178021.179001.fwd	PATRIC	CDS	178021	179001	981	+	PGF_10482923	326	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1760	PATRIC.2.9855.2.9855.con.0001.CDS.1783744.1784019.fwd	PATRIC	CDS	1783744	1784019	276	+	PGF_08065547	91	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1766	PATRIC.2.9855.2.9855.con.0001.CDS.1792567.1792734.fwd	PATRIC	CDS	1792567	1792734	168	+	PGF_01285451	55	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1767	PATRIC.2.9855.2.9855.con.0001.CDS.1792943.1793083.rev	PATRIC	CDS	1792943	1793083	141	-	PGF_01285061	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1768	PATRIC.2.9855.2.9855.con.0001.CDS.1793375.1793545.fwd	PATRIC	CDS	1793375	1793545	171	+	PGF_01286006	56	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1770	PATRIC.2.9855.2.9855.con.0001.CDS.1794686.1794814.rev	PATRIC	CDS	1794686	1794814	129	-	PGF_06909830	42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1771	PATRIC.2.9855.2.9855.con.0001.CDS.1795070.1795387.rev	PATRIC	CDS	1795070	1795387	318	-	PGF_01285318	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1772	PATRIC.2.9855.2.9855.con.0001.CDS.1795685.1795822.fwd	PATRIC	CDS	1795685	1795822	138	+		45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1774	PATRIC.2.9855.2.9855.con.0001.CDS.1797099.1797929.fwd	PATRIC	CDS	1797099	1797929	831	+	PGF_12877955	276	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1784	PATRIC.2.9855.2.9855.con.0001.CDS.1806350.1806493.fwd	PATRIC	CDS	1806350	1806493	144	+		47	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1786	PATRIC.2.9855.2.9855.con.0001.CDS.1807992.1808471.rev	PATRIC	CDS	1807992	1808471	480	-	PGF_01326781	159	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1787	PATRIC.2.9855.2.9855.con.0001.CDS.1808656.1809318.rev	PATRIC	CDS	1808656	1809318	663	-	PGF_10566978	220	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1788	PATRIC.2.9855.2.9855.con.0001.CDS.1809350.1810504.rev	PATRIC	CDS	1809350	1810504	1155	-	PGF_00669990	384	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1791	PATRIC.2.9855.2.9855.con.0001.CDS.1815582.1815932.fwd	PATRIC	CDS	1815582	1815932	351	+	PGF_01284355	116	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1794	PATRIC.2.9855.2.9855.con.0001.CDS.1818330.1818698.fwd	PATRIC	CDS	1818330	1818698	369	+	PGF_07461887	122	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1795	PATRIC.2.9855.2.9855.con.0001.CDS.1818977.1819732.fwd	PATRIC	CDS	1818977	1819732	756	+	PGF_08225224	251	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1797	PATRIC.2.9855.2.9855.con.0001.CDS.1821402.1821947.rev	PATRIC	CDS	1821402	1821947	546	-	PGF_01304545	181	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1798	PATRIC.2.9855.2.9855.con.0001.CDS.1822289.1822402.fwd	PATRIC	CDS	1822289	1822402	114	+		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1800	PATRIC.2.9855.2.9855.con.0001.CDS.1823599.1823928.fwd	PATRIC	CDS	1823599	1823928	330	+	PGF_01285450	109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1810	PATRIC.2.9855.2.9855.con.0001.CDS.1836007.1836315.fwd	PATRIC	CDS	1836007	1836315	309	+	PGF_00013373	102	Hypothetical protein, CF-29 family
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1818	PATRIC.2.9855.2.9855.con.0001.CDS.1844619.1845437.fwd	PATRIC	CDS	1844619	1845437	819	+	PGF_06209011	272	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1821	PATRIC.2.9855.2.9855.con.0001.CDS.1848963.1849850.fwd	PATRIC	CDS	1848963	1849850	888	+	PGF_00128945	295	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1822	PATRIC.2.9855.2.9855.con.0001.CDS.1850080.1850523.fwd	PATRIC	CDS	1850080	1850523	444	+	PGF_01281391	147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1823	PATRIC.2.9855.2.9855.con.0001.CDS.1850592.1850798.fwd	PATRIC	CDS	1850592	1850798	207	+	PGF_01284239	68	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1837	PATRIC.2.9855.2.9855.con.0001.CDS.1863792.1864295.fwd	PATRIC	CDS	1863792	1864295	504	+	PGF_08225224	167	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1838	PATRIC.2.9855.2.9855.con.0001.CDS.1864463.1864693.fwd	PATRIC	CDS	1864463	1864693	231	+	PGF_01272223	76	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1839	PATRIC.2.9855.2.9855.con.0001.CDS.1864724.1865005.fwd	PATRIC	CDS	1864724	1865005	282	+	PGF_03140318	93	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1845	PATRIC.2.9855.2.9855.con.0001.CDS.1869968.1870162.fwd	PATRIC	CDS	1869968	1870162	195	+	PGF_08225224	64	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1849	PATRIC.2.9855.2.9855.con.0001.CDS.1873285.1873425.fwd	PATRIC	CDS	1873285	1873425	141	+		46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1852	PATRIC.2.9855.2.9855.con.0001.CDS.1875489.1875983.fwd	PATRIC	CDS	1875489	1875983	495	+	PGF_08225224	164	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1853	PATRIC.2.9855.2.9855.con.0001.CDS.1876061.1876600.fwd	PATRIC	CDS	1876061	1876600	540	+	PGF_12911669	179	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1865	PATRIC.2.9855.2.9855.con.0001.CDS.1885731.1885886.fwd	PATRIC	CDS	1885731	1885886	156	+		51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1866	PATRIC.2.9855.2.9855.con.0001.CDS.1885944.1886102.fwd	PATRIC	CDS	1885944	1886102	159	+	PGF_01285626	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1867	PATRIC.2.9855.2.9855.con.0001.CDS.1886123.1886428.rev	PATRIC	CDS	1886123	1886428	306	-	PGF_01310663	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1870	PATRIC.2.9855.2.9855.con.0001.CDS.1889627.1889746.rev	PATRIC	CDS	1889627	1889746	120	-	PGF_00915583	39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1871	PATRIC.2.9855.2.9855.con.0001.CDS.1889773.1890027.fwd	PATRIC	CDS	1889773	1890027	255	+	PGF_01280862	84	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1874	PATRIC.2.9855.2.9855.con.0001.CDS.1892388.1892861.fwd	PATRIC	CDS	1892388	1892861	474	+	PGF_00261890	157	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1875	PATRIC.2.9855.2.9855.con.0001.CDS.1893100.1893645.fwd	PATRIC	CDS	1893100	1893645	546	+	PGF_08225224	181	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1876	PATRIC.2.9855.2.9855.con.0001.CDS.1893654.1893776.fwd	PATRIC	CDS	1893654	1893776	123	+	PGF_08225224	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1878	PATRIC.2.9855.2.9855.con.0001.CDS.1896539.1897915.rev	PATRIC	CDS	1896539	1897915	1377	-	PGF_03237127	458	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1880	PATRIC.2.9855.2.9855.con.0001.CDS.1901414.1901776.fwd	PATRIC	CDS	1901414	1901776	363	+	PGF_02013948	120	Blr3520 protein homolog, hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1881	PATRIC.2.9855.2.9855.con.0001.CDS.1901837.1902202.rev	PATRIC	CDS	1901837	1902202	366	-	PGF_01264807	121	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1884	PATRIC.2.9855.2.9855.con.0001.CDS.1904442.1904840.rev	PATRIC	CDS	1904442	1904840	399	-	PGF_00113841	132	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1887	PATRIC.2.9855.2.9855.con.0001.CDS.1907126.1907272.rev	PATRIC	CDS	1907126	1907272	147	-		48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1891	PATRIC.2.9855.2.9855.con.0001.CDS.1911016.1911138.rev	PATRIC	CDS	1911016	1911138	123	-	PGF_10426466	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1893	PATRIC.2.9855.2.9855.con.0001.CDS.1912202.1912336.fwd	PATRIC	CDS	1912202	1912336	135	+	PGF_01088118	44	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.160	PATRIC.2.9855.2.9855.con.0001.CDS.191966.192409.rev	PATRIC	CDS	191966	192409	444	-	PGF_08225224	147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.161	PATRIC.2.9855.2.9855.con.0001.CDS.192593.192748.fwd	PATRIC	CDS	192593	192748	156	+		51	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1904	PATRIC.2.9855.2.9855.con.0001.CDS.1926374.1927717.fwd	PATRIC	CDS	1926374	1927717	1344	+		PGF_08225224	447	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.162	PATRIC.2.9855.2.9855.con.0001.CDS.192781.193608.fwd	PATRIC	CDS	192781	193608	828	+		PGF_04034218	275	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1917	PATRIC.2.9855.2.9855.con.0001.CDS.1945738.1945917.fwd	PATRIC	CDS	1945738	1945917	180	+		PGF_01284989	59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1918	PATRIC.2.9855.2.9855.con.0001.CDS.1948039.1948491.rev	PATRIC	CDS	1948039	1948491	453	-		PGF_08225224	150	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1925	PATRIC.2.9855.2.9855.con.0001.CDS.1959519.1959638.fwd	PATRIC	CDS	1959519	1959638	120	+			39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1936	PATRIC.2.9855.2.9855.con.0001.CDS.1974752.1975399.rev	PATRIC	CDS	1974752	1975399	648	-		PGF_08225224	215	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1937	PATRIC.2.9855.2.9855.con.0001.CDS.1975612.1975824.fwd	PATRIC	CDS	1975612	1975824	213	+		PGF_01285103	70	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1939	PATRIC.2.9855.2.9855.con.0001.CDS.1977361.1978251.rev	PATRIC	CDS	1977361	1978251	891	-		PGF_08225224	296	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1944	PATRIC.2.9855.2.9855.con.0001.CDS.1985276.1986613.fwd	PATRIC	CDS	1985276	1986613	1338	+		PGF_00940642	445	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1949	PATRIC.2.9855.2.9855.con.0001.CDS.1992417.1992545.rev	PATRIC	CDS	1992417	1992545	129	-		PGF_07165829	42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1952	PATRIC.2.9855.2.9855.con.0001.CDS.1996211.1996366.rev	PATRIC	CDS	1996211	1996366	156	-		PGF_12955838	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1960	PATRIC.2.9855.2.9855.con.0001.CDS.2008421.2008966.rev	PATRIC	CDS	2008421	2008966	546	-		PGF_08225224	181	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1961	PATRIC.2.9855.2.9855.con.0001.CDS.2009113.2009226.rev	PATRIC	CDS	2009113	2009226	114	-			37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1964	PATRIC.2.9855.2.9855.con.0001.CDS.2011665.2011973.fwd	PATRIC	CDS	2011665	2011973	309	+		PGF_08225224	102	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1968	PATRIC.2.9855.2.9855.con.0001.CDS.2015826.2016488.fwd	PATRIC	CDS	2015826	2016488	663	+		PGF_08225224	220	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1969	PATRIC.2.9855.2.9855.con.0001.CDS.2016880.2016999.fwd	PATRIC	CDS	2016880	2016999	120	+			39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1971	PATRIC.2.9855.2.9855.con.0001.CDS.2019325.2020863.fwd	PATRIC	CDS	2019325	2020863	1539	+		PGF_10456559	512	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1972	PATRIC.2.9855.2.9855.con.0001.CDS.2021493.2022155.fwd	PATRIC	CDS	2021493	2022155	663	+		PGF_08225224	220	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1976	PATRIC.2.9855.2.9855.con.0001.CDS.2025625.2026608.fwd	PATRIC	CDS	2025625	2026608	984	+		PGF_12704131	327	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1978	PATRIC.2.9855.2.9855.con.0001.CDS.2027931.2028812.fwd	PATRIC	CDS	2027931	2028812	882	+		PGF_08225224	293	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1982	PATRIC.2.9855.2.9855.con.0001.CDS.2032686.2032802.fwd	PATRIC	CDS	2032686	2032802	117	+			38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.172	PATRIC.2.9855.2.9855.con.0001.CDS.203609.205786.fwd	PATRIC	CDS	203609	205786	2178	+		PGF_08225224	725	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1993	PATRIC.2.9855.2.9855.con.0001.CDS.2046763.2046900.fwd	PATRIC	CDS	2046763	2046900	138	+			45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1996	PATRIC.2.9855.2.9855.con.0001.CDS.2051307.2051429.fwd	PATRIC	CDS	2051307	2051429	123	+			40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1997	PATRIC.2.9855.2.9855.con.0001.CDS.2051940.2053307.fwd	PATRIC	CDS	2051940	2053307	1368	+		PGF_07359272	455	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.1999	PATRIC.2.9855.2.9855.con.0001.CDS.2054403.2055575.fwd	PATRIC	CDS	2054403	2055575	1173	+		PGF_08225224	390	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2000	PATRIC.2.9855.2.9855.con.0001.CDS.2055722.2056138.fwd	PATRIC	CDS	2055722	2056138	417	+		PGF_01313152	138	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2002	PATRIC.2.9855.2.9855.con.0001.CDS.2057301.2057636.fwd	PATRIC	CDS	2057301	2057636	336	+			111	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.173	PATRIC.2.9855.2.9855.con.0001.CDS.205844.206269.fwd	PATRIC	CDS	205844	206269	426	+		PGF_08225224	141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2004	PATRIC.2.9855.2.9855.con.0001.CDS.2058663.2058836.fwd	PATRIC	CDS	2058663	2058836	174	+		PGF_00830184	57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2006	PATRIC.2.9855.2.9855.con.0001.CDS.2060112.2060372.fwd	PATRIC	CDS	2060112	2060372	261	+		PGF_08225224	86	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2007	PATRIC.2.9855.2.9855.con.0001.CDS.2060515.2060688.fwd	PATRIC	CDS	2060515	2060688	174	+		PGF_08225224	57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2008	PATRIC.2.9855.2.9855.con.0001.CDS.2060779.2061294.fwd	PATRIC	CDS	2060779	2061294	516	+		PGF_00381299	171	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2009	PATRIC.2.9855.2.9855.con.0001.CDS.2061518.2062027.fwd	PATRIC	CDS	2061518	2062027	510	+		PGF_00381299	169	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2010	PATRIC.2.9855.2.9855.con.0001.CDS.2062073.2064880.fwd	PATRIC	CDS	2062073	2064880	2808	+		PGF_08225224	935	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.174	PATRIC.2.9855.2.9855.con.0001.CDS.206297.206722.fwd	PATRIC	CDS	206297	206722	426	+		PGF_08225224	141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2011	PATRIC.2.9855.2.9855.con.0001.CDS.2064870.2066954.fwd	PATRIC	CDS	2064870	2066954	2085	+		PGF_08225224	694	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2012	PATRIC.2.9855.2.9855.con.0001.CDS.2066954.2067892.fwd	PATRIC	CDS	2066954	2067892	939	+		PGF_00392542	312	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2013	PATRIC.2.9855.2.9855.con.0001.CDS.2067901.2068605.fwd	PATRIC	CDS	2067901	2068605	705	+		PGF_01322510	234	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2014	PATRIC.2.9855.2.9855.con.0001.CDS.2068646.2069545.fwd	PATRIC	CDS	2068646	2069545	900	+		PGF_00217252	299	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2015	PATRIC.2.9855.2.9855.con.0001.CDS.2069859.2070422.fwd	PATRIC	CDS	2069859	2070422	564	+			187	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2018	PATRIC.2.9855.2.9855.con.0001.CDS.2073454.2074695.fwd	PATRIC	CDS	2073454	2074695	1242	+			413	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.176	PATRIC.2.9855.2.9855.con.0001.CDS.207425.207994.fwd	PATRIC	CDS	207425	207994	570	+		PGF_01312055	189	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2020	PATRIC.2.9855.2.9855.con.0001.CDS.2076896.2078215.fwd	PATRIC	CDS	2076896	2078215	1320	+			439	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2021	PATRIC.2.9855.2.9855.con.0001.CDS.2078398.2078547.fwd	PATRIC	CDS	2078398	2078547	150	+			49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2022	PATRIC.2.9855.2.9855.con.0001.CDS.2078876.2079949.fwd	PATRIC	CDS	2078876	2079949	1074	+		PGF_00646585	357	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.177	PATRIC.2.9855.2.9855.con.0001.CDS.208077.208577.fwd	PATRIC	CDS	208077	208577	501	+		PGF_08268603	166	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2025	PATRIC.2.9855.2.9855.con.0001.CDS.2084611.2087031.fwd	PATRIC	CDS	2084611	2087031	2421	+		PGF_08225224	806	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2027	PATRIC.2.9855.2.9855.con.0001.CDS.2088153.2088569.fwd	PATRIC	CDS	2088153	2088569	417	+		PGF_08225224	138	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2029	PATRIC.2.9855.2.9855.con.0001.CDS.2089636.2091177.fwd	PATRIC	CDS	2089636	2091177	1542	+		PGF_08225224	513	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.179	PATRIC.2.9855.2.9855.con.0001.CDS.209500.211338.fwd	PATRIC	CDS	209500	211338	1839	+		PGF_08225224	612	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2032	PATRIC.2.9855.2.9855.con.0001.CDS.2095189.2095278.rev	PATRIC	CDS	2095189	2095278	90	-			29	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2033	PATRIC.2.9855.2.9855.con.0001.CDS.2095416.2095541.fwd	PATRIC	CDS	2095416	2095541	126	+			41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2034	PATRIC.2.9855.2.9855.con.0001.CDS.2095666.2095983.fwd	PATRIC	CDS	2095666	2095983	318	+		PGF_08225224	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2035	PATRIC.2.9855.2.9855.con.0001.CDS.2096081.2096236.fwd	PATRIC	CDS	2096081	2096236	156	+			51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2036	PATRIC.2.9855.2.9855.con.0001.CDS.2096307.2097476.fwd	PATRIC	CDS	2096307	2097476	1170	+		PGF_01284237	389	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2040	PATRIC.2.9855.2.9855.con.0001.CDS.2103076.2103321.fwd	PATRIC	CDS	2103076	2103321	246	+		PGF_01292863	81	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2041	PATRIC.2.9855.2.9855.con.0001.CDS.2103318.2103698.fwd	PATRIC	CDS	2103318	2103698	381	+		PGF_01282620	126	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2045	PATRIC.2.9855.2.9855.con.0001.CDS.2108270.2108449.rev	PATRIC	CDS	2108270	2108449	180	-		PGF_01281633	59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2051	PATRIC.2.9855.2.9855.con.0001.CDS.2113325.2114254.rev	PATRIC	CDS	2113325	2114254	930	-		PGF_08225224	309	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.180	PATRIC.2.9855.2.9855.con.0001.CDS.211411.212691.fwd	PATRIC	CDS	211411	212691	1281	+		PGF_08225224	426	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2054	PATRIC.2.9855.2.9855.con.0001.CDS.2117571.2118671.rev	PATRIC	CDS	2117571	2118671	1101	-		PGF_01023927	366	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2063	PATRIC.2.9855.2.9855.con.0001.CDS.2126489.2127562.fwd	PATRIC	CDS	2126489	2127562	1074	+		PGF_08225224	357	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.181	PATRIC.2.9855.2.9855.con.0001.CDS.212688.213386.fwd	PATRIC	CDS	212688	213386	699	+		PGF_05095511	232	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.182	PATRIC.2.9855.2.9855.con.0001.CDS.213460.216090.fwd	PATRIC	CDS	213460	216090	2631	+		PGF_08225224	876	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2072	PATRIC.2.9855.2.9855.con.0001.CDS.2135513.2135662.fwd	PATRIC	CDS	2135513	2135662	150	+			49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2074	PATRIC.2.9855.2.9855.con.0001.CDS.2139402.2139902.fwd	PATRIC	CDS	2139402	2139902	501	+		PGF_01283163	166	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2075	PATRIC.2.9855.2.9855.con.0001.CDS.2139933.2140046.fwd	PATRIC	CDS	2139933	2140046	114	+			37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2077	PATRIC.2.9855.2.9855.con.0001.CDS.2143737.2144540.fwd	PATRIC	CDS	2143737	2144540	804	+		PGF_01253939	267	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2079	PATRIC.2.9855.2.9855.con.0001.CDS.2145655.2148102.fwd	PATRIC	CDS	2145655	2148102	2448	+		PGF_08225224	815	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2081	PATRIC.2.9855.2.9855.con.0001.CDS.2149346.2151112.fwd	PATRIC	CDS	2149346	2151112	1767	+		PGF_08225224	588	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2082	PATRIC.2.9855.2.9855.con.0001.CDS.2151135.2151524.fwd	PATRIC	CDS	2151135	2151524	390	+		PGF_01283215	129	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2093	PATRIC.2.9855.2.9855.con.0001.CDS.2164010.2165284.rev	PATRIC	CDS	2164010	2165284	1275	-	PGF_12906558	424	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.183	PATRIC.2.9855.2.9855.con.0001.CDS.216905.217684.fwd	PATRIC	CDS	216905	217684	780	+	PGF_07046483	259	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2104	PATRIC.2.9855.2.9855.con.0001.CDS.2181304.2181666.fwd	PATRIC	CDS	2181304	2181666	363	+	PGF_08225224	120	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2107	PATRIC.2.9855.2.9855.con.0001.CDS.2183490.2184110.fwd	PATRIC	CDS	2183490	2184110	621	+	PGF_08225224	206	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2108	PATRIC.2.9855.2.9855.con.0001.CDS.2184173.2184631.fwd	PATRIC	CDS	2184173	2184631	459	+	PGF_01283631	152	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2110	PATRIC.2.9855.2.9855.con.0001.CDS.2185651.2185989.rev	PATRIC	CDS	2185651	2185989	339	-	PGF_01282315	112	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2111	PATRIC.2.9855.2.9855.con.0001.CDS.2186236.2186523.fwd	PATRIC	CDS	2186236	2186523	288	+	PGF_01321888	95	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2113	PATRIC.2.9855.2.9855.con.0001.CDS.2188744.2188950.rev	PATRIC	CDS	2188744	2188950	207	-	PGF_00291811	68	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2115	PATRIC.2.9855.2.9855.con.0001.CDS.2190532.2190711.fwd	PATRIC	CDS	2190532	2190711	180	+	PGF_01308916	59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2123	PATRIC.2.9855.2.9855.con.0001.CDS.2198364.2198963.fwd	PATRIC	CDS	2198364	2198963	600	+	PGF_01286890	199	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.186	PATRIC.2.9855.2.9855.con.0001.CDS.219852.220451.fwd	PATRIC	CDS	219852	220451	600	+	PGF_01303729	199	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.187	PATRIC.2.9855.2.9855.con.0001.CDS.220495.221022.fwd	PATRIC	CDS	220495	221022	528	+	PGF_02687704	175	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2128	PATRIC.2.9855.2.9855.con.0001.CDS.2206690.2207853.fwd	PATRIC	CDS	2206690	2207853	1164	+	PGF_01253486	387	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2130	PATRIC.2.9855.2.9855.con.0001.CDS.2208640.2208738.fwd	PATRIC	CDS	2208640	2208738	99	+	PGF_00862695	32	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2131	PATRIC.2.9855.2.9855.con.0001.CDS.2208761.2209153.fwd	PATRIC	CDS	2208761	2209153	393	+	PGF_00125879	130	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2132	PATRIC.2.9855.2.9855.con.0001.CDS.2209232.2209372.fwd	PATRIC	CDS	2209232	2209372	141	+	PGF_01326908	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2133	PATRIC.2.9855.2.9855.con.0001.CDS.2209369.2209557.fwd	PATRIC	CDS	2209369	2209557	189	+	PGF_01286736	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2135	PATRIC.2.9855.2.9855.con.0001.CDS.2209882.2210115.fwd	PATRIC	CDS	2209882	2210115	234	+	PGF_00173938	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2136	PATRIC.2.9855.2.9855.con.0001.CDS.2210129.2210392.fwd	PATRIC	CDS	2210129	2210392	264	+	PGF_01282346	87	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.188	PATRIC.2.9855.2.9855.con.0001.CDS.221052.221411.fwd	PATRIC	CDS	221052	221411	360	+	PGF_01313776	119	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2138	PATRIC.2.9855.2.9855.con.0001.CDS.2211477.2212169.fwd	PATRIC	CDS	2211477	2212169	693	+	PGF_10452192	230	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2139	PATRIC.2.9855.2.9855.con.0001.CDS.2212281.2212388.fwd	PATRIC	CDS	2212281	2212388	108	+	PGF_09699570	35	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2140	PATRIC.2.9855.2.9855.con.0001.CDS.2212342.2212629.fwd	PATRIC	CDS	2212342	2212629	288	+	PGF_09699570	95	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2142	PATRIC.2.9855.2.9855.con.0001.CDS.2213593.2214069.fwd	PATRIC	CDS	2213593	2214069	477	+	PGF_06156504	158	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.189	PATRIC.2.9855.2.9855.con.0001.CDS.221437.222915.fwd	PATRIC	CDS	221437	222915	1479	+	PGF_08225224	492	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2146	PATRIC.2.9855.2.9855.con.0001.CDS.2217232.2220594.fwd	PATRIC	CDS	2217232	2220594	3363	+	PGF_08225224	1120	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2147	PATRIC.2.9855.2.9855.con.0001.CDS.2220808.2221359.rev	PATRIC	CDS	2220808	2221359	552	-	PGF_01129740	183	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2156	PATRIC.2.9855.2.9855.con.0001.CDS.2232000.2232632.fwd	PATRIC	CDS	2232000	2232632	633	+	PGF_01281360	210	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2157	PATRIC.2.9855.2.9855.con.0001.CDS.2232829.2233077.fwd	PATRIC	CDS	2232829	2233077	249	+	PGF_01283336	82	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2158	PATRIC.2.9855.2.9855.con.0001.CDS.2233238.2233375.rev	PATRIC	CDS	2233238	2233375	138	-	PGF_01322995	45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2159	PATRIC.2.9855.2.9855.con.0001.CDS.2234034.2236289.rev	PATRIC	CDS	2234034	2236289	2256	-	PGF_00425984	751	FIG00441814: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2171	PATRIC.2.9855.2.9855.con.0001.CDS.2249014.2249352.fwd	PATRIC	CDS	2249014	2249352	339	+	PGF_08225224	112	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.191	PATRIC.2.9855.2.9855.con.0001.CDS.224977.225351.fwd	PATRIC	CDS	224977	225351	375	+		124	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.192	PATRIC.2.9855.2.9855.con.0001.CDS.225576.225824.fwd	PATRIC	CDS	225576	225824	249	+	PGF_08225224	82	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2187	PATRIC.2.9855.2.9855.con.0001.CDS.2266193.2266342.fwd	PATRIC	CDS	2266193	2266342	150	+	PGF_10382523	49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2190	PATRIC.2.9855.2.9855.con.0001.CDS.2269571.2269690.fwd	PATRIC	CDS	2269571	2269690	120	+		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2192	PATRIC.2.9855.2.9855.con.0001.CDS.2271866.2272075.fwd	PATRIC	CDS	2271866	2272075	210	+	PGF_01271576	69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.194	PATRIC.2.9855.2.9855.con.0001.CDS.227532.227975.fwd	PATRIC	CDS	227532	227975	444	+	PGF_01304758	147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2197	PATRIC.2.9855.2.9855.con.0001.CDS.2278342.2278455.rev	PATRIC	CDS	2278342	2278455	114	-		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2200	PATRIC.2.9855.2.9855.con.0001.CDS.2280248.2280577.rev	PATRIC	CDS	2280248	2280577	330	-	PGF_01285616	109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2201	PATRIC.2.9855.2.9855.con.0001.CDS.2280991.2281512.fwd	PATRIC	CDS	2280991	2281512	522	+	PGF_01285517	173	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2202	PATRIC.2.9855.2.9855.con.0001.CDS.2281700.2282140.fwd	PATRIC	CDS	2281700	2282140	441	+	PGF_02870548	146	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2204	PATRIC.2.9855.2.9855.con.0001.CDS.2284399.2284641.rev	PATRIC	CDS	2284399	2284641	243	-	PGF_08225224	80	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2205	PATRIC.2.9855.2.9855.con.0001.CDS.2284791.2286347.rev	PATRIC	CDS	2284791	2286347	1557	-	PGF_08225224	518	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2208	PATRIC.2.9855.2.9855.con.0001.CDS.2288487.2289260.fwd	PATRIC	CDS	2288487	2289260	774	+	PGF_08225224	257	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2212	PATRIC.2.9855.2.9855.con.0001.CDS.2293805.2294329.rev	PATRIC	CDS	2293805	2294329	525	-	PGF_12871472	174	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.196	PATRIC.2.9855.2.9855.con.0001.CDS.229451.229675.fwd	PATRIC	CDS	229451	229675	225	+	PGF_01295563	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2215	PATRIC.2.9855.2.9855.con.0001.CDS.2295761.2296546.rev	PATRIC	CDS	2295761	2296546	786	-	PGF_08225224	261	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.197	PATRIC.2.9855.2.9855.con.0001.CDS.229732.229848.fwd	PATRIC	CDS	229732	229848	117	+	PGF_01297015	38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.198	PATRIC.2.9855.2.9855.con.0001.CDS.229935.230060.fwd	PATRIC	CDS	229935	230060	126	+		41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2218	PATRIC.2.9855.2.9855.con.0001.CDS.2299875.2305724.rev	PATRIC	CDS	2299875	2305724	5850	-	PGF_04122317	1949	hypothetical protein formerly called flagellar hook-length control protein FliK
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.199	PATRIC.2.9855.2.9855.con.0001.CDS.230412.231854.fwd	PATRIC	CDS	230412	231854	1443	+	PGF_08225224	480	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2219	PATRIC.2.9855.2.9855.con.0001.CDS.2305971.2306120.fwd	PATRIC	CDS	2305971	2306120	150	+	PGF_05760067	49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2225	PATRIC.2.9855.2.9855.con.0001.CDS.2313930.2314430.rev	PATRIC	CDS	2313930	2314430	501	-	PGF_01994131	166	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2226	PATRIC.2.9855.2.9855.con.0001.CDS.2314698.2315462.rev	PATRIC	CDS	2314698	2315462	765	-	PGF_08225224	254	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2227	PATRIC.2.9855.2.9855.con.0001.CDS.2315635.2317158.fwd	PATRIC	CDS	2315635	2317158	1524	+	PGF_00649975	507	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2228	PATRIC.2.9855.2.9855.con.0001.CDS.2317245.2317514.fwd	PATRIC	CDS	2317245	2317514	270	+	PGF_01322121	89	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2234	PATRIC.2.9855.2.9855.con.0001.CDS.2323456.2324406.fwd	PATRIC	CDS	2323456	2324406	951	+	PGF_01293816	316	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2235	PATRIC.2.9855.2.9855.con.0001.CDS.2324408.2325136.fwd	PATRIC	CDS	2324408	2325136	729	+	PGF_01293186	242	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2236	PATRIC.2.9855.2.9855.con.0001.CDS.2325183.2325368.rev	PATRIC	CDS	2325183	2325368	186	-	PGF_01293825	61	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2237	PATRIC.2.9855.2.9855.con.0001.CDS.2325489.2325938.fwd	PATRIC	CDS	2325489	2325938	450	+	PGF_01293810	149	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.201	PATRIC.2.9855.2.9855.con.0001.CDS.232629.232727.fwd	PATRIC	CDS	232629	232727	99	+	PGF_08225224	32	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.202	PATRIC.2.9855.2.9855.con.0001.CDS.232747.233535.fwd	PATRIC	CDS	232747	233535	789	+	PGF_08225224	262	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2240	PATRIC.2.9855.2.9855.con.0001.CDS.2328602.2329387.fwd	PATRIC	CDS	2328602	2329387	786	+	PGF_01293809	261	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2241	PATRIC.2.9855.2.9855.con.0001.CDS.2329392.2330033.fwd	PATRIC	CDS	2329392	2330033	642	+	PGF_01301723	213	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2242	PATRIC.2.9855.2.9855.con.0001.CDS.2330145.2331287.rev	PATRIC	CDS	2330145	2331287	1143	-	PGF_01283471	380	hypothetical protein formerly called flagellar hook-length control protein FliK
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.203	PATRIC.2.9855.2.9855.con.0001.CDS.233567.234073.fwd	PATRIC	CDS	233567	234073	507	+	PGF_08225224	168	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2247	PATRIC.2.9855.2.9855.con.0001.CDS.2335674.2335790.rev	PATRIC	CDS	2335674	2335790	117	-		38	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2249	PATRIC.2.9855.2.9855.con.0001.CDS.2337724.2338092.fwd	PATRIC	CDS	2337724	2338092	369	+	PGF_01280885	122	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2255	PATRIC.2.9855.2.9855.con.0001.CDS.2345473.2345628.rev	PATRIC	CDS	2345473	2345628	156	-	PGF_01283957	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.205	PATRIC.2.9855.2.9855.con.0001.CDS.235230.235751.fwd	PATRIC	CDS	235230	235751	522	+	PGF_01283237	173	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2263	PATRIC.2.9855.2.9855.con.0001.CDS.2352818.2353537.fwd	PATRIC	CDS	2352818	2353537	720	+	PGF_00305439	239	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.206	PATRIC.2.9855.2.9855.con.0001.CDS.235754.236527.fwd	PATRIC	CDS	235754	236527	774	+	PGF_08225224	257	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2267	PATRIC.2.9855.2.9855.con.0001.CDS.2358033.2358134.rev	PATRIC	CDS	2358033	2358134	102	-		33	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2269	PATRIC.2.9855.2.9855.con.0001.CDS.2359315.2359485.rev	PATRIC	CDS	2359315	2359485	171	-	PGF_01271300	56	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2270	PATRIC.2.9855.2.9855.con.0001.CDS.2359534.2359755.rev	PATRIC	CDS	2359534	2359755	222	-	PGF_01312118	73	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2271	PATRIC.2.9855.2.9855.con.0001.CDS.2359826.2360317.rev	PATRIC	CDS	2359826	2360317	492	-	PGF_01270727	163	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2272	PATRIC.2.9855.2.9855.con.0001.CDS.2360511.2361149.rev	PATRIC	CDS	2360511	2361149	639	-	PGF_08225224	212	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2273	PATRIC.2.9855.2.9855.con.0001.CDS.2361414.2361557.rev	PATRIC	CDS	2361414	2361557	144	-	PGF_01282798	47	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.207	PATRIC.2.9855.2.9855.con.0001.CDS.236717.244516.fwd	PATRIC	CDS	236717	244516	7800	+	PGF_08225224	2599	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2286	PATRIC.2.9855.2.9855.con.0001.CDS.2373690.2374649.fwd	PATRIC	CDS	2373690	2374649	960	+	PGF_01086216	319	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2288	PATRIC.2.9855.2.9855.con.0001.CDS.2375438.2375626.rev	PATRIC	CDS	2375438	2375626	189	-	PGF_00735450	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2291	PATRIC.2.9855.2.9855.con.0001.CDS.2378244.2378354.rev	PATRIC	CDS	2378244	2378354	111	-		36	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2292	PATRIC.2.9855.2.9855.con.0001.CDS.2378402.2379220.rev	PATRIC	CDS	2378402	2379220	819	-	PGF_01289928	272	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2299	PATRIC.2.9855.2.9855.con.0001.CDS.2387798.2388058.rev	PATRIC	CDS	2387798	2388058	261	-	PGF_08225224	86	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2305	PATRIC.2.9855.2.9855.con.0001.CDS.2395777.2397144.fwd	PATRIC	CDS	2395777	2397144	1368	+	PGF_01703213	455	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2318	PATRIC.2.9855.2.9855.con.0001.CDS.2410860.2411159.rev	PATRIC	CDS	2410860	2411159	300	-	PGF_01282476	99	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2320	PATRIC.2.9855.2.9855.con.0001.CDS.2412689.2412817.rev	PATRIC	CDS	2412689	2412817	129	-		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2322	PATRIC.2.9855.2.9855.con.0001.CDS.2414518.2414748.fwd	PATRIC	CDS	2414518	2414748	231	+	PGF_07329939	76	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2337	PATRIC.2.9855.2.9855.con.0001.CDS.2433051.2433968.rev	PATRIC	CDS	2433051	2433968	918	-	PGF_00150726	305	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2342	PATRIC.2.9855.2.9855.con.0001.CDS.2439058.2439744.rev	PATRIC	CDS	2439058	2439744	687	-	PGF_07557571	228	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2344	PATRIC.2.9855.2.9855.con.0001.CDS.2441209.2441910.rev	PATRIC	CDS	2441209	2441910	702	-	PGF_07375251	233	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2346	PATRIC.2.9855.2.9855.con.0001.CDS.2444215.2444364.fwd	PATRIC	CDS	2444215	2444364	150	+		49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.208	PATRIC.2.9855.2.9855.con.0001.CDS.244531.245115.fwd	PATRIC	CDS	244531	245115	585	+	PGF_01307860	194	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2349	PATRIC.2.9855.2.9855.con.0001.CDS.2446129.2447409.rev	PATRIC	CDS	2446129	2447409	1281	-	PGF_10027474	426	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2355	PATRIC.2.9855.2.9855.con.0001.CDS.2455224.2455616.rev	PATRIC	CDS	2455224	2455616	393	-	PGF_02006588	130	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2356	PATRIC.2.9855.2.9855.con.0001.CDS.2455766.2456227.fwd	PATRIC	CDS	2455766	2456227	462	+	PGF_01286809	153	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.209	PATRIC.2.9855.2.9855.con.0001.CDS.245898.246302.fwd	PATRIC	CDS	245898	246302	405	+	PGF_01304757	134	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.210	PATRIC.2.9855.2.9855.con.0001.CDS.246318.246557.fwd	PATRIC	CDS	246318	246557	240	+	PGF_01304757	79	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.211	PATRIC.2.9855.2.9855.con.0001.CDS.246573.247019.fwd	PATRIC	CDS	246573	247019	447	+	PGF_06899023	148	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2365	PATRIC.2.9855.2.9855.con.0001.CDS.2466028.2466192.fwd	PATRIC	CDS	2466028	2466192	165	+		54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2367	PATRIC.2.9855.2.9855.con.0001.CDS.2468228.2469193.fwd	PATRIC	CDS	2468228	2469193	966	+	PGF_05038169	321	COG1683: Uncharacterized conserved protein / FIG143828: Hypothetical protein YbgA
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.212	PATRIC.2.9855.2.9855.con.0001.CDS.247318.247434.fwd	PATRIC	CDS	247318	247434	117	+	PGF_08256783	38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2373	PATRIC.2.9855.2.9855.con.0001.CDS.2477244.2477633.fwd	PATRIC	CDS	2477244	2477633	390	+	PGF_08225224	129	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.214	PATRIC.2.9855.2.9855.con.0001.CDS.248609.249445.fwd	PATRIC	CDS	248609	249445	837	+	PGF_08225224	278	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2387	PATRIC.2.9855.2.9855.con.0001.CDS.2490022.2490549.rev	PATRIC	CDS	2490022	2490549	528	-	PGF_01304246	175	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2388	PATRIC.2.9855.2.9855.con.0001.CDS.2490716.2491273.rev	PATRIC	CDS	2490716	2491273	558	-	PGF_01284275	185	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2389	PATRIC.2.9855.2.9855.con.0001.CDS.2491624.2492169.fwd	PATRIC	CDS	2491624	2492169	546	+	PGF_01263496	181	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2396	PATRIC.2.9855.2.9855.con.0001.CDS.2500217.2500486.fwd	PATRIC	CDS	2500217	2500486	270	+	PGF_01284375	89	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2400	PATRIC.2.9855.2.9855.con.0001.CDS.2505011.2505268.fwd	PATRIC	CDS	2505011	2505268	258	+	PGF_01281781	85	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2407	PATRIC.2.9855.2.9855.con.0001.CDS.2516502.2517359.rev	PATRIC	CDS	2516502	2517359	858	-	PGF_07046483	285	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.217	PATRIC.2.9855.2.9855.con.0001.CDS.251950.253086.fwd	PATRIC	CDS	251950	253086	1137	+	PGF_01283078	378	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2418	PATRIC.2.9855.2.9855.con.0001.CDS.2532418.2533053.rev	PATRIC	CDS	2532418	2533053	636	-	PGF_08225224	211	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2421	PATRIC.2.9855.2.9855.con.0001.CDS.2534573.2535343.rev	PATRIC	CDS	2534573	2535343	771	-	PGF_00978873	256	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2422	PATRIC.2.9855.2.9855.con.0001.CDS.2535537.2536604.rev	PATRIC	CDS	2535537	2536604	1068	-	PGF_09466613	355	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2429	PATRIC.2.9855.2.9855.con.0001.CDS.2545773.2545898.rev	PATRIC	CDS	2545773	2545898	126	-	PGF_01293197	41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.219	PATRIC.2.9855.2.9855.con.0001.CDS.255030.255335.rev	PATRIC	CDS	255030	255335	306	-	PGF_08225224	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2434	PATRIC.2.9855.2.9855.con.0001.CDS.2550477.2551409.rev	PATRIC	CDS	2550477	2551409	933	-	PGF_08225224	310	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.220	PATRIC.2.9855.2.9855.con.0001.CDS.255351.255821.rev	PATRIC	CDS	255351	255821	471	-	PGF_01282439	156	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2442	PATRIC.2.9855.2.9855.con.0001.CDS.2560248.2560871.rev	PATRIC	CDS	2560248	2560871	624	-	PGF_08225224	207	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.221	PATRIC.2.9855.2.9855.con.0001.CDS.256296.256814.fwd	PATRIC	CDS	256296	256814	519	+	PGF_08225224	172	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2457	PATRIC.2.9855.2.9855.con.0001.CDS.2579583.2580104.rev	PATRIC	CDS	2579583	2580104	522	-	PGF_01295334	173	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2460	PATRIC.2.9855.2.9855.con.0001.CDS.2581217.2581768.rev	PATRIC	CDS	2581217	2581768	552	-	PGF_08225224	183	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.223	PATRIC.2.9855.2.9855.con.0001.CDS.258159.258479.fwd	PATRIC	CDS	258159	258479	321	+	PGF_00422478	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2461	PATRIC.2.9855.2.9855.con.0001.CDS.2581772.2581891.rev	PATRIC	CDS	2581772	2581891	120	-		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2476	PATRIC.2.9855.2.9855.con.0001.CDS.2598593.2599270.fwd	PATRIC	CDS	2598593	2599270	678	+	PGF_08225224	225	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2480	PATRIC.2.9855.2.9855.con.0001.CDS.2603872.2604021.fwd	PATRIC	CDS	2603872	2604021	150	+	PGF_07073118	49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2483	PATRIC.2.9855.2.9855.con.0001.CDS.2605827.2605946.rev	PATRIC	CDS	2605827	2605946	120	-	PGF_01283840	39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2485	PATRIC.2.9855.2.9855.con.0001.CDS.2607573.2607878.rev	PATRIC	CDS	2607573	2607878	306	-	PGF_01297260	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2486	PATRIC.2.9855.2.9855.con.0001.CDS.2608197.2608703.rev	PATRIC	CDS	2608197	2608703	507	-	PGF_01283227	168	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2487	PATRIC.2.9855.2.9855.con.0001.CDS.2609291.2609521.rev	PATRIC	CDS	2609291	2609521	231	-	PGF_08225224	76	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2488	PATRIC.2.9855.2.9855.con.0001.CDS.2609672.2609833.rev	PATRIC	CDS	2609672	2609833	162	-	PGF_01281405	53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2490	PATRIC.2.9855.2.9855.con.0001.CDS.2610502.2610690.rev	PATRIC	CDS	2610502	2610690	189	-	PGF_01286194	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2491	PATRIC.2.9855.2.9855.con.0001.CDS.2611084.2611314.rev	PATRIC	CDS	2611084	2611314	231	-	PGF_01284861	76	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2492	PATRIC.2.9855.2.9855.con.0001.CDS.2611653.2611826.rev	PATRIC	CDS	2611653	2611826	174	-		57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2493	PATRIC.2.9855.2.9855.con.0001.CDS.2612205.2612435.rev	PATRIC	CDS	2612205	2612435	231	-	PGF_01310674	76	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2496	PATRIC.2.9855.2.9855.con.0001.CDS.2615367.2616044.rev	PATRIC	CDS	2615367	2616044	678	-	PGF_01282316	225	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2497	PATRIC.2.9855.2.9855.con.0001.CDS.2616142.2616501.rev	PATRIC	CDS	2616142	2616501	360	-	PGF_01282438	119	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2505	PATRIC.2.9855.2.9855.con.0001.CDS.2621342.2621863.rev	PATRIC	CDS	2621342	2621863	522	-		PGF_08225224	173	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2506	PATRIC.2.9855.2.9855.con.0001.CDS.2622350.2623114.rev	PATRIC	CDS	2622350	2623114	765	-		PGF_01286624	254	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2514	PATRIC.2.9855.2.9855.con.0001.CDS.2630300.2630620.fwd	PATRIC	CDS	2630300	2630620	321	+		PGF_04007746	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2515	PATRIC.2.9855.2.9855.con.0001.CDS.2630772.2631212.rev	PATRIC	CDS	2630772	2631212	441	-		PGF_05654159	146	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2520	PATRIC.2.9855.2.9855.con.0001.CDS.2636837.2637469.rev	PATRIC	CDS	2636837	2637469	633	-		PGF_01280912	210	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2528	PATRIC.2.9855.2.9855.con.0001.CDS.2643624.2644334.rev	PATRIC	CDS	2643624	2644334	711	-		PGF_08225224	236	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2531	PATRIC.2.9855.2.9855.con.0001.CDS.2647282.2647533.rev	PATRIC	CDS	2647282	2647533	252	-		PGF_08225224	83	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2533	PATRIC.2.9855.2.9855.con.0001.CDS.2649160.2649759.rev	PATRIC	CDS	2649160	2649759	600	-		PGF_01314781	199	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2534	PATRIC.2.9855.2.9855.con.0001.CDS.2649762.2650502.rev	PATRIC	CDS	2649762	2650502	741	-		PGF_06884747	246	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2535	PATRIC.2.9855.2.9855.con.0001.CDS.2650638.2651276.fwd	PATRIC	CDS	2650638	2651276	639	+		PGF_01284625	212	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2537	PATRIC.2.9855.2.9855.con.0001.CDS.2651991.2652137.rev	PATRIC	CDS	2651991	2652137	147	-		PGF_08225224	48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2538	PATRIC.2.9855.2.9855.con.0001.CDS.2652641.2653243.fwd	PATRIC	CDS	2652641	2653243	603	+		PGF_08225224	200	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2539	PATRIC.2.9855.2.9855.con.0001.CDS.2653619.2653900.fwd	PATRIC	CDS	2653619	2653900	282	+		PGF_01289085	93	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2542	PATRIC.2.9855.2.9855.con.0001.CDS.2657870.2658259.rev	PATRIC	CDS	2657870	2658259	390	-		PGF_12838797	129	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2543	PATRIC.2.9855.2.9855.con.0001.CDS.2658335.2658493.rev	PATRIC	CDS	2658335	2658493	159	-		PGF_12838797	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2544	PATRIC.2.9855.2.9855.con.0001.CDS.2658551.2658793.rev	PATRIC	CDS	2658551	2658793	243	-		PGF_00210048	80	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2545	PATRIC.2.9855.2.9855.con.0001.CDS.2659151.2659678.fwd	PATRIC	CDS	2659151	2659678	528	+		PGF_12951167	175	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2547	PATRIC.2.9855.2.9855.con.0001.CDS.2660786.2660893.rev	PATRIC	CDS	2660786	2660893	108	-		PGF_08225224	35	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2549	PATRIC.2.9855.2.9855.con.0001.CDS.2661623.2661736.rev	PATRIC	CDS	2661623	2661736	114	-			37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2550	PATRIC.2.9855.2.9855.con.0001.CDS.2661740.2662369.rev	PATRIC	CDS	2661740	2662369	630	-		PGF_01280928	209	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2556	PATRIC.2.9855.2.9855.con.0001.CDS.2666797.2666976.rev	PATRIC	CDS	2666797	2666976	180	-		PGF_01290688	59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2561	PATRIC.2.9855.2.9855.con.0001.CDS.2669994.2670221.fwd	PATRIC	CDS	2669994	2670221	228	+			75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2564	PATRIC.2.9855.2.9855.con.0001.CDS.2672866.2672991.rev	PATRIC	CDS	2672866	2672991	126	-		PGF_01287472	41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2566	PATRIC.2.9855.2.9855.con.0001.CDS.2675901.2676536.rev	PATRIC	CDS	2675901	2676536	636	-		PGF_12881293	211	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2568	PATRIC.2.9855.2.9855.con.0001.CDS.2677566.2677808.rev	PATRIC	CDS	2677566	2677808	243	-		PGF_00210048	80	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2580	PATRIC.2.9855.2.9855.con.0001.CDS.2690216.2690440.fwd	PATRIC	CDS	2690216	2690440	225	+		PGF_01282349	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2581	PATRIC.2.9855.2.9855.con.0001.CDS.2690524.2690742.fwd	PATRIC	CDS	2690524	2690742	219	+		PGF_00915583	72	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2585	PATRIC.2.9855.2.9855.con.0001.CDS.2694781.2695083.rev	PATRIC	CDS	2694781	2695083	303	-		PGF_08225224	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2591	PATRIC.2.9855.2.9855.con.0001.CDS.2700035.2700163.rev	PATRIC	CDS	2700035	2700163	129	-			42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2592	PATRIC.2.9855.2.9855.con.0001.CDS.2700536.2700733.rev	PATRIC	CDS	2700536	2700733	198	-		PGF_01280971	65	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2598	PATRIC.2.9855.2.9855.con.0001.CDS.2705863.2706051.rev	PATRIC	CDS	2705863	2706051	189	-		PGF_01326833	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2599	PATRIC.2.9855.2.9855.con.0001.CDS.2706351.2706779.rev	PATRIC	CDS	2706351	2706779	429	-		PGF_01304742	142	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2600	PATRIC.2.9855.2.9855.con.0001.CDS.2707142.2707483.rev	PATRIC	CDS	2707142	2707483	342	-		PGF_01307338	113	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2601	PATRIC.2.9855.2.9855.con.0001.CDS.2707748.2708596.fwd	PATRIC	CDS	2707748	2708596	849	+		PGF_01289569	282	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2603	PATRIC.2.9855.2.9855.con.0001.CDS.2709464.2709760.fwd	PATRIC	CDS	2709464	2709760	297	+			98	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2614	PATRIC.2.9855.2.9855.con.0001.CDS.2719420.2720292.rev	PATRIC	CDS	2719420	2720292	873	-		PGF_00333600	290	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2626	PATRIC.2.9855.2.9855.con.0001.CDS.2731824.2732042.rev	PATRIC	CDS	2731824	2732042	219	-		PGF_01284897	72	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2628	PATRIC.2.9855.2.9855.con.0001.CDS.2734610.2734759.rev	PATRIC	CDS	2734610	2734759	150	-			49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2629	PATRIC.2.9855.2.9855.con.0001.CDS.2734865.2735098.rev	PATRIC	CDS	2734865	2735098	234	-		PGF_01283327	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2635	PATRIC.2.9855.2.9855.con.0001.CDS.2744600.2744767.rev	PATRIC	CDS	2744600	2744767	168	-		PGF_01285094	55	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2636	PATRIC.2.9855.2.9855.con.0001.CDS.2745049.2745468.rev	PATRIC	CDS	2745049	2745468	420	-		PGF_10395756	139	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2637	PATRIC.2.9855.2.9855.con.0001.CDS.2745535.2745768.rev	PATRIC	CDS	2745535	2745768	234	-		PGF_01284294	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2638	PATRIC.2.9855.2.9855.con.0001.CDS.2745801.2746019.rev	PATRIC	CDS	2745801	2746019	219	-		PGF_01284293	72	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2642	PATRIC.2.9855.2.9855.con.0001.CDS.2750155.2750403.rev	PATRIC	CDS	2750155	2750403	249	-		PGF_00102303	82	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2643	PATRIC.2.9855.2.9855.con.0001.CDS.2750685.2751809.rev	PATRIC	CDS	2750685	2751809	1125	-		PGF_01283229	374	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2645	PATRIC.2.9855.2.9855.con.0001.CDS.2755686.2755874.rev	PATRIC	CDS	2755686	2755874	189	-		PGF_01282359	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2646	PATRIC.2.9855.2.9855.con.0001.CDS.2755916.2756110.rev	PATRIC	CDS	2755916	2756110	195	-		PGF_01285617	64	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2647	PATRIC.2.9855.2.9855.con.0001.CDS.2756182.2756388.rev	PATRIC	CDS	2756182	2756388	207	-		PGF_01284333	68	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2648	PATRIC.2.9855.2.9855.con.0001.CDS.2756927.2757340.rev	PATRIC	CDS	2756927	2757340	414	-		PGF_08368006	137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2649	PATRIC.2.9855.2.9855.con.0001.CDS.2757935.2758327.rev	PATRIC	CDS	2757935	2758327	393	-		PGF_02926107	130	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2651	PATRIC.2.9855.2.9855.con.0001.CDS.2759482.2759706.rev	PATRIC	CDS	2759482	2759706	225	-		PGF_01284232	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2652	PATRIC.2.9855.2.9855.con.0001.CDS.2759753.2759959.rev	PATRIC	CDS	2759753	2759959	207	-		PGF_01285112	68	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2653	PATRIC.2.9855.2.9855.con.0001.CDS.2760314.2760466.rev	PATRIC	CDS	2760314	2760466	153	-		PGF_01286192	50	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2654	PATRIC.2.9855.2.9855.con.0001.CDS.2760547.2760678.fwd	PATRIC	CDS	2760547	2760678	132	+			43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2656	PATRIC.2.9855.2.9855.con.0001.CDS.2761406.2762098.rev	PATRIC	CDS	2761406	2762098	693	-		PGF_00335595	230	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2662	PATRIC.2.9855.2.9855.con.0001.CDS.2770096.2770668.fwd	PATRIC	CDS	2770096	2770668	573	+		PGF_08225224	190	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.243	PATRIC.2.9855.2.9855.con.0001.CDS.279782.280780.fwd	PATRIC	CDS	279782	280780	999	+		PGF_01317514	332	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2684	PATRIC.2.9855.2.9855.con.0001.CDS.2798937.2799092.rev	PATRIC	CDS	2798937	2799092	156	-		PGF_01282326	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2687	PATRIC.2.9855.2.9855.con.0001.CDS.2802430.2804301.rev	PATRIC	CDS	2802430	2804301	1872	-		PGF_01280848	623	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2692	PATRIC.2.9855.2.9855.con.0001.CDS.2809821.2810375.rev	PATRIC	CDS	2809821	2810375	555	-		PGF_10398610	184	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2697	PATRIC.2.9855.2.9855.con.0001.CDS.2815601.2815942.rev	PATRIC	CDS	2815601	2815942	342	-		PGF_01300089	113	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2698	PATRIC.2.9855.2.9855.con.0001.CDS.2816123.2816302.rev	PATRIC	CDS	2816123	2816302	180	-		PGF_00123911	59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2701	PATRIC.2.9855.2.9855.con.0001.CDS.2819903.2821156.rev	PATRIC	CDS	2819903	2821156	1254	-		PGF_00135284	417	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2704	PATRIC.2.9855.2.9855.con.0001.CDS.2826408.2826668.rev	PATRIC	CDS	2826408	2826668	261	-		PGF_01282404	86	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2710	PATRIC.2.9855.2.9855.con.0001.CDS.2831392.2831997.rev	PATRIC	CDS	2831392	2831997	606	-		PGF_05019237	201	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2715	PATRIC.2.9855.2.9855.con.0001.CDS.2836391.2836654.rev	PATRIC	CDS	2836391	2836654	264	-		PGF_01283230	87	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2722	PATRIC.2.9855.2.9855.con.0001.CDS.2844608.2844850.rev	PATRIC	CDS	2844608	2844850	243	-		PGF_01284402	80	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2732	PATRIC.2.9855.2.9855.con.0001.CDS.2857383.2857607.rev	PATRIC	CDS	2857383	2857607	225	-		PGF_01284967	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2737	PATRIC.2.9855.2.9855.con.0001.CDS.2863791.2864714.rev	PATRIC	CDS	2863791	2864714	924	-		PGF_08225224	307	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2738	PATRIC.2.9855.2.9855.con.0001.CDS.2864741.2865781.rev	PATRIC	CDS	2864741	2865781	1041	-		PGF_01282327	346	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2739	PATRIC.2.9855.2.9855.con.0001.CDS.2865818.2866648.rev	PATRIC	CDS	2865818	2866648	831	-		PGF_08225224	276	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2745	PATRIC.2.9855.2.9855.con.0001.CDS.2872663.2872770.rev	PATRIC	CDS	2872663	2872770	108	-		PGF_07056092	35	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2752	PATRIC.2.9855.2.9855.con.0001.CDS.2879519.2879647.rev	PATRIC	CDS	2879519	2879647	129	-		PGF_08276117	42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2753	PATRIC.2.9855.2.9855.con.0001.CDS.2879887.2881983.rev	PATRIC	CDS	2879887	2881983	2097	-		PGF_06939704	698	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2754	PATRIC.2.9855.2.9855.con.0001.CDS.2882551.2882955.rev	PATRIC	CDS	2882551	2882955	405	-			134	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2755	PATRIC.2.9855.2.9855.con.0001.CDS.2883269.2883571.fwd	PATRIC	CDS	2883269	2883571	303	+		PGF_01259102	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2756	PATRIC.2.9855.2.9855.con.0001.CDS.2883805.2883945.fwd	PATRIC	CDS	2883805	2883945	141	+			46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2757	PATRIC.2.9855.2.9855.con.0001.CDS.2884031.2884552.rev	PATRIC	CDS	2884031	2884552	522	-		PGF_10674380	173	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2759	PATRIC.2.9855.2.9855.con.0001.CDS.2885392.2885826.rev	PATRIC	CDS	2885392	2885826	435	-		PGF_04001193	144	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2760	PATRIC.2.9855.2.9855.con.0001.CDS.2885886.2886320.rev	PATRIC	CDS	2885886	2886320	435	-		PGF_08225224	144	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2761	PATRIC.2.9855.2.9855.con.0001.CDS.2886555.2887769.rev	PATRIC	CDS	2886555	2887769	1215	-		PGF_03152613	404	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2762	PATRIC.2.9855.2.9855.con.0001.CDS.2887892.2888191.rev	PATRIC	CDS	2887892	2888191	300	-		PGF_10438005	99	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2763	PATRIC.2.9855.2.9855.con.0001.CDS.2888228.2888548.rev	PATRIC	CDS	2888228	2888548	321	-			106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2764	PATRIC.2.9855.2.9855.con.0001.CDS.2888611.2888793.rev	PATRIC	CDS	2888611	2888793	183	-		PGF_10327607	60	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2765	PATRIC.2.9855.2.9855.con.0001.CDS.2888777.2888938.rev	PATRIC	CDS	2888777	2888938	162	-		PGF_08225224	53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2766	PATRIC.2.9855.2.9855.con.0001.CDS.2889183.2889866.rev	PATRIC	CDS	2889183	2889866	684	-			227	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2770	PATRIC.2.9855.2.9855.con.0001.CDS.2893855.2894016.rev	PATRIC	CDS	2893855	2894016	162	-		PGF_01301885	53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2775	PATRIC.2.9855.2.9855.con.0001.CDS.2901110.2901505.rev	PATRIC	CDS	2901110	2901505	396	-		PGF_01285374	131	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2777	PATRIC.2.9855.2.9855.con.0001.CDS.2903779.2903916.fwd	PATRIC	CDS	2903779	2903916	138	+		PGF_01287471	45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2778	PATRIC.2.9855.2.9855.con.0001.CDS.2904125.2904733.rev	PATRIC	CDS	2904125	2904733	609	-		PGF_01269351	202	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2779	PATRIC.2.9855.2.9855.con.0001.CDS.2904985.2906304.rev	PATRIC	CDS	2904985	2906304	1320	-		PGF_08225224	439	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2791	PATRIC.2.9855.2.9855.con.0001.CDS.2920391.2920570.rev	PATRIC	CDS	2920391	2920570	180	-			59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2792	PATRIC.2.9855.2.9855.con.0001.CDS.2920770.2921351.fwd	PATRIC	CDS	2920770	2921351	582	+		PGF_01285706	193	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2796	PATRIC.2.9855.2.9855.con.0001.CDS.2924929.2925051.rev	PATRIC	CDS	2924929	2925051	123	-			40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.255	PATRIC.2.9855.2.9855.con.0001.CDS.292550.292963.rev	PATRIC	CDS	292550	292963	414	-		PGF_01281812	137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.256	PATRIC.2.9855.2.9855.con.0001.CDS.293375.293776.fwd	PATRIC	CDS	293375	293776	402	+		PGF_01317772	133	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2805	PATRIC.2.9855.2.9855.con.0001.CDS.2936194.2936553.rev	PATRIC	CDS	2936194	2936553	360	-		PGF_01668636	119	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2806	PATRIC.2.9855.2.9855.con.0001.CDS.2936891.2937022.fwd	PATRIC	CDS	2936891	2937022	132	+		PGF_12951167	43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2810	PATRIC.2.9855.2.9855.con.0001.CDS.2942854.2943198.rev	PATRIC	CDS	2942854	2943198	345	-		PGF_08225224	114	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2811	PATRIC.2.9855.2.9855.con.0001.CDS.2943604.2943909.rev	PATRIC	CDS	2943604	2943909	306	-		PGF_08225224	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2814	PATRIC.2.9855.2.9855.con.0001.CDS.2946485.2946796.rev	PATRIC	CDS	2946485	2946796	312	-		PGF_01280915	103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2817	PATRIC.2.9855.2.9855.con.0001.CDS.2948589.2949440.fwd	PATRIC	CDS	2948589	2949440	852	+		PGF_08225224	283	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2818	PATRIC.2.9855.2.9855.con.0001.CDS.2949669.2949833.rev	PATRIC	CDS	2949669	2949833	165	-		PGF_01280890	54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2820	PATRIC.2.9855.2.9855.con.0001.CDS.2953209.2953637.rev	PATRIC	CDS	2953209	2953637	429	-		PGF_01305270	142	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2821	PATRIC.2.9855.2.9855.con.0001.CDS.2953634.2954053.rev	PATRIC	CDS	2953634	2954053	420	-		PGF_01283645	139	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2829	PATRIC.2.9855.2.9855.con.0001.CDS.2960592.2960723.rev	PATRIC	CDS	2960592	2960723	132	-		PGF_07295428	43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2832	PATRIC.2.9855.2.9855.con.0001.CDS.2965099.2965275.rev	PATRIC	CDS	2965099	2965275	177	-		PGF_01290293	58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2837	PATRIC.2.9855.2.9855.con.0001.CDS.2969951.2970094.rev	PATRIC	CDS	2969951	2970094	144	-		PGF_06806179	47	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2839	PATRIC.2.9855.2.9855.con.0001.CDS.2971409.2972383.rev	PATRIC	CDS	2971409	2972383	975	-		PGF_08225224	324	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2875	PATRIC.2.9855.2.9855.con.0001.CDS.3014593.3014808.rev	PATRIC	CDS	3014593	3014808	216	-			71	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2876	PATRIC.2.9855.2.9855.con.0001.CDS.3014805.3014969.rev	PATRIC	CDS	3014805	3014969	165	-			54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2877	PATRIC.2.9855.2.9855.con.0001.CDS.3015193.3015408.rev	PATRIC	CDS	3015193	3015408	216	-		PGF_07639480	71	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2878	PATRIC.2.9855.2.9855.con.0001.CDS.3015610.3015843.rev	PATRIC	CDS	3015610	3015843	234	-		PGF_01283972	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2885	PATRIC.2.9855.2.9855.con.0001.CDS.3020921.3021427.fwd	PATRIC	CDS	3020921	3021427	507	+		PGF_08225224	168	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2888	PATRIC.2.9855.2.9855.con.0001.CDS.3023694.3023834.fwd	PATRIC	CDS	3023694	3023834	141	+		PGF_04710333	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2889	PATRIC.2.9855.2.9855.con.0001.CDS.3024943.3025152.fwd	PATRIC	CDS	3024943	3025152	210	+			69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2890	PATRIC.2.9855.2.9855.con.0001.CDS.3025226.3025393.fwd	PATRIC	CDS	3025226	3025393	168	+			55	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2891	PATRIC.2.9855.2.9855.con.0001.CDS.3027665.3028141.rev	PATRIC	CDS	3027665	3028141	477	-		PGF_01281808	158	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2895	PATRIC.2.9855.2.9855.con.0001.CDS.3031718.3033286.rev	PATRIC	CDS	3031718	3033286	1569	-		PGF_08225224	522	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2897	PATRIC.2.9855.2.9855.con.0001.CDS.3036438.3036890.fwd	PATRIC	CDS	3036438	3036890	453	+			150	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2899	PATRIC.2.9855.2.9855.con.0001.CDS.3040731.3042296.rev	PATRIC	CDS	3040731	3042296	1566	-		PGF_08225224	521	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2901	PATRIC.2.9855.2.9855.con.0001.CDS.3043482.3044045.rev	PATRIC	CDS	3043482	3044045	564	-		PGF_12850942	187	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2902	PATRIC.2.9855.2.9855.con.0001.CDS.3044200.3045024.fwd	PATRIC	CDS	3044200	3045024	825	+		PGF_01273912	274	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2915	PATRIC.2.9855.2.9855.con.0001.CDS.3059242.3059601.rev	PATRIC	CDS	3059242	3059601	360	-		PGF_00718326	119	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2918	PATRIC.2.9855.2.9855.con.0001.CDS.3062885.3063343.rev	PATRIC	CDS	3062885	3063343	459	-		PGF_03127849	152	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2919	PATRIC.2.9855.2.9855.con.0001.CDS.3063510.3063878.rev	PATRIC	CDS	3063510	3063878	369	-		PGF_01323605	122	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2921	PATRIC.2.9855.2.9855.con.0001.CDS.3065812.3066918.rev	PATRIC	CDS	3065812	3066918	1107	-		PGF_10485374	368	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2924	PATRIC.2.9855.2.9855.con.0001.CDS.3070208.3070726.fwd	PATRIC	CDS	3070208	3070726	519	+		PGF_00255984	172	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2934	PATRIC.2.9855.2.9855.con.0001.CDS.3083098.3083562.rev	PATRIC	CDS	3083098	3083562	465	-		PGF_00175945	154	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2937	PATRIC.2.9855.2.9855.con.0001.CDS.3085579.3085752.rev	PATRIC	CDS	3085579	3085752	174	-		PGF_01285571	57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2938	PATRIC.2.9855.2.9855.con.0001.CDS.3085844.3085939.rev	PATRIC	CDS	3085844	3085939	96	-			31	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2939	PATRIC.2.9855.2.9855.con.0001.CDS.3085964.3086167.rev	PATRIC	CDS	3085964	3086167	204	-		PGF_01284449	67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2940	PATRIC.2.9855.2.9855.con.0001.CDS.3087222.3088616.rev	PATRIC	CDS	3087222	3088616	1395	-		PGF_07548162	464	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2941	PATRIC.2.9855.2.9855.con.0001.CDS.3088993.3089604.rev	PATRIC	CDS	3088993	3089604	612	-		PGF_08198982	203	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2943	PATRIC.2.9855.2.9855.con.0001.CDS.3091363.3091644.rev	PATRIC	CDS	3091363	3091644	282	-		PGF_01314177	93	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2948	PATRIC.2.9855.2.9855.con.0001.CDS.3094442.3094933.rev	PATRIC	CDS	3094442	3094933	492	-		PGF_01282357	163	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2956	PATRIC.2.9855.2.9855.con.0001.CDS.3103231.3103500.rev	PATRIC	CDS	3103231	3103500	270	-		PGF_01314147	89	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2958	PATRIC.2.9855.2.9855.con.0001.CDS.3104710.3105741.rev	PATRIC	CDS	3104710	3105741	1032	-		PGF_01023927	343	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2963	PATRIC.2.9855.2.9855.con.0001.CDS.3109891.3110958.rev	PATRIC	CDS	3109891	3110958	1068	-		PGF_01262568	355	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2966	PATRIC.2.9855.2.9855.con.0001.CDS.3112210.3112860.rev	PATRIC	CDS	3112210	3112860	651	-		PGF_08225224	216	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2968	PATRIC.2.9855.2.9855.con.0001.CDS.3114980.3115384.rev	PATRIC	CDS	3114980	3115384	405	-		PGF_08225224	134	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2972	PATRIC.2.9855.2.9855.con.0001.CDS.3119093.3119635.fwd	PATRIC	CDS	3119093	3119635	543	+		PGF_03077139	180	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2980	PATRIC.2.9855.2.9855.con.0001.CDS.3126165.3126656.fwd	PATRIC	CDS	3126165	3126656	492	+		PGF_01281763	163	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2982	PATRIC.2.9855.2.9855.con.0001.CDS.3127098.3127346.rev	PATRIC	CDS	3127098	3127346	249	-		PGF_03974086	82	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.267	PATRIC.2.9855.2.9855.con.0001.CDS.312965.313300.fwd	PATRIC	CDS	312965	313300	336	+		PGF_08225224	111	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2985	PATRIC.2.9855.2.9855.con.0001.CDS.3129792.3130550.fwd	PATRIC	CDS	3129792	3130550	759	+		PGF_08225224	252	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2987	PATRIC.2.9855.2.9855.con.0001.CDS.3131075.3131632.rev	PATRIC	CDS	3131075	3131632	558	-		PGF_06656301	185	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2988	PATRIC.2.9855.2.9855.con.0001.CDS.3131722.3132381.rev	PATRIC	CDS	3131722	3132381	660	-		PGF_01280914	219	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.2989	PATRIC.2.9855.2.9855.con.0001.CDS.3132607.3133170.fwd	PATRIC	CDS	3132607	3133170	564	+		PGF_08225224	187	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.269	PATRIC.2.9855.2.9855.con.0001.CDS.314911.315030.fwd	PATRIC	CDS	314911	315030	120	+			39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.270	PATRIC.2.9855.2.9855.con.0001.CDS.315288.315428.fwd	PATRIC	CDS	315288	315428	141	+			46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3025	PATRIC.2.9855.2.9855.con.0001.CDS.3176213.3176758.rev	PATRIC	CDS	3176213	3176758	546	-		PGF_06515169	181	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3027	PATRIC.2.9855.2.9855.con.0001.CDS.3178776.3179912.rev	PATRIC	CDS	3178776	3179912	1137	-		PGF_08225224	378	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3035	PATRIC.2.9855.2.9855.con.0001.CDS.3188954.3189532.fwd	PATRIC	CDS	3188954	3189532	579	+		PGF_01281806	192	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3042	PATRIC.2.9855.2.9855.con.0001.CDS.3195752.3195940.rev	PATRIC	CDS	3195752	3195940	189	-			62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3050	PATRIC.2.9855.2.9855.con.0001.CDS.3204064.3205308.rev	PATRIC	CDS	3204064	3205308	1245	-		PGF_08225224	414	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3051	PATRIC.2.9855.2.9855.con.0001.CDS.3205398.3205526.rev	PATRIC	CDS	3205398	3205526	129	-		PGF_01277895	42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3054	PATRIC.2.9855.2.9855.con.0001.CDS.3207811.3208140.rev	PATRIC	CDS	3207811	3208140	330	-		PGF_05180549	109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3056	PATRIC.2.9855.2.9855.con.0001.CDS.3209252.3210007.rev	PATRIC	CDS	3209252	3210007	756	-		PGF_08225224	251	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3058	PATRIC.2.9855.2.9855.con.0001.CDS.3211056.3211793.rev	PATRIC	CDS	3211056	3211793	738	-		PGF_03126660	245	FIG145533: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3069	PATRIC.2.9855.2.9855.con.0001.CDS.3220397.3220921.fwd	PATRIC	CDS	3220397	3220921	525	+		PGF_08225224	174	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3071	PATRIC.2.9855.2.9855.con.0001.CDS.3222270.3222527.fwd	PATRIC	CDS	3222270	3222527	258	+		PGF_03260965	85	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3072	PATRIC.2.9855.2.9855.con.0001.CDS.3222656.3224635.rev	PATRIC	CDS	3222656	3224635	1980	-		PGF_04442645	659	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3078	PATRIC.2.9855.2.9855.con.0001.CDS.3232782.3233159.rev	PATRIC	CDS	3232782	3233159	378	-		PGF_08225224	125	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3079	PATRIC.2.9855.2.9855.con.0001.CDS.3233304.3233420.rev	PATRIC	CDS	3233304	3233420	117	-			38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3081	PATRIC.2.9855.2.9855.con.0001.CDS.3234367.3235563.rev	PATRIC	CDS	3234367	3235563	1197	-		PGF_08225224	398	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3091	PATRIC.2.9855.2.9855.con.0001.CDS.3245448.3245840.rev	PATRIC	CDS	3245448	3245840	393	-		PGF_08225224	130	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3101	PATRIC.2.9855.2.9855.con.0001.CDS.3262716.3263135.rev	PATRIC	CDS	3262716	3263135	420	-		PGF_01291816	139	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3102	PATRIC.2.9855.2.9855.con.0001.CDS.3263251.3263550.rev	PATRIC	CDS	3263251	3263550	300	-		PGF_04771191	99	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3103	PATRIC.2.9855.2.9855.con.0001.CDS.3263632.3263748.rev	PATRIC	CDS	3263632	3263748	117	-			38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3104	PATRIC.2.9855.2.9855.con.0001.CDS.3263841.3264254.fwd	PATRIC	CDS	3263841	3264254	414	+		PGF_00745987	137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3112	PATRIC.2.9855.2.9855.con.0001.CDS.3271508.3271633.rev	PATRIC	CDS	3271508	3271633	126	-			41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3113	PATRIC.2.9855.2.9855.con.0001.CDS.3271745.3271930.fwd	PATRIC	CDS	3271745	3271930	186	+		PGF_01282676	61	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3128	PATRIC.2.9855.2.9855.con.0001.CDS.3285404.3286636.rev	PATRIC	CDS	3285404	3286636	1233	-		PGF_01282310	410	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3129	PATRIC.2.9855.2.9855.con.0001.CDS.3287113.3287415.fwd	PATRIC	CDS	3287113	3287415	303	+		PGF_01286656	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3136	PATRIC.2.9855.2.9855.con.0001.CDS.3293600.3295351.rev	PATRIC	CDS	3293600	3295351	1752	-		PGF_08225224	583	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3144	PATRIC.2.9855.2.9855.con.0001.CDS.3305973.3306374.rev	PATRIC	CDS	3305973	3306374	402	-		PGF_08225224	133	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3147	PATRIC.2.9855.2.9855.con.0001.CDS.3309025.3309252.rev	PATRIC	CDS	3309025	3309252	228	-		PGF_01035965	75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3149	PATRIC.2.9855.2.9855.con.0001.CDS.3310192.3310305.rev	PATRIC	CDS	3310192	3310305	114	-		PGF_01286234	37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3150	PATRIC.2.9855.2.9855.con.0001.CDS.3310550.3310645.rev	PATRIC	CDS	3310550	3310645	96	-			31	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3173	PATRIC.2.9855.2.9855.con.0001.CDS.3329130.3329495.rev	PATRIC	CDS	3329130	3329495	366	-		PGF_01288468	121	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3175	PATRIC.2.9855.2.9855.con.0001.CDS.3330465.3330833.rev	PATRIC	CDS	3330465	3330833	369	-		PGF_01283340	122	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3176	PATRIC.2.9855.2.9855.con.0001.CDS.3330826.3331236.rev	PATRIC	CDS	3330826	3331236	411	-		PGF_01283339	136	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3177	PATRIC.2.9855.2.9855.con.0001.CDS.3331187.3331852.rev	PATRIC	CDS	3331187	3331852	666	-		PGF_00805927	221	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3178	PATRIC.2.9855.2.9855.con.0001.CDS.3331917.3332339.rev	PATRIC	CDS	3331917	3332339	423	-		PGF_01284273	140	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3179	PATRIC.2.9855.2.9855.con.0001.CDS.3332330.3332794.rev	PATRIC	CDS	3332330	3332794	465	-		PGF_01280883	154	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3180	PATRIC.2.9855.2.9855.con.0001.CDS.3332784.3333209.rev	PATRIC	CDS	3332784	3333209	426	-		PGF_08119168	141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3181	PATRIC.2.9855.2.9855.con.0001.CDS.3333206.3333652.rev	PATRIC	CDS	3333206	3333652	447	-		PGF_01282350	148	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3184	PATRIC.2.9855.2.9855.con.0001.CDS.3335392.3335610.fwd	PATRIC	CDS	3335392	3335610	219	+		PGF_08225224	72	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3186	PATRIC.2.9855.2.9855.con.0001.CDS.3336752.3337126.rev	PATRIC	CDS	3336752	3337126	375	-		PGF_07372253	124	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3187	PATRIC.2.9855.2.9855.con.0001.CDS.3337147.3337248.rev	PATRIC	CDS	3337147	3337248	102	-			33	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3188	PATRIC.2.9855.2.9855.con.0001.CDS.3337407.3337805.fwd	PATRIC	CDS	3337407	3337805	399	+		PGF_06969150	132	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3191	PATRIC.2.9855.2.9855.con.0001.CDS.3339777.3339998.rev	PATRIC	CDS	3339777	3339998	222	-		PGF_01289287	73	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3192	PATRIC.2.9855.2.9855.con.0001.CDS.3340181.3340360.rev	PATRIC	CDS	3340181	3340360	180	-		PGF_04033534	59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3193	PATRIC.2.9855.2.9855.con.0001.CDS.3340375.3340464.rev	PATRIC	CDS	3340375	3340464	90	-			29	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3194	PATRIC.2.9855.2.9855.con.0001.CDS.3340548.3340667.rev	PATRIC	CDS	3340548	3340667	120	-		PGF_08306013	39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3195	PATRIC.2.9855.2.9855.con.0001.CDS.3340860.3341573.rev	PATRIC	CDS	3340860	3341573	714	-			237	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3196	PATRIC.2.9855.2.9855.con.0001.CDS.3341698.3342135.rev	PATRIC	CDS	3341698	3342135	438	-			145	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3198	PATRIC.2.9855.2.9855.con.0001.CDS.3343030.3343812.rev	PATRIC	CDS	3343030	3343812	783	-			260	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3199	PATRIC.2.9855.2.9855.con.0001.CDS.3344006.3345013.fwd	PATRIC	CDS	3344006	3345013	1008	+			335	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3201	PATRIC.2.9855.2.9855.con.0001.CDS.3345921.3346364.rev	PATRIC	CDS	3345921	3346364	444	-		PGF_01270000	147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3202	PATRIC.2.9855.2.9855.con.0001.CDS.3346380.3346616.rev	PATRIC	CDS	3346380	3346616	237	-		PGF_00013376	78	Hypothetical protein, CF-8 family
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3203	PATRIC.2.9855.2.9855.con.0001.CDS.3346640.3346765.rev	PATRIC	CDS	3346640	3346765	126	-		PGF_01273247	41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3204	PATRIC.2.9855.2.9855.con.0001.CDS.3347056.3347229.rev	PATRIC	CDS	3347056	3347229	174	-		PGF_01253927	57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3205	PATRIC.2.9855.2.9855.con.0001.CDS.3347264.3347527.rev	PATRIC	CDS	3347264	3347527	264	-		PGF_01284291	87	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3206	PATRIC.2.9855.2.9855.con.0001.CDS.3347549.3348505.rev	PATRIC	CDS	3347549	3348505	957	-		PGF_08225224	318	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.292	PATRIC.2.9855.2.9855.con.0001.CDS.335090.335380.fwd	PATRIC	CDS	335090	335380	291	+		PGF_07727091	96	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3210	PATRIC.2.9855.2.9855.con.0001.CDS.3352488.3352922.rev	PATRIC	CDS	3352488	3352922	435	-		PGF_01290120	144	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3211	PATRIC.2.9855.2.9855.con.0001.CDS.3352915.3353265.rev	PATRIC	CDS	3352915	3353265	351	-		PGF_01257335	116	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3212	PATRIC.2.9855.2.9855.con.0001.CDS.3353277.3355328.rev	PATRIC	CDS	3353277	3355328	2052	-		PGF_01059666	683	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3213	PATRIC.2.9855.2.9855.con.0001.CDS.3355337.3355966.rev	PATRIC	CDS	3355337	3355966	630	-		PGF_06811686	209	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3214	PATRIC.2.9855.2.9855.con.0001.CDS.3355986.3357920.rev	PATRIC	CDS	3355986	3357920	1935	-		PGF_00681212	644	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3215	PATRIC.2.9855.2.9855.con.0001.CDS.3357921.3358076.rev	PATRIC	CDS	3357921	3358076	156	-		PGF_01288340	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3216	PATRIC.2.9855.2.9855.con.0001.CDS.3358097.3358483.rev	PATRIC	CDS	3358097	3358483	387	-		PGF_06937657	128	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3217	PATRIC.2.9855.2.9855.con.0001.CDS.3358540.3358965.rev	PATRIC	CDS	3358540	3358965	426	-		PGF_01294445	141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3218	PATRIC.2.9855.2.9855.con.0001.CDS.3358980.3360050.rev	PATRIC	CDS	3358980	3360050	1071	-		PGF_00199463	356	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3219	PATRIC.2.9855.2.9855.con.0001.CDS.3360050.3360517.rev	PATRIC	CDS	3360050	3360517	468	-		PGF_06852105	155	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3220	PATRIC.2.9855.2.9855.con.0001.CDS.3360518.3360913.rev	PATRIC	CDS	3360518	3360913	396	-		PGF_00774388	131	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3221	PATRIC.2.9855.2.9855.con.0001.CDS.3360906.3361244.rev	PATRIC	CDS	3360906	3361244	339	-		PGF_01307361	112	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3222	PATRIC.2.9855.2.9855.con.0001.CDS.3361260.3361589.rev	PATRIC	CDS	3361260	3361589	330	-			109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3223	PATRIC.2.9855.2.9855.con.0001.CDS.3361589.3361711.rev	PATRIC	CDS	3361589	3361711	123	-		PGF_11433618	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3225	PATRIC.2.9855.2.9855.con.0001.CDS.3362744.3363334.rev	PATRIC	CDS	3362744	3363334	591	-		PGF_08225224	196	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3226	PATRIC.2.9855.2.9855.con.0001.CDS.3363465.3363767.rev	PATRIC	CDS	3363465	3363767	303	-		PGF_08225224	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3227	PATRIC.2.9855.2.9855.con.0001.CDS.3363834.3363992.rev	PATRIC	CDS	3363834	3363992	159	-			52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3228	PATRIC.2.9855.2.9855.con.0001.CDS.3364007.3365479.rev	PATRIC	CDS	3364007	3365479	1473	-		PGF_01305455	490	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3229	PATRIC.2.9855.2.9855.con.0001.CDS.3365472.3366794.rev	PATRIC	CDS	3365472	3366794	1323	-		PGF_08225224	440	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3230	PATRIC.2.9855.2.9855.con.0001.CDS.3366812.3367951.rev	PATRIC	CDS	3366812	3367951	1140	-		PGF_07210384	379	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3231	PATRIC.2.9855.2.9855.con.0001.CDS.3368169.3368867.rev	PATRIC	CDS	3368169	3368867	699	-		PGF_00426414	232	FIG00515055: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3232	PATRIC.2.9855.2.9855.con.0001.CDS.3368899.3369402.rev	PATRIC	CDS	3368899	3369402	504	-			167	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3233	PATRIC.2.9855.2.9855.con.0001.CDS.3369524.3370354.rev	PATRIC	CDS	3369524	3370354	831	-			276	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3234	PATRIC.2.9855.2.9855.con.0001.CDS.3370413.3371087.rev	PATRIC	CDS	3370413	3371087	675	-			224	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3235	PATRIC.2.9855.2.9855.con.0001.CDS.3371229.3371522.rev	PATRIC	CDS	3371229	3371522	294	-			97	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3236	PATRIC.2.9855.2.9855.con.0001.CDS.3371624.3372049.rev	PATRIC	CDS	3371624	3372049	426	-			141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3237	PATRIC.2.9855.2.9855.con.0001.CDS.3372620.3373042.rev	PATRIC	CDS	3372620	3373042	423	-			140	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3238	PATRIC.2.9855.2.9855.con.0001.CDS.3373329.3373793.rev	PATRIC	CDS	3373329	3373793	465	-			154	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3239	PATRIC.2.9855.2.9855.con.0001.CDS.3374354.3374854.rev	PATRIC	CDS	3374354	3374854	501	-			166	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3240	PATRIC.2.9855.2.9855.con.0001.CDS.3375070.3375489.rev	PATRIC	CDS	3375070	3375489	420	-			139	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3241	PATRIC.2.9855.2.9855.con.0001.CDS.3375696.3376541.rev	PATRIC	CDS	3375696	3376541	846	-			281	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3242	PATRIC.2.9855.2.9855.con.0001.CDS.3376910.3377167.fwd	PATRIC	CDS	3376910	3377167	258	+			85	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3243	PATRIC.2.9855.2.9855.con.0001.CDS.3377353.3377964.rev	PATRIC	CDS	3377353	3377964	612	-			203	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3245	PATRIC.2.9855.2.9855.con.0001.CDS.3380726.3380953.rev	PATRIC	CDS	3380726	3380953	228	-			75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3246	PATRIC.2.9855.2.9855.con.0001.CDS.3380963.3381562.rev	PATRIC	CDS	3380963	3381562	600	-			199	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3247	PATRIC.2.9855.2.9855.con.0001.CDS.3381562.3381837.rev	PATRIC	CDS	3381562	3381837	276	-			91	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3248	PATRIC.2.9855.2.9855.con.0001.CDS.3381861.3382019.rev	PATRIC	CDS	3381861	3382019	159	-			52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3250	PATRIC.2.9855.2.9855.con.0001.CDS.3382748.3383026.rev	PATRIC	CDS	3382748	3383026	279	-			92	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3251	PATRIC.2.9855.2.9855.con.0001.CDS.3383033.3383656.rev	PATRIC	CDS	3383033	3383656	624	-		PGF_03258151	207	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.295	PATRIC.2.9855.2.9855.con.0001.CDS.338352.338681.fwd	PATRIC	CDS	338352	338681	330	+			109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3253	PATRIC.2.9855.2.9855.con.0001.CDS.3384424.3385257.rev	PATRIC	CDS	3384424	3385257	834	-		PGF_07272403	277	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3254	PATRIC.2.9855.2.9855.con.0001.CDS.3385241.3385480.rev	PATRIC	CDS	3385241	3385480	240	-			79	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3255	PATRIC.2.9855.2.9855.con.0001.CDS.3385523.3385702.rev	PATRIC	CDS	3385523	3385702	180	-			59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3256	PATRIC.2.9855.2.9855.con.0001.CDS.3385699.3386142.rev	PATRIC	CDS	3385699	3386142	444	-		PGF_06264237	147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3257	PATRIC.2.9855.2.9855.con.0001.CDS.3386211.3386420.fwd	PATRIC	CDS	3386211	3386420	210	+			69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3258	PATRIC.2.9855.2.9855.con.0001.CDS.3386417.3386593.rev	PATRIC	CDS	3386417	3386593	177	-			58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3259	PATRIC.2.9855.2.9855.con.0001.CDS.3386590.3386805.rev	PATRIC	CDS	3386590	3386805	216	-			71	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3260	PATRIC.2.9855.2.9855.con.0001.CDS.3386832.3387071.rev	PATRIC	CDS	3386832	3387071	240	-		PGF_06981507	79	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3262	PATRIC.2.9855.2.9855.con.0001.CDS.3387888.3388139.rev	PATRIC	CDS	3387888	3388139	252	-		PGF_05668206	83	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3263	PATRIC.2.9855.2.9855.con.0001.CDS.3388308.3388877.fwd	PATRIC	CDS	3388308	3388877	570	+		PGF_05961997	189	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3264	PATRIC.2.9855.2.9855.con.0001.CDS.3388893.3389351.fwd	PATRIC	CDS	3388893	3389351	459	+			152	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3265	PATRIC.2.9855.2.9855.con.0001.CDS.3389432.3389752.fwd	PATRIC	CDS	3389432	3389752	321	+		PGF_04520850	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3266	PATRIC.2.9855.2.9855.con.0001.CDS.3389746.3390591.fwd	PATRIC	CDS	3389746	3390591	846	+			281	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3267	PATRIC.2.9855.2.9855.con.0001.CDS.3390657.3390806.rev	PATRIC	CDS	3390657	3390806	150	-			49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3268	PATRIC.2.9855.2.9855.con.0001.CDS.3391354.3391755.rev	PATRIC	CDS	3391354	3391755	402	-		PGF_01281805	133	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3269	PATRIC.2.9855.2.9855.con.0001.CDS.3391885.3392643.rev	PATRIC	CDS	3391885	3392643	759	-			252	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3270	PATRIC.2.9855.2.9855.con.0001.CDS.3393075.3393299.rev	PATRIC	CDS	3393075	3393299	225	-		PGF_01289287	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3272	PATRIC.2.9855.2.9855.con.0001.CDS.3393955.3394137.rev	PATRIC	CDS	3393955	3394137	183	-		PGF_04032346	60	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3275	PATRIC.2.9855.2.9855.con.0001.CDS.3396278.3396541.rev	PATRIC	CDS	3396278	3396541	264	-		PGF_01298707	87	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3276	PATRIC.2.9855.2.9855.con.0001.CDS.3396734.3397147.rev	PATRIC	CDS	3396734	3397147	414	-		PGF_08225224	137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3277	PATRIC.2.9855.2.9855.con.0001.CDS.3397654.3397776.rev	PATRIC	CDS	3397654	3397776	123	-			40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3279	PATRIC.2.9855.2.9855.con.0001.CDS.3398936.3399376.rev	PATRIC	CDS	3398936	3399376	441	-		PGF_01270000	146	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3280	PATRIC.2.9855.2.9855.con.0001.CDS.3399392.3399628.rev	PATRIC	CDS	3399392	3399628	237	-		PGF_00013376	78	Hypothetical protein, CF-8 family
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3282	PATRIC.2.9855.2.9855.con.0001.CDS.3401258.3401431.rev	PATRIC	CDS	3401258	3401431	174	-		PGF_01253927	57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3283	PATRIC.2.9855.2.9855.con.0001.CDS.3401466.3401741.rev	PATRIC	CDS	3401466	3401741	276	-		PGF_01284291	91	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3284	PATRIC.2.9855.2.9855.con.0001.CDS.3401767.3403143.rev	PATRIC	CDS	3401767	3403143	1377	-		PGF_08225224	458	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3285	PATRIC.2.9855.2.9855.con.0001.CDS.3403156.3403791.rev	PATRIC	CDS	3403156	3403791	636	-		PGF_01293804	211	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3288	PATRIC.2.9855.2.9855.con.0001.CDS.3405356.3405703.rev	PATRIC	CDS	3405356	3405703	348	-		PGF_01292654	115	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3291	PATRIC.2.9855.2.9855.con.0001.CDS.3407481.3408008.rev	PATRIC	CDS	3407481	3408008	528	-		PGF_07340489	175	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3293	PATRIC.2.9855.2.9855.con.0001.CDS.3411694.3411825.rev	PATRIC	CDS	3411694	3411825	132	-		PGF_01284146	43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3294	PATRIC.2.9855.2.9855.con.0001.CDS.3411870.3412301.rev	PATRIC	CDS	3411870	3412301	432	-		PGF_01288985	143	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3297	PATRIC.2.9855.2.9855.con.0001.CDS.3414251.3414574.rev	PATRIC	CDS	3414251	3414574	324	-		PGF_00850797	107	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3298	PATRIC.2.9855.2.9855.con.0001.CDS.3414580.3415410.rev	PATRIC	CDS	3414580	3415410	831	-		PGF_01284452	276	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3299	PATRIC.2.9855.2.9855.con.0001.CDS.3415418.3415822.rev	PATRIC	CDS	3415418	3415822	405	-		PGF_00346964	134	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3300	PATRIC.2.9855.2.9855.con.0001.CDS.3415836.3415991.rev	PATRIC	CDS	3415836	3415991	156	-		PGF_01018015	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3301	PATRIC.2.9855.2.9855.con.0001.CDS.3416210.3416542.rev	PATRIC	CDS	3416210	3416542	333	-		PGF_00371742	110	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3302	PATRIC.2.9855.2.9855.con.0001.CDS.3416570.3417607.rev	PATRIC	CDS	3416570	3417607	1038	-		PGF_08225224	345	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3303	PATRIC.2.9855.2.9855.con.0001.CDS.3417632.3418009.rev	PATRIC	CDS	3417632	3418009	378	-		PGF_08225224	125	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3304	PATRIC.2.9855.2.9855.con.0001.CDS.3418028.3419422.rev	PATRIC	CDS	3418028	3419422	1395	-		PGF_01653347	464	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3305	PATRIC.2.9855.2.9855.con.0001.CDS.3419545.3420555.rev	PATRIC	CDS	3419545	3420555	1011	-		PGF_08225224	336	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3306	PATRIC.2.9855.2.9855.con.0001.CDS.3420548.3422047.rev	PATRIC	CDS	3420548	3422047	1500	-		PGF_10317027	499	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3309	PATRIC.2.9855.2.9855.con.0001.CDS.3424389.3425078.rev	PATRIC	CDS	3424389	3425078	690	-		PGF_01074669	229	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3310	PATRIC.2.9855.2.9855.con.0001.CDS.3425169.3425552.rev	PATRIC	CDS	3425169	3425552	384	-		PGF_08225224	127	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3311	PATRIC.2.9855.2.9855.con.0001.CDS.3425612.3425923.rev	PATRIC	CDS	3425612	3425923	312	-		PGF_00426422	103	FIG00515420: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3313	PATRIC.2.9855.2.9855.con.0001.CDS.3427531.3428820.rev	PATRIC	CDS	3427531	3428820	1290	-			429	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3314	PATRIC.2.9855.2.9855.con.0001.CDS.3429224.3429727.rev	PATRIC	CDS	3429224	3429727	504	-			167	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3315	PATRIC.2.9855.2.9855.con.0001.CDS.3429854.3430375.rev	PATRIC	CDS	3429854	3430375	522	-			173	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3316	PATRIC.2.9855.2.9855.con.0001.CDS.3430487.3430654.rev	PATRIC	CDS	3430487	3430654	168	-		PGF_00719970	55	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3317	PATRIC.2.9855.2.9855.con.0001.CDS.3430731.3431375.rev	PATRIC	CDS	3430731	3431375	645	-		PGF_08225224	214	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3318	PATRIC.2.9855.2.9855.con.0001.CDS.3431379.3431807.rev	PATRIC	CDS	3431379	3431807	429	-		PGF_00013380	142	Hypothetical protein, Lmo2306 homolog [Bacteriophage A118]
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3319	PATRIC.2.9855.2.9855.con.0001.CDS.3431823.3432035.rev	PATRIC	CDS	3431823	3432035	213	-		PGF_01292402	70	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3320	PATRIC.2.9855.2.9855.con.0001.CDS.3432035.3432172.rev	PATRIC	CDS	3432035	3432172	138	-			45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3321	PATRIC.2.9855.2.9855.con.0001.CDS.3432188.3432955.rev	PATRIC	CDS	3432188	3432955	768	-		PGF_00774504	255	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3322	PATRIC.2.9855.2.9855.con.0001.CDS.3432948.3433808.rev	PATRIC	CDS	3432948	3433808	861	-		PGF_08225224	286	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3325	PATRIC.2.9855.2.9855.con.0001.CDS.3435464.3435880.rev	PATRIC	CDS	3435464	3435880	417	-		PGF_01292401	138	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3327	PATRIC.2.9855.2.9855.con.0001.CDS.3437906.3438247.rev	PATRIC	CDS	3437906	3438247	342	-		PGF_01304741	113	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3328	PATRIC.2.9855.2.9855.con.0001.CDS.3438262.3438420.rev	PATRIC	CDS	3438262	3438420	159	-		PGF_01309295	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3329	PATRIC.2.9855.2.9855.con.0001.CDS.3438420.3438929.rev	PATRIC	CDS	3438420	3438929	510	-		PGF_01282442	169	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3330	PATRIC.2.9855.2.9855.con.0001.CDS.3438986.3439186.fwd	PATRIC	CDS	3438986	3439186	201	+			66	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3331	PATRIC.2.9855.2.9855.con.0001.CDS.3439188.3439481.rev	PATRIC	CDS	3439188	3439481	294	-		PGF_06915397	97	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3332	PATRIC.2.9855.2.9855.con.0001.CDS.3439592.3439819.rev	PATRIC	CDS	3439592	3439819	228	-		PGF_01290151	75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3334	PATRIC.2.9855.2.9855.con.0001.CDS.3440324.3440470.rev	PATRIC	CDS	3440324	3440470	147	-			48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3335	PATRIC.2.9855.2.9855.con.0001.CDS.3440605.3440721.fwd	PATRIC	CDS	3440605	3440721	117	+		PGF_12726692	38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3336	PATRIC.2.9855.2.9855.con.0001.CDS.3440837.3443941.rev	PATRIC	CDS	3440837	3443941	3105	-		PGF_08225224	1034	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3338	PATRIC.2.9855.2.9855.con.0001.CDS.3445318.3445980.rev	PATRIC	CDS	3445318	3445980	663	-			220	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3339	PATRIC.2.9855.2.9855.con.0001.CDS.3446048.3446164.rev	PATRIC	CDS	3446048	3446164	117	-			38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3340	PATRIC.2.9855.2.9855.con.0001.CDS.3446202.3447611.rev	PATRIC	CDS	3446202	3447611	1410	-			469	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3341	PATRIC.2.9855.2.9855.con.0001.CDS.3447644.3448909.rev	PATRIC	CDS	3447644	3448909	1266	-		PGF_08225224	421	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3342	PATRIC.2.9855.2.9855.con.0001.CDS.3448949.3450442.rev	PATRIC	CDS	3448949	3450442	1494	-			497	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3343	PATRIC.2.9855.2.9855.con.0001.CDS.3450605.3451300.rev	PATRIC	CDS	3450605	3451300	696	-			231	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3344	PATRIC.2.9855.2.9855.con.0001.CDS.3451576.3452046.rev	PATRIC	CDS	3451576	3452046	471	-			156	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3345	PATRIC.2.9855.2.9855.con.0001.CDS.3452051.3453313.rev	PATRIC	CDS	3452051	3453313	1263	-			420	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3346	PATRIC.2.9855.2.9855.con.0001.CDS.3454626.3454772.rev	PATRIC	CDS	3454626	3454772	147	-			48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3347	PATRIC.2.9855.2.9855.con.0001.CDS.3455156.3455467.fwd	PATRIC	CDS	3455156	3455467	312	+			103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3348	PATRIC.2.9855.2.9855.con.0001.CDS.3455514.3455957.fwd	PATRIC	CDS	3455514	3455957	444	+			147	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3349	PATRIC.2.9855.2.9855.con.0001.CDS.3456078.3457088.rev	PATRIC	CDS	3456078	3457088	1011	-		PGF_08099168	336	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3351	PATRIC.2.9855.2.9855.con.0001.CDS.3458990.3459682.rev	PATRIC	CDS	3458990	3459682	693	-		PGF_04818097	230	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3352	PATRIC.2.9855.2.9855.con.0001.CDS.3459890.3460111.rev	PATRIC	CDS	3459890	3460111	222	-		PGF_01282436	73	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3353	PATRIC.2.9855.2.9855.con.0001.CDS.3460203.3460625.rev	PATRIC	CDS	3460203	3460625	423	-		PGF_08225224	140	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3354	PATRIC.2.9855.2.9855.con.0001.CDS.3460872.3461879.rev	PATRIC	CDS	3460872	3461879	1008	-		PGF_08225224	335	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.299	PATRIC.2.9855.2.9855.con.0001.CDS.346442.347368.fwd	PATRIC	CDS	346442	347368	927	+		PGF_05426577	308	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.300	PATRIC.2.9855.2.9855.con.0001.CDS.347381.348214.fwd	PATRIC	CDS	347381	348214	834	+			277	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3381	PATRIC.2.9855.2.9855.con.0001.CDS.3488811.3488963.rev	PATRIC	CDS	3488811	3488963	153	-		PGF_01288115	50	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.302	PATRIC.2.9855.2.9855.con.0001.CDS.349309.349977.fwd	PATRIC	CDS	349309	349977	669	+			222	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3388	PATRIC.2.9855.2.9855.con.0001.CDS.3495680.3496579.rev	PATRIC	CDS	3495680	3496579	900	-		PGF_01327941	299	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3389	PATRIC.2.9855.2.9855.con.0001.CDS.3496805.3497509.fwd	PATRIC	CDS	3496805	3497509	705	+		PGF_01983435	234	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3390	PATRIC.2.9855.2.9855.con.0001.CDS.3497615.3497782.rev	PATRIC	CDS	3497615	3497782	168	-		PGF_01281861	55	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.303	PATRIC.2.9855.2.9855.con.0001.CDS.349985.350704.fwd	PATRIC	CDS	349985	350704	720	+		PGF_08225224	239	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3395	PATRIC.2.9855.2.9855.con.0001.CDS.3503091.3503705.rev	PATRIC	CDS	3503091	3503705	615	-		PGF_01301656	204	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3398	PATRIC.2.9855.2.9855.con.0001.CDS.3505338.3506150.rev	PATRIC	CDS	3505338	3506150	813	-		PGF_08225224	270	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3404	PATRIC.2.9855.2.9855.con.0001.CDS.3511922.3513268.rev	PATRIC	CDS	3511922	3513268	1347	-		PGF_08225224	448	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3409	PATRIC.2.9855.2.9855.con.0001.CDS.3517386.3518093.fwd	PATRIC	CDS	3517386	3518093	708	+		PGF_01282400	235	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3420	PATRIC.2.9855.2.9855.con.0001.CDS.3530609.3530977.rev	PATRIC	CDS	3530609	3530977	369	-		PGF_02680547	122	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3427	PATRIC.2.9855.2.9855.con.0001.CDS.3536550.3537284.rev	PATRIC	CDS	3536550	3537284	735	-		PGF_01668610	244	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3431	PATRIC.2.9855.2.9855.con.0001.CDS.3540264.3540623.fwd	PATRIC	CDS	3540264	3540623	360	+		PGF_01005358	119	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.307	PATRIC.2.9855.2.9855.con.0001.CDS.354300.354548.fwd	PATRIC	CDS	354300	354548	249	+			82	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.308	PATRIC.2.9855.2.9855.con.0001.CDS.354716.354895.fwd	PATRIC	CDS	354716	354895	180	+		PGF_01313654	59	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3438	PATRIC.2.9855.2.9855.con.0001.CDS.3547736.3547852.rev	PATRIC	CDS	3547736	3547852	117	-		PGF_01288045	38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.309	PATRIC.2.9855.2.9855.con.0001.CDS.354926.355756.fwd	PATRIC	CDS	354926	355756	831	+		PGF_10353643	276	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3443	PATRIC.2.9855.2.9855.con.0001.CDS.3553173.3553325.fwd	PATRIC	CDS	3553173	3553325	153	+			50	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3444	PATRIC.2.9855.2.9855.con.0001.CDS.3553473.3553658.fwd	PATRIC	CDS	3553473	3553658	186	+		PGF_08225224	61	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3447	PATRIC.2.9855.2.9855.con.0001.CDS.3556038.3556214.fwd	PATRIC	CDS	3556038	3556214	177	+		PGF_01296872	58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3451	PATRIC.2.9855.2.9855.con.0001.CDS.3560273.3561373.fwd	PATRIC	CDS	3560273	3561373	1101	+		PGF_08225224	366	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3456	PATRIC.2.9855.2.9855.con.0001.CDS.3566076.3566381.rev	PATRIC	CDS	3566076	3566381	306	-		PGF_01286135	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3457	PATRIC.2.9855.2.9855.con.0001.CDS.3566411.3566629.rev	PATRIC	CDS	3566411	3566629	219	-		PGF_01285942	72	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3462	PATRIC.2.9855.2.9855.con.0001.CDS.3570771.3570974.rev	PATRIC	CDS	3570771	3570974	204	-		PGF_01283216	67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3466	PATRIC.2.9855.2.9855.con.0001.CDS.3573218.3573592.rev	PATRIC	CDS	3573218	3573592	375	-		PGF_08225224	124	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3467	PATRIC.2.9855.2.9855.con.0001.CDS.3573592.3574008.rev	PATRIC	CDS	3573592	3574008	417	-		PGF_08461705	138	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3468	PATRIC.2.9855.2.9855.con.0001.CDS.3573968.3574354.rev	PATRIC	CDS	3573968	3574354	387	-		PGF_08461705	128	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3469	PATRIC.2.9855.2.9855.con.0001.CDS.3575152.3575640.fwd	PATRIC	CDS	3575152	3575640	489	+		PGF_01284288	162	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3470	PATRIC.2.9855.2.9855.con.0001.CDS.3575729.3575920.fwd	PATRIC	CDS	3575729	3575920	192	+		PGF_01284288	63	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3471	PATRIC.2.9855.2.9855.con.0001.CDS.3577482.3578036.rev	PATRIC	CDS	3577482	3578036	555	-			184	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3472	PATRIC.2.9855.2.9855.con.0001.CDS.3578103.3578225.rev	PATRIC	CDS	3578103	3578225	123	-		40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3475	PATRIC.2.9855.2.9855.con.0001.CDS.3581095.3581796.rev	PATRIC	CDS	3581095	3581796	702	-	PGF_08078960	233	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3479	PATRIC.2.9855.2.9855.con.0001.CDS.3586593.3587090.fwd	PATRIC	CDS	3586593	3587090	498	+	PGF_01317646	165	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3481	PATRIC.2.9855.2.9855.con.0001.CDS.3588125.3588526.fwd	PATRIC	CDS	3588125	3588526	402	+	PGF_01280882	133	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3491	PATRIC.2.9855.2.9855.con.0001.CDS.3598243.3599007.fwd	PATRIC	CDS	3598243	3599007	765	+	PGF_08225224	254	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3492	PATRIC.2.9855.2.9855.con.0001.CDS.3599062.3599514.rev	PATRIC	CDS	3599062	3599514	453	-	PGF_00175945	150	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3499	PATRIC.2.9855.2.9855.con.0001.CDS.3607809.3607937.rev	PATRIC	CDS	3607809	3607937	129	-	PGF_10519086	42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3500	PATRIC.2.9855.2.9855.con.0001.CDS.3607939.3608406.rev	PATRIC	CDS	3607939	3608406	468	-	PGF_10519086	155	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3501	PATRIC.2.9855.2.9855.con.0001.CDS.3608706.3609197.rev	PATRIC	CDS	3608706	3609197	492	-	PGF_01281777	163	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3502	PATRIC.2.9855.2.9855.con.0001.CDS.3609587.3609736.rev	PATRIC	CDS	3609587	3609736	150	-	PGF_01282102	49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3504	PATRIC.2.9855.2.9855.con.0001.CDS.3611143.3611448.rev	PATRIC	CDS	3611143	3611448	306	-	PGF_01307601	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3511	PATRIC.2.9855.2.9855.con.0001.CDS.3622991.3623350.rev	PATRIC	CDS	3622991	3623350	360	-	PGF_00174834	119	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3525	PATRIC.2.9855.2.9855.con.0001.CDS.3640231.3640587.rev	PATRIC	CDS	3640231	3640587	357	-	PGF_08225224	118	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3526	PATRIC.2.9855.2.9855.con.0001.CDS.3640661.3641890.rev	PATRIC	CDS	3640661	3641890	1230	-	PGF_01317309	409	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3532	PATRIC.2.9855.2.9855.con.0001.CDS.3650209.3650442.rev	PATRIC	CDS	3650209	3650442	234	-	PGF_08225224	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3540	PATRIC.2.9855.2.9855.con.0001.CDS.3661943.3662584.rev	PATRIC	CDS	3661943	3662584	642	-	PGF_00122285	213	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3543	PATRIC.2.9855.2.9855.con.0001.CDS.3664996.3665253.rev	PATRIC	CDS	3664996	3665253	258	-	PGF_08225224	85	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3544	PATRIC.2.9855.2.9855.con.0001.CDS.3665366.3666406.rev	PATRIC	CDS	3665366	3666406	1041	-	PGF_09466613	346	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3547	PATRIC.2.9855.2.9855.con.0001.CDS.3669898.3670164.fwd	PATRIC	CDS	3669898	3670164	267	+	PGF_00224157	88	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3550	PATRIC.2.9855.2.9855.con.0001.CDS.3672106.3673011.fwd	PATRIC	CDS	3672106	3673011	906	+	PGF_08225224	301	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3553	PATRIC.2.9855.2.9855.con.0001.CDS.3674459.3675481.rev	PATRIC	CDS	3674459	3675481	1023	-	PGF_06148711	340	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3554	PATRIC.2.9855.2.9855.con.0001.CDS.3675626.3676108.fwd	PATRIC	CDS	3675626	3676108	483	+	PGF_01326646	160	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3558	PATRIC.2.9855.2.9855.con.0001.CDS.3679698.3679898.rev	PATRIC	CDS	3679698	3679898	201	-	PGF_01054406	66	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3559	PATRIC.2.9855.2.9855.con.0001.CDS.3680204.3680416.fwd	PATRIC	CDS	3680204	3680416	213	+	PGF_00694130	70	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3560	PATRIC.2.9855.2.9855.con.0001.CDS.3680849.3681247.rev	PATRIC	CDS	3680849	3681247	399	-	PGF_02872192	132	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3561	PATRIC.2.9855.2.9855.con.0001.CDS.3681265.3681510.rev	PATRIC	CDS	3681265	3681510	246	-	PGF_08225224	81	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3571	PATRIC.2.9855.2.9855.con.0001.CDS.3692491.3693045.rev	PATRIC	CDS	3692491	3693045	555	-	PGF_00148848	184	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3580	PATRIC.2.9855.2.9855.con.0001.CDS.3704894.3705523.fwd	PATRIC	CDS	3704894	3705523	630	+	PGF_01324719	209	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3587	PATRIC.2.9855.2.9855.con.0001.CDS.3716742.3716966.rev	PATRIC	CDS	3716742	3716966	225	-		74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3590	PATRIC.2.9855.2.9855.con.0001.CDS.3718406.3719329.fwd	PATRIC	CDS	3718406	3719329	924	+	PGF_01283606	307	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3591	PATRIC.2.9855.2.9855.con.0001.CDS.3719619.3720143.rev	PATRIC	CDS	3719619	3720143	525	-	PGF_08225224	174	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3592	PATRIC.2.9855.2.9855.con.0001.CDS.3720258.3720512.rev	PATRIC	CDS	3720258	3720512	255	-	PGF_01291576	84	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3593	PATRIC.2.9855.2.9855.con.0001.CDS.3720544.3721032.rev	PATRIC	CDS	3720544	3721032	489	-	PGF_08225224	162	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3599	PATRIC.2.9855.2.9855.con.0001.CDS.3726214.3726417.rev	PATRIC	CDS	3726214	3726417	204	-	PGF_07337644	67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3603	PATRIC.2.9855.2.9855.con.0001.CDS.3729870.3730685.rev	PATRIC	CDS	3729870	3730685	816	-	PGF_08225224	271	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3604	PATRIC.2.9855.2.9855.con.0001.CDS.3730815.3731009.rev	PATRIC	CDS	3730815	3731009	195	-		64	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3615	PATRIC.2.9855.2.9855.con.0001.CDS.3739938.3740687.fwd	PATRIC	CDS	3739938	3740687	750	+	PGF_08225224	249	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3625	PATRIC.2.9855.2.9855.con.0001.CDS.3751269.3751388.rev	PATRIC	CDS	3751269	3751388	120	-		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3626	PATRIC.2.9855.2.9855.con.0001.CDS.3751393.3752343.rev	PATRIC	CDS	3751393	3752343	951	-	PGF_01321985	316	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3629	PATRIC.2.9855.2.9855.con.0001.CDS.3754945.3756018.rev	PATRIC	CDS	3754945	3756018	1074	-	PGF_08225224	357	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3631	PATRIC.2.9855.2.9855.con.0001.CDS.3757151.3758290.rev	PATRIC	CDS	3757151	3758290	1140	-	PGF_08225224	379	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3632	PATRIC.2.9855.2.9855.con.0001.CDS.3758883.3759224.fwd	PATRIC	CDS	3758883	3759224	342	+	PGF_05762615	113	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3633	PATRIC.2.9855.2.9855.con.0001.CDS.3759526.3760191.rev	PATRIC	CDS	3759526	3760191	666	-	PGF_00335595	221	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3634	PATRIC.2.9855.2.9855.con.0001.CDS.3760630.3761184.rev	PATRIC	CDS	3760630	3761184	555	-	PGF_01283220	184	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3638	PATRIC.2.9855.2.9855.con.0001.CDS.3764364.3765302.rev	PATRIC	CDS	3764364	3765302	939	-	PGF_01258756	312	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3640	PATRIC.2.9855.2.9855.con.0001.CDS.3767311.3767868.rev	PATRIC	CDS	3767311	3767868	558	-	PGF_00083457	185	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3650	PATRIC.2.9855.2.9855.con.0001.CDS.3777700.3778308.rev	PATRIC	CDS	3777700	3778308	609	-	PGF_08225224	202	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.333	PATRIC.2.9855.2.9855.con.0001.CDS.377908.378528.fwd	PATRIC	CDS	377908	378528	621	+	PGF_03114042	206	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3652	PATRIC.2.9855.2.9855.con.0001.CDS.3779820.3780878.fwd	PATRIC	CDS	3779820	3780878	1059	+	PGF_00350914	352	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.334	PATRIC.2.9855.2.9855.con.0001.CDS.378567.378722.fwd	PATRIC	CDS	378567	378722	156	+	PGF_01284009	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3657	PATRIC.2.9855.2.9855.con.0001.CDS.3786469.3786984.rev	PATRIC	CDS	3786469	3786984	516	-	PGF_01305468	171	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3664	PATRIC.2.9855.2.9855.con.0001.CDS.3793043.3793429.rev	PATRIC	CDS	3793043	3793429	387	-	PGF_01283349	128	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3670	PATRIC.2.9855.2.9855.con.0001.CDS.3798096.3798320.rev	PATRIC	CDS	3798096	3798320	225	-	PGF_07319434	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3672	PATRIC.2.9855.2.9855.con.0001.CDS.3798645.3798821.rev	PATRIC	CDS	3798645	3798821	177	-		58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3673	PATRIC.2.9855.2.9855.con.0001.CDS.3799314.3799766.rev	PATRIC	CDS	3799314	3799766	453	-	PGF_06509468	150	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3681	PATRIC.2.9855.2.9855.con.0001.CDS.3807176.3807310.rev	PATRIC	CDS	3807176	3807310	135	-		44	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3682	PATRIC.2.9855.2.9855.con.0001.CDS.3807366.3807761.rev	PATRIC	CDS	3807366	3807761	396	-	PGF_00991263	131	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3683	PATRIC.2.9855.2.9855.con.0001.CDS.3807854.3808261.rev	PATRIC	CDS	3807854	3808261	408	-	PGF_06274330	135	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3688	PATRIC.2.9855.2.9855.con.0001.CDS.3812248.3812403.rev	PATRIC	CDS	3812248	3812403	156	-	PGF_01310426	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3689	PATRIC.2.9855.2.9855.con.0001.CDS.3812594.3812734.rev	PATRIC	CDS	3812594	3812734	141	-		46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3691	PATRIC.2.9855.2.9855.con.0001.CDS.3815226.3815594.rev	PATRIC	CDS	3815226	3815594	369	-	PGF_09361040	122	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3694	PATRIC.2.9855.2.9855.con.0001.CDS.3819429.3819785.rev	PATRIC	CDS	3819429	3819785	357	-	PGF_05802972	118	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3699	PATRIC.2.9855.2.9855.con.0001.CDS.3823917.3824150.rev	PATRIC	CDS	3823917	3824150	234	-		77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3713	PATRIC.2.9855.2.9855.con.0001.CDS.3844397.3845647.rev	PATRIC	CDS	3844397	3845647	1251	-	PGF_08225224	416	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3714	PATRIC.2.9855.2.9855.con.0001.CDS.3846107.3847102.fwd	PATRIC	CDS	3846107	3847102	996	+	PGF_10406873	331	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.339	PATRIC.2.9855.2.9855.con.0001.CDS.385847.386278.rev	PATRIC	CDS	385847	386278	432	-	PGF_08225224	143	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3726	PATRIC.2.9855.2.9855.con.0001.CDS.3860346.3860627.rev	PATRIC	CDS	3860346	3860627	282	-	PGF_10397663	93	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3765	PATRIC.2.9855.2.9855.con.0001.CDS.3901549.3901647.rev	PATRIC	CDS	3901549	3901647	99	-	PGF_07256643	32	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.343	PATRIC.2.9855.2.9855.con.0001.CDS.391298.392152.fwd	PATRIC	CDS	391298	392152	855	+	PGF_01281320	284	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.346	PATRIC.2.9855.2.9855.con.0001.CDS.394686.396887.fwd	PATRIC	CDS	394686	396887	2202	+	PGF_06775043	733	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3817	PATRIC.2.9855.2.9855.con.0001.CDS.3952157.3952426.rev	PATRIC	CDS	3952157	3952426	270	-	PGF_01170416	89	FIG011856: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.42	PATRIC.2.9855.2.9855.con.0001.CDS.39689.39808.fwd	PATRIC	CDS	39689	39808	120	+		39	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3833	PATRIC.2.9855.2.9855.con.0001.CDS.3969972.3970250.rev	PATRIC	CDS	3969972	3970250	279	-	PGF_01307815	92	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3834	PATRIC.2.9855.2.9855.con.0001.CDS.3970243.3970425.rev	PATRIC	CDS	3970243	3970425	183	-		60	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3839	PATRIC.2.9855.2.9855.con.0001.CDS.3975833.3976333.rev	PATRIC	CDS	3975833	3976333	501	-	PGF_01057507	166	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3840	PATRIC.2.9855.2.9855.con.0001.CDS.3976938.3977234.rev	PATRIC	CDS	3976938	3977234	297	-	PGF_08225224	98	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3841	PATRIC.2.9855.2.9855.con.0001.CDS.3977231.3977344.rev	PATRIC	CDS	3977231	3977344	114	-		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3847	PATRIC.2.9855.2.9855.con.0001.CDS.3982796.3982972.rev	PATRIC	CDS	3982796	3982972	177	-	PGF_10465435	58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3848	PATRIC.2.9855.2.9855.con.0001.CDS.3983170.3983496.rev	PATRIC	CDS	3983170	3983496	327	-	PGF_01288945	108	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3849	PATRIC.2.9855.2.9855.con.0001.CDS.3983794.3984327.rev	PATRIC	CDS	3983794	3984327	534	-	PGF_01288945	177	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3850	PATRIC.2.9855.2.9855.con.0001.CDS.3984421.3984969.rev	PATRIC	CDS	3984421	3984969	549	-	PGF_08225224	182	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3851	PATRIC.2.9855.2.9855.con.0001.CDS.3985148.3985375.rev	PATRIC	CDS	3985148	3985375	228	-	PGF_04460157	75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3853	PATRIC.2.9855.2.9855.con.0001.CDS.3987308.3988672.rev	PATRIC	CDS	3987308	3988672	1365	-	PGF_06364304	454	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3856	PATRIC.2.9855.2.9855.con.0001.CDS.3993004.3993117.rev	PATRIC	CDS	3993004	3993117	114	-	PGF_12918941	37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3857	PATRIC.2.9855.2.9855.con.0001.CDS.3993592.3994146.fwd	PATRIC	CDS	3993592	3994146	555	+	PGF_08141806	184	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3859	PATRIC.2.9855.2.9855.con.0001.CDS.3995450.3995737.rev	PATRIC	CDS	3995450	3995737	288	-	PGF_00900030	95	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3860	PATRIC.2.9855.2.9855.con.0001.CDS.3995798.3996001.rev	PATRIC	CDS	3995798	3996001	204	-	PGF_01290081	67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3861	PATRIC.2.9855.2.9855.con.0001.CDS.3996105.3996947.rev	PATRIC	CDS	3996105	3996947	843	-	PGF_01282556	280	similar to (EMBL:AL117211) YPMT1.20C, Yersinia pestis CO-92 hypothetical protein from plasmid pMT1; similar to (EMBL:AF074611) Y1035, Yersinia pestis KIM5 hypothetical protein from plasmid pMT1; blastn and dotplot analyses suggest that an insertion event has taken place at this point as compared to Yersinia pestis pMT1
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.350	PATRIC.2.9855.2.9855.con.0001.CDS.399701.400561.fwd	PATRIC	CDS	399701	400561	861	+	PGF_08496569	286	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3862	PATRIC.2.9855.2.9855.con.0001.CDS.3997103.3997225.rev	PATRIC	CDS	3997103	3997225	123	-	PGF_08225224	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3878	PATRIC.2.9855.2.9855.con.0001.CDS.4012176.4012787.fwd	PATRIC	CDS	4012176	4012787	612	+	PGF_08225224	203	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3879	PATRIC.2.9855.2.9855.con.0001.CDS.4013083.4013616.rev	PATRIC	CDS	4013083	4013616	534	-	PGF_05872322	177	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3883	PATRIC.2.9855.2.9855.con.0001.CDS.4018719.4019021.rev	PATRIC	CDS	4018719	4019021	303	-	PGF_08225224	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.353	PATRIC.2.9855.2.9855.con.0001.CDS.403238.403909.fwd	PATRIC	CDS	403238	403909	672	+	PGF_08225224	223	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3897	PATRIC.2.9855.2.9855.con.0001.CDS.4035379.4036197.rev	PATRIC	CDS	4035379	4036197	819	-	PGF_08225224	272	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3902	PATRIC.2.9855.2.9855.con.0001.CDS.4041721.4042152.fwd	PATRIC	CDS	4041721	4042152	432	+	PGF_01283178	143	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3904	PATRIC.2.9855.2.9855.con.0001.CDS.4044009.4044260.fwd	PATRIC	CDS	4044009	4044260	252	+	PGF_01287284	83	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3910	PATRIC.2.9855.2.9855.con.0001.CDS.4050809.4051111.fwd	PATRIC	CDS	4050809	4051111	303	+	PGF_01288473	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3915	PATRIC.2.9855.2.9855.con.0001.CDS.4056623.4057633.fwd	PATRIC	CDS	4056623	4057633	1011	+	PGF_02995647	336	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3916	PATRIC.2.9855.2.9855.con.0001.CDS.4057844.4058164.rev	PATRIC	CDS	4057844	4058164	321	-	PGF_06788215	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3922	PATRIC.2.9855.2.9855.con.0001.CDS.4063350.4064108.rev	PATRIC	CDS	4063350	4064108	759	-	PGF_08225224	252	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3927	PATRIC.2.9855.2.9855.con.0001.CDS.4069172.4069813.rev	PATRIC	CDS	4069172	4069813	642	-	PGF_08225224	213	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3928	PATRIC.2.9855.2.9855.con.0001.CDS.4070297.4071337.rev	PATRIC	CDS	4070297	4071337	1041	-	PGF_08225224	346	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.356	PATRIC.2.9855.2.9855.con.0001.CDS.407315.407857.fwd	PATRIC	CDS	407315	407857	543	+	PGF_00689871	180	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3938	PATRIC.2.9855.2.9855.con.0001.CDS.4083252.4084634.fwd	PATRIC	CDS	4083252	4084634	1383	+	PGF_03237127	460	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.357	PATRIC.2.9855.2.9855.con.0001.CDS.408384.409304.fwd	PATRIC	CDS	408384	409304	921	+	PGF_03029761	306	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3954	PATRIC.2.9855.2.9855.con.0001.CDS.4102589.4103086.rev	PATRIC	CDS	4102589	4103086	498	-	PGF_05873024	165	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3955	PATRIC.2.9855.2.9855.con.0001.CDS.4103330.4103482.fwd	PATRIC	CDS	4103330	4103482	153	+	PGF_01282507	50	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3957	PATRIC.2.9855.2.9855.con.0001.CDS.4104264.4105487.rev	PATRIC	CDS	4104264	4105487	1224	-	PGF_03136537	407	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.361	PATRIC.2.9855.2.9855.con.0001.CDS.413072.413989.fwd	PATRIC	CDS	413072	413989	918	+	PGF_08225224	305	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.362	PATRIC.2.9855.2.9855.con.0001.CDS.414711.416303.fwd	PATRIC	CDS	414711	416303	1593	+		530	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.3999	PATRIC.2.9855.2.9855.con.0001.CDS.4159686.4160321.fwd	PATRIC	CDS	4159686	4160321	636	+	PGF_10339942	211	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.363	PATRIC.2.9855.2.9855.con.0001.CDS.416838.417038.fwd	PATRIC	CDS	416838	417038	201	+	PGF_11719864	66	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.364	PATRIC.2.9855.2.9855.con.0001.CDS.417112.417261.rev	PATRIC	CDS	417112	417261	150	-		49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4009	PATRIC.2.9855.2.9855.con.0001.CDS.4174310.4175446.rev	PATRIC	CDS	4174310	4175446	1137	-	PGF_07441531	378	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4015	PATRIC.2.9855.2.9855.con.0001.CDS.4179324.4179746.fwd	PATRIC	CDS	4179324	4179746	423	+	PGF_01285370	140	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4016	PATRIC.2.9855.2.9855.con.0001.CDS.4179889.4180470.rev	PATRIC	CDS	4179889	4180470	582	-	PGF_02954476	193	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.366	PATRIC.2.9855.2.9855.con.0001.CDS.418001.421069.fwd	PATRIC	CDS	418001	421069	3069	+	PGF_00205103	1022	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4018	PATRIC.2.9855.2.9855.con.0001.CDS.4181848.4182243.rev	PATRIC	CDS	4181848	4182243	396	-	PGF_01270000	131	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4019	PATRIC.2.9855.2.9855.con.0001.CDS.4182259.4182495.rev	PATRIC	CDS	4182259	4182495	237	-	PGF_00013376	78	Hypothetical protein, CF-8 family
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4020	PATRIC.2.9855.2.9855.con.0001.CDS.4182492.4182620.rev	PATRIC	CDS	4182492	4182620	129	-		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4021	PATRIC.2.9855.2.9855.con.0001.CDS.4182716.4183090.rev	PATRIC	CDS	4182716	4183090	375	-		124	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4022	PATRIC.2.9855.2.9855.con.0001.CDS.4183361.4184518.rev	PATRIC	CDS	4183361	4184518	1158	-		385	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4023	PATRIC.2.9855.2.9855.con.0001.CDS.4184789.4184920.rev	PATRIC	CDS	4184789	4184920	132	-		43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4024	PATRIC.2.9855.2.9855.con.0001.CDS.4184913.4185320.rev	PATRIC	CDS	4184913	4185320	408	-	PGF_00369477	135	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4025	PATRIC.2.9855.2.9855.con.0001.CDS.4185339.4186421.rev	PATRIC	CDS	4185339	4186421	1083	-	PGF_07413190	360	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4026	PATRIC.2.9855.2.9855.con.0001.CDS.4186437.4187162.rev	PATRIC	CDS	4186437	4187162	726	-	PGF_01258756	241	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4028	PATRIC.2.9855.2.9855.con.0001.CDS.4188865.4189569.rev	PATRIC	CDS	4188865	4189569	705	-	PGF_06888704	234	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4029	PATRIC.2.9855.2.9855.con.0001.CDS.4189571.4192846.rev	PATRIC	CDS	4189571	4192846	3276	-	PGF_12833299	1091	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4030	PATRIC.2.9855.2.9855.con.0001.CDS.4193094.4193477.rev	PATRIC	CDS	4193094	4193477	384	-		127	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4031	PATRIC.2.9855.2.9855.con.0001.CDS.4193548.4194132.rev	PATRIC	CDS	4193548	4194132	585	-	PGF_12717751	194	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4032	PATRIC.2.9855.2.9855.con.0001.CDS.4194139.4194495.rev	PATRIC	CDS	4194139	4194495	357	-	PGF_04030238	118	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4033	PATRIC.2.9855.2.9855.con.0001.CDS.4194506.4194862.rev	PATRIC	CDS	4194506	4194862	357	-	PGF_05011140	118	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4035	PATRIC.2.9855.2.9855.con.0001.CDS.4195258.4196340.rev	PATRIC	CDS	4195258	4196340	1083	-	PGF_08225224	360	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4039	PATRIC.2.9855.2.9855.con.0001.CDS.4198524.4198739.rev	PATRIC	CDS	4198524	4198739	216	-		71	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4043	PATRIC.2.9855.2.9855.con.0001.CDS.4201460.4201939.rev	PATRIC	CDS	4201460	4201939	480	-		159	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4044	PATRIC.2.9855.2.9855.con.0001.CDS.4202208.4202825.rev	PATRIC	CDS	4202208	4202825	618	-	PGF_07602525	205	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4045	PATRIC.2.9855.2.9855.con.0001.CDS.4202822.4203049.rev	PATRIC	CDS	4202822	4203049	228	-	PGF_12891832	75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4046	PATRIC.2.9855.2.9855.con.0001.CDS.4203090.4203488.rev	PATRIC	CDS	4203090	4203488	399	-	PGF_00951936	132	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4047	PATRIC.2.9855.2.9855.con.0001.CDS.4203654.4203983.rev	PATRIC	CDS	4203654	4203983	330	-	PGF_06943129	109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4048	PATRIC.2.9855.2.9855.con.0001.CDS.4204225.4204524.rev	PATRIC	CDS	4204225	4204524	300	-	PGF_00074201	99	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4049	PATRIC.2.9855.2.9855.con.0001.CDS.4204790.4205182.rev	PATRIC	CDS	4204790	4205182	393	-	PGF_01307443	130	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4050	PATRIC.2.9855.2.9855.con.0001.CDS.4205547.4205978.rev	PATRIC	CDS	4205547	4205978	432	-	PGF_00343391	143	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4051	PATRIC.2.9855.2.9855.con.0001.CDS.4206036.4206218.rev	PATRIC	CDS	4206036	4206218	183	-	PGF_10392770	60	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4052	PATRIC.2.9855.2.9855.con.0001.CDS.4206329.4206610.rev	PATRIC	CDS	4206329	4206610	282	-		93	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4053	PATRIC.2.9855.2.9855.con.0001.CDS.4206822.4207133.fwd	PATRIC	CDS	4206822	4207133	312	+	PGF_08058392	103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4054	PATRIC.2.9855.2.9855.con.0001.CDS.4207177.4207494.fwd	PATRIC	CDS	4207177	4207494	318	+	PGF_08058392	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4055	PATRIC.2.9855.2.9855.con.0001.CDS.4207547.4207705.rev	PATRIC	CDS	4207547	4207705	159	-	PGF_01284265	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4056	PATRIC.2.9855.2.9855.con.0001.CDS.4207912.4208229.fwd	PATRIC	CDS	4207912	4208229	318	+	PGF_01296568	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4057	PATRIC.2.9855.2.9855.con.0001.CDS.4208252.4208575.fwd	PATRIC	CDS	4208252	4208575	324	+	PGF_01284229	107	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4058	PATRIC.2.9855.2.9855.con.0001.CDS.4208845.4209624.rev	PATRIC	CDS	4208845	4209624	780	-	PGF_00774504	259	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4059	PATRIC.2.9855.2.9855.con.0001.CDS.4209617.4210450.rev	PATRIC	CDS	4209617	4210450	834	-	PGF_08225224	277	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4060	PATRIC.2.9855.2.9855.con.0001.CDS.4210498.4210683.rev	PATRIC	CDS	4210498	4210683	186	-	PGF_01282437	61	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.367	PATRIC.2.9855.2.9855.con.0001.CDS.421062.421190.fwd	PATRIC	CDS	421062	421190	129	+		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4061	PATRIC.2.9855.2.9855.con.0001.CDS.4210774.4211073.rev	PATRIC	CDS	4210774	4211073	300	-	PGF_01283221	99	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4062	PATRIC.2.9855.2.9855.con.0001.CDS.4211109.4211273.rev	PATRIC	CDS	4211109	4211273	165	-	PGF_01281864	54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4063	PATRIC.2.9855.2.9855.con.0001.CDS.4211330.4211761.rev	PATRIC	CDS	4211330	4211761	432	-	PGF_08225224	143	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4064	PATRIC.2.9855.2.9855.con.0001.CDS.4211804.4212007.rev	PATRIC	CDS	4211804	4212007	204	-		67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4066	PATRIC.2.9855.2.9855.con.0001.CDS.4212617.4214494.rev	PATRIC	CDS	4212617	4214494	1878	-		625	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.368	PATRIC.2.9855.2.9855.con.0001.CDS.421413.422054.fwd	PATRIC	CDS	421413	422054	642	+		213	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4067	PATRIC.2.9855.2.9855.con.0001.CDS.4214491.4214940.rev	PATRIC	CDS	4214491	4214940	450	-		149	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4068	PATRIC.2.9855.2.9855.con.0001.CDS.4214933.4216195.rev	PATRIC	CDS	4214933	4216195	1263	-		420	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.369	PATRIC.2.9855.2.9855.con.0001.CDS.422170.423066.fwd	PATRIC	CDS	422170	423066	897	+		298	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4078	PATRIC.2.9855.2.9855.con.0001.CDS.4230319.4231185.rev	PATRIC	CDS	4230319	4231185	867	-	PGF_10384892	288	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4081	PATRIC.2.9855.2.9855.con.0001.CDS.4234911.4235795.rev	PATRIC	CDS	4234911	4235795	885	-	PGF_01283170	294	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.370	PATRIC.2.9855.2.9855.con.0001.CDS.423714.423812.fwd	PATRIC	CDS	423714	423812	99	+		32	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.371	PATRIC.2.9855.2.9855.con.0001.CDS.423946.425559.fwd	PATRIC	CDS	423946	425559	1614	+		537	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4093	PATRIC.2.9855.2.9855.con.0001.CDS.4252358.4253620.rev	PATRIC	CDS	4252358	4253620	1263	-	PGF_08225224	420	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4094	PATRIC.2.9855.2.9855.con.0001.CDS.4253613.4255418.rev	PATRIC	CDS	4253613	4255418	1806	-	PGF_10677061	601	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4095	PATRIC.2.9855.2.9855.con.0001.CDS.4255558.4256886.rev	PATRIC	CDS	4255558	4256886	1329	-	PGF_12663335	442	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.372	PATRIC.2.9855.2.9855.con.0001.CDS.425561.428005.fwd	PATRIC	CDS	425561	428005	2445	+	PGF_10339942	814	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4097	PATRIC.2.9855.2.9855.con.0001.CDS.4259503.4259808.rev	PATRIC	CDS	4259503	4259808	306	-	PGF_00199989	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4113	PATRIC.2.9855.2.9855.con.0001.CDS.4278289.4278567.rev	PATRIC	CDS	4278289	4278567	279	-	PGF_01299889	92	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.373	PATRIC.2.9855.2.9855.con.0001.CDS.428216.429130.fwd	PATRIC	CDS	428216	429130	915	+		304	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.374	PATRIC.2.9855.2.9855.con.0001.CDS.429155.429523.fwd	PATRIC	CDS	429155	429523	369	+		122	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4127	PATRIC.2.9855.2.9855.con.0001.CDS.4293465.4293905.rev	PATRIC	CDS	4293465	4293905	441	-	PGF_01280886	146	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4129	PATRIC.2.9855.2.9855.con.0001.CDS.4296064.4296393.rev	PATRIC	CDS	4296064	4296393	330	-	PGF_01282505	109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.45	PATRIC.2.9855.2.9855.con.0001.CDS.43066.43377.fwd	PATRIC	CDS	43066	43377	312	+	PGF_01317997	103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.376	PATRIC.2.9855.2.9855.con.0001.CDS.430902.431063.fwd	PATRIC	CDS	430902	431063	162	+		53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.377	PATRIC.2.9855.2.9855.con.0001.CDS.431144.431308.fwd	PATRIC	CDS	431144	431308	165	+		54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.378	PATRIC.2.9855.2.9855.con.0001.CDS.431431.432249.fwd	PATRIC	CDS	431431	432249	819	+		272	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.379	PATRIC.2.9855.2.9855.con.0001.CDS.432384.432521.fwd	PATRIC	CDS	432384	432521	138	+		45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.380	PATRIC.2.9855.2.9855.con.0001.CDS.432693.432974.fwd	PATRIC	CDS	432693	432974	282	+		93	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4153	PATRIC.2.9855.2.9855.con.0001.CDS.4329298.4329753.rev	PATRIC	CDS	4329298	4329753	456	-	PGF_01280970	151	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.381	PATRIC.2.9855.2.9855.con.0001.CDS.433016.433255.fwd	PATRIC	CDS	433016	433255	240	+		79	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4155	PATRIC.2.9855.2.9855.con.0001.CDS.4330835.4331080.rev	PATRIC	CDS	4330835	4331080	246	-	PGF_01285251	81	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.382	PATRIC.2.9855.2.9855.con.0001.CDS.433367.434092.fwd	PATRIC	CDS	433367	434092	726	+	PGF_07132671	241	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4163	PATRIC.2.9855.2.9855.con.0001.CDS.4337383.4338186.fwd	PATRIC	CDS	4337383	4338186	804	+	PGF_08225224	267	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.383	PATRIC.2.9855.2.9855.con.0001.CDS.434423.435103.fwd	PATRIC	CDS	434423	435103	681	+	PGF_07112604	226	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4178	PATRIC.2.9855.2.9855.con.0001.CDS.4352608.4353375.rev	PATRIC	CDS	4352608	4353375	768	-	PGF_12866473	255	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.384	PATRIC.2.9855.2.9855.con.0001.CDS.435305.435613.fwd	PATRIC	CDS	435305	435613	309	+		102	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.385	PATRIC.2.9855.2.9855.con.0001.CDS.435670.436308.fwd	PATRIC	CDS	435670	436308	639	+		212	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.386	PATRIC.2.9855.2.9855.con.0001.CDS.436460.436669.fwd	PATRIC	CDS	436460	436669	210	+	PGF_01289047	69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4190	PATRIC.2.9855.2.9855.con.0001.CDS.4368847.4368987.fwd	PATRIC	CDS	4368847	4368987	141	+	PGF_04710333	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4191	PATRIC.2.9855.2.9855.con.0001.CDS.4370099.4370551.fwd	PATRIC	CDS	4370099	4370551	453	+	PGF_08225224	150	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4192	PATRIC.2.9855.2.9855.con.0001.CDS.4372634.4372747.rev	PATRIC	CDS	4372634	4372747	114	-		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4194	PATRIC.2.9855.2.9855.con.0001.CDS.4374562.4375470.rev	PATRIC	CDS	4374562	4375470	909	-	PGF_01260600	302	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.388	PATRIC.2.9855.2.9855.con.0001.CDS.438576.438752.fwd	PATRIC	CDS	438576	438752	177	+	PGF_01293789	58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.390	PATRIC.2.9855.2.9855.con.0001.CDS.439754.440038.fwd	PATRIC	CDS	439754	440038	285	+	PGF_12844699	94	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4213	PATRIC.2.9855.2.9855.con.0001.CDS.4403307.4403516.rev	PATRIC	CDS	4403307	4403516	210	-	PGF_01296786	69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4224	PATRIC.2.9855.2.9855.con.0001.CDS.4416520.4417860.rev	PATRIC	CDS	4416520	4417860	1341	-	PGF_08225224	446	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4225	PATRIC.2.9855.2.9855.con.0001.CDS.4417987.4418100.rev	PATRIC	CDS	4417987	4418100	114	-		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4231	PATRIC.2.9855.2.9855.con.0001.CDS.4425062.4426504.fwd	PATRIC	CDS	4425062	4426504	1443	+	PGF_08225224	480	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4241	PATRIC.2.9855.2.9855.con.0001.CDS.4436927.4437193.rev	PATRIC	CDS	4436927	4437193	267	-	PGF_01293194	88	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4246	PATRIC.2.9855.2.9855.con.0001.CDS.4442004.4443614.rev	PATRIC	CDS	4442004	4443614	1611	-	PGF_00901798	536	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4247	PATRIC.2.9855.2.9855.con.0001.CDS.4443617.4445425.rev	PATRIC	CDS	4443617	4445425	1809	-	PGF_01254697	602	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4251	PATRIC.2.9855.2.9855.con.0001.CDS.4449957.4450274.rev	PATRIC	CDS	4449957	4450274	318	-	PGF_08063424	105	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4254	PATRIC.2.9855.2.9855.con.0001.CDS.4454599.4455417.rev	PATRIC	CDS	4454599	4455417	819	-	PGF_08053408	272	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4263	PATRIC.2.9855.2.9855.con.0001.CDS.4465317.4467290.rev	PATRIC	CDS	4465317	4467290	1974	-	PGF_02784966	657	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4267	PATRIC.2.9855.2.9855.con.0001.CDS.4471120.4471941.rev	PATRIC	CDS	4471120	4471941	822	-	PGF_01286739	273	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4268	PATRIC.2.9855.2.9855.con.0001.CDS.4472381.4473169.fwd	PATRIC	CDS	4472381	4473169	789	+	PGF_00939026	262	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4269	PATRIC.2.9855.2.9855.con.0001.CDS.4473169.4474920.fwd	PATRIC	CDS	4473169	4474920	1752	+	PGF_00245257	583	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4272	PATRIC.2.9855.2.9855.con.0001.CDS.4477550.4478593.rev	PATRIC	CDS	4477550	4478593	1044	-	PGF_00112747	347	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4273	PATRIC.2.9855.2.9855.con.0001.CDS.4478593.4479225.rev	PATRIC	CDS	4478593	4479225	633	-	PGF_01282659	210	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4278	PATRIC.2.9855.2.9855.con.0001.CDS.4484816.4485295.fwd	PATRIC	CDS	4484816	4485295	480	+	PGF_00378224	159	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.398	PATRIC.2.9855.2.9855.con.0001.CDS.448961.449917.fwd	PATRIC	CDS	448961	449917	957	+	PGF_01319073	318	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4286	PATRIC.2.9855.2.9855.con.0001.CDS.4492959.4493087.rev	PATRIC	CDS	4492959	4493087	129	-		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4289	PATRIC.2.9855.2.9855.con.0001.CDS.4494842.4495666.fwd	PATRIC	CDS	4494842	4495666	825	+		274	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4290	PATRIC.2.9855.2.9855.con.0001.CDS.4495686.4496735.rev	PATRIC	CDS	4495686	4496735	1050	-	PGF_08225224	349	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4291	PATRIC.2.9855.2.9855.con.0001.CDS.4496905.4499664.rev	PATRIC	CDS	4496905	4499664	2760	-		919	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.399	PATRIC.2.9855.2.9855.con.0001.CDS.449965.452445.fwd	PATRIC	CDS	449965	452445	2481	+	PGF_08225224	826	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4292	PATRIC.2.9855.2.9855.con.0001.CDS.4499657.4502107.rev	PATRIC	CDS	4499657	4502107	2451	-		816	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4293	PATRIC.2.9855.2.9855.con.0001.CDS.4502205.4503206.rev	PATRIC	CDS	4502205	4503206	1002	-		333	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4303	PATRIC.2.9855.2.9855.con.0001.CDS.4517598.4518860.rev	PATRIC	CDS	4517598	4518860	1263	-	PGF_08225224	420	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4304	PATRIC.2.9855.2.9855.con.0001.CDS.4518895.4519023.rev	PATRIC	CDS	4518895	4519023	129	-	PGF_01255167	42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4305	PATRIC.2.9855.2.9855.con.0001.CDS.4519079.4519636.rev	PATRIC	CDS	4519079	4519636	558	-	PGF_09152153	185	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4306	PATRIC.2.9855.2.9855.con.0001.CDS.4520220.4520780.fwd	PATRIC	CDS	4520220	4520780	561	+	PGF_01307519	186	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4308	PATRIC.2.9855.2.9855.con.0001.CDS.4521440.4521946.rev	PATRIC	CDS	4521440	4521946	507	-	PGF_01307767	168	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.400	PATRIC.2.9855.2.9855.con.0001.CDS.452461.453030.fwd	PATRIC	CDS	452461	453030	570	+	PGF_00727983	189	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.401	PATRIC.2.9855.2.9855.con.0001.CDS.453092.455980.fwd	PATRIC	CDS	453092	455980	2889	+	PGF_00399704	962	hypothetical protein formerly called flagellar hook-length control protein FliK
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4313	PATRIC.2.9855.2.9855.con.0001.CDS.4531115.4531234.fwd	PATRIC	CDS	4531115	4531234	120	+	PGF_01310347	39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4323	PATRIC.2.9855.2.9855.con.0001.CDS.4541805.4541978.rev	PATRIC	CDS	4541805	4541978	174	-	PGF_00386109	57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4325	PATRIC.2.9855.2.9855.con.0001.CDS.4543252.4544214.rev	PATRIC	CDS	4543252	4544214	963	-	PGF_08225224	320	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4326	PATRIC.2.9855.2.9855.con.0001.CDS.4544751.4544999.fwd	PATRIC	CDS	4544751	4544999	249	+		82	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4347	PATRIC.2.9855.2.9855.con.0001.CDS.4569693.4569818.rev	PATRIC	CDS	4569693	4569818	126	-	PGF_01287724	41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4369	PATRIC.2.9855.2.9855.con.0001.CDS.4595093.4595572.rev	PATRIC	CDS	4595093	4595572	480	-	PGF_01260980	159	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4384	PATRIC.2.9855.2.9855.con.0001.CDS.4610753.4610872.rev	PATRIC	CDS	4610753	4610872	120	-		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4386	PATRIC.2.9855.2.9855.con.0001.CDS.4611660.4612004.rev	PATRIC	CDS	4611660	4612004	345	-	PGF_08225224	114	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4387	PATRIC.2.9855.2.9855.con.0001.CDS.4612090.4612446.rev	PATRIC	CDS	4612090	4612446	357	-	PGF_01283294	118	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4392	PATRIC.2.9855.2.9855.con.0001.CDS.4618092.4618229.rev	PATRIC	CDS	4618092	4618229	138	-	PGF_00302810	45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4393	PATRIC.2.9855.2.9855.con.0001.CDS.4618314.4618739.rev	PATRIC	CDS	4618314	4618739	426	-	PGF_07312044	141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4394	PATRIC.2.9855.2.9855.con.0001.CDS.4618894.4619040.rev	PATRIC	CDS	4618894	4619040	147	-	PGF_01303906	48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4398	PATRIC.2.9855.2.9855.con.0001.CDS.4622008.4623414.rev	PATRIC	CDS	4622008	4623414	1407	-	PGF_07208491	468	FIG099352: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4415	PATRIC.2.9855.2.9855.con.0001.CDS.4640748.4641050.rev	PATRIC	CDS	4640748	4641050	303	-	PGF_01057039	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4418	PATRIC.2.9855.2.9855.con.0001.CDS.4644760.4645167.fwd	PATRIC	CDS	4644760	4645167	408	+	PGF_00112218	135	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4419	PATRIC.2.9855.2.9855.con.0001.CDS.4645544.4645801.rev	PATRIC	CDS	4645544	4645801	258	-	PGF_01283647	85	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4425	PATRIC.2.9855.2.9855.con.0001.CDS.4652212.4652610.rev	PATRIC	CDS	4652212	4652610	399	-	PGF_01280866	132	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4426	PATRIC.2.9855.2.9855.con.0001.CDS.4652631.4653323.rev	PATRIC	CDS	4652631	4653323	693	-	PGF_10397066	230	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4441	PATRIC.2.9855.2.9855.con.0001.CDS.4666733.4667434.rev	PATRIC	CDS	4666733	4667434	702	-	PGF_05843198	233	FIG017108: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4443	PATRIC.2.9855.2.9855.con.0001.CDS.4669526.4673761.rev	PATRIC	CDS	4669526	4673761	4236	-	PGF_08225224	1411	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4445	PATRIC.2.9855.2.9855.con.0001.CDS.4676360.4676869.rev	PATRIC	CDS	4676360	4676869	510	-	PGF_01281389	169	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4447	PATRIC.2.9855.2.9855.con.0001.CDS.4678044.4678520.rev	PATRIC	CDS	4678044	4678520	477	-	PGF_06987973	158	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4448	PATRIC.2.9855.2.9855.con.0001.CDS.4678739.4678879.rev	PATRIC	CDS	4678739	4678879	141	-	PGF_01288030	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.408	PATRIC.2.9855.2.9855.con.0001.CDS.468289.468411.fwd	PATRIC	CDS	468289	468411	123	+		40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4460	PATRIC.2.9855.2.9855.con.0001.CDS.4690025.4690699.rev	PATRIC	CDS	4690025	4690699	675	-	PGF_01283297	224	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4465	PATRIC.2.9855.2.9855.con.0001.CDS.4696634.4697311.fwd	PATRIC	CDS	4696634	4697311	678	+	PGF_08225224	225	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.410	PATRIC.2.9855.2.9855.con.0001.CDS.469794.470084.fwd	PATRIC	CDS	469794	470084	291	+	PGF_08225224	96	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4467	PATRIC.2.9855.2.9855.con.0001.CDS.4697994.4698653.fwd	PATRIC	CDS	4697994	4698653	660	+	PGF_07131539	219	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.411	PATRIC.2.9855.2.9855.con.0001.CDS.470273.470413.fwd	PATRIC	CDS	470273	470413	141	+	PGF_01276909	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4474	PATRIC.2.9855.2.9855.con.0001.CDS.4706393.4706515.rev	PATRIC	CDS	4706393	4706515	123	-	PGF_01286009	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4477	PATRIC.2.9855.2.9855.con.0001.CDS.4708276.4709292.rev	PATRIC	CDS	4708276	4709292	1017	-	PGF_01260402	338	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4500	PATRIC.2.9855.2.9855.con.0001.CDS.4731707.4732492.rev	PATRIC	CDS	4731707	4732492	786	-	PGF_08225224	261	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4512	PATRIC.2.9855.2.9855.con.0001.CDS.4748907.4749242.rev	PATRIC	CDS	4748907	4749242	336	-	PGF_01284233	111	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4516	PATRIC.2.9855.2.9855.con.0001.CDS.4752752.4753084.fwd	PATRIC	CDS	4752752	4753084	333	+	PGF_01294963	110	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.417	PATRIC.2.9855.2.9855.con.0001.CDS.476320.476484.fwd	PATRIC	CDS	476320	476484	165	+	PGF_01322036	54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.418	PATRIC.2.9855.2.9855.con.0001.CDS.476684.476869.fwd	PATRIC	CDS	476684	476869	186	+	PGF_07212195	61	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4531	PATRIC.2.9855.2.9855.con.0001.CDS.4771984.4772634.rev	PATRIC	CDS	4771984	4772634	651	-	PGF_00002441	216	FIG013354: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4540	PATRIC.2.9855.2.9855.con.0001.CDS.4779121.4779486.rev	PATRIC	CDS	4779121	4779486	366	-	PGF_01282733	121	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4549	PATRIC.2.9855.2.9855.con.0001.CDS.4787768.4789528.rev	PATRIC	CDS	4787768	4789528	1761	-	PGF_00003270	586	FIG069887: hypothetical protein / Peptide chain release factor N(5)-glutamine methyltransferase (EC 2.1.1.297)
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4555	PATRIC.2.9855.2.9855.con.0001.CDS.4795427.4795735.rev	PATRIC	CDS	4795427	4795735	309	-	PGF_01260311	102	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4561	PATRIC.2.9855.2.9855.con.0001.CDS.4801647.4801850.rev	PATRIC	CDS	4801647	4801850	204	-		67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4572	PATRIC.2.9855.2.9855.con.0001.CDS.4813548.4814702.rev	PATRIC	CDS	4813548	4814702	1155	-	PGF_01324494	384	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4580	PATRIC.2.9855.2.9855.con.0001.CDS.4821567.4822139.rev	PATRIC	CDS	4821567	4822139	573	-	PGF_01874968	190	Hypothetical protein Cj1505c
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4587	PATRIC.2.9855.2.9855.con.0001.CDS.4832130.4832582.fwd	PATRIC	CDS	4832130	4832582	453	+	PGF_08225224	150	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4589	PATRIC.2.9855.2.9855.con.0001.CDS.4837040.4837249.rev	PATRIC	CDS	4837040	4837249	210	-	PGF_00200465	69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4591	PATRIC.2.9855.2.9855.con.0001.CDS.4839895.4840209.rev	PATRIC	CDS	4839895	4840209	315	-	PGF_08150122	104	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4592	PATRIC.2.9855.2.9855.con.0001.CDS.4840209.4840838.rev	PATRIC	CDS	4840209	4840838	630	-	PGF_12745521	209	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4593	PATRIC.2.9855.2.9855.con.0001.CDS.4840845.4841228.rev	PATRIC	CDS	4840845	4841228	384	-	PGF_00390083	127	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4595	PATRIC.2.9855.2.9855.con.0001.CDS.4843676.4844833.rev	PATRIC	CDS	4843676	4844833	1158	-	PGF_08225224	385	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4596	PATRIC.2.9855.2.9855.con.0001.CDS.4844923.4845060.rev	PATRIC	CDS	4844923	4845060	138	-	PGF_02782326	45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4598	PATRIC.2.9855.2.9855.con.0001.CDS.4846169.4846444.rev	PATRIC	CDS	4846169	4846444	276	-	PGF_08065547	91	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4599	PATRIC.2.9855.2.9855.con.0001.CDS.4846851.4847027.rev	PATRIC	CDS	4846851	4847027	177	-	PGF_01308972	58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4603	PATRIC.2.9855.2.9855.con.0001.CDS.4851619.4853358.fwd	PATRIC	CDS	4851619	4853358	1740	+	PGF_08225224	579	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4605	PATRIC.2.9855.2.9855.con.0001.CDS.4855161.4855433.rev	PATRIC	CDS	4855161	4855433	273	-	PGF_03121020	90	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4625	PATRIC.2.9855.2.9855.con.0001.CDS.4877423.4877746.rev	PATRIC	CDS	4877423	4877746	324	-	PGF_01282441	107	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4639	PATRIC.2.9855.2.9855.con.0001.CDS.4894648.4895229.rev	PATRIC	CDS	4894648	4895229	582	-	PGF_01288736	193	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.431	PATRIC.2.9855.2.9855.con.0001.CDS.490047.490781.fwd	PATRIC	CDS	490047	490781	735	+	PGF_08225224	244	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4644	PATRIC.2.9855.2.9855.con.0001.CDS.4901209.4902120.rev	PATRIC	CDS	4901209	4902120	912	-	PGF_01284296	303	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.432	PATRIC.2.9855.2.9855.con.0001.CDS.490778.491098.fwd	PATRIC	CDS	490778	491098	321	+	PGF_12708186	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4658	PATRIC.2.9855.2.9855.con.0001.CDS.4919712.4920467.rev	PATRIC	CDS	4919712	4920467	756	-	PGF_08225224	251	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4661	PATRIC.2.9855.2.9855.con.0001.CDS.4923017.4923187.fwd	PATRIC	CDS	4923017	4923187	171	+		56	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4663	PATRIC.2.9855.2.9855.con.0001.CDS.4923842.4924597.rev	PATRIC	CDS	4923842	4924597	756	-	PGF_01324146	251	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4664	PATRIC.2.9855.2.9855.con.0001.CDS.4924868.4925272.fwd	PATRIC	CDS	4924868	4925272	405	+	PGF_01291809	134	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4667	PATRIC.2.9855.2.9855.con.0001.CDS.4930804.4933413.rev	PATRIC	CDS	4930804	4933413	2610	-	PGF_08225224	869	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4670	PATRIC.2.9855.2.9855.con.0001.CDS.4935023.4935439.rev	PATRIC	CDS	4935023	4935439	417	-	PGF_01291436	138	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4675	PATRIC.2.9855.2.9855.con.0001.CDS.4942032.4942739.rev	PATRIC	CDS	4942032	4942739	708	-	PGF_08225224	235	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4677	PATRIC.2.9855.2.9855.con.0001.CDS.4943376.4944074.rev	PATRIC	CDS	4943376	4944074	699	-	PGF_08225224	232	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4678	PATRIC.2.9855.2.9855.con.0001.CDS.4944104.4944937.rev	PATRIC	CDS	4944104	4944937	834	-	PGF_01285572	277	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4679	PATRIC.2.9855.2.9855.con.0001.CDS.4944980.4945405.rev	PATRIC	CDS	4944980	4945405	426	-	PGF_01285375	141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4684	PATRIC.2.9855.2.9855.con.0001.CDS.4948751.4949002.fwd	PATRIC	CDS	4948751	4949002	252	+	PGF_01285838	83	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4690	PATRIC.2.9855.2.9855.con.0001.CDS.4954077.4954241.rev	PATRIC	CDS	4954077	4954241	165	-		54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4691	PATRIC.2.9855.2.9855.con.0001.CDS.4954299.4954460.rev	PATRIC	CDS	4954299	4954460	162	-	PGF_01321975	53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4693	PATRIC.2.9855.2.9855.con.0001.CDS.4955058.4955174.rev	PATRIC	CDS	4955058	4955174	117	-	PGF_08181261	38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.51	PATRIC.2.9855.2.9855.con.0001.CDS.49581.50618.fwd	PATRIC	CDS	49581	50618	1038	+	PGF_08225224	345	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4697	PATRIC.2.9855.2.9855.con.0001.CDS.4958503.4958634.rev	PATRIC	CDS	4958503	4958634	132	-	PGF_01309906	43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4698	PATRIC.2.9855.2.9855.con.0001.CDS.4958631.4958885.rev	PATRIC	CDS	4958631	4958885	255	-	PGF_10027474	84	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4699	PATRIC.2.9855.2.9855.con.0001.CDS.4959154.4959276.rev	PATRIC	CDS	4959154	4959276	123	-	PGF_10027474	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4709	PATRIC.2.9855.2.9855.con.0001.CDS.4972340.4973458.rev	PATRIC	CDS	4972340	4973458	1119	-	PGF_08225224	372	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4716	PATRIC.2.9855.2.9855.con.0001.CDS.4994885.4995007.rev	PATRIC	CDS	4994885	4995007	123	-		40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4725	PATRIC.2.9855.2.9855.con.0001.CDS.5007949.5008077.rev	PATRIC	CDS	5007949	5008077	129	-		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4755	PATRIC.2.9855.2.9855.con.0001.CDS.5040513.5040938.rev	PATRIC	CDS	5040513	5040938	426	-	PGF_01260392	141	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.444	PATRIC.2.9855.2.9855.con.0001.CDS.504287.504670.fwd	PATRIC	CDS	504287	504670	384	+	PGF_01283368	127	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.445	PATRIC.2.9855.2.9855.con.0001.CDS.504758.504880.fwd	PATRIC	CDS	504758	504880	123	+	PGF_01299703	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4778	PATRIC.2.9855.2.9855.con.0001.CDS.5066809.5066985.fwd	PATRIC	CDS	5066809	5066985	177	+	PGF_05432122	58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.450	PATRIC.2.9855.2.9855.con.0001.CDS.512238.514706.fwd	PATRIC	CDS	512238	514706	2469	+	PGF_08225224	822	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4850	PATRIC.2.9855.2.9855.con.0001.CDS.5124728.5124931.rev	PATRIC	CDS	5124728	5124931	204	-	PGF_01273426	67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4855	PATRIC.2.9855.2.9855.con.0001.CDS.5127901.5128083.rev	PATRIC	CDS	5127901	5128083	183	-	PGF_01280945	60	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4860	PATRIC.2.9855.2.9855.con.0001.CDS.5135800.5136213.fwd	PATRIC	CDS	5135800	5136213	414	+	PGF_08225224	137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4864	PATRIC.2.9855.2.9855.con.0001.CDS.5143688.5143801.rev	PATRIC	CDS	5143688	5143801	114	-	PGF_01310607	37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4865	PATRIC.2.9855.2.9855.con.0001.CDS.5143944.5144081.fwd	PATRIC	CDS	5143944	5144081	138	+		45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4892	PATRIC.2.9855.2.9855.con.0001.CDS.5176280.5176417.rev	PATRIC	CDS	5176280	5176417	138	-	PGF_01285093	45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4895	PATRIC.2.9855.2.9855.con.0001.CDS.5179139.5179837.fwd	PATRIC	CDS	5179139	5179837	699	+	PGF_08991923	232	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4900	PATRIC.2.9855.2.9855.con.0001.CDS.5185718.5185915.rev	PATRIC	CDS	5185718	5185915	198	-	PGF_10484453	65	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4907	PATRIC.2.9855.2.9855.con.0001.CDS.5194825.5195031.fwd	PATRIC	CDS	5194825	5195031	207	+		68	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4912	PATRIC.2.9855.2.9855.con.0001.CDS.5197314.5198150.rev	PATRIC	CDS	5197314	5198150	837	-	PGF_08225224	278	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.53	PATRIC.2.9855.2.9855.con.0001.CDS.51984.54221.fwd	PATRIC	CDS	51984	54221	2238	+	PGF_08225224	745	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4915	PATRIC.2.9855.2.9855.con.0001.CDS.5199714.5201810.rev	PATRIC	CDS	5199714	5201810	2097	-	PGF_08225224	698	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4918	PATRIC.2.9855.2.9855.con.0001.CDS.5203385.5203516.fwd	PATRIC	CDS	5203385	5203516	132	+		43	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4926	PATRIC.2.9855.2.9855.con.0001.CDS.5213132.5213317.fwd	PATRIC	CDS	5213132	5213317	186	+	PGF_01317928	61	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4931	PATRIC.2.9855.2.9855.con.0001.CDS.5220397.5220699.fwd	PATRIC	CDS	5220397	5220699	303	+	PGF_08225224	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4935	PATRIC.2.9855.2.9855.con.0001.CDS.5223534.5223752.fwd	PATRIC	CDS	5223534	5223752	219	+	PGF_08225224	72	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4942	PATRIC.2.9855.2.9855.con.0001.CDS.5231232.5231900.rev	PATRIC	CDS	5231232	5231900	669	-	PGF_10463191	222	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4943	PATRIC.2.9855.2.9855.con.0001.CDS.5231902.5232273.rev	PATRIC	CDS	5231902	5232273	372	-	PGF_10361365	123	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4947	PATRIC.2.9855.2.9855.con.0001.CDS.5235443.5235676.rev	PATRIC	CDS	5235443	5235676	234	-	PGF_01303873	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4955	PATRIC.2.9855.2.9855.con.0001.CDS.5245663.5246256.fwd	PATRIC	CDS	5245663	5246256	594	+	PGF_08225224	197	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4961	PATRIC.2.9855.2.9855.con.0001.CDS.5252455.5252937.rev	PATRIC	CDS	5252455	5252937	483	-	PGF_10457215	160	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4966	PATRIC.2.9855.2.9855.con.0001.CDS.5263089.5263316.rev	PATRIC	CDS	5263089	5263316	228	-	PGF_01298363	75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.462	PATRIC.2.9855.2.9855.con.0001.CDS.526731.526967.fwd	PATRIC	CDS	526731	526967	237	+		78	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4971	PATRIC.2.9855.2.9855.con.0001.CDS.5268775.5269086.fwd	PATRIC	CDS	5268775	5269086	312	+		103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4990	PATRIC.2.9855.2.9855.con.0001.CDS.5290090.5290599.fwd	PATRIC	CDS	5290090	5290599	510	+	PGF_00354504	169	FIG072699: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4991	PATRIC.2.9855.2.9855.con.0001.CDS.5290753.5290881.fwd	PATRIC	CDS	5290753	5290881	129	+	PGF_01288153	42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4992	PATRIC.2.9855.2.9855.con.0001.CDS.5291048.5291161.fwd	PATRIC	CDS	5291048	5291161	114	+		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4993	PATRIC.2.9855.2.9855.con.0001.CDS.5291804.5291950.rev	PATRIC	CDS	5291804	5291950	147	-	PGF_01288945	48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4996	PATRIC.2.9855.2.9855.con.0001.CDS.5294245.5294892.rev	PATRIC	CDS	5294245	5294892	648	-	PGF_12752218	215	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.4997	PATRIC.2.9855.2.9855.con.0001.CDS.5295061.5295303.fwd	PATRIC	CDS	5295061	5295303	243	+	PGF_01275907	80	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5003	PATRIC.2.9855.2.9855.con.0001.CDS.5297751.5298071.fwd	PATRIC	CDS	5297751	5298071	321	+	PGF_01299586	106	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5008	PATRIC.2.9855.2.9855.con.0001.CDS.5303970.5304308.rev	PATRIC	CDS	5303970	5304308	339	-	PGF_01281841	112	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5010	PATRIC.2.9855.2.9855.con.0001.CDS.5305317.5305850.rev	PATRIC	CDS	5305317	5305850	534	-	PGF_00260352	177	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5016	PATRIC.2.9855.2.9855.con.0001.CDS.5311826.5312374.fwd	PATRIC	CDS	5311826	5312374	549	+	PGF_02010655	182	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5023	PATRIC.2.9855.2.9855.con.0001.CDS.5319611.5320150.rev	PATRIC	CDS	5319611	5320150	540	-	PGF_08225224	179	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5034	PATRIC.2.9855.2.9855.con.0001.CDS.5334666.5335556.fwd	PATRIC	CDS	5334666	5335556	891	+	PGF_01300174	296	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5035	PATRIC.2.9855.2.9855.con.0001.CDS.5335598.5336017.rev	PATRIC	CDS	5335598	5336017	420	-	PGF_00275965	139	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5037	PATRIC.2.9855.2.9855.con.0001.CDS.5338662.5338811.rev	PATRIC	CDS	5338662	5338811	150	-	PGF_01300418	49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5038	PATRIC.2.9855.2.9855.con.0001.CDS.5339105.5339344.fwd	PATRIC	CDS	5339105	5339344	240	+	PGF_00247500	79	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5039	PATRIC.2.9855.2.9855.con.0001.CDS.5339509.5339757.fwd	PATRIC	CDS	5339509	5339757	249	+	PGF_01283260	82	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5045	PATRIC.2.9855.2.9855.con.0001.CDS.5344691.5345662.fwd	PATRIC	CDS	5344691	5345662	972	+	PGF_08225224	323	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.472	PATRIC.2.9855.2.9855.con.0001.CDS.535552.535710.fwd	PATRIC	CDS	535552	535710	159	+	PGF_00156311	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5049	PATRIC.2.9855.2.9855.con.0001.CDS.5359883.5359996.fwd	PATRIC	CDS	5359883	5359996	114	+		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5052	PATRIC.2.9855.2.9855.con.0001.CDS.5362944.5363903.fwd	PATRIC	CDS	5362944	5363903	960	+	PGF_08225224	319	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5057	PATRIC.2.9855.2.9855.con.0001.CDS.5369706.5370218.fwd	PATRIC	CDS	5369706	5370218	513	+	PGF_06086981	170	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5063	PATRIC.2.9855.2.9855.con.0001.CDS.5378828.5378962.fwd	PATRIC	CDS	5378828	5378962	135	+		44	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5065	PATRIC.2.9855.2.9855.con.0001.CDS.5380294.5380641.fwd	PATRIC	CDS	5380294	5380641	348	+	PGF_01285454	115	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5066	PATRIC.2.9855.2.9855.con.0001.CDS.5381333.5382283.fwd	PATRIC	CDS	5381333	5382283	951	+	PGF_08225224	316	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5067	PATRIC.2.9855.2.9855.con.0001.CDS.5382351.5382788.fwd	PATRIC	CDS	5382351	5382788	438	+	PGF_12779907	145	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.475	PATRIC.2.9855.2.9855.con.0001.CDS.538516.538989.rev	PATRIC	CDS	538516	538989	474	-	PGF_01326986	157	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5073	PATRIC.2.9855.2.9855.con.0001.CDS.5387994.5388179.fwd	PATRIC	CDS	5387994	5388179	186	+	PGF_01261160	61	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5074	PATRIC.2.9855.2.9855.con.0001.CDS.5388416.5389309.fwd	PATRIC	CDS	5388416	5389309	894	+	PGF_08225224	297	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5075	PATRIC.2.9855.2.9855.con.0001.CDS.5389302.5389568.fwd	PATRIC	CDS	5389302	5389568	267	+	PGF_10316679	88	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5076	PATRIC.2.9855.2.9855.con.0001.CDS.5389853.5390326.fwd	PATRIC	CDS	5389853	5390326	474	+	PGF_05192035	157	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5077	PATRIC.2.9855.2.9855.con.0001.CDS.5390513.5390629.fwd	PATRIC	CDS	5390513	5390629	117	+		38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5082	PATRIC.2.9855.2.9855.con.0001.CDS.5395633.5395806.fwd	PATRIC	CDS	5395633	5395806	174	+		57	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5086	PATRIC.2.9855.2.9855.con.0001.CDS.5397643.5398230.fwd	PATRIC	CDS	5397643	5398230	588	+	PGF_00199126	195	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5094	PATRIC.2.9855.2.9855.con.0001.CDS.5406971.5407129.fwd	PATRIC	CDS	5406971	5407129	159	+	PGF_02006588	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5095	PATRIC.2.9855.2.9855.con.0001.CDS.5407338.5407598.rev	PATRIC	CDS	5407338	5407598	261	-	PGF_01289659	86	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5103	PATRIC.2.9855.2.9855.con.0001.CDS.5416057.5416203.fwd	PATRIC	CDS	5416057	5416203	147	+	PGF_06915483	48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5118	PATRIC.2.9855.2.9855.con.0001.CDS.5433756.5434307.fwd	PATRIC	CDS	5433756	5434307	552	+	PGF_01316589	183	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5125	PATRIC.2.9855.2.9855.con.0001.CDS.5440716.5440994.fwd	PATRIC	CDS	5440716	5440994	279	+	PGF_01304400	92	FIG015094: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5129	PATRIC.2.9855.2.9855.con.0001.CDS.5445071.5445193.fwd	PATRIC	CDS	5445071	5445193	123	+		40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5141	PATRIC.2.9855.2.9855.con.0001.CDS.5454431.5455183.rev	PATRIC	CDS	5454431	5455183	753	-	PGF_01313946	250	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5143	PATRIC.2.9855.2.9855.con.0001.CDS.5456949.5457944.fwd	PATRIC	CDS	5456949	5457944	996	+	PGF_00819593	331	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5151	PATRIC.2.9855.2.9855.con.0001.CDS.5467371.5467487.fwd	PATRIC	CDS	5467371	5467487	117	+		38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5153	PATRIC.2.9855.2.9855.con.0001.CDS.5469955.5470077.fwd	PATRIC	CDS	5469955	5470077	123	+	PGF_01297157	40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5154	PATRIC.2.9855.2.9855.con.0001.CDS.5470268.5470390.fwd	PATRIC	CDS	5470268	5470390	123	+		40	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.481	PATRIC.2.9855.2.9855.con.0001.CDS.547089.547910.rev	PATRIC	CDS	547089	547910	822	-	PGF_12766250	273	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5157	PATRIC.2.9855.2.9855.con.0001.CDS.5472581.5473504.rev	PATRIC	CDS	5472581	5473504	924	-	PGF_10491990	307	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5159	PATRIC.2.9855.2.9855.con.0001.CDS.5475213.5475824.fwd	PATRIC	CDS	5475213	5475824	612	+	PGF_01316046	203	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5170	PATRIC.2.9855.2.9855.con.0001.CDS.5490866.5491318.rev	PATRIC	CDS	5490866	5491318	453	-	PGF_08225224	150	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5172	PATRIC.2.9855.2.9855.con.0001.CDS.5496774.5497079.rev	PATRIC	CDS	5496774	5497079	306	-	PGF_08225224	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5181	PATRIC.2.9855.2.9855.con.0001.CDS.5513973.5514281.rev	PATRIC	CDS	5513973	5514281	309	-	PGF_08225224	102	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5182	PATRIC.2.9855.2.9855.con.0001.CDS.5515544.5515684.rev	PATRIC	CDS	5515544	5515684	141	-	PGF_04710333	46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5185	PATRIC.2.9855.2.9855.con.0001.CDS.5518937.5519686.rev	PATRIC	CDS	5518937	5519686	750	-	PGF_00734670	249	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5191	PATRIC.2.9855.2.9855.con.0001.CDS.5531876.5532112.fwd	PATRIC	CDS	5531876	5532112	237	+	PGF_01289694	78	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5195	PATRIC.2.9855.2.9855.con.0001.CDS.5536406.5536816.rev	PATRIC	CDS	5536406	5536816	411	-	PGF_01293981	136	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5203	PATRIC.2.9855.2.9855.con.0001.CDS.5544076.5544666.fwd	PATRIC	CDS	5544076	5544666	591	+	PGF_01308101	196	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5210	PATRIC.2.9855.2.9855.con.0001.CDS.5552914.5553243.fwd	PATRIC	CDS	5552914	5553243	330	+	PGF_01305357	109	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.489	PATRIC.2.9855.2.9855.con.0001.CDS.558742.559179.fwd	PATRIC	CDS	558742	559179	438	+	PGF_08225224	145	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5257	PATRIC.2.9855.2.9855.con.0001.CDS.5613508.5613699.fwd	PATRIC	CDS	5613508	5613699	192	+	PGF_01308749	63	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5265	PATRIC.2.9855.2.9855.con.0001.CDS.5621460.5621687.fwd	PATRIC	CDS	5621460	5621687	228	+	PGF_01282506	75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5267	PATRIC.2.9855.2.9855.con.0001.CDS.5622466.5622828.rev	PATRIC	CDS	5622466	5622828	363	-	PGF_01283176	120	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5269	PATRIC.2.9855.2.9855.con.0001.CDS.5625839.5626228.rev	PATRIC	CDS	5625839	5626228	390	-	PGF_01281838	129	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5291	PATRIC.2.9855.2.9855.con.0001.CDS.5650639.5651565.rev	PATRIC	CDS	5650639	5651565	927	-	PGF_07679919	308	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5292	PATRIC.2.9855.2.9855.con.0001.CDS.5651562.5652557.rev	PATRIC	CDS	5651562	5652557	996	-	PGF_04975304	331	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5297	PATRIC.2.9855.2.9855.con.0001.CDS.5657923.5658147.fwd	PATRIC	CDS	5657923	5658147	225	+	PGF_01282353	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5300	PATRIC.2.9855.2.9855.con.0001.CDS.5663347.5663475.fwd	PATRIC	CDS	5663347	5663475	129	+		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5304	PATRIC.2.9855.2.9855.con.0001.CDS.5666952.5667758.rev	PATRIC	CDS	5666952	5667758	807	-	PGF_01280864	268	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5312	PATRIC.2.9855.2.9855.con.0001.CDS.5687184.5687450.rev	PATRIC	CDS	5687184	5687450	267	-	PGF_00355644	88	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5313	PATRIC.2.9855.2.9855.con.0001.CDS.5687495.5687746.rev	PATRIC	CDS	5687495	5687746	252	-	PGF_01283225	83	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5314	PATRIC.2.9855.2.9855.con.0001.CDS.5687845.5688066.rev	PATRIC	CDS	5687845	5688066	222	-	PGF_01283226	73	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5315	PATRIC.2.9855.2.9855.con.0001.CDS.5688079.5688345.rev	PATRIC	CDS	5688079	5688345	267	-	PGF_01281779	88	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5319	PATRIC.2.9855.2.9855.con.0001.CDS.5693603.5693722.rev	PATRIC	CDS	5693603	5693722	120	-		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5324	PATRIC.2.9855.2.9855.con.0001.CDS.5701891.5703723.rev	PATRIC	CDS	5701891	5703723	1833	-	PGF_00899388	610	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5325	PATRIC.2.9855.2.9855.con.0001.CDS.5704020.5705156.rev	PATRIC	CDS	5704020	5705156	1137	-	PGF_08225224	378	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5327	PATRIC.2.9855.2.9855.con.0001.CDS.5706984.5708003.fwd	PATRIC	CDS	5706984	5708003	1020	+	PGF_05195214	339	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5328	PATRIC.2.9855.2.9855.con.0001.CDS.5707955.5709328.fwd	PATRIC	CDS	5707955	5709328	1374	+	PGF_08225224	457	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5329	PATRIC.2.9855.2.9855.con.0001.CDS.5709458.5710261.fwd	PATRIC	CDS	5709458	5710261	804	+	PGF_07172830	267	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5331	PATRIC.2.9855.2.9855.con.0001.CDS.5711562.5712683.fwd	PATRIC	CDS	5711562	5712683	1122	+	PGF_01292668	373	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5332	PATRIC.2.9855.2.9855.con.0001.CDS.5712705.5715812.fwd	PATRIC	CDS	5712705	5715812	3108	+	PGF_08225224	1035	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5333	PATRIC.2.9855.2.9855.con.0001.CDS.5715817.5717994.fwd	PATRIC	CDS	5715817	5717994	2178	+		725	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5334	PATRIC.2.9855.2.9855.con.0001.CDS.5718022.5718459.fwd	PATRIC	CDS	5718022	5718459	438	+		145	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5335	PATRIC.2.9855.2.9855.con.0001.CDS.5718486.5719295.fwd	PATRIC	CDS	5718486	5719295	810	+		269	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5336	PATRIC.2.9855.2.9855.con.0001.CDS.5719285.5720169.fwd	PATRIC	CDS	5719285	5720169	885	+		294	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5337	PATRIC.2.9855.2.9855.con.0001.CDS.5720159.5721619.fwd	PATRIC	CDS	5720159	5721619	1461	+	PGF_02683098	486	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5338	PATRIC.2.9855.2.9855.con.0001.CDS.5721612.5722007.fwd	PATRIC	CDS	5721612	5722007	396	+	PGF_01987043	131	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5339	PATRIC.2.9855.2.9855.con.0001.CDS.5722030.5722767.fwd	PATRIC	CDS	5722030	5722767	738	+		245	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5340	PATRIC.2.9855.2.9855.con.0001.CDS.5722796.5724397.fwd	PATRIC	CDS	5722796	5724397	1602	+		533	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5341	PATRIC.2.9855.2.9855.con.0001.CDS.5724681.5727644.fwd	PATRIC	CDS	5724681	5727644	2964	+		987	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5342	PATRIC.2.9855.2.9855.con.0001.CDS.5728267.5730222.fwd	PATRIC	CDS	5728267	5730222	1956	+	PGF_10346395	651	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5343	PATRIC.2.9855.2.9855.con.0001.CDS.5730243.5730710.fwd	PATRIC	CDS	5730243	5730710	468	+	PGF_01253473	155	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5349	PATRIC.2.9855.2.9855.con.0001.CDS.5735941.5737074.rev	PATRIC	CDS	5735941	5737074	1134	-	PGF_07656290	377	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5352	PATRIC.2.9855.2.9855.con.0001.CDS.5740134.5740271.fwd	PATRIC	CDS	5740134	5740271	138	+		45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5358	PATRIC.2.9855.2.9855.con.0001.CDS.5745142.5745282.fwd	PATRIC	CDS	5745142	5745282	141	+		46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5364	PATRIC.2.9855.2.9855.con.0001.CDS.5749602.5749721.rev	PATRIC	CDS	5749602	5749721	120	-		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5383	PATRIC.2.9855.2.9855.con.0001.CDS.5784442.5785401.rev	PATRIC	CDS	5784442	5785401	960	-	PGF_01280887	319	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5384	PATRIC.2.9855.2.9855.con.0001.CDS.5785815.5786099.rev	PATRIC	CDS	5785815	5786099	285	-	PGF_01284400	94	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5388	PATRIC.2.9855.2.9855.con.0001.CDS.5791022.5792059.fwd	PATRIC	CDS	5791022	5792059	1038	+	PGF_00985218	345	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5398	PATRIC.2.9855.2.9855.con.0001.CDS.5804345.5804671.fwd	PATRIC	CDS	5804345	5804671	327	+	PGF_01281449	108	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5401	PATRIC.2.9855.2.9855.con.0001.CDS.5810016.5810414.fwd	PATRIC	CDS	5810016	5810414	399	+	PGF_08225224	132	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5405	PATRIC.2.9855.2.9855.con.0001.CDS.5817248.5817943.rev	PATRIC	CDS	5817248	5817943	696	-	PGF_01295441	231	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5409	PATRIC.2.9855.2.9855.con.0001.CDS.5822030.5822296.fwd	PATRIC	CDS	5822030	5822296	267	+	PGF_00426416	88	FIG00515214: hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.507	PATRIC.2.9855.2.9855.con.0001.CDS.583372.584778.fwd	PATRIC	CDS	583372	584778	1407	+	PGF_01273174	468	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5435	PATRIC.2.9855.2.9855.con.0001.CDS.5861758.5862546.rev	PATRIC	CDS	5861758	5862546	789	-	PGF_03078387	262	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5461	PATRIC.2.9855.2.9855.con.0001.CDS.5898674.5898898.fwd	PATRIC	CDS	5898674	5898898	225	+	PGF_01262750	74	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5476	PATRIC.2.9855.2.9855.con.0001.CDS.5917813.5919522.fwd	PATRIC	CDS	5917813	5919522	1710	+	PGF_08225224	569	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5481	PATRIC.2.9855.2.9855.con.0001.CDS.5924428.5924586.rev	PATRIC	CDS	5924428	5924586	159	-	PGF_06553016	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5486	PATRIC.2.9855.2.9855.con.0001.CDS.5929451.5929687.rev	PATRIC	CDS	5929451	5929687	237	-	PGF_00282391	78	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5487	PATRIC.2.9855.2.9855.con.0001.CDS.5929736.5930011.rev	PATRIC	CDS	5929736	5930011	276	-	PGF_01283662	91	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5488	PATRIC.2.9855.2.9855.con.0001.CDS.5930048.5930236.rev	PATRIC	CDS	5930048	5930236	189	-	PGF_08225224	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5490	PATRIC.2.9855.2.9855.con.0001.CDS.5930902.5931051.rev	PATRIC	CDS	5930902	5931051	150	-	PGF_01290489	49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5492	PATRIC.2.9855.2.9855.con.0001.CDS.5932444.5934327.fwd	PATRIC	CDS	5932444	5934327	1884	+	PGF_08225224	627	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5497	PATRIC.2.9855.2.9855.con.0001.CDS.5937589.5938269.rev	PATRIC	CDS	5937589	5938269	681	-	PGF_08225224	226	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5499	PATRIC.2.9855.2.9855.con.0001.CDS.5939797.5940576.fwd	PATRIC	CDS	5939797	5940576	780	+	PGF_08102871	259	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5501	PATRIC.2.9855.2.9855.con.0001.CDS.5941738.5943072.fwd	PATRIC	CDS	5941738	5943072	1335	+	PGF_04133490	444	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5502	PATRIC.2.9855.2.9855.con.0001.CDS.5943152.5943823.fwd	PATRIC	CDS	5943152	5943823	672	+	PGF_02880270	223	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5504	PATRIC.2.9855.2.9855.con.0001.CDS.5944532.5945275.fwd	PATRIC	CDS	5944532	5945275	744	+	PGF_01291256	247	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.516	PATRIC.2.9855.2.9855.con.0001.CDS.594479.594790.fwd	PATRIC	CDS	594479	594790	312	+	PGF_01281863	103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5507	PATRIC.2.9855.2.9855.con.0001.CDS.5947593.5948270.fwd	PATRIC	CDS	5947593	5948270	678	+	PGF_01280909	225	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5508	PATRIC.2.9855.2.9855.con.0001.CDS.5948298.5948501.fwd	PATRIC	CDS	5948298	5948501	204	+		67	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5514	PATRIC.2.9855.2.9855.con.0001.CDS.5957271.5957432.fwd	PATRIC	CDS	5957271	5957432	162	+	PGF_08225224	53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5516	PATRIC.2.9855.2.9855.con.0001.CDS.5960534.5961250.fwd	PATRIC	CDS	5960534	5961250	717	+	PGF_10425289	238	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.518	PATRIC.2.9855.2.9855.con.0001.CDS.596100.596255.fwd	PATRIC	CDS	596100	596255	156	+	PGF_01312215	51	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.5520	PATRIC.2.9855.2.9855.con.0001.CDS.5965292.5966695.fwd	PATRIC	CDS	5965292	5966695	1404	+	PGF_12877465	467	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.520	PATRIC.2.9855.2.9855.con.0001.CDS.597124.597420.rev	PATRIC	CDS	597124	597420	297	-	PGF_00839702	98	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.534	PATRIC.2.9855.2.9855.con.0001.CDS.618091.618402.fwd	PATRIC	CDS	618091	618402	312	+	PGF_04008796	103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.535	PATRIC.2.9855.2.9855.con.0001.CDS.618802.619008.fwd	PATRIC	CDS	618802	619008	207	+	PGF_01283217	68	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.544	PATRIC.2.9855.2.9855.con.0001.CDS.628211.628663.rev	PATRIC	CDS	628211	628663	453	-	PGF_00013175	150	Hypothetical protein PA1329
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.552	PATRIC.2.9855.2.9855.con.0001.CDS.635417.636190.fwd	PATRIC	CDS	635417	636190	774	+	PGF_03001320	257	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.570	PATRIC.2.9855.2.9855.con.0001.CDS.655030.655146.fwd	PATRIC	CDS	655030	655146	117	+		38	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.571	PATRIC.2.9855.2.9855.con.0001.CDS.655143.655613.fwd	PATRIC	CDS	655143	655613	471	+	PGF_08225224	156	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.572	PATRIC.2.9855.2.9855.con.0001.CDS.655613.656971.fwd	PATRIC	CDS	655613	656971	1359	+	PGF_08225224	452	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.576	PATRIC.2.9855.2.9855.con.0001.CDS.661420.661548.fwd	PATRIC	CDS	661420	661548	129	+		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.577	PATRIC.2.9855.2.9855.con.0001.CDS.661947.662912.fwd	PATRIC	CDS	661947	662912	966	+	PGF_08225224	321	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.578	PATRIC.2.9855.2.9855.con.0001.CDS.663252.663584.fwd	PATRIC	CDS	663252	663584	333	+	PGF_01281436	110	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.581	PATRIC.2.9855.2.9855.con.0001.CDS.665833.666024.fwd	PATRIC	CDS	665833	666024	192	+	PGF_10541011	63	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.582	PATRIC.2.9855.2.9855.con.0001.CDS.666120.666266.fwd	PATRIC	CDS	666120	666266	147	+		48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.584	PATRIC.2.9855.2.9855.con.0001.CDS.667740.667859.fwd	PATRIC	CDS	667740	667859	120	+	PGF_07753010	39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.602	PATRIC.2.9855.2.9855.con.0001.CDS.691882.692304.rev	PATRIC	CDS	691882	692304	423	-	PGF_03476288	140	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.618	PATRIC.2.9855.2.9855.con.0001.CDS.708147.708473.rev	PATRIC	CDS	708147	708473	327	-	PGF_00908688	108	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.619	PATRIC.2.9855.2.9855.con.0001.CDS.708939.709400.fwd	PATRIC	CDS	708939	709400	462	+	PGF_00809459	153	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.621	PATRIC.2.9855.2.9855.con.0001.CDS.710664.710879.rev	PATRIC	CDS	710664	710879	216	-	PGF_01283757	71	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.622	PATRIC.2.9855.2.9855.con.0001.CDS.711015.711173.fwd	PATRIC	CDS	711015	711173	159	+	PGF_01281634	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.624	PATRIC.2.9855.2.9855.con.0001.CDS.713252.713893.rev	PATRIC	CDS	713252	713893	642	-	PGF_08225224	213	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.628	PATRIC.2.9855.2.9855.con.0001.CDS.717992.718492.fwd	PATRIC	CDS	717992	718492	501	+	PGF_08225224	166	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.68	PATRIC.2.9855.2.9855.con.0001.CDS.71867.72247.rev	PATRIC	CDS	71867	72247	381	-	PGF_00241612	126	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.629	PATRIC.2.9855.2.9855.con.0001.CDS.718774.718893.fwd	PATRIC	CDS	718774	718893	120	+		39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.69	PATRIC.2.9855.2.9855.con.0001.CDS.72244.72942.rev	PATRIC	CDS	72244	72942	699	-	PGF_08225224	232	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.639	PATRIC.2.9855.2.9855.con.0001.CDS.731404.731757.fwd	PATRIC	CDS	731404	731757	354	+	PGF_01280943	117	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.644	PATRIC.2.9855.2.9855.con.0001.CDS.737188.737364.rev	PATRIC	CDS	737188	737364	177	-	PGF_00280414	58	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.646	PATRIC.2.9855.2.9855.con.0001.CDS.739469.739627.rev	PATRIC	CDS	739469	739627	159	-	PGF_01283347	52	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.648	PATRIC.2.9855.2.9855.con.0001.CDS.741558.742703.fwd	PATRIC	CDS	741558	742703	1146	+	PGF_12768589	381	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.653	PATRIC.2.9855.2.9855.con.0001.CDS.752921.753163.fwd	PATRIC	CDS	752921	753163	243	+	PGF_01282402	80	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.656	PATRIC.2.9855.2.9855.con.0001.CDS.757948.758607.rev	PATRIC	CDS	757948	758607	660	-	PGF_01268268	219	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.658	PATRIC.2.9855.2.9855.con.0001.CDS.759115.759912.fwd	PATRIC	CDS	759115	759912	798	+	PGF_00942398	265	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.659	PATRIC.2.9855.2.9855.con.0001.CDS.760201.760593.fwd	PATRIC	CDS	760201	760593	393	+	PGF_08225224	130	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.660	PATRIC.2.9855.2.9855.con.0001.CDS.760868.761185.rev	PATRIC	CDS	760868	761185	318	-	PGF_01281386	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.661	PATRIC.2.9855.2.9855.con.0001.CDS.761236.761547.rev	PATRIC	CDS	761236	761547	312	-	PGF_01281762	103	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.667	PATRIC.2.9855.2.9855.con.0001.CDS.766474.766797.rev	PATRIC	CDS	766474	766797	324	-	PGF_01280863	107	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.670	PATRIC.2.9855.2.9855.con.0001.CDS.769711.769959.fwd	PATRIC	CDS	769711	769959	249	+	PGF_08087891	82	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.671	PATRIC.2.9855.2.9855.con.0001.CDS.770299.770445.fwd	PATRIC	CDS	770299	770445	147	+	PGF_01189671	48	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.672	PATRIC.2.9855.2.9855.con.0001.CDS.770569.770886.rev	PATRIC	CDS	770569	770886	318	-	PGF_03051711	105	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.675	PATRIC.2.9855.2.9855.con.0001.CDS.772459.772935.rev	PATRIC	CDS	772459	772935	477	-	PGF_01284318	158	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.678	PATRIC.2.9855.2.9855.con.0001.CDS.775140.775334.fwd	PATRIC	CDS	775140	775334	195	+	PGF_01284745	64	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.679	PATRIC.2.9855.2.9855.con.0001.CDS.775552.775839.fwd	PATRIC	CDS	775552	775839	288	+	PGF_01283222	95	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.683	PATRIC.2.9855.2.9855.con.0001.CDS.778486.778806.rev	PATRIC	CDS	778486	778806	321	-	PGF_08225224	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.684	PATRIC.2.9855.2.9855.con.0001.CDS.779156.779539.fwd	PATRIC	CDS	779156	779539	384	+	PGF_01281803	127	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.687	PATRIC.2.9855.2.9855.con.0001.CDS.783957.784232.fwd	PATRIC	CDS	783957	784232	276	+	PGF_01283173	91	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.688	PATRIC.2.9855.2.9855.con.0001.CDS.784341.784484.rev	PATRIC	CDS	784341	784484	144	-		47	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.692	PATRIC.2.9855.2.9855.con.0001.CDS.787295.787435.fwd	PATRIC	CDS	787295	787435	141	+		46	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.695	PATRIC.2.9855.2.9855.con.0001.CDS.788900.789028.fwd	PATRIC	CDS	788900	789028	129	+		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.698	PATRIC.2.9855.2.9855.con.0001.CDS.792297.792872.fwd	PATRIC	CDS	792297	792872	576	+	PGF_01283174	191	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.700	PATRIC.2.9855.2.9855.con.0001.CDS.794867.795157.fwd	PATRIC	CDS	794867	795157	291	+	PGF_01283223	96	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.702	PATRIC.2.9855.2.9855.con.0001.CDS.796070.796330.fwd	PATRIC	CDS	796070	796330	261	+	PGF_00957978	86	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.708	PATRIC.2.9855.2.9855.con.0001.CDS.800903.801520.fwd	PATRIC	CDS	800903	801520	618	+	PGF_01283224	205	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.711	PATRIC.2.9855.2.9855.con.0001.CDS.802994.803227.fwd	PATRIC	CDS	802994	803227	234	+	PGF_01295561	77	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.716	PATRIC.2.9855.2.9855.con.0001.CDS.806602.806772.fwd	PATRIC	CDS	806602	806772	171	+	PGF_08225224	56	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.717	PATRIC.2.9855.2.9855.con.0001.CDS.806989.807525.fwd	PATRIC	CDS	806989	807525	537	+	PGF_08225224	178	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.718	PATRIC.2.9855.2.9855.con.0001.CDS.807515.808540.fwd	PATRIC	CDS	807515	808540	1026	+	PGF_01297644	341	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.722	PATRIC.2.9855.2.9855.con.0001.CDS.811518.812231.fwd	PATRIC	CDS	811518	812231	714	+	PGF_08225224	237	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.724	PATRIC.2.9855.2.9855.con.0001.CDS.813637.814182.fwd	PATRIC	CDS	813637	814182	546	+	PGF_08225224	181	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.727	PATRIC.2.9855.2.9855.con.0001.CDS.815519.815932.rev	PATRIC	CDS	815519	815932	414	-	PGF_01281398	137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.728	PATRIC.2.9855.2.9855.con.0001.CDS.816314.817426.fwd	PATRIC	CDS	816314	817426	1113	+	PGF_08225224	370	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.76	PATRIC.2.9855.2.9855.con.0001.CDS.81778.82131.fwd	PATRIC	CDS	81778	82131	354	+	PGF_08225224	117	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.733	PATRIC.2.9855.2.9855.con.0001.CDS.821964.822101.rev	PATRIC	CDS	821964	822101	138	-		45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.734	PATRIC.2.9855.2.9855.con.0001.CDS.822304.823632.fwd	PATRIC	CDS	822304	823632	1329	+	PGF_00940642	442	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.735	PATRIC.2.9855.2.9855.con.0001.CDS.824122.825108.fwd	PATRIC	CDS	824122	825108	987	+	PGF_01324091	328	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.736	PATRIC.2.9855.2.9855.con.0001.CDS.825865.827166.fwd	PATRIC	CDS	825865	827166	1302	+	PGF_01293189	433	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.738	PATRIC.2.9855.2.9855.con.0001.CDS.828326.829165.fwd	PATRIC	CDS	828326	829165	840	+	PGF_00248506	279	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.742	PATRIC.2.9855.2.9855.con.0001.CDS.833511.833834.rev	PATRIC	CDS	833511	833834	324	-	PGF_10483925	107	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.743	PATRIC.2.9855.2.9855.con.0001.CDS.834112.834402.rev	PATRIC	CDS	834112	834402	291	-	PGF_08225224	96	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.79	PATRIC.2.9855.2.9855.con.0001.CDS.84173.84334.fwd	PATRIC	CDS	84173	84334	162	+		53	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.80	PATRIC.2.9855.2.9855.con.0001.CDS.84427.84711.rev	PATRIC	CDS	84427	84711	285	-	PGF_01290947	94	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.758	PATRIC.2.9855.2.9855.con.0001.CDS.851782.852129.fwd	PATRIC	CDS	851782	852129	348	+	PGF_00127017	115	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.760	PATRIC.2.9855.2.9855.con.0001.CDS.853121.853858.fwd	PATRIC	CDS	853121	853858	738	+	PGF_12895615	245	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.762	PATRIC.2.9855.2.9855.con.0001.CDS.855115.855360.rev	PATRIC	CDS	855115	855360	246	-	PGF_07056387	81	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.763	PATRIC.2.9855.2.9855.con.0001.CDS.855493.855993.fwd	PATRIC	CDS	855493	855993	501	+	PGF_01030799	166	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.764	PATRIC.2.9855.2.9855.con.0001.CDS.856159.856386.rev	PATRIC	CDS	856159	856386	228	-	PGF_07345813	75	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.767	PATRIC.2.9855.2.9855.con.0001.CDS.857809.858096.fwd	PATRIC	CDS	857809	858096	288	+	PGF_08225224	95	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.768	PATRIC.2.9855.2.9855.con.0001.CDS.858360.858806.rev	PATRIC	CDS	858360	858806	447	-	PGF_01299701	148	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.771	PATRIC.2.9855.2.9855.con.0001.CDS.860472.861119.fwd	PATRIC	CDS	860472	861119	648	+	PGF_08225224	215	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.777	PATRIC.2.9855.2.9855.con.0001.CDS.866236.866349.rev	PATRIC	CDS	866236	866349	114	-		37	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.778	PATRIC.2.9855.2.9855.con.0001.CDS.867104.867496.fwd	PATRIC	CDS	867104	867496	393	+	PGF_01284230	130	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.780	PATRIC.2.9855.2.9855.con.0001.CDS.868367.868687.fwd	PATRIC	CDS	868367	868687	321	+	PGF_01258443	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.787	PATRIC.2.9855.2.9855.con.0001.CDS.875150.875521.fwd	PATRIC	CDS	875150	875521	372	+	PGF_01284227	123	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.788	PATRIC.2.9855.2.9855.con.0001.CDS.876008.876868.fwd	PATRIC	CDS	876008	876868	861	+	PGF_00239530	286	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.789	PATRIC.2.9855.2.9855.con.0001.CDS.877522.878340.fwd	PATRIC	CDS	877522	878340	819	+	PGF_00771326	272	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.796	PATRIC.2.9855.2.9855.con.0001.CDS.884760.884975.fwd	PATRIC	CDS	884760	884975	216	+	PGF_10372143	71	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.797	PATRIC.2.9855.2.9855.con.0001.CDS.884977.885882.fwd	PATRIC	CDS	884977	885882	906	+	PGF_06369888	301	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.799	PATRIC.2.9855.2.9855.con.0001.CDS.886489.888201.fwd	PATRIC	CDS	886489	888201	1713	+	PGF_08225224	570	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.800	PATRIC.2.9855.2.9855.con.0001.CDS.888235.888969.fwd	PATRIC	CDS	888235	888969	735	+	PGF_01292516	244	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.84	PATRIC.2.9855.2.9855.con.0001.CDS.88889.90463.fwd	PATRIC	CDS	88889	90463	1575	+	PGF_00013079	524	Hypothetical iron-sulfur cluster binding protein YccM
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.803	PATRIC.2.9855.2.9855.con.0001.CDS.892112.892462.fwd	PATRIC	CDS	892112	892462	351	+	PGF_02686762	116	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.817	PATRIC.2.9855.2.9855.con.0001.CDS.905756.906061.rev	PATRIC	CDS	905756	906061	306	-	PGF_01307608	101	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.819	PATRIC.2.9855.2.9855.con.0001.CDS.906583.907548.rev	PATRIC	CDS	906583	907548	966	-	PGF_01270738	321	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.822	PATRIC.2.9855.2.9855.con.0001.CDS.909921.910688.fwd	PATRIC	CDS	909921	910688	768	+	PGF_08225224	255	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.830	PATRIC.2.9855.2.9855.con.0001.CDS.919234.919383.fwd	PATRIC	CDS	919234	919383	150	+	PGF_01286134	49	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.841	PATRIC.2.9855.2.9855.con.0001.CDS.931662.932066.rev	PATRIC	CDS	931662	932066	405	-	PGF_08225224	134	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.849	PATRIC.2.9855.2.9855.con.0001.CDS.941842.943776.rev	PATRIC	CDS	941842	943776	1935	-	PGF_04121229	644	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.855	PATRIC.2.9855.2.9855.con.0001.CDS.950441.950605.fwd	PATRIC	CDS	950441	950605	165	+	PGF_07018364	54	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.858	PATRIC.2.9855.2.9855.con.0001.CDS.956374.956712.fwd	PATRIC	CDS	956374	956712	339	+	PGF_08225224	112	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.862	PATRIC.2.9855.2.9855.con.0001.CDS.959049.959435.fwd	PATRIC	CDS	959049	959435	387	+	PGF_01059613	128	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.864	PATRIC.2.9855.2.9855.con.0001.CDS.960220.960741.fwd	PATRIC	CDS	960220	960741	522	+	PGF_08225224	173	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.866	PATRIC.2.9855.2.9855.con.0001.CDS.962110.962430.fwd	PATRIC	CDS	962110	962430	321	+	PGF_01304698	106	hypothetical protein

Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.867	PATRIC.2.9855.2.9855.con.0001.CDS.962527.962829.fwd	PATRIC	CDS	962527	962829	303	+	PGF_01284384	100	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.868	PATRIC.2.9855.2.9855.con.0001.CDS.962891.963211.rev	PATRIC	CDS	962891	963211	321	-	PGF_01282405	106	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.869	PATRIC.2.9855.2.9855.con.0001.CDS.963614.964147.rev	PATRIC	CDS	963614	964147	534	-	PGF_01283252	177	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.870	PATRIC.2.9855.2.9855.con.0001.CDS.964360.964581.rev	PATRIC	CDS	964360	964581	222	-	PGF_04951118	73	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.871	PATRIC.2.9855.2.9855.con.0001.CDS.964586.965122.rev	PATRIC	CDS	964586	965122	537	-	PGF_00246801	178	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.872	PATRIC.2.9855.2.9855.con.0001.CDS.965270.965398.fwd	PATRIC	CDS	965270	965398	129	+		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.874	PATRIC.2.9855.2.9855.con.0001.CDS.966323.966511.fwd	PATRIC	CDS	966323	966511	189	+	PGF_01301707	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.876	PATRIC.2.9855.2.9855.con.0001.CDS.967296.968444.rev	PATRIC	CDS	967296	968444	1149	-	PGF_08225224	382	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.877	PATRIC.2.9855.2.9855.con.0001.CDS.968574.969233.rev	PATRIC	CDS	968574	969233	660	-	PGF_01301706	219	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.878	PATRIC.2.9855.2.9855.con.0001.CDS.969790.971448.fwd	PATRIC	CDS	969790	971448	1659	+	PGF_08225224	552	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.882	PATRIC.2.9855.2.9855.con.0001.CDS.976324.976530.fwd	PATRIC	CDS	976324	976530	207	+	PGF_01323220	68	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.883	PATRIC.2.9855.2.9855.con.0001.CDS.976625.976813.fwd	PATRIC	CDS	976625	976813	189	+	PGF_01282477	62	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.886	PATRIC.2.9855.2.9855.con.0001.CDS.978327.978983.fwd	PATRIC	CDS	978327	978983	657	+	PGF_10554413	218	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.887	PATRIC.2.9855.2.9855.con.0001.CDS.980304.980717.fwd	PATRIC	CDS	980304	980717	414	+	PGF_01312018	137	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.888	PATRIC.2.9855.2.9855.con.0001.CDS.980937.981872.rev	PATRIC	CDS	980937	981872	936	-	PGF_00234409	311	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.889	PATRIC.2.9855.2.9855.con.0001.CDS.981869.981997.rev	PATRIC	CDS	981869	981997	129	-		42	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.890	PATRIC.2.9855.2.9855.con.0001.CDS.982154.982273.fwd	PATRIC	CDS	982154	982273	120	+	PGF_01310346	39	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.892	PATRIC.2.9855.2.9855.con.0001.CDS.983393.983860.fwd	PATRIC	CDS	983393	983860	468	+		155	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.893	PATRIC.2.9855.2.9855.con.0001.CDS.983905.984030.fwd	PATRIC	CDS	983905	984030	126	+		41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.894	PATRIC.2.9855.2.9855.con.0001.CDS.984084.984557.fwd	PATRIC	CDS	984084	984557	474	+	PGF_08225224	157	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.895	PATRIC.2.9855.2.9855.con.0001.CDS.984609.985142.fwd	PATRIC	CDS	984609	985142	534	+	PGF_01283200	177	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.898	PATRIC.2.9855.2.9855.con.0001.CDS.988920.989207.fwd	PATRIC	CDS	988920	989207	288	+	PGF_06956273	95	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.899	PATRIC.2.9855.2.9855.con.0001.CDS.989379.989813.rev	PATRIC	CDS	989379	989813	435	-	PGF_01284297	144	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.900	PATRIC.2.9855.2.9855.con.0001.CDS.989830.990267.rev	PATRIC	CDS	989830	990267	438	-	PGF_08225224	145	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.903	PATRIC.2.9855.2.9855.con.0001.CDS.992546.992755.fwd	PATRIC	CDS	992546	992755	210	+	PGF_01281567	69	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.904	PATRIC.2.9855.2.9855.con.0001.CDS.992815.992952.fwd	PATRIC	CDS	992815	992952	138	+		45	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.905	PATRIC.2.9855.2.9855.con.0001.CDS.993283.993702.fwd	PATRIC	CDS	993283	993702	420	+	PGF_08225224	139	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.907	PATRIC.2.9855.2.9855.con.0001.CDS.995070.995195.fwd	PATRIC	CDS	995070	995195	126	+	PGF_01287376	41	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.908	PATRIC.2.9855.2.9855.con.0001.CDS.995371.995652.fwd	PATRIC	CDS	995371	995652	282	+	PGF_01298562	93	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.909	PATRIC.2.9855.2.9855.con.0001.CDS.996191.996517.fwd	PATRIC	CDS	996191	996517	327	+	PGF_08225224	108	hypothetical protein
Bacteria DY20_complete	2.9855	2.9855.con.0001	fig|2.9855.peg.910	PATRIC.2.9855.2.9855.con.0001.CDS.997133.997282.fwd	PATRIC	CDS	997133	997282	150	+	PGF_10382523	49	hypothetical protein

ATTACHMENT 12

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

In Vitro Hemolytic Assay

Hemolysis Testing of [redacted] (b) (4) Dairy Strain *C. beijerinckii* ASCUSDY20
JE 14Apr21

1. Purpose
   1.1. To determine *C. beijerinckii* ASCUSDY20's ability to induce hemolysis via production of hemloysin.
2. Methods
   2.1. Media Preparation

[redacted] (b) (4)

   2.2. Inoculation

[redacted] (b) (4)

   2.3. Interpretation

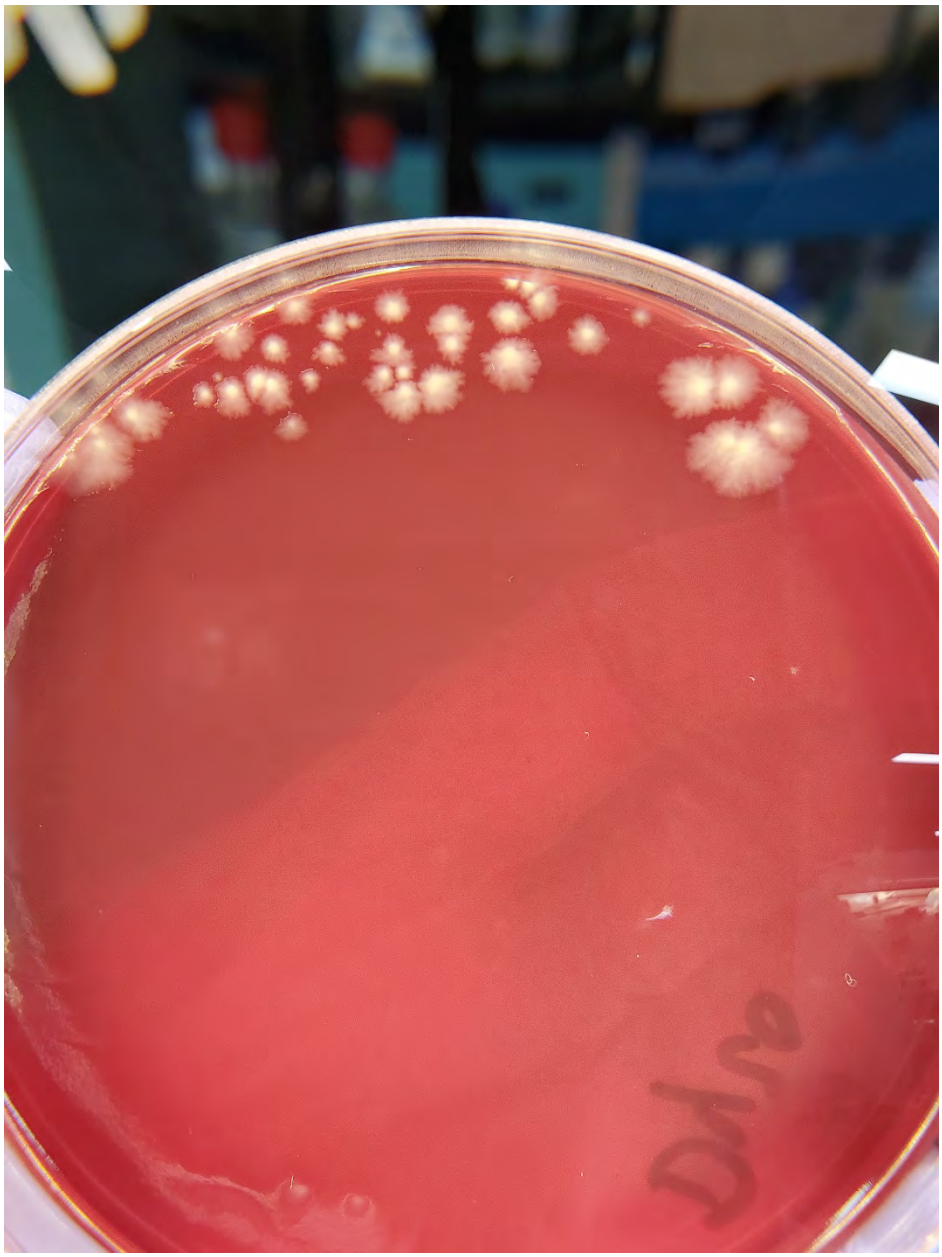
[redacted] (b) (4)

[redacted] (b) (4)

[redacted] (b) (4)

3. Results

3.1. *C. beijerinckii* ASCUSDY20 possesses gamma hemolysis. *C. beijerinckii* ASCUSDY20 lacks the ability to lyse red blood cells.



(b) (4)

(b) (4)

ATTACHMENT 13

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

CSV of the Genes in Each Island in IslandViewer4

(b) (4)

IslandViewer_AMR: Virulence_Annotations

Protein ID	Type	Source

Island start	Island end	Length	Method	Gene name	Gene ID	Locus	Gene start	Gene end	Strand	Product	External Annotations
245898	250269	4371	Predicted by at least one method				245898	246302	1	hypothetical protein	
245898	250269	4371	Predicted by at least one method				246318	246557	1	hypothetical protein	
245898	250269	4371	Predicted by at least one method				246573	247019	1	unknown	
245898	250269	4371	Predicted by at least one method				247318	247434	1	hypothetical protein	
245898	250269	4371	Predicted by at least one method				247652	248362	1	Endonuclease V (EC 3.1.21.7)	
245898	250269	4371	Predicted by at least one method				248609	249445	1	hypothetical protein	
245898	250269	4371	Predicted by at least one method				249916	250269	1	Permeases of the major facilitator superfamily	
413952	436519	22567	Predicted by at least one method				413072	413989	1	integrase/recombinase XerD	
413952	436519	22567	Predicted by at least one method				414711	416303	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				416838	417038	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				417112	417261	-1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				417263	417415	-1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				418001	421069	1	putative large ATP-binding protein	
413952	436519	22567	Predicted by at least one method				421413	422054	1	site-specific recombinase, resolvase family	
413952	436519	22567	Predicted by at least one method				422170	423066	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				423946	425559	1	5-methylcytosine-specific restriction related enzyme	
413952	436519	22567	Predicted by at least one method				425561	428005	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				428216	429130	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				429155	429523	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				429754	430767	1	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)	
413952	436519	22567	Predicted by at least one method				430902	431063	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				431144	431308	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				431431	432249	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				432384	432521	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				432693	432974	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				433016	433255	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				433367	434092	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				434423	435103	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				435305	435613	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				435670	436308	1	hypothetical protein	
413952	436519	22567	Predicted by at least one method				436460	436669	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				418001	421069	1	putative large ATP-binding protein	
418001	436308	18307	Predicted by at least one method				421413	422054	1	site-specific recombinase, resolvase family	
418001	436308	18307	Predicted by at least one method				422170	423066	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				423946	425559	1	5-methylcytosine-specific restriction related enzyme	
418001	436308	18307	Predicted by at least one method				425561	428005	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				428216	429130	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				429155	429523	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				429754	430767	1	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)	
418001	436308	18307	Predicted by at least one method				430902	431063	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				431144	431308	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				431431	432249	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				432384	432521	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				432693	432974	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				433016	433255	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				433367	434092	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				434423	435103	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				435305	435613	1	hypothetical protein	
418001	436308	18307	Predicted by at least one method				435670	436308	1	hypothetical protein	
941544	949009	7465	Predicted by at least one method				940744	941550	1	Iron compound ABC uptake transporter ATP-binding protein PiaD	
941544	949009	7465	Predicted by at least one method				941842	943776	-1	FIG00513656: hypothetical protein	
941544	949009	7465	Predicted by at least one method				944064	944513	1	PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB compon	
941544	949009	7465	Predicted by at least one method				944516	944827	1	PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC compon	
941544	949009	7465	Predicted by at least one method				944984	946096	1	PTS system, fructose-specific IIBC component (EC 2.7.1.69)	
941544	949009	7465	Predicted by at least one method				946181	948853	1	Alpha-mannosidase (EC 3.2.1.24)	
941544	949009	7465	Predicted by at least one method				948997	949875	1	Hexokinase (EC 2.7.1.1)	
963614	974114	10500	Predicted by at least one method				963614	964147	-1	hypothetical protein	
963614	974114	10500	Predicted by at least one method				964360	964581	-1	phage related protein	
963614	974114	10500	Predicted by at least one method				964586	965122	-1	FIG00516522: hypothetical protein	
963614	974114	10500	Predicted by at least one method				965270	965398	1	hypothetical protein	
963614	974114	10500	Predicted by at least one method				965448	966110	1	Phosphoglycolate phosphatase (EC 3.1.3.18)	
963614	974114	10500	Predicted by at least one method				966323	966511	1	hypothetical protein	
963614	974114	10500	Predicted by at least one method				966626	967108	1	Transcriptional regulator, MarR family	
963614	974114	10500	Predicted by at least one method				967296	968444	-1	Carboxylic ester hydrolase	
963614	974114	10500	Predicted by at least one method				968574	969233	-1	Transcriptional regulator, TetR family	
963614	974114	10500	Predicted by at least one method				969790	971448	1	FIG00530160: hypothetical protein	

963614	974114	10500	Predicted by at least one method	971560	972780	1	Integral membrane protein
963614	974114	10500	Predicted by at least one method	973473	974114	1	Iron-sulfur flavoprotein
1034760	1046884	12124	Predicted by at least one method	1032298	1034763	1	Protein tyrosine phosphatase II superfamily protein
1034760	1046884	12124	Predicted by at least one method	1035123	1036136	1	Ribose operon repressor
1034760	1046884	12124	Predicted by at least one method	1036236	1036667	1	L-fucose mutarotase
1034760	1046884	12124	Predicted by at least one method	1036711	1038225	1	Xylulose kinase (EC 2.7.1.17)
1034760	1046884	12124	Predicted by at least one method	1038228	1039259	1	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)
1034760	1046884	12124	Predicted by at least one method	1039386	1040396	1	Aldehyde reductase(EC:1.1.1.21)
1034760	1046884	12124	Predicted by at least one method	1040565	1041497	1	2-keto-3-deoxygluconate permease (KDG permease)
1034760	1046884	12124	Predicted by at least one method	1041642	1043138	1	Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)
1034760	1046884	12124	Predicted by at least one method	1043157	1044137	1	Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)
1034760	1046884	12124	Predicted by at least one method	1044325	1045323	1	periplasmic ribose-binding protein, sugar ABC transporter
1034760	1046884	12124	Predicted by at least one method	1045649	1047343	1	methyl-accepting chemotaxis sensory transducer
1049883	1059072	9189	Predicted by at least one method	1049707	1050585	1	Aldose 1-epimerase
1049883	1059072	9189	Predicted by at least one method	1050722	1051483	-1	Two-component response regulator yesN
1049883	1059072	9189	Predicted by at least one method	1051480	1053297	-1	Two-component sensor kinase YesM (EC 2.7.3.-)
1049883	1059072	9189	Predicted by at least one method	1053444	1054757	1	Xylose ABC transporter, substrate-binding component
1049883	1059072	9189	Predicted by at least one method	1054825	1055703	1	Predicted rhamnose oligosaccharide ABC transport system, permease component
1049883	1059072	9189	Predicted by at least one method	1055703	1056530	1	putative transport system permease ABC transporter protein
1049883	1059072	9189	Predicted by at least one method	1056547	1058988	1	Alpha-xylosidase (EC 3.2.1.-)
1246399	1264370	17971	Predicted by at least one method	1246399	1246647	1	Phenazine biosynthesis protein PhzF like
1246399	1264370	17971	Predicted by at least one method	1246655	1248193	-1	Site-specific recombinases, DNA invertase Pin homolog
1246399	1264370	17971	Predicted by at least one method	1248274	1248393	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1248398	1248760	-1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1248979	1249179	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1249140	1249262	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1249273	1249434	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1249434	1250159	1	Phage antirepressor protein
1246399	1264370	17971	Predicted by at least one method	1250162	1250278	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1250534	1250950	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1251039	1251206	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1251211	1251894	1	phage protein
1246399	1264370	17971	Predicted by at least one method	1252139	1252588	1	DNA replication protein DnaC
1246399	1264370	17971	Predicted by at least one method	1252602	1253015	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1253029	1253490	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1253501	1254304	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1254316	1254822	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1254837	1254953	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1254955	1255827	1	Phage protein
1246399	1264370	17971	Predicted by at least one method	1256141	1256335	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1256342	1256680	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1256733	1256894	-1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1257136	1257309	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1257453	1258163	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1258240	1258443	-1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1258622	1258909	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1258914	1259063	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1259131	1259295	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1259298	1259576	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1259589	1259768	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1259773	1260276	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1260326	1260484	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1260477	1260908	1	Single-stranded DNA-binding protein
1246399	1264370	17971	Predicted by at least one method	1261031	1261150	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1261338	1261523	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1261665	1261841	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1261842	1262150	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1262291	1262668	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1262796	1263698	1	hypothetical protein
1246399	1264370	17971	Predicted by at least one method	1263714	1264370	1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1246399	1246647	1	Phenazine biosynthesis protein PhzF like
1246627	1252612	5985	Predicted by at least one method	1246655	1248193	-1	Site-specific recombinases, DNA invertase Pin homolog
1246627	1252612	5985	Predicted by at least one method	1248274	1248393	1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1248398	1248760	-1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1248979	1249179	1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1249140	1249262	1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1249273	1249434	1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1249434	1250159	1	Phage antirepressor protein

1246627	1252612	5985	Predicted by at least one method	1250162	1250278	1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1250534	1250950	1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1251039	1251206	1	hypothetical protein
1246627	1252612	5985	Predicted by at least one method	1251211	1251894	1	phage protein
1246627	1252612	5985	Predicted by at least one method	1252139	1252588	1	DNA replication protein DnaC
1246627	1252612	5985	Predicted by at least one method	1252602	1253015	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1252602	1253015	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1253029	1253490	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1253501	1254304	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1254316	1254822	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1254837	1254953	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1254955	1255827	1	Phage protein
1252812	1287884	35072	Predicted by at least one method	1256141	1256335	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1256342	1256680	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1256733	1256894	-1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1257136	1257309	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1257453	1258163	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1258240	1258443	-1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1258622	1258909	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1258914	1259063	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1259131	1259295	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1259298	1259576	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1259589	1259768	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1259773	1260276	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1260326	1260484	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1260477	1260908	1	Single-stranded DNA-binding protein
1252812	1287884	35072	Predicted by at least one method	1261031	1261150	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1261338	1261523	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1261665	1261841	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1261842	1262150	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1262291	1262668	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1262796	1263698	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1263714	1264370	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1264373	1264678	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1264678	1264869	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1265265	1266203	1	Phage terminase small subunit
1252812	1287884	35072	Predicted by at least one method	1266169	1267560	1	Phage terminase, large subunit
1252812	1287884	35072	Predicted by at least one method	1267578	1267730	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1267884	1269335	1	Phage minor capsid protein
1252812	1287884	35072	Predicted by at least one method	1269611	1270216	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1270420	1271106	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1271167	1272327	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1272431	1273555	1	Minor capsid protein [Bacteriophage A118]
1252812	1287884	35072	Predicted by at least one method	1273729	1273998	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1274203	1274844	1	Phage capsid and scaffold
1252812	1287884	35072	Predicted by at least one method	1274871	1275764	1	Phage tail fiber protein
1252812	1287884	35072	Predicted by at least one method	1275780	1276061	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1276074	1276475	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1276475	1276918	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1276920	1277300	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1277300	1277740	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1277763	1278578	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1278600	1279259	1	hypothetical protein
1252812	1287884	35072	Predicted by at least one method	1279320	1284785	1	Phage tail length tape-measure protein
1252812	1287884	35072	Predicted by at least one method	1284799	1285485	1	Phage protein
1252812	1287884	35072	Predicted by at least one method	1285485	1287266	1	Phage-related protein
1252812	1287884	35072	Predicted by at least one method	1287336	1287737	1	Choline binding protein A
1252812	1287884	35072	Predicted by at least one method	1287780	1288598	-1	Phage protein
1272431	1300309	27878	Predicted by at least one method	1272431	1273555	1	Minor capsid protein [Bacteriophage A118]
1272431	1300309	27878	Predicted by at least one method	1273729	1273998	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1274203	1274844	1	Phage capsid and scaffold
1272431	1300309	27878	Predicted by at least one method	1274871	1275764	1	Phage tail fiber protein
1272431	1300309	27878	Predicted by at least one method	1275780	1276061	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1276074	1276475	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1276475	1276918	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1276920	1277300	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1277300	1277740	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1277763	1278578	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1278600	1279259	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1279320	1284785	1	Phage tail length tape-measure protein
1272431	1300309	27878	Predicted by at least one method	1284799	1285485	1	Phage protein
1272431	1300309	27878	Predicted by at least one method	1285485	1287266	1	Phage-related protein
1272431	1300309	27878	Predicted by at least one method	1287336	1287737	1	Choline binding protein A

1272431	1300309	27878	Predicted by at least one method	1287780	1288598	-1	Phage protein
1272431	1300309	27878	Predicted by at least one method	1288797	1289633	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1289651	1291132	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1291145	1291555	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1291555	1291710	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1291832	1292071	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1292090	1292599	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1292659	1293420	1	Choline binding protein A
1272431	1300309	27878	Predicted by at least one method	1294079	1294204	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1294225	1294488	-1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1294680	1294865	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1294881	1295096	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1295086	1297065	1	ATPase involved in DNA repair, phage associated
1272431	1300309	27878	Predicted by at least one method	1297065	1297979	1	Recombinational DNA repair protein RecT (prophage associated)
1272431	1300309	27878	Predicted by at least one method	1297979	1298686	1	Metallo-beta-lactamase superfamily domain protein in prophage
1272431	1300309	27878	Predicted by at least one method	1298798	1299025	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1299169	1299657	1	hypothetical protein
1272431	1300309	27878	Predicted by at least one method	1299932	1300309	-1	hypothetical protein
1293165	1299796	6631	Predicted by at least one method	1292659	1293420	1	Choline binding protein A
1293165	1299796	6631	Predicted by at least one method	1294079	1294204	1	hypothetical protein
1293165	1299796	6631	Predicted by at least one method	1294225	1294488	-1	hypothetical protein
1293165	1299796	6631	Predicted by at least one method	1294680	1294865	1	hypothetical protein
1293165	1299796	6631	Predicted by at least one method	1294881	1295096	1	hypothetical protein
1293165	1299796	6631	Predicted by at least one method	1295086	1297065	1	ATPase involved in DNA repair, phage associated
1293165	1299796	6631	Predicted by at least one method	1297065	1297979	1	Recombinational DNA repair protein RecT (prophage associated)
1293165	1299796	6631	Predicted by at least one method	1297979	1298686	1	Metallo-beta-lactamase superfamily domain protein in prophage
1293165	1299796	6631	Predicted by at least one method	1298798	1299025	1	hypothetical protein
1293165	1299796	6631	Predicted by at least one method	1299169	1299657	1	hypothetical protein
1397326	1402256	4930	Predicted by at least one method	1396227	1397333	1	Phage-like element PBSX protein xkdT
1397326	1402256	4930	Predicted by at least one method	1397326	1398030	1	Phage-like element pbsx protein xkdT
1397326	1402256	4930	Predicted by at least one method	1398032	1398685	1	FIG00514630: hypothetical protein
1397326	1402256	4930	Predicted by at least one method	1398859	1399020	1	Flagellar hook-length control protein FliK
1397326	1402256	4930	Predicted by at least one method	1399099	1399452	1	Flagellar hook-length control protein FliK
1397326	1402256	4930	Predicted by at least one method	1399654	1401324	1	Structural protein
1397326	1402256	4930	Predicted by at least one method	1401342	1401653	1	FIG00521056: hypothetical protein
1397326	1402256	4930	Predicted by at least one method	1401688	1401861	1	hypothetical protein
1397326	1402256	4930	Predicted by at least one method	1402023	1402256	1	hypothetical protein, CF-8 family
1522091	1528343	6252	Predicted by at least one method	1522091	1522351	1	hypothetical protein
1522091	1528343	6252	Predicted by at least one method	1522695	1522952	1	Holin, phage associated
1522091	1528343	6252	Predicted by at least one method	1523050	1524084	1	Choline binding protein A
1522091	1528343	6252	Predicted by at least one method	1525004	1525174	1	hypothetical protein
1522091	1528343	6252	Predicted by at least one method	1525436	1526074	1	hypothetical protein
1522091	1528343	6252	Predicted by at least one method	1526510	1526899	1	hypothetical protein
1522091	1528343	6252	Predicted by at least one method	1527035	1527241	1	Small acid-soluble spore protein, alpha-type SASP
1522091	1528343	6252	Predicted by at least one method	1527606	1528343	1	Choline binding protein A
1862127	1883445	21318	Predicted by at least one method	1861447	1862130	1	Two-component response regulator
1862127	1883445	21318	Predicted by at least one method	1862127	1863500	1	Two component system histidine kinase (EC 2.7.3.-)
1862127	1883445	21318	Predicted by at least one method	1863792	1864295	1	Heavy-metal-associated domain (N-terminus) and membrane-bounded cytochrome biogenesis cycZ-like doma
1862127	1883445	21318	Predicted by at least one method	1864463	1864693	1	hypothetical protein
1862127	1883445	21318	Predicted by at least one method	1864724	1865005	1	hypothetical protein
1862127	1883445	21318	Predicted by at least one method	1865130	1866035	-1	Multicopper oxidase
1862127	1883445	21318	Predicted by at least one method	1866376	1866585	1	hypothetical protein
1862127	1883445	21318	Predicted by at least one method	1866811	1867380	1	membrane protein, putative
1862127	1883445	21318	Predicted by at least one method	1867436	1867810	-1	Thiol:disulfide oxidoreductase related to ResA
1862127	1883445	21318	Predicted by at least one method	1868104	1869816	1	Methyl-accepting chemotaxis protein
1862127	1883445	21318	Predicted by at least one method	1869968	1870162	1	surface antigen gene
1862127	1883445	21318	Predicted by at least one method	1870310	1871203	-1	Cell division protein FtsX
1862127	1883445	21318	Predicted by at least one method	1871193	1871879	-1	Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1)
1862127	1883445	21318	Predicted by at least one method	1872111	1873214	1	NLP/P60 family protein
1862127	1883445	21318	Predicted by at least one method	1873288	1873425	1	hypothetical protein
1862127	1883445	21318	Predicted by at least one method	1873467	1874300	1	Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)
1862127	1883445	21318	Predicted by at least one method	1874620	1875447	1	Octaprenyl diphosphate synthase (EC 2.5.1.90)
1862127	1883445	21318	Predicted by at least one method	1875489	1875983	1	hypothetical protein
1862127	1883445	21318	Predicted by at least one method	1876061	1876600	1	hypothetical protein
1862127	1883445	21318	Predicted by at least one method	1876627	1878018	1	Nitrogen assimilation regulatory protein

1862127	1883445	21318	Predicted by at least one method	1878145	1879044	1	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74)
1862127	1883445	21318	Predicted by at least one method	1879060	1879686	1	CAAX amino terminal protease family protein
1862127	1883445	21318	Predicted by at least one method	1879803	1880507	1	2-heptaprenyl-1,4-naphthoquinone methyltransferase (EC 2.1.1.163)
1862127	1883445	21318	Predicted by at least one method	1880743	1881216	1	Mobile element protein
1862127	1883445	21318	Predicted by at least one method	1881575	1882021	1	HTH DNA-binding protein
1862127	1883445	21318	Predicted by at least one method	1882110	1882466	-1	MTH1175-like domain family protein
1862127	1883445	21318	Predicted by at least one method	1882768	1883445	1	Cytochrome c-type biogenesis protein CcdA (DsbD analog)
2294872	2312538	17666	Predicted by at least one method	2294872	2295669	-1	transferase hexapeptide repeat
2294872	2312538	17666	Predicted by at least one method	2295761	2296546	-1	glycosyl transferase, family 2
2294872	2312538	17666	Predicted by at least one method	2296765	2298363	-1	FIG00517471: hypothetical protein
2294872	2312538	17666	Predicted by at least one method	2298625	2299698	-1	Glycosyl transferase, group 2 family protein
2294872	2312538	17666	Predicted by at least one method	2299875	2305724	-1	Flagellar hook-length control protein FliK
2294872	2312538	17666	Predicted by at least one method	2305971	2306120	1	Transposase
2294872	2312538	17666	Predicted by at least one method	2306201	2306818	1	Mobile element protein
2294872	2312538	17666	Predicted by at least one method	2307863	2309668	1	glutamine synthetase family protein
2294872	2312538	17666	Predicted by at least one method	2310751	2310975	1	Mobile element protein
2294872	2312538	17666	Predicted by at least one method	2311126	2312538	-1	Glycosyl transferase, group 2 family protein
2351636	2359755	8119	Predicted by at least one method	2351636	2352139	1	Free methionine-(R)-sulfoxide reductase, contains GAF domain
2351636	2359755	8119	Predicted by at least one method	2352287	2352721	1	Protein containing Zn-finger domain
2351636	2359755	8119	Predicted by at least one method	2352818	2353537	1	FIG00527899: hypothetical protein
2351636	2359755	8119	Predicted by at least one method	2353668	2354657	-1	Probable integrase/recombinase
2351636	2359755	8119	Predicted by at least one method	2355458	2355946	1	Cys-tRNA(Pro) deacylase YbaK
2351636	2359755	8119	Predicted by at least one method	2356666	2358033	-1	tRNA-i(6)A37 methylthiotransferase
2351636	2359755	8119	Predicted by at least one method	2358154	2359023	-1	Acetyltransferase Iojap substitute?
2351636	2359755	8119	Predicted by at least one method	2359315	2359485	-1	hypothetical protein
2351636	2359755	8119	Predicted by at least one method	2359534	2359755	-1	hypothetical protein
2665757	2689914	24157	Predicted by at least one method	2665757	2665909	1	hypothetical protein
2665757	2689914	24157	Predicted by at least one method	2666104	2666439	-1	DSBH domain containing protein
2665757	2689914	24157	Predicted by at least one method	2666797	2666976	-1	Mobile element protein
2665757	2689914	24157	Predicted by at least one method	2666988	2667344	-1	Transcriptional regulator, HxlR family
2665757	2689914	24157	Predicted by at least one method	2667489	2668526	1	putative zinc-binding oxidoreductase
2665757	2689914	24157	Predicted by at least one method	2669084	2669347	1	Transcriptional regulator, HxlR family
2665757	2689914	24157	Predicted by at least one method	2669412	2669852	-1	Auxin-binding protein, putative
2665757	2689914	24157	Predicted by at least one method	2669994	2670221	1	iron-sulfur flavoprotein
2665757	2689914	24157	Predicted by at least one method	2670520	2670915	1	NimC/NimA family protein
2665757	2689914	24157	Predicted by at least one method	2671236	2672681	-1	Lincomycin resistance protein lmrB
2665757	2689914	24157	Predicted by at least one method	2672866	2672991	-1	hypothetical protein
2665757	2689914	24157	Predicted by at least one method	2673666	2675732	1	Chloride channel protein
2665757	2689914	24157	Predicted by at least one method	2675901	2676536	-1	hypothetical protein
2665757	2689914	24157	Predicted by at least one method	2676924	2677496	1	RNA polymerase, sigma-24 subunit, ECF subfamily
2665757	2689914	24157	Predicted by at least one method	2677566	2677808	-1	hypothetical protein
2665757	2689914	24157	Predicted by at least one method	2678495	2678680	1	hypothetical protein
2665757	2689914	24157	Predicted by at least one method	2678677	2679246	-1	Dihydrofolate reductase (EC 1.5.1.3)
2665757	2689914	24157	Predicted by at least one method	2679384	2681084	-1	Methyl-accepting chemotaxis protein
2665757	2689914	24157	Predicted by at least one method	2681675	2682883	-1	L-serine dehydratase (EC 4.3.1.17)
2665757	2689914	24157	Predicted by at least one method	2683024	2683860	-1	Probable enoyl-CoA hydratase (EC 4.2.1.17)
2665757	2689914	24157	Predicted by at least one method	2684003	2684833	-1	Enoyl-CoA hydratase (EC 4.2.1.17)
2665757	2689914	24157	Predicted by at least one method	2684865	2686079	-1	Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate, subunit A
2665757	2689914	24157	Predicted by at least one method	2686315	2687628	1	Regulatory protein (induces abgABT, used to catabolize p-aminobenzoyl-glutamate)
2665757	2689914	24157	Predicted by at least one method	2687686	2688510	-1	Transcriptional regulator, TrmB family
2665757	2689914	24157	Predicted by at least one method	2688651	2689568	1	Permease of the drug/metabolite transporter (DMT) superfamily
2665757	2689914	24157	Predicted by at least one method	2689708	2689914	-1	Small acid-soluble spore protein, alpha-type SASP
2681675	2687628	5953	Predicted by at least one method	2681675	2682883	-1	L-serine dehydratase (EC 4.3.1.17)
2681675	2687628	5953	Predicted by at least one method	2683024	2683860	-1	Probable enoyl-CoA hydratase (EC 4.2.1.17)
2681675	2687628	5953	Predicted by at least one method	2684003	2684833	-1	Enoyl-CoA hydratase (EC 4.2.1.17)
2681675	2687628	5953	Predicted by at least one method	2684865	2686079	-1	Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate, subunit A
2681675	2687628	5953	Predicted by at least one method	2686315	2687628	1	Regulatory protein (induces abgABT, used to catabolize p-aminobenzoyl-glutamate)
3340056	3345198	5142	Predicted by at least one method	3340181	3340360	-1	hypothetical protein
3340056	3345198	5142	Predicted by at least one method	3340548	3340667	-1	hypothetical protein
3340056	3345198	5142	Predicted by at least one method	3340860	3341573	-1	hypothetical protein
3340056	3345198	5142	Predicted by at least one method	3341613	3341726	-1	hypothetical protein
3340056	3345198	5142	Predicted by at least one method	3341698	3342135	-1	hypothetical protein
3340056	3345198	5142	Predicted by at least one method	3342132	3343013	-1	Chromosome (plasmid) partitioning protein ParA
3340056	3345198	5142	Predicted by at least one method	3343030	3343812	-1	hypothetical protein

3340056	3345198	5142	Predicted by at least one method	3344006	3345013	1	hypothetical protein
3340056	3345198	5142	Predicted by at least one method	3345076	3345861	-1	Choline binding protein A
3354579	3363124	8545	Predicted by at least one method	3353277	3355328	-1	NLP/P60 family protein
3354579	3363124	8545	Predicted by at least one method	3355337	3355966	-1	Phage-like element PBSX protein xkdP
3354579	3363124	8545	Predicted by at least one method	3355986	3357890	-1	Phage protein
3354579	3363124	8545	Predicted by at least one method	3357921	3358076	-1	hypothetical protein
3354579	3363124	8545	Predicted by at least one method	3358097	3358483	-1	hypothetical protein
3354579	3363124	8545	Predicted by at least one method	3358540	3358965	-1	hypothetical protein
3354579	3363124	8545	Predicted by at least one method	3358980	3360050	-1	Phage-like element PBSX protein xkdK
3354579	3363124	8545	Predicted by at least one method	3360050	3360517	-1	hypothetical protein
3354579	3363124	8545	Predicted by at least one method	3360518	3360913	-1	Phage protein
3354579	3363124	8545	Predicted by at least one method	3360906	3361244	-1	hypothetical protein
3354579	3363124	8545	Predicted by at least one method	3361260	3361589	-1	hypothetical protein
3354579	3363124	8545	Predicted by at least one method	3361589	3361711	-1	hypothetical protein
3354579	3363124	8545	Predicted by at least one method	3361759	3362709	-1	FIG00523353: hypothetical protein
3354579	3363124	8545	Predicted by at least one method	3362744	3363334	-1	FIG00515289: hypothetical protein
3394539	3403791	9252	Predicted by at least one method	3394539	3395489	-1	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)
3394539	3403791	9252	Predicted by at least one method	3395651	3396100	-1	Surface protein PspC
3394539	3403791	9252	Predicted by at least one method	3396734	3397147	-1	hypothetical protein
3394539	3403791	9252	Predicted by at least one method	3398087	3398872	-1	Choline binding protein A
3394539	3403791	9252	Predicted by at least one method	3398936	3399376	-1	hypothetical protein
3394539	3403791	9252	Predicted by at least one method	3399392	3399628	-1	hypothetical protein, CF-8 family
3394539	3403791	9252	Predicted by at least one method	3399759	3400940	-1	Protein of unknown function DUF11
3394539	3403791	9252	Predicted by at least one method	3401258	3401431	-1	hypothetical protein
3394539	3403791	9252	Predicted by at least one method	3401466	3401741	-1	FIG00521056: hypothetical protein
3394539	3403791	9252	Predicted by at least one method	3401767	3403143	-1	putative phage structural protein
3394539	3403791	9252	Predicted by at least one method	3403156	3403791	-1	Phage-like element pbsx protein xkdT
3394539	3403791	9252	Predicted by at least one method	3403788	3404918	-1	Phage baseplate
3433836	3440470	6634	Predicted by at least one method	3433836	3434543	-1	Metallo-beta-lactamase superfamily domain protein in prophage
3433836	3440470	6634	Predicted by at least one method	3434543	3435463	-1	Recombinational DNA repair protein RecT (prophage associated)
3433836	3440470	6634	Predicted by at least one method	3435464	3435880	-1	hypothetical protein
3433836	3440470	6634	Predicted by at least one method	3435934	3437925	-1	ATPase involved in DNA repair, phage associated
3433836	3440470	6634	Predicted by at least one method	3437906	3438247	-1	hypothetical protein
3433836	3440470	6634	Predicted by at least one method	3438262	3438420	-1	hypothetical protein
3433836	3440470	6634	Predicted by at least one method	3438420	3438929	-1	hypothetical protein
3433836	3440470	6634	Predicted by at least one method	3438986	3439186	1	hypothetical protein
3433836	3440470	6634	Predicted by at least one method	3439188	3439481	-1	hypothetical protein
3433836	3440470	6634	Predicted by at least one method	3439592	3439819	-1	hypothetical protein
3433836	3440470	6634	Predicted by at least one method	3439956	3440327	1	Transcriptional regulator
3433836	3440470	6634	Predicted by at least one method	3440324	3440470	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4179324	4179746	1	transcriptional regulator, XRE family
4179324	4195206	15882	Predicted by at least one method	4179889	4180470	-1	FIG01236936: hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4180989	4181777	-1	Choline binding protein A
4179324	4195206	15882	Predicted by at least one method	4181848	4182243	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4182259	4182495	-1	hypothetical protein, CF-8 family
4179324	4195206	15882	Predicted by at least one method	4182492	4182620	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4182716	4183132	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4183361	4184518	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4184789	4184920	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4184913	4185320	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4185339	4186421	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4186437	4187162	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4187180	4188865	-1	Phage endopeptidase
4179324	4195206	15882	Predicted by at least one method	4188865	4189569	-1	Phage-related protein
4179324	4195206	15882	Predicted by at least one method	4189571	4192846	-1	Phage tail length tape-measure protein
4179324	4195206	15882	Predicted by at least one method	4193094	4193477	-1	hypothetical protein
4179324	4195206	15882	Predicted by at least one method	4193548	4194132	-1	Phage major tail protein
4179324	4195206	15882	Predicted by at least one method	4194139	4194495	-1	Phage protein
4179324	4195206	15882	Predicted by at least one method	4194506	4194862	-1	Phage protein, HK97 gp10 family
4179324	4195206	15882	Predicted by at least one method	4194859	4195206	-1	Phage protein
4201017	4217236	16219	Predicted by at least one method	4201017	4201445	-1	FIG00513960: hypothetical protein
4201017	4217236	16219	Predicted by at least one method	4201460	4201939	-1	FIG00513910: hypothetical protein
4201017	4217236	16219	Predicted by at least one method	4202208	4202825	-1	prophage LambdaSa2, site-specific recombinase, phage integrase family
4201017	4217236	16219	Predicted by at least one method	4202822	4203097	-1	conserved hypothetical protein
4201017	4217236	16219	Predicted by at least one method	4203090	4203488	-1	hypothetical protein
4201017	4217236	16219	Predicted by at least one method	4203654	4203983	-1	hypothetical protein
4201017	4217236	16219	Predicted by at least one method	4204225	4204524	-1	hypothetical protein
4201017	4217236	16219	Predicted by at least one method	4204790	4205182	-1	hypothetical protein
4201017	4217236	16219	Predicted by at least one method	4205547	4205927	-1	hypothetical protein
4201017	4217236	16219	Predicted by at least one method	4206036	4206218	-1	hypothetical protein

4201017	4217236	16219	Predicted by at least one method
4201017	4217236	16219	Predicted by at least one method
4201017	4217236	16219	Predicted by at least one method
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4201017	4217236	16219	Predicted by at least one method
4201017	4217236	16219	Predicted by at least one method
4201017	4217236	16219	Predicted by at least one method
4201017	4217236	16219	Predicted by at least one method
4201017	4217236	16219	Predicted by at least one method
4201017	4217236	16219	Predicted by at least one method
4250802	4258863	8061	Predicted by at least one method
4250802	4258863	8061	Predicted by at least one method
4250802	4258863	8061	Predicted by at least one method
4250802	4258863	8061	Predicted by at least one method
4250802	4258863	8061	Predicted by at least one method
4440203	4445910	5707	Predicted by at least one method
4440203	4445910	5707	Predicted by at least one method
4440203	4445910	5707	Predicted by at least one method
4440203	4445910	5707	Predicted by at least one method
4494715	4503576	8861	Predicted by at least one method
4494715	4503576	8861	Predicted by at least one method
4494715	4503576	8861	Predicted by at least one method
4494715	4503576	8861	Predicted by at least one method
4494715	4503576	8861	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4533265	4544999	11734	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
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4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
4695112	4711042	15930	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method

4206329	4206610	-1	hypothetical protein
4206822	4207133	1	hypothetical protein
4207547	4207705	-1	hypothetical protein
4208384	4208575	1	hypothetical protein
4208845	4209624	-1	hypothetical protein
4209617	4210450	-1	phage protein
4210498	4210683	-1	hypothetical protein
4210774	4211073	-1	hypothetical protein
4211109	4211273	-1	hypothetical protein
4211330	4211761	-1	FIG00532806: hypothetical protein
4211804	4212007	-1	hypothetical protein
4212174	4212512	1	Transcriptional regulator, Cro/CI family
4212617	4214461	-1	plasmid-related protein
4214491	4214940	-1	hypothetical protein
4214933	4216195	-1	hypothetical protein
4216739	4217236	1	putative phage-related protein
4250766	4252337	-1	Beta-xylosidase (EC 3.2.1.37)
4252358	4253620	-1	Two-component response regulator yesN
4253613	4255418	-1	two-component sensor histidine kinase
4255558	4256811	-1	ABC-type sugar transport system, periplasmic binding protein ycjN
4257085	4258476	-1	Xyloside transporter XynT
4439648	4440454	-1	Xylose ABC transporter, permease component
4440593	4441894	-1	similar to ABC-type sugar transport system periplasmic component
4442004	4443614	-1	DNA-binding response regulator, AraC family
4443617	4445425	-1	Autolysis histidine kinase LytS
4445891	4448176	-1	Beta-galactosidase (EC 3.2.1.23)
4494842	4495666	1	hypothetical protein
4495686	4496726	-1	FIG00443277: hypothetical protein
4496905	4499664	-1	Adenosine deaminase (EC 3.5.4.5)
4499657	4502104	-1	hypothetical protein
4502205	4503206	-1	Radical SAM domain heme biosynthesis protein
4533265	4534068	-1	Sulfur carrier protein adenylyltransferase ThiF
4534694	4535290	1	Substrate-specific component PanT of predicted pantothenate ECF transporter
4535558	4538149	-1	ClpB protein
4538414	4538800	1	CBS domain protein
4538958	4540223	-1	Xre family DNA-binding domain and TPR-repeat-containing protein
4540241	4541551	-1	Xre family DNA-binding domain and TPR-repeat-containing protein
4541805	4541978	-1	FIG00515074: hypothetical protein
4542200	4543150	-1	Ribonuclease HI-related protein
4543252	4544214	-1	Conserved protein
4544751	4544999	1	hypothetical protein
4544967	4545362	-1	Methionine ABC transporter substrate-binding protein
4695112	4696266	-1	SSU ribosomal protein S1p
4696627	4696755	-1	hypothetical protein
4696724	4697311	1	hypothetical protein
4697333	4697983	1	Phage shock protein A
4697994	4698653	1	FIG00513465: hypothetical protein
4698840	4699289	-1	CBS domain protein
4699408	4700319	-1	exonuclease family protein
4700367	4702157	-1	MutS-related protein, family 1
4702662	4703273	-1	Zinc ABC transporter, periplasmic-binding protein ZnuA
4703316	4703558	-1	Zinc ABC transporter, periplasmic-binding protein ZnuA
4703668	4706403	-1	DNA double-strand break repair Rad50 ATPase
4706393	4706515	-1	hypothetical protein
4706505	4707638	-1	DNA double-strand break repair protein Mre11
4707870	4708061	-1	Small acid-soluble spore protein, alpha-type SASP
4708276	4709292	-1	FIG00517086: hypothetical protein
4709975	4711042	1	Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9)
5115773	5117149	-1	DNA repair protein RadA
5117635	5117862	1	Glutaredoxin
5117938	5118873	-1	Thioredoxin reductase (EC 1.8.1.9)
5119004	5121478	-1	ATP-dependent Clp protease, ATP-binding subunit ClpC / Negative regulator of genetic competence clcC
5121504	5122517	-1	Putative ATP:guanido phosphotransferase YacI (EC 2.7.3.-)
5122510	5123088	-1	Nucleotide excision repair protein, with UvrB/UvrC motif
5123103	5123558	-1	Transcriptional regulator CtsR

5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method
5115773	5128083	12310	Predicted by at least one method

5123728	5124378	1	Zn-dependent hydrolases of the metallo-beta-lactamase superfamily
5124435	5124605	-1	Ferredoxin
5124728	5124931	-1	Predicted metal-binding protein of ferredoxin fold
5124943	5125848	-1	Signal peptidase-like protein
5125852	5126784	-1	DNA polymerase III delta prime subunit (EC 2.7.7.7)
5126804	5127136	-1	protein from nitrogen regulatory protein P-II (GLNB) family, ortholog YAAQ B. subtilis
5127210	5127851	-1	Thymidylate kinase (EC 2.7.4.9)
5127901	5128083	-1	Zn-finger containing protein, csfB B.subtilis homolog

ATTACHMENT 14

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

(Revised) Safety Narrative

(b) (4)

PART 6 – NARRATIVE (REVISED)

The conclusion that *C. beijerinckii* ASCUSDY20 spray dried powder, as described herein, is GRAS under the conditions of intended use as a direct fed microbial in feed for dairy cattle is based on scientific procedures using product-specific characterization data on the microbial strain together with a body of published information on the prevalence and potential pathogenicity and toxigenicity of the *Clostridium* species.

As mentioned in Part 1.3, *C. beijerinckii* ASCUSDY20 will be provided to dairy cattle as a spray dried powder with starch, either alone or in combination with other direct fed microbials. The strain was isolated from the rumen content of a healthy mid-lactation Holstein cow and is intended as a source of commensal microorganisms. In this respect, *C. beijerinckii* ASCUSDY20 spray dried powder will contribute to the native microbial population in the rumen and the functionality of the direct fed microbial strain is considered in Part 6.1.

The safety of *C. beijerinckii* ASCUSDY20 for use as a direct fed microbial for dairy cattle is evaluated using several different pieces of data regarding strain characterization and the evaluation of its pathogenic and toxigenic potential. In order to understand the pathogenic and toxigenic potential, the microbial strain must be fully characterized and the body of knowledge pertaining to safety based on its taxonomic unit considered. Full details of the characterization of *C. beijerinckii* ASCUSDY20 are detailed in Part 2. The microbial has been unambiguously characterized as *Clostridium beijerinckii* (see Part 2.1.4). Furthermore, whole genome sequence analysis indicates the absence of any genetic element sequences that code for virulence factors or protein toxins (see Part 2.1.8). Whole genome sequence analysis together with phenotypic testing indicate that *C. beijerinckii* ASCUSDY20 is susceptible to antimicrobials and should not increase the risk of transfer of resistance to other microorganisms (see Part 2.1.5 and 2.1.6). Testing also confirms *C. beijerinckii* ASCUSDY20 does not produce antimicrobial substances (see Part 2.1.7 and Appendix 005).

In addition to the characterization data, a body of information is available in the public domain pertaining to (a) the identity of *C. beijerinckii* (see Part 6.2); (b) the history of exposure of the species by animals and humans (see Parts 6.4 and 6.5); and (c) the potential for toxigenicity and pathogenicity (see Part 6.6). These data represent another important component of the safety evaluation of *C. beijerinckii* ASCUSDY20 spray dried powder and are summarized below.

6.1 Functionality

The microbial population of the rumen plays an important role in the utilization of feed by dairy cattle. Manipulation of rumen microbiota by dietary supplementation with sources of viable microorganisms is common practice in the dairy cattle industry in the U.S. in order to facilitate fermentation and contribute to the general digestive health of the animal (Yoon & Stern, 1995; Chaucheyras-Durand & Durand, 2010; El-Tawab *et al*., 2016). The contribution of bacteria to the fermentation characteristics of the rumen have been extensively evaluated in the published literature, with important functions reported to be stabilization of the rumen pH, increase in volatile fatty acid production, reduction in ammonia concentrations, improved microbial protein synthesis and fiber digestibility (*e.g*., McAllister et al., 2011, Nocek et al., 2002, Henning et al., 2010, Krehbiel et al., 2003, Qiao et al., 2009, Weinberg et al., 2007, Jeyanathan et al., 2019, Yoon & Stern, 1995). As mentioned in Part 2, *C. beijerinckii*

ASCUSDY20 was isolated from the rumen content of a healthy mid-lactation Holstein and is expected to contribute in the same way as other bacteria to digestion and metabolism in the ruminal environment.

In particular, *C. beijerinckii* ASCUSDY20 was shown to utilize various carbon sources including simple carbohydrates (e.g., glucose and fructose) as well as reducing sugar derived from plant materials such as xylose and cellobiose (see Part 2.1). Similar phenotypes are reported in the published literature for other *C. beijerinckii* strains (*e.g.*, Zhang *et al.*, 2012; Ezeji *et al.*, 2007). Zhang et al (2012) found that *C. beijerinckii* NCIMB 8052 could ferment corncobs and produce butanol, acetone, ethanol, acetate, and butyrate. Ezeji et al. (2007) reported that *C. beijerinckii* BA101 was able to grow on major reducing sugars of lignocellulose (glucose, xylose, cellobiose, mannose, arabinose, galactose) and produce acetone, butanol, and ethanol. Thus, the microorganism has the potential to support digestion by aiding fermentation of forages and partially degraded digesta in the rumen.

Similar to other *Clostridium* species, *C. beijerinckii* ASCUSDY20 has been shown to utilize a range of monosaccharides including glucose, fructose and xylose to produce relatively high levels of butyric acid and acetic acid (Ho *et al.*, 2011). Volatile fatty acids (VFAs) are the main source of energy in ruminants and are produced predominantly through microbial fermentation of feed in the rumen (Bergman, 1990; NRC, 2001). The three major VFAs produced by anaerobic microbial fermentation in the rumen are acetate, propionate and butyrate with the relative ratios largely depending on the nature of the feed. The VFAs are readily absorbed and utilized by ruminants accounting for up to 80% of their maintenance energy requirements. Butyrate in particular acts as the major energy source for epithelial cells in ruminants and is recognized to play an important role in maintaining colonic health in the animal. Studies have also linked butyrate to the development of rumen papillary and calf gastrointestinal tracts (Weigand et al., 1975; Górka et al., 2018). Seymour *et al.* (2005) reviewed the results of 20 studies evaluating the relationship between VFAs and production-related variables in Holstein cows. The strongest associations identified were between rumen butyrate concentration, which displayed a significant positive linear regression relationship with dry matter intake, and milk yield. The authors concluded that butyrate indirectly supports the milk yield and production although the relationship is complex. Similarly, a number of other studies in the published literature indicate that butyrate can support the general production performance of the animals (Rook and Balch, 1961; Huhtanen *et al.*, 1993; Miettinen and Huhtanen, 1996). Similarly, acetate is considered essential for milk fat production and low levels of rumen acetate have been reported to lead to depressed milk fat content (Bergman, 1990; Gäbel *et al.*, 2002; Aluwong *et al.*, 2010). The role of VFAs as energy sources for dairy cattle also is supported by the existing food additive listing for the ammonium or calcium salts of isobutyric acid, iso-valeric acid, 2-methylbutyric acid and n-valeric acid as sources of energy in dairy cattle feeds under 21 CFR §573.914.

C. beijerinckii can also undergo mixotrophic growth to recapture carbon during fermentation processes. Sandoval-Espinola et al (2017) monitored biogas availability and the transcriptomes of *C. beijerinckii* in batch fermentation systems. The study found that in the presence of external electron sinks (eg., CO/CO2), the production of acetyl-coA along with the acetone-butanol-alcohol pathway in *C. beijerinckii* lead to better sugar utilization and could recover 17-27% more carbon. This suggests that *C. beijerinckii* may play a unique role in improving sugar utilization and carbon-energy recapture in rumen.

Taken together, these examples of the potential functionality of anaerobic *Clostridium* species in the rumen support the proposed role of *C. beijerinckii* ASCUSDY20 as a source of viable microorganisms in the diet to positively influence the production of VFAs. While *C. beijerinckii* ASCUSDY20 may contribute to the native population of *Clostridium* species in the gut of the animal, the technical function has no bearing on the safety when used as a direct fed microbial in feed for dairy cattle. Should *C. beijerinckii* ASCUSDY20 fail, other members of the existing rumen microbiome will continue to ferment feed, thus supplying the animal with sufficient nutrients. On this basis, no further demonstration of the technical effect (utility) of *C. beijerinckii* ASCUSDY20 was required for the safety evaluation (see Part 2.5).

6.2 Identity

The genus *Clostridium* consists of a heterogeneous set of species which are not phylogenetically coherent. Many species were assigned to the genus based only on their being gram positive anaerobic rods which are capable of endospore formation. Phylogenetic and comparative analyses indicate that of the >150 *Clostridium* species identified, fewer than half are part of cluster I, the distinct cluster in the 16S rRNA tree which are generally regarded as the true representatives of the genus *Clostridium* and which includes *C. beijerinckii* (Johnson & Francis, 1975; Collins *et al*., 1994; Stackebrandt *et al*., 1999; Gupta & Gao, 2009; Lawson & Rainey, 2016; Udaondo *et al*., 2017). *Clostridium* cluster I is recognized as *Clostridium sensu stricto* and includes the medically important *Clostridium botulinum* but not *Clostridium difficile*. The species assigned to *Clostridium* cluster I are metabolically and physiologically diverse species capable of utilizing carbohydrates and peptones to produce organic acids and alcohols. The G+C content of cluster I species varies from between 22 and 37 mol%, and the 16S rRNA gene sequence similarities range from 92 to 99% (Wiegel *et al*., 2006; Rainey *et al*., 1993).

In the past, *Clostridium* species were extensively used for the industrial production of butanol and acetone from starch-based substrates (Jones and Woods, 1986; Jones and Keis, 1995; Keis *et al*., 2001). The first strains isolated and developed for large scale production of these solvents were identified as *Clostridium acetobutylicum* but were later assigned to four species, *C. acetobutylicum*, *C. beijerinckii*, *Clostridium saccharoperbutylacetonicum* and *Clostridium saccharobutylicum* (Johnson *et al*., 1997; Keis *et al*., 1995; Wilkinson and Young, 1995; Keis *et al*., 2001). Similarly, strains historically assigned to the species *Clostridium butylicum* have been subsequently shown to members of *C. beijerinckii* (George and Chen, 1983).

Additionally, some strains originally designated as *C. butyricum* have been renamed *C. beijerinckii*. While challenging to distinguish phenotypically, these species can largely be (Cummins & Johnson, 1971; Ikeda *et al*., 1998) differentiated based on electrophoretic patterns of cellular proteins or by testing nutritional requirements (Brandle *et al*., 2016).

From the perspective of the safety assessment, it is therefore acknowledged that some strains of *C. beijerinckii* were formerly classified as *C. acetobutylicum*, *C. butylicum* and *C. butyricum* and all species were included in the literature search and subsequent review of published information.

6.3 Literature Search

A comprehensive literature search was conducted in order to identify all publicly available information pertaining to the safety of *C. beijerinckii* for the intended use as a source of viable cells for dairy cows.

As mentioned in Part 6.2, all potential nomenclature was included in the literature search (*i.e.*, *Clostridium acetobutylicum*, *Clostridium butylicum, Clostridium butyricum* and *Clostridium beijerinckii*) and details of the search strategy are provided in updated Appendix 017 (Attachment 15).

The results of the literature search form the basis of the safety assessment, in keeping with the general recognition requirements for GRAS notices.

6.4 Natural Occurrence

6.4.1 Prevalence in Animals

C. beijerinckii is ubiquitous in nature and routinely isolated from livestock feces and soil samples (Sankar *et al*. 2003; Pan *et al*., 2008; Hussain and El Sanousi, 2011; Brandle *et al*., 2016; Driehuis *et al*., 2016). It was one of the major populations of butyric acid bacteria isolated in 296 samples of soil, maize and grass silage, dairy cow feces and farm tank milk collected from dairy farms in the Netherlands (Driehuis *et al*., 2016). Similarly, in a study by Hussain and El sanousi*,* 210 fecal samples were collected from 7 different animals (cattle, sheep, goats, camels, horses, donkeys, and chickens) to investigate the prevalence of *Clostridium*-like species. The prevalence of *C. beijerinckii* among these samples was 3.3% (Hussain and El Sanousi, 2011). Isolation and characterization of xylanolytic solventogenic bacteria from cow rumen fluid identified 5 strains of *C. beijerinckii* to be present, in combination with *C. acetobutylicum*, *C. butyricum* and *C. bifermentans* strains (Sankar *et al*., 2003). Dutta, et al. (1983) isolated members of Clostridia, Lactobacilli, and Streptococci from pigs, cattle, and poultry to investigate their antibiotic susceptibility. The group was able to isolate 3 *C. beijerinckii* strains, and found that all three did not possess any acquired antimicrobial resistance.

A total of 207 different strains of *C. beijerinckii* have been isolated, sequenced, and analyzed in the JGI genome portal to date (https://genome.jgi.doe.gov/portal/). Many strains within this database represent industrial fermentation strains, however, several of the isolates were obtained from rumen content as part of the Hungate1000 project (http://www.rmgnetwork.org/hungate1000.html; Seshadri *et al.,* 2018*)*. The Hungate1000 project attempted to isolate taxonomically diverse microorganisms from rumen content. In total, 410 bacteria and archaea were isolated, representing ~75% of the genera present in the rumen. Similarly, the Global Rumen Census found that Clostridiales were present in all ruminants surveyed, and were found to comprise 15.3% of the rumen microbial community on average (Henderson *et al.,* 2015). The *Clostridium* genus was found to comprise an average of 0.71% of the rumen microbial community. *Clostridium* was detected in 98% of the 742 samples from 32 animal species across 35 countries. The samples in which *Clostridium* was not detected were primarily male crossbreed cattle being fed 100% concentrate diets. Thus, *Clostridium* and *C. beijerinckii* are highly prevalent as a commensal organism of the rumen microbial ecosystem.

6.4.2 Microbiome Safety

The rumen microbiome is crucial for the digestion of feed and supplies necessary nutrients to ruminants (Faichney, 1996 ; Huws et al., 2018). The rumen hosts a diverse group of microorganisms that work closely to degrade plant materials. The fermentation process converts nearly all dietary carbohydrates to volatile fatty acids (VFA), predominantly butyrate, acetate, and propionate. It has been widely recognized that the rumen VFAs are crucial for digestive system development and animal carbon and nitrogen needs

(Storm and Orskov, 1984; Wallace et al., 1997; Broudiscou and Jouany, 1995; Weigand et al., 1975; Górka et al., 2018; Leng et al., 1967; Young, 1977; Huws et al., 2018; Bach et al., 2005; Edwards et al., 2008). Direction infusion of VFAs into the rumen can also improve animal performances. For example, direct infusion of butyrate into the rumen increased milk fat production without changing milk yield (Huhtanen *et al*., 1993) and direct infusion of propionate into the rumen increased milk protein production (Rook and Balch, 1961).

The contribution of DFMs to the fermentation characteristics of the rumen has been extensively evaluated (Elghandour *et al*., 2015). Specific species within the genera *Lactobacillus, Bifidobacterium, Enterococcus, Streptococcus, Bacillus, Propionibacterium, Megasphaera and Prevotella* have been fed to animals (Nocek *et al*., 2002; Yoon and Stern, 1995; Ghorbani *et al*., 2002; Stein *et al*., 2006; Yang *et al*., 2004; Nagaraja *et al*., 1997; Chiquette *et al*., 2008; Mohammed *et al*., 2012; Weiss *et al*., 2008; Aikman *et al*., 2011). There are several studies, for example, that describe the fermentation patterns and feed digestibility of ruminants fed a standard diet supplemented with a DFM compared to ruminants only on a standard diet. Feeding of *Lactobacillus plantarum* via silage in Mohammed *et al*., (2012) showed no changes in production, but no deleterious effects on the animal. Similar results were observed in studies feeding *Lactobacillus acidophilus* (Raeth-Knight *et al*., 2007; Abu-Tarboush *et al*. 1996; Higginbotham and Bath, 1993; McGilliard and Stallings, 1997). In Weiss *et al*. (2008), dairy cows were supplemented with *Propionibacterium* P169 2 weeks before anticipated calving to 119 days in milk. Cows fed *Propionibacterium* P169 had lower concentrations of acetate and greater concentrations of propionate and butyrate compared to control cows. Treatment cows also produced similar amounts of milk with similar composition as cows fed the control diet and had similar body weights throughout the trial. Chiquette *et al*. (2008) fed *Prevotella bryantii* 25A to dairy cows in early lactation, and found that administration did not change milk yield, but tended to increase milk fat. This is in alignment with the increased acetate and butyrate concentrations observed in the rumen of treatment animals. In Chiquette *et al*. (2007), *Ruminococcus flavefaciens* NJ was fed to non-lactating dairy cows on either a high concentrate or a high forage diet daily. Cows fed *R. flavefaciens* NJ exhibited improved *in sacco* digestibility of hay in the rumen when fed as part of a high concentrate diet. Several experiments have fed *Megasphaera elsdenii* with various results on digestibility and performance, but no deleterious impacts were observed (Aikman *et al*., 2011; Hagg *et al*., 2010; Zebeli *et al*., 2012; Hagg , 2008; Kung and Hession, 1995).

Bacteria catabolism also plays an important role in animal nutrient cycling. Hoogenraad et al (1969) studied how model organisms of gram-negative bacterium (*Escherichia coli*) and gram-positive bacterium (*Bacillus subtilis*) were utilized in adult sheep digestive tract. The study found that the freeze-dried whole cells of either bacteria were quickly digested by rumen microbiome and cell carbons were incorporated into VFAs. A large amount of the bacterial carbon (70%) was captured by the host animal. Bacterial whole cells and cell components such as cell wall and content were also readily digested and metabolized in abomasum. Despite the common belief that gram-positive cells are more difficult to metabolize due to the presence of peptidoglycan, 73-86% of *B. subtilis* cell and cell component carbon was captured by the animal through lower gut digestion. In contrast, a smaller portion (66-78%) of *E. coli* carbon was captured by the host animal. Notably, although *B. subtilis* cells contain a greater amount of glucose than *E. coli*, a much greater amount of *E. coli* carbon was incorporated into the lower gut glucose pool. The findings suggest that bacteria turnover in ruminant digestive tract is an important process and supplying building blocks to support the host metabolism.

The rumen microbiome is dynamic. Moraïs and Mizrahi (2019) summarized that multiple microbial community states exist within the rumen depending on the rumen metabolic needs. The flow of

metabolites and energy were passed on from one functional group to the next rather than from one group to another. Thus, microbial interactions could drive larger changes in overall fermentation patterns and identifying the optimal microbial interactions could improve digestibility (Weimer, 2015). Published studies showed that diet contributes to the greatest rumen microbiome shifts observed (Kumar et al., 2015; Deusch et al., 2017; Mizrahi and Jami, 2018; Belanche et al., 2019; Johnson and Johnson, 1995; Brulc et al., 2009; Carberry et al., 2014). Under the same diet, the addition of DFMs does not change the rumen microbiome significantly but can improve rumen digestibility. Westergaard (2015) fed a *Bacillus pumilus* DFM to 21 dairy cows and compared the composition of their rumen microbiomes to 22 control animals. The study reported an insignificant increase in Firmicutes from 14.1% to 15.8% and an insignificant decrease of Bacteroidetes from 64.1% to 62.3% in rumen fluid of animals received the DFM. Its companion study reported that the animals receiving the DFM were more efficient at feed conversion (ECM:DMI) than the control animals, although not significantly ($p = 0.06$) (Luan et al., 2015). Le and colleagues (2016) conducted a study comparing the growth performance of 4 week-old dairy calves with and without DFM *Bacillus amyloliquefaciens* in feed. *B. amyloliquefaciens* was administered daily for 9 weeks to 12 calves and another 12 calves were used as controls. The study found that dairy calves administered *B. amyloliquefaciens* gained 20% more weight and suffered less diarrhea than the control group. Notably, its companion study observed that *B. amyloliquefaciens* supplementation did not change the dairy calf rumen microbiomes significantly, despite confirmation of colonization of the DFM strain in rumen (Schofield et al., 2018). In another study, Fomenky and colleagues (2018) compared the rumen digesta microbiome of pre- (33 days old) and post-weaned calves (96 days old) fed with control diet alone and control diet supplemented with *S. cerevisiae* (SCB) or *L. acidophilus* (LA) (8 per treatment). The study found that supplementing DFMs did not significantly change the overall rumen microbial community structure, where the p-values for alpha diversity indices ranged from 0.051 to 0.992 and the p-value for beta diversity (PERMANOVA) was 0.512. The study also predicted that pathways involved in lipid and protein metabolism and cellular processes were more abundant in pre-weaned rumen administered DFMs. Once weaned, no predicted pathways in rumen digesta were significantly different between control and LA fed animals. Riboflavin metabolism was the only significantly more abundant pathway in SCB fed animal rumen digesta than control. These studies demonstrated that DFMs could promote better microbial interactions and improve the overall rumen feed digestibility without significantly changing microbial community structures.

The use of *C. beijerinckii* augments the digestion of carbohydrates by increasing the utilization of simple carbohydrates in animal feed within the rumen. *C. beijerinckii* has been frequently isolated from hemicellulose rich environments (Jones and Woods, 1986; Trudeau *et al.,* 1992; Noparat *et al.,* 2011; Thi Hoang *et al.,* 2020). Studies conducted on different *C. beijerinckii* strains revealed a high level of amylase production when grown on starch (Qureshi and Blaschek, 2001; Taguchi *et al.,* 1993). *C. beijerinckii* is frequently found in rumen content globally (Kameshwar *et al*., 2019; Avila and Carvaho, 2019; Thi Hoang *et al*., 2020; Seshadri *et al*., 2018) and is also commonly found in monogastric animals (Vanbelle *et al.,* 1990, Prosekov*et et al.,* 2015). Although it has not been used as a DFM in ruminants, *C. beijerinckii* is a common commensal rumen microorganism.

ASCUS Biosciences conducted a series of experiments in order to obtain a representative sampling of the rumen microbial community in dairy cows under farm-like conditions in the U.S. The full study report is provided in Appendix 018. In two general survey experiments, animals were cannulated and sampling of the rumen was conducted across the different regions over a number of days. In a third study, *C. beijerinckii* ASCUSDY20 along with another native rumen microorganism was administered to lactating dairy cows via injection and rumen sampling conducted over a number of days. In all of the

experiments, the typical abundance of *C. beijerinckii* specifically, in the rumen of dairy cows was found to vary from approximately 0.0001% to 2% of the bacterial population. General observations indicated that all animals were in good health. *C. beijerinckii* ASCUSDY20 inoculation was not observed to have a significant impact on the ruminal microbial community. Taken together, these studies provide corroborative experimental evidence that *C. beijerinckii* is naturally abundant in the rumen of dairy cattle and not associated with any health concerns.

6.4.3 Environmental Occurrence

C. beijerinckii occurs extensively in nature. It can be found in a variety of environments, including soil (Wu *et al.,* 2019; Bhutada and Shrivastava, 2018; Dobbin *et al.,* 1999; Montoya *et al.,* 2000; Abd-Alla *et al.* 2015), insects (Taguchi *et al.,* 1993; Cruden *et al.,* 1987) wastewater (Fonesca *et al.,* 2019; Rosewarne *et al.,* 2013), manure (Ostling and Lindgren. 1991; Scott *et al.,* 2018; An *et al.,* 2014; Pandey *et al.,* 2009; Islas-Espinoza *et al.,* 2012; Lin *et al.,* 2013; Scott and Murano 2007), as well as anaerobic sludge (Fonesca *et al.*, 2016; Pan *et al.,* 2008; Scott and Murano, 2007; Zhao *et al.,* 2011). A *C. beijerinckii* that is capable of coupling dechlorination of pentachlorophenol with Fe(III) reduction has been isolated from rice paddy fields in Zhejiang, China (Xu *et al.,* 2013). Eighteen different strains of *C. beijerinckii* have been deposited in the open collection of the American Type Culture Collection (ATCC) to date. Similarly, a total of 207 different strains of *C. beijerinckii* have been isolated, sequenced, and analyzed in the JGI genome portal to date (https://genome.jgi.doe.gov/portal/). Many strains within this database represent industrial fermentation strains, however, several of the isolates were obtained from rumen content as part of the Hungate 1000 project (http://www.rmgnetwork.org/hungate1000.html; Seshadri *et al.,* 2018*)*.

Clostridium species are extensively used for the industrial production of butanol and acetone from starch-based substrates (Jones and Woods, 1986; Jones and Keis, 1995; Keis *et al*., 2001; Valdez-Vazquez *et al*., 2015). The first strains isolated and developed for large scale production of these solvents were identified as *Clostridium acetobutylicum* but were later assigned to four species, *C. acetobutylicum*, *C. beijerinckii*, *Clostridium saccharoperbutylacetonicum* and *Clostridium saccharobutylicum* (Johnson *et al*., 1997; Keis *et al*., 1995; Wilkinson and Young, 1995; Keis *et al*., 2001). New strains of these species (including *C. beijerinckii*) capable of more efficient industrial production of solvents, particularly acetone, butanol, and ethanol, are still being screened for in environmental samples for industrial applications (Abd-Alla *et al.* 2015). Abd-Alla, *et al.*, for example, isolated 107 *Clostridium* isolates from agriculture soil, several of which were *C. beijerinckii*.

6.4.4 Section Summary

C. beijerinckii occurs widely in the environment and is prevalent as a commensal member of the rumen microbiome. Supplementation of the diet with *C. beijerinckii* ASCUSDY20 will not negatively impact the function of the rumen nor negatively impact the well-being of the animal.

6.5 History of Use in Manufacture of Food and Feed Ingredients

Along with *C. butyricum*, *C. sporogens* and *C. tyrobutyricum*, the species is one of the anaerobic spore forming, butyric acid bacteria reported to spoil foodstuffs, including dairy products, meat products, and fresh and canned vegetables (EFSA, 2005). These butyric acid bacteria have been frequently isolated from milk and cheeses, where *C. tyrobutyricum* is considered the primary cause of the late-blowing effect (Drouin and Lafreniere, 2012; Brandle *et al*., 2016). The expected exposure of Clostridial spores in

milk is < 10^1 – 10^2 spores/gram (Pahlow *et al.* 2003, Queiroz *et al.,* 2018). Use of *C. beijerinckii* ASCUSYDY20 in feed is not expected to increase the load of *C. beijerinckii* spores observed in milk beyond the typically observed values. *Clostridium* spp. are common livestock commensal microorganisms, and thus animal feces are the primary source of *Clostridium* contamination of milk as feces can readily contaminate the cow's udder leading to spores entering the milk (Pahlow *et al.* 2003). While these species are associated with spoilage, they are not generally considered to pose a safety concern to human health (Ghoddusi and Sherburn, 2010). Based on genomic data, *C. beijerinckii* ASCUSDY20 does not contain genes capable of producing botulinum toxins and previous mouse testing supports that the strain is not capable of producing botulinum toxins and thus should not cause human food safety concerns.

C. beijerinckii has been proposed as a downstream biorefinery process to follow fermentation of seaweed for animal feed (Bikker *et al*., 2016). *Ulva lactuca*, a type of green seaweed, can be fractionated and the subsequent liquid fraction can leverage *C. beijerinckii* for fermentative production of chemicals. Similarly, *C. beijerinckii* can also be found in silage. The presence of *Clostridium* spp. in silage is mainly from soil contamination or slurry application and this can lead to contamination of animal feeds and products. It has been reported that the central part of a corn silage bunker silo had less than 10^3 spores of *Clostridium* spp. per gram of silage, whereas the peripheral area had more than 10^6 spores per gram (Queiroz *et al.,* 2018).

Thus, although *C. beijerinckii* and other closely related members of *Clostridium* are typically associated with spoilage in feed and food, they are generally always present in these environments at low abundance (Queiroz *et al.,* 2018). Despite the continuous consumption of these low levels of spores, no deleterious impacts on health are observed (Ghoddusi and Sherburn, 2010).

6.6 Toxigenicity and Pathogenicity

The potential pathogenicity of *Clostridium*, including *C. beijerinckii*, is widely reported in the published literature. Unlike known pathogenic *Clostridium,* such as *C. difficile* and *C. perfringens, C. beijerinckii* is considered an opportunistic pathogen in humans and animals. This classification suggests that *C. beijerinckii* is normally harmless, as it rarely causes disease. The American Type Culture Collection (ATCC) lists *C. beijerinckii* as BSL-1, indicating that it is a low-risk microorganism that poses little to no threat of infection in healthy humans and animals. DSMZ also classifies *C. beijerinckii* as BSL-1.

Large scale genome analysis of both pathogenic and nonpathogenic *Clostridium* has revealed that there were only 169 orthologous gene groups shared by all *Clostridium* strains, and a pangenome of 22,668 genes (Zhou *et al.,* 2014). This finding suggests that *Clostridium* contains a diverse gene pool that enables adaptation to different environments. Many of the Clostridia are normally harmless and ubiquitously found in soil and in the gastrointestinal tract of healthy animals, including humans. Clinical cases are only rarely seen (Moore, and Lacey, 2019). Disease generally occurs when there is some tissue damage to the skin or gastrointestinal tract that results in proliferation of *Clostridium* and opportunistic infection. This bimodal lifestyle, split between a free-living, otherwise harmless existence in the environment and host colonization and pathogenesis is reflected in the genomes of the Clostridia. The spore-forming machinery encoded Clostridial genomes increases resilience and survival in the environment, and the wide array of toxins and degradative enzymes that are encoded assist in nutrient scavenging. Many of

the toxins produced by Clostridia are encoded on large plasmids (Moore,and Lacey, 2019). The genomes of normally harmless *Clostridium* tend to be larger, suggesting that they are generalists that can survive in a range of ecological niches and use a wider variety of substrates for growth (Suen, *et al.* 2007). Different levels of genomic plasticity have been noted amongst Clostridial species, with sequence variation being driven primarily by mobile elements, chromosomal rearrangement, deletions and insertions, and SNPs (Moore and Lacey, 2019). The genomes of true Clostridia (cluster I), including *C. beijerinckii,* were found to be more stable than other clusters of Clostridia, with plasmids playing a large role in determining strain variation. Large conjugative toxin gene carrying plasmids, in particular, often determine the virulence of *Clostridium* isolates (Moore and Lacey, 2019).

The Google Scholar literature search revealed 2,000+ hits when searching for "*Clostridium beijerinckii"* and various forms of the word "toxins" and "toxicity". Google Scholar provided 5,000+ hits when all safety related terms (various forms of the words "toxin", "pathogen", "safety", "infection", "disease", or "mortality") were included. Further investigation of these results revealed that the vast majority of hits (>75%) were related to butanol toxicity, a physiological by-product inhibition common in the industrial production of butanol with *Clostridium beijerinckii.* When these results (butanol-related; -"butanol" added to search criteria) were removed, only 775 hits remained. These hits formed the basis of the *C. beijerinckii* safety summary provided below.

While Clostridia are part of the commensal microbiota and normally harmless, epidemiology studies have implicated some species with human disease, specifically in opportunistic infections. Reports of *C. beijerinckii* causing endophthalmitis secondary to an initial injury have been reported (Newton, *et al.* 1999). *Clostridium* have also been implicated as one of the causative agents of necrotizing enterocolitis in premature infants (EFSA, 2014; Cassir *et al*., 2016; Schönherr-Hellec *et al*., 2018). No studies were identified in the published literature associating *C. beijerinckii* with necrotizing enterocolitis.

To further address the safety of *C. beijerinckii*, neurotoxins and other known *Clostridium*-related toxins were investigated directly by performing an additional literature search based on the Clostridial virulence genes identified using the virulence factor database (VFDB; http://www.mgc.ac.cn/cgi-bin/VFs/compvfs.cgi?Genus=Clostridium; 42 genes) cross referenced with Victor's database. Victor's database includes animal pathogens as well as human pathogens, making it the most appropriate and relevant database to assess animal-related pathogenicity and toxigenicity of *C. beijerinckii* ASCUSDY20. However, VFDB contains more *Clostridium*-specific genes. Thus, both databases were leveraged to identify gene names to use in the literature search. A total of 42 Clostridial virulence genes and the terms "hemolysin" and "neurotoxin" were used in combination with *C. beijerinckii, C. acetobutylicum*, *C. butylicum,* and *C. butyricum* in Google Scholar. These results are reported in Appendix 17, Table 3. Fifty-four results were identified across all four organisms searched, with the bulk of the results (49) arising for *C. butyricum*. Three relevant results were identified for *C. beijerinckii* and are summarized below:

1. "Clostridial genetics: Genetic manipulation of the pathogenic Clostridia" (Kuehne et al., 2019)

   > "If used without the Gram positive replicon, they act as suicide vectors in the Clostridia and have been effectively used in this capacity in studies involving the nonpathogenic species *C. beijerinckii* and *Clostridium autoethanogenum*.

Most recently, CRISPR-gene editing technologies were successfully used in the clostridia. Initially developed in nonpathogenic Clostridia, such as *C. pasteurianum*, *C. beijerinckii*, and *C. cellulolyticum*, this emerging technology was used in 2017 to generate deletion mutants in *C. difficile*."

Although *C. beijerinckii* is mentioned in this article about pathogenic Clostridia, it is only discussed as an example of nonpathogenic Clostridia (see excerpts above).

2. "Development of a reporter system for the study of gene expression for solvent production in *Clostridium beijerinckii* NRRL B592 and *Clostridium acetobutylicum* ATCC 824" (Li, 1998)

   This document is a dissertation discussing the development of a reporter system to control the expression of solvent-producing genes in *C. beijerinckii.* Although it appeared in the search results, it does not discuss pathogenicity of *C. beijerinckii.*

3. "Microbial hazards in the dairy chain: A literature study" (Veen et al., 2015)

   "Most butyric acid bacteria are spoilage microorganisms like *Clostridium butyricum, Clostridium tyrobutyricum,* and *Clostridium beijerinckii*, however, the ability of some strains of *C. butyricum* to produce botulinum toxin makes the detection of this group of microbes in milk important. Control of butyric acid bacterial spore counts in silage is therefore considered important in prevention of surface contamination of teats and eventually to limit spore counts in milk storage tanks."

   Thus, although *C. beijerinckii* is mentioned in this document, it is presented in context of food spoilage rather than pathogenicity and toxicity. Food spoilage and human safety is addressed in Section 6.5 of the Dossier, and question 7 of the AGRN-41 response.

No hits for *C. acetobutylicum* were relevant. However, there were several relevant hits for *C. butyricum.* There are some rare instances of *C. butyricum* causing human disease, including necrotizing enterocolitis in premature infants when associated with very specific risk factors (Howard *et al*., 1977; Sturm *et al*., 1980; Caya and Truant, 2000; Gardner *et al*., 2008; Morowitz *et al*., 2010; EFSA, 2014; Cassir *et al*., 2016). For example, Caya and Truant (2000) reported the diagnosis of 53 infant pediatric patients with Clostridial bacteremia, of which 25.9% cases were identified as being associated with *C. butyricum*. Necrotizing enterocolitis-related lesions were also induced by *C. butyricum* in chicken and quail experimental models (Popoff and Dodin, 1985; Butel *et al*., 1998; Waligora-Dupriet *et al*., 2009). The toxigenic mechanism responsible for the pathogenesis of necrotizing enterocolitis is not fully understood but β-haemolysin production has been proposed as a primary virulence factor (Cassir *et al*., 2015). *C. butyricum* has also been shown to produce type E botulinum toxin (Aureli *et al.,* 1986; Tsukamoto *et al.,* 2002; Hill *et al.,* 2012; Fu *et al.,* 2008; Rovira *et al.,* 2011). The ability of the host to ferment lactose and the production of high levels of butyric acid by intestinal *C. butyricum* are also suggested by other researchers in the development of necrotic lesions (Waligora-Dupriet *et al*., 2009; Azcarate-Peril *et al*., 2011; Cassir *et al*., 2016). Recently, a systematic characterization of necrotizing enterocolitis and control strains was conducted by Schönherr-Hellec *et al*., (2018) suggested the existence of a specific signature associated with pathogenicity and that a unifying causative mechanism for development of the disease may be activation of an innate immune response. The presence of neuraminidase was investigated in several *Clostridium* strains belonging to *C. butyricum, C. difficile,* and *C. beijerinckii* (Popoff and Dodin, 1985). Neurominidase-production has been implicated in the pathogenesis of neonatal necrotizing

enterocolitis. Of the 98 strains tested, including 16 *C. beijerinckii*, only a few *C. butyricum* strains were found to produce neuraminidase.

The pathogenic Clostridial species with the greatest impacts on human and animal health are *C. difficile, C. perfringens, C. tetani, C. botulinum*, and other species that produce botulinum toxins and other neurotoxins (Moore and Lacey, 2019). Cattle, in particular, are primarily affected by botulinum toxins B, C, and D. Type B animal poisonings are typically found in the eastern US and Europe, type C poisoning is typically found in the western US, and type D poisoning is most common in South Africa, South America and Australia (Moeller *et al*., 2007). Humans tend to be impacted by botulinum toxins A, B, E, and F (Moeller *et al.,* 2007). The Clostridial species that produce botulinum toxins are well studied. Botulism, caused by botulinum neurotoxin (BoNT) is most frequently associated with *Clostridium botulinum* but can occasionally arise from *C. butyricum* (Peck, 2002; Cassir *et al.*, 2016). The disease can occur when BoNT-producing *Clostridium* species colonize the intestine or wounds of animals or humans and subsequently produce the toxin, or alternatively, when contaminated foods are ingested in which the toxin has already been formed. No reports of BoNT-producing *C. beijerinckii* were identified in the published literature. However, as mentioned above, a minority of closely-related *C. butyricum* strains harbor the *BoNT/E* gene and are capable of producing botulinum neurotoxin E (Hauser *et al*., 1992; Peck, 2002; Dupuy *et al*., 2006; Cassir *et al*., 2015; EFSA, 2011; Ghoddusi and Sherburn, 2010). The operon harboring the *BoNT/E* gene in *C. butyricum* is reportedly similar to that carried by type II E toxin-producing *C. botulinum* strains consistent with horizontal transfer events and recombinant events mediated by mobile genetic elements. Toxigenic *C. butyricum* have been responsible for a number of cases of infantile and infantile-like botulism arising from the production of the toxin in the intestine after germination and colonization of *C. butyricum* (*e.g*., Abe *et al*., 2008; Aureli *et al*., 1986; Fenicia *et al*., 1999 and Dykes *et al.,* 2015). The reports of infantile-like botulism are generally isolated cases (single or few cases) in immunocompromised individuals (*e.g*., following intestinal surgery). Likewise, cases of food-borne botulism from the ingestion of *C. butyricum*-derived toxin type E are rare (Anniballi *et al*., 2002; Peck, 2002). The first report of an outbreak of food-borne botulism caused by toxin type E produced by *C. butyricum* was in China in 1994, when 6 people became ill after consuming a home-made salted and fermented paste of soybeans and wax gourds (Meng *et al*., 1997 and 1999). Subsequently, *C. butyricum* has been implicated in two earlier outbreaks of botulism following the consumption of soybeans in China and an incident in which 34 students contracted botulism after eating gram-flour based crisps in India (Peck, 2002). Thus, although *Clostridium* can produce medically important toxins, neurotoxins are rarely found and have not been reported in *C. beijerinckii.* Tetanus toxin (*Clostridium tetani*) and botulinum toxin (*Clostridium botulinum*) have not been associated with *C. beijerinckii.* Type E botulinum toxin has been observed in rare cases in *C. butyricum,* but it has not been associated with *C. beijerinckii.*

Overall, the available data indicate that *C. beijerinckii* strains are not associated with botulinum toxin or other neurotoxins, and only rarely cause infection in humans and animals. Under normal circumstances, it is a harmless organism. These data are consistent with the whole genome analyses (see Part 2.1.8) which confirmed the absence of the botulinum toxin and tetanus toxin biosynthetic operons.

6.6.1 Summary

Overall, the available information indicates that *C. beijerinckii* is a prevalent organism in the environment and in the microbiome of animals. Although generally harmless, it can be an opportunistic pathogen and has been associated with infections in immunocompromised humans and animals. Despite the wide prevalence and exposure to *C. beijerinckii* in the environment and food, the invasive infection caused by *C. beijerinckii* is rare (see Appendix 17). As indicated in Part 2.1.8, interrogation of the whole genome sequence of *C. beijerinckii* ASCUSDY20 did not reveal the presence of any genetic element sequences that code for virulence factors or protein toxins. *C. beijerinckii* is not known to produce neurotoxins.

6.7 Studies in Target Animals

The determination that *C. beijerinckii* ASCUSDY20 is GRAS under the intended conditions is based on product-specific characterization data together with the body of information in the published literature. The organism is a commensal rumen organism.

Three investigative studies in which dairy cattle were inoculated with *C. beijerinckii* ASCUSDY20 were conducted by ASCUS Biosciences corroborate the target animal safety determination. The first study is published (Goetz, et al. 2021). *C. beijerinckii* ASCUSDY20 was fed to twenty-three lactating primiparous and multiparous Holstein cows for 60 days. Another twenty-three cows served as the control and were fed carrier with no cells daily. No adverse effects were observed, providing experimental evidence of the safety of *C. beijerinckii* ASCUSDY20 under the intended conditions of use as a direct fed microbial.

The two unpublished studies, summarized in turn below, were of short duration and were designed primarily to assess the potential value of *C. beijerinckii* ASCUSDY20 and other microorganisms as potential direct fed microbials. In both studies, *C. beijerinckii* ASCUSDY20 was administered via ruminal cannulation in combination with at least one other microorganism. Overall, the study findings provide corroborative evidence that *C. beijerinckii* ASCUSDY20 is well-tolerated and without adverse effects but are of limited relevance to the assessment of safety.

6.7.1 Study DUS1601 (Unpublished Study Report – Appendix 019)

In the first study, 16 multiparous Holstein cows were individually housed for a total of 52 days at DairyExperts (Tulare, CA). Animals underwent ruminal cannulation surgery followed by a 10-day recovery and adaptation period. After this time, the cows were allocated at random to one of 2 treatment groups (8 cows/treatment; 1 cow/replicate) and administered either buffer (control) or buffer containing a selection of microorganisms including *C. beijerinckii* ASCUSDY20 once daily via ruminal cannulation for 32 days. Cows were monitored for a further 10 days after the last inoculation day. Observations included feed intake, body weight, milk yield, rumen digesta microbial content and pH, and fecal analysis. No adverse effects were reported for any of the variables measured over the duration of the study. Overall, the findings of the study corroborate the safety of *C. beijerinckii* ASCUSDY20 for dairy cattle.

6.7.2 Study DUS1701 (Unpublished Study Report – Appendix 020)

In the second study, 32 Holstein cows approximately 100 days in milk were assigned to one of 3 treatment groups (8 cows/treatment; 1 cow/replicate; mean days in milk, approximately 100). Cows were administered a buffer containing either 2 (treatment group 1), 3 (treatment group 2) or no (treatment group 3; control) microorganisms once daily via direct injection into the rumen for 28 days.

The microorganisms fed to the cows in treatment groups 1 and 2 included *C. beijerinckii* ASCUSDY20. Fecal samples were taken at Days 1, 8, 16, 24 and 28 and analyzed for neutral detergent fiber (NDF), acid detergent fiber (ADF) and DM content. Rumen contents also were sampled from each cow at Days 1, 8, 18, 24 and 28. From Day -7 to Day 38 of the study, observations included milk yield, general health and clinical udder evaluation.

Abnormal clinical udder findings and abnormal clinical health observations were considered minimal, incidental and not related to treatment for the duration of the study. No adverse effects were reported in any of the other variables measured for the duration of the study. Overall, the findings of the study corroborate the safety of *C. beijerinckii* ASCUSDY20 for dairy cattle.

6.8 Summary and Critical Evaluation of Target Animal Safety

C. beijerinckii is a commensal bacteria in the gut of humans and animals. It occurs widely in soil and is commonly found in food. No reports of toxigenicity or pathogenicity associated with *C. beijerinckii* were identified in the published literature. The species is not known to produce neurotoxins, and is typically a harmless microorganism. However, a minority of strains of related species *C. butyricum* is capable of producing botulinum-type toxin E, and there are occasional reports of toxigenicity and pathogenicity. ASCUS Biosciences has conducted an assessment of *C. beijerinckii* ASCUSDY20 and confirmed the absence of any genes encoding for toxin production or other virulence factors known to be associated with pathogenicity (see Part 2.1.8). Furthermore, the susceptibility of *C. beijerinckii* ASCUSDY20 strains to antibiotics of veterinary and pharmaceutical relevance, and the absence of antimicrobial production has been demonstrated (see Parts 2.1.6 and 2.1.7, and Appendices 004 and 005). *C. beijerinckii* ASCUSYDY20 has also been fed to twenty-three lactating, Holstein cows for 60 days in a controlled academic setting. No adverse health effects were observed. Collectively, these data indicate that *C. beijerinckii* ASCUSDY20 spray dried powder (the notified substance) should not be associated with any safety concerns for dairy cattle under the intended conditions of use as a direct fed microbial.

6.9 Summary and Critical Evaluation of Human Food Safety

As mentioned in Part 3.2, no transfer of viable *C. beijerinckii* ASCUSDY20 from the rumen to milk or other edible species is anticipated under the conditions of intended use as a direct fed microbial in the feed of dairy cattle. Furthermore, the strain has been unambiguously characterized as *C. beijerinckii* and whole genome sequence analysis indicates the absence of any genetic element sequences that code for virulence factors or protein toxins (see Part 2.1.8). The absence of pathogenicity or toxigenicity is supported by the ubiquitous nature of *C. beijerinckii* and its natural occurrence in the rumen and gastrointestinal tract of animals. Under normal circumstances, *C. beijerinckii* is a harmless organism that rarely causes disease. Taken together, these data indicate that *C. beijerinckii* ASCUSDY20 spray dried powder should not be associated with any human food safety concerns under the intended conditions of use as a direct fed microbial in the feed of dairy cattle.

In this safety assessment we identified, discussed and placed into context data and information that are, or may appear to be inconsistent with the GRAS status (21 CFR 570.250(c)(1)). Based on the preponderance of evidence, ASCUS' conclusion of safety is scientifically justified.

ATTACHMENT 15

AGRN 41 *Clostridium beijeirinckii* ASCUSDY20 GRAS Dossier Amendment

(Revised) Dossier Appendix 17: Literature Search Done in Google Scholar

A literature search was conducted by [redacted] (b) (4) on April 13, 2021 in order to identify potential information related to the safety and utility of *Clostridium beijerinckii* as a direct fed microbial (DFM) strain for cattle. The overall search strategy is described in Table 1. The Google Scholar database was searched using the keyword/search terms listed in Table 2. The search was verified by reviewing the primary hits from a Google Scholar search.

Considering the number of articles identified (>500), the search results were reviewed to identify articles representative of the body of available data relating to the safety of the genus. In particular, the review focused on identifying comprehensive reviews, widely cited articles and recent articles of relevance.

Nomenclature

The NCBI database was reviewed as well as published literature to identify all recognized taxonomic classification of the species Strains falling in this species have previously been classified as *Clostridium acetobutylicum* and *Clostridium butylicum*. Moreover, data on the closely related species, *Clostridium butyricum* was also considered relevant. The relevant database was searched using the keyword/search terms listed in Tables 2A, B, C, and D. There were many duplicates identified between the different searches on account of the different nomenclature being widely acknowledged in publications, and of there being a number of pertinent reviews on closely related *Clostridia* species. Considering the relatively large body of available information on closely related *Clostridia* species, the objective of the search was to identify a representative body of information on the species.

We also performed a literature search based on the Clostridial virulence genes identified using the virulence factor database (http://www.mgc.ac.cn/cgi-bin/VFs/compvfs.cgi?Genus=Clostridium).
A total number of 42 Clostridial virulence genes and terms “hemolysin” and “neurotoxin” in combination with *C. beijerinckii, C. acetobutylicum*, *C. butylicum,* and *C. butyricum* were searched in Google Scholar. The number of results are reported in Table 3.

Table 1: Literature Search and Selection Strategy		
Step 1	Records identified using selected literature databases	Google Scholar
	Total records (titles/abstracts) identified through electronic search (exclude patents and citations)	
Step 2	Exclude duplicates by searching Google Scholar using conditional terms	
Step 3	Screen titles/abstracts and exclude obviously irrelevant records	
Step 4	Review full texts and assess for relevance and eligibility for inclusion	

Table 2A: Topic Specific Search Terms using Species [*Clostridium beijerinckii*]

	Google Scholar Search		Google Scholar Search (exclude duplicates)	
	Input terms in search box	Results	Input terms in search box	Results
Search strategy for safety of species [Safety Search]	“Clostridium beijerinckii”+”tox”	72	“Clostridium beijerinckii”+”tox” OR “toxin” OR “toxins” OR “toxicity” OR “toxicities”	5,330
	“Clostridium beijerinckii”+”toxin”	708		
	“Clostridium beijerinckii”+”toxins”	571		
	“Clostridium beijerinckii”+”toxicity”	2,710		

	"Clostridium beijerinckii"+"toxicities"	75	OR "pathogen" OR "pathogens" OR "safe" OR "safety" OR "infection" OR "infections" OR "disease" OR "diseases" OR "mortality" OR "mortalities"	
	"Clostridium beijerinckii"+"pathogen"	1,010		
	"Clostridium beijerinckii"+"pathogens"	1,320		
	"Clostridium beijerinckii"+"safe"	913		
	"Clostridium beijerinckii"+"safety"	1,210		
	"Clostridium beijerinckii"+"infection"	1,300		
	"Clostridium beijerinckii"+"infections"	864		
	"Clostridium beijerinckii"+"disease"	1,450		
	"Clostridium beijerinckii"+"diseases"	1,240		
	"Clostridium beijerinckii"+"mortality"	296		
	"Clostridium beijerinckii"+"mortalities"	12		
Search strategy for safety Clostridium beijerinckii [Target Animal]	"Clostridium beijerinckii"+"cattle"	729	"Clostridium beijerinckii"+"cattle" OR "cow" OR "cows" OR "bovine" OR "bovines" OR "ruminant" OR "ruminants" OR "calves" OR "calf"	2,130
	"Clostridium beijerinckii"+"cow"	657		
	"Clostridium beijerinckii"+"cows"	213		
	"Clostridium beijerinckii"+"bovine"	1,050		
	"Clostridium beijerinckii"+"bovines"	11		
	"Clostridium beijerinckii"+"ruminant"	182		
	"Clostridium beijerinckii"+"ruminants"	171		
	"Clostridium beijerinckii"+"calves"	61		
	"Clostridium beijerinckii"+"calf"	132		
Search strategy for history of use of Clostridium beijerinckii	"Clostridium beijerinckii"+"food"	5,130	"Clostridium beijerinckii"+"food" OR "foods" OR "feed" OR "feeds"	5,750
	"Clostridium beijerinckii"+"foods"	984		
	"Clostridium beijerinckii"+ "feed"	2,750		
	"Clostridium beijerinckii"+"feeds"	506		

Search: Must include quotes. Quotes ensure words being included in the search, although the words are not guaranteed to be in the found results. Exclude patents and citations.

Table 2B: Topic Specific Search Terms using Species [*Clostridium acetobutylicum*]

	Google Scholar Search		Google Scholar Search (exclude duplicates)	
	Input terms in search box	Results	Input terms in search box	Results
Search strategy for safety of species [Safety Search]	"Clostridium acetobutylicum"+"tox"	226	"Clostridium acetobutylicum"+"tox" OR "toxin" OR "toxins" OR "toxicity" OR "toxicities" OR "pathogen" OR "pathogens" OR "safe"	13,400
	"Clostridium acetobutylicum"+"toxin"	2,210		
	"Clostridium acetobutylicum"+"toxins"	1,640		
	"Clostridium acetobutylicum"+"toxicity"	6,070		
	"Clostridium acetobutylicum"+"toxicities"	206		
	"Clostridium acetobutylicum"+"pathogen"	3,040		

	“Clostridium acetobutylicum”+”pathogens”	3,470	OR “safety” OR “infection” OR “infections” OR “disease” OR “diseases” OR “mortality” OR “mortalities”	
	“Clostridium acetobutylicum”+”safe”	1,960		
	“Clostridium acetobutylicum”+”safety”	2,480		
	“Clostridium acetobutylicum”+”infection”	3,910		
	“Clostridium acetobutylicum”+”infections”	2,250		
	“Clostridium acetobutylicum”+”disease”	4,180		
	“Clostridium acetobutylicum”+”diseases”	3,260		
	“Clostridium acetobutylicum”+”mortality”	832		
	“Clostridium acetobutylicum”+”mortalities”	38		
Search strategy for safety Clostridium acetobutylicum [Target Animal]	“Clostridium acetobutylicum”+”cattle”	1,400	“Clostridium acetobutylicum”+”cattle” OR “cow” OR “cows” OR “bovine” OR “bovines” OR “ruminant” OR “ruminants” OR “calves” OR “calf”	5,560
	“Clostridium acetobutylicum”+”cow”	1,110		
	“Clostridium acetobutylicum”+”cows”	420		
	“Clostridium acetobutylicum”+”bovine”	3,200		
	“Clostridium acetobutylicum”+”bovines”	44		
	“Clostridium acetobutylicum”+”ruminant”	417		
	“Clostridium acetobutylicum”+”ruminants”	516		
	“Clostridium acetobutylicum”+”calves”	157		
	“Clostridium acetobutylicum”+”calf”	503		
Search strategy for history of use of Clostridium acetobutylicum	“Clostridium acetobutylicum”+”food”	10,800	“Clostridium acetobutylicum”+”food” OR “foods” OR “feed” OR “feeds”	12,900
	“Clostridium acetobutylicum”+”foods”	2,100		
	“Clostridium acetobutylicum”+”feed”	6,510		
	“Clostridium acetobutylicum”+”feeds”	1,330		

Search: Must include quotes. Quotes ensure words being included in the search, although the words are not guaranteed to be in the found results. Exclude patents and citations.

Table 2C: Topic Specific Search Terms using Species [*Clostridium butylicum*]

	Google Scholar Search		Google Scholar Search (exclude duplicates)	
	Input terms in search box	Results	Input terms in search box	Results
Search strategy for safety of species [Safety Search]	“Clostridium butylicum”+”tox”	9	“Clostridium butylicum”+”tox” OR “toxin” OR “toxins” OR “toxicity” OR “toxicities” OR “pathogen” OR “pathogens” OR “safe” OR “safety” OR “infection” OR “infections” OR “disease” OR	536
	“Clostridium butylicum”+”toxin”	97		
	“Clostridium butylicum”+”toxins”	62		
	“Clostridium butylicum”+”toxicity”	4,950		
	“Clostridium butylicum”+”toxicities”	4		
	“Clostridium butylicum”+”pathogen”	78		
	“Clostridium butylicum”+”pathogens”	87		
	“Clostridium butylicum”+”safe”	90		
	“Clostridium butylicum”+”safety”	103		

	“Clostridium butylicum”+”infection”	133	“diseases” OR “mortality” OR “mortalities”	
	“Clostridium butylicum”+”infections”	87		
	“Clostridium butylicum”+”disease”	139		
	“Clostridium butylicum”+”diseases”	128		
	“Clostridium butylicum”+”mortality”	38		
	“Clostridium butylicum”+”mortalities”	0		
Search strategy for safety Clostridium butylicum [Target Animal]	“Clostridium butylicum”+”cattle”	92	“Clostridium butylicum”+”cattle” OR “cow” OR “cows” OR “bovine” OR “bovines” OR “ruminant” OR “ruminants” OR “calves” OR “calf”	285
	“Clostridium butylicum”+”cow”	75		
	“Clostridium butylicum”+”cows”	30		
	“Clostridium butylicum”+”bovine”	144		
	“Clostridium butylicum”+”bovines”	1		
	“Clostridium butylicum”+”ruminant”	11		
	“Clostridium butylicum”+”ruminants”	34		
	“Clostridium butylicum”+”calves”	24		
	“Clostridium butylicum”+”calf”	41		
Search strategy for history of use of Clostridium butylicum	“Clostridium butylicum”+”food”	475	“Clostridium butylicum”+”food” OR “foods” OR “feed” OR “feeds”	546
	“Clostridium butylicum”+”foods”	104		
	“Clostridium butylicum”+”feed”	615		
	“Clostridium butylicum”+”feeds”	60		

Search: Must include quotes. Quotes ensure words being included in the search, although the words are not guaranteed to be in the found results. Exclude patents and citations.

Table 2D: Topic Specific Search Terms using Species [*Clostridium butyricum*]

	Google Scholar Search		Google Scholar Search (exclude duplicates)	
	Input terms in search box	Results	Input terms in search box	Results
Search strategy for safety of species [Safety Search]	“Clostridium butyricum”+”tox”	360	“Clostridium butyricum”+”tox” OR “toxin” OR “toxins” OR “toxicity” OR “toxicities” OR “pathogen” OR “pathogens” OR “safe” OR “safety” OR “infection” OR “infections” OR “disease” OR “diseases” OR “mortality” OR “mortalities”	14,500
	“Clostridium butyricum”+”toxin”	3,680		
	“Clostridium butyricum”+”toxins”	3,170		
	“Clostridium butyricum”+”toxicity”	4,510		
	“Clostridium butyricum”+”toxicities”	300		
	“Clostridium butyricum”+”pathogen”	4,420		
	“Clostridium butyricum”+”pathogens”	5,620		
	“Clostridium butyricum”+”safe”	3,330		
	“Clostridium butyricum”+”safety”	4,920		
	“Clostridium butyricum”+”infection”	5,880		
	“Clostridium butyricum”+”infections”	4,190		
	“Clostridium butyricum”+”disease”	8,570		

	“Clostridium butyricum”+”diseases”	7,180		
	“Clostridium butyricum”+”mortality”	2,970		
	“Clostridium butyricum”+”mortalities”	233		
Search strategy for safety Clostridium butyricum [Target Animal]	“Clostridium butyricum”+”cattle”	2,280	“Clostridium butyricum”+”cattle” OR “cow” OR “cows” OR “bovine” OR “bovines” OR “ruminant” OR “ruminants” OR “calves” OR “calf”	6,390
	“Clostridium butyricum”+”cow”	2,050		
	“Clostridium butyricum”+”cows”	937		
	“Clostridium butyricum”+”bovine”	2,910		
	“Clostridium butyricum”+”bovines”	85		
	“Clostridium butyricum”+”ruminant”	635		
	“Clostridium butyricum”+”ruminants”	700		
	“Clostridium butyricum”+”calves”	580		
	“Clostridium butyricum”+”calf”	581		
Search strategy for history of use of Clostridium butyricum	“Clostridium butyricum”+”food”	13,400	“Clostridium butyricum”+”food” OR “foods” OR “feed” OR “feeds”	14,900
	“Clostridium butyricum”+”foods”	4,290		
	“Clostridium butyricum”+“feed”	7,330		
	“Clostridium butyricum”+”feeds”	1,640		

Search: Must include quotes. Quotes ensure words being included in the search, although the words are not guaranteed to be in the found results. Exclude patents and citations.

Table 3

Keywords/search terms [Database: Google Scholar]										
Species	Clostridium virulence factor groups		Input terms in search box	Dispalyed Counts❖	Retrievable Counts◆	With Combination of the Keywords ₸	Combined (dereplicated by titles)	Results containing pathogen keywords [A]	Results containing pathogen keywords and animal keywords [B]	Final relevant results
Clostridium beijerinckii	Adherence factors		"Clostridium beijerinckii"+"cbpA" OR "CD0873" OR "CD2831" OR "CD3246" OR "cna" OR "cwp66" OR "cwp84" OR "cwpV" OR "fbpA" OR "fbp68" OR "groEL" OR "slpA"	392	388	16	118	57	5	3
	Exoenzyme factors		"Clostridium beijerinckii"+"zmp1"	2	2	0				
	Regulation factors		"Clostridium beijerinckii"+"virS" OR "virR"	39	29	0				
	Toxin factors (2 searches due to terms were too long)	search 1	"Clostridium beijerinckii"+"cloSI" OR "plc" OR "cpb2" OR "atx" OR "tcnA" OR "cpe" OR "cdtA" OR "cdtB" OR "entA" OR "entC" OR "entD" OR "entB" OR "Hemolysin"	319	310	63				
		search 2	"Clostridium beijerinckii"+"colA" OR "nagH" OR "nagI" OR "nagJ" OR "nagK" OR "nagL" OR "pfoA" OR "nanH" OR "nanI" OR "nanJ" OR "tetX" OR "toxA" OR "toxB"	153	130	3				
	neurotoxin		"Clostridium beijerinckii"+"neurotoxin" OR "neurotoxins"	174	162	49				
Clostridium acetobutylicum	Adherence factors (2 searches due to too many outputs)	search 1	"Clostridium acetobutylicum"+"cbpA" OR "CD0873" OR "CD2831" OR "CD3246" OR "cna" OR "cwp66" OR "cwp84" OR "cwpV"	513	507	33	322	128	14	2
		search 2	"Clostridium acetobutylicum"+"fbpA" OR "fbp68" OR "groEL" OR "slpA"	909	910	28				
	Exoenzyme factors		"Clostridium acetobutylicum"+"zmp1"	7	7	0				
	Regulation factors		"Clostridium acetobutylicum"+"virS" OR "virR"	125	115	0				
	Toxin factors (2 searches due to terms were too long)	search 1	"Clostridium acetobutylicum"+"cloSI" OR "plc" OR "cpb2" OR "atx" OR "tcnA" OR "cpe" OR "cdtA" OR "cdtB" OR "entA" OR "entC" OR "entD" OR "entB" OR "Hemolysin"	976	929	185				
		search 2	"Clostridium acetobutylicum"+"colA" OR "nagH" OR "nagI" OR "nagJ" OR "nagK" OR "nagL" OR "pfoA" OR "nanH" OR "nanI" OR "nanJ" OR "tetX" OR "toxA" OR "toxB"	435	400	6				
	neurotoxin		"Clostridium acetobutylicum"+"neurotoxin" OR "neurotoxins"	402	379	105				
Clostridium butylicum	Adherence factors		"Clostridium butylicum"+"cbpA" OR "CD0873" OR "CD2831" OR "CD3246" OR "cna" OR "cwp66" OR "cwp84" OR "cwpV" OR "fbpA" OR "fbp68" OR "groEL" OR "slpA"	24	24	1	14	4	0	0
	Exoenzyme factors		"Clostridium butylicum"+"zmp1"	0	0	0				
	Regulation factors		"Clostridium butylicum"+"virS" OR "virR"	1	1	0				
	Toxin factors (2 searches due to terms were too long)	search 1	"Clostridium butylicum"+"cloSI" OR "plc" OR "cpb2" OR "atx" OR "tcnA" OR "cpe" OR "cdtA" OR "cdtB" OR "entA" OR "entC" OR "entD" OR "entB" OR "Hemolysin"	34	34	9				
		search 2	"Clostridium butylicum"+"colA" OR "nagH" OR "nagI" OR "nagJ" OR "nagK" OR "nagL" OR "pfoA" OR "nanH" OR "nanI" OR "nanJ" OR "tetX" OR "toxA" OR "toxB"	17	18	0				
	neurotoxin		"Clostridium butylicum"+"neurotoxin" OR "neurotoxins"	25	14	4				
Clostridium butyricum	Adherence factors		"Clostridium butyricum"+"cbpA" OR "CD0873" OR "CD2831" OR "CD3246" OR "cna" OR "cwp66" OR "cwp84" OR "cwpV" OR "fbpA" OR "fbp68" OR "groEL" OR "slpA"	328	324	27	296	166	97	49
	Exoenzyme factors		"Clostridium butyricum"+"zmp1"	2	0	0				
	Regulation factors		"Clostridium butyricum"+"virS" OR "virR"	70	60	0				
	Toxin factors (2 searches due to terms were too long)	search 1	"Clostridium butyricum"+"cloSI" OR "plc" OR "cpb2" OR "atx" OR "tcnA" OR "cpe" OR "cdtA" OR "cdtB" OR "entA" OR "entC" OR "entD" OR "entB" OR "Hemolysin"	819	790	181				
		search 2	"Clostridium butyricum"+"colA" OR "nagH" OR "nagI" OR "nagJ" OR "nagK" OR "nagL" OR "pfoA" OR "nanH" OR "nanI" OR "nanJ" OR "tetX" OR "toxA" OR "toxB"	425	360	3				
	neurotoxin*		Clostridium butyricum+"neurotoxin" OR "neurotoxins"+"cow" OR "cows" OR "cattle" OR "ruminant" OR "ruminants" OR "bovine" OR "bovines"	569	580	114				

* Search "Clostridium butyricum"+"neurotoxin" alone produced 1330 results. Google Scholar does not allow the download beyond 1000 results. Therefore the search terms were altered for ruminants specific.

❖Number of results displayed on the first page under the search field. It is a number of estimation.

◆The retrievable counts are the number of results that were actually obtained in pdf or electronic form. Only results in English (English title at the very minimum) are retrieved.

₸ Must contain the second half of the species names (eg., beijerinckii) and at least one of the conditional terms connected with "OR".

A. pathogen keywords are any words containing 'pathogen', 'tox', 'infect', 'diseas', 'bacteremia'.

B. animal keywords are any words containing 'homo', 'patient', 'man', 'woman', 'men', 'women', 'male', 'female', 'child', 'infant' , 'cow', 'ruminant', 'bovine', 'cattle', 'calf', 'calves', 'animal', 'mammal'.