Supplemental Table S3. Table of gene orthologs in JCVI SC001 across the available P. gingivalis genomes.

Reference Gene Name	Reference Locus Tag	Reference Genome	Query Gene Name	Query Genome	Locus Tag	Coordinates	% ID	Bit Score	E-value
MiaB-like tRNA modifying enzyme	Pgjcvi_00001	PG JCVI SC001	MiaB-like tRNA modifying enzyme	PG W83	PG2221	1, 444	99.8	891	0
MiaB-like tRNA modifying enzyme	Pgjcvi_00001	PG JCVI SC001	putative Fe-S oxidoreductases	PG ATCC 33277	PGN_2085	1, 444	99.1	886.3	0
MiaB-like tRNA modifying enzyme	Pgjcvi_00001	PG JCVI SC001	MiaB-like tRNA modifying enzyme	PG TDC60	PGTDC60_2248	4, 447	99.1	886.7	0
Lauroyl/myristoyl acyltransferase	Pgjcvi_00002	PG JCVI SC001	acyltransferase	PG TDC60	PGTDC60_2249	1, 305	99	611.7	0
Lauroyl/myristoyl acyltransferase	Pgjcvi_00002	PG JCVI SC001	acyltransferase, HtrB/MsbB family	PG W83	PG2222	1, 305	98.7	609.4	0
Lauroyl/myristoyl acyltransferase	Pgjcvi_00002	PG JCVI SC001	probable acetyltransferase	PG ATCC 33277	PGN_2086	1, 287	97.6	570.5	0
Predicted glycosyltransferases	Pgjcvi_00003	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG2223	1, 322	99.7	648.7	0
Predicted glycosyltransferases	Pgjcvi_00003	PG JCVI SC001	glycosyltransferase	PG ATCC 33277	PGN_2087	1, 322	99.1	647.5	0
Predicted glycosyltransferases	Pgjcvi_00003	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_2250	1, 336	98.8	671.8	0
hypothetical protein	Pgjcvi_00004	PG JCVI SC001	hypothetical protein	PG W83	PG2224	1, 185	100	370.5	0
hypothetical protein	Pgjcvi_00004	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2251	1, 198	100	395.2	0
hypothetical protein	Pgjcvi_00004	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2088	1, 198	99	391.7	0
hypothetical protein	Pgjcvi_00005	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2089	1, 97	99	189.9	0
hypothetical protein	Pgjcvi_00005	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2252	1, 98	99	191.8	0
hypothetical protein	Pgjcvi_00005	PG JCVI SC001	hypothetical protein	PG W83	PG2225	1, 88	98.9	172.2	1.00E-41
hypothetical protein	Pgjcvi_00006	PG JCVI SC001	hypothetical protein	PG W83	PG2226	1, 740	98.9	1476.1	0
hypothetical protein	Pgjcvi_00006	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2090	1, 740	98.8	1468	0
hypothetical protein	Pgjcvi_00006	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2253	1, 721	98.2	1430.6	0
hypothetical protein	Pgjcvi_00007	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2091	1, 218	99.5	432.6	0
hypothetical protein	Pgjcvi_00007	PG JCVI SC001	hypothetical protein	PG W83	PG2227	1, 218	99.5	431.4	0
hypothetical protein	Pgjcvi_00007	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2254	1, 218	99.1	428.7	0
chromosomal replication initiator protein DnaA	Pgjcvi_00008	PG JCVI SC001	chromosomal replication initiator protein DnaA	PG ATCC 33277	PGN_0001	1, 473	100	937.6	0
chromosomal replication initiator protein DnaA	Pgjcvi_00008	PG JCVI SC001	chromosomal replication initiation protein	PG W83	PG0001	1, 473	100	937.6	0
chromosomal replication initiator protein DnaA	Pgjcvi_00008	PG JCVI SC001	chromosomal replication initiation protein	PG TDC60	PGTDC60_0001	1, 473	99.6	932.2	0
N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)	Pgjcvi_00009	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0002	1, 190	100	396.7	0
N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)	Pgjcvi_00009	PG JCVI SC001	hexapeptide transferase family protein	PG TDC60	PGTDC60_0002	1, 190	100	396.7	0
N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)	Pgjcvi_00009	PG JCVI SC001	hexapeptide transferase family protein	PG W83	PG0002	1, 190	99.5	396.4	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00010	PG JCVI SC001	hypothetical protein	PG W83	PG0003	1, 339	100	694.1	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00010	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0003	1, 339	99.4	688.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00010	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0003	1, 320	99.1	652.9	0
NAD-dependent protein deacetylases, SIR2 family	Pgjcvi_00011	PG JCVI SC001	NAD-dependent deacetylase	PG TDC60	PGTDC60_0004	1, 232	100	472.2	0
NAD-dependent protein deacetylases, SIR2 family	Pgjcvi_00011	PG JCVI SC001	putative nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase	PG ATCC 33277	PGN_0004	1, 234	99.6	474.6	0
NAD-dependent protein deacetylases, SIR2 family	Pgjcvi_00011	PG JCVI SC001	NAD-dependent deacetylase	PG W83	PG0004	1, 234	99.6	474.6	0
Predicted phosphohydrolases	Pgjcvi_00012	PG JCVI SC001	hypothetical protein	PG W83	PG0005	1, 384	99.5	768.1	0
Predicted phosphohydrolases	Pgjcvi_00012	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0005	1, 384	99.5	768.1	0
Predicted phosphohydrolases	Pgjcvi_00012	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0005	1, 384	99.2	767.7	0
putative efflux protein, MATE family	Pgjcvi_00013	PG JCVI SC001	putative Na+driven multidrug efflux pump	PG ATCC 33277	PGN_0006	1, 459	99.8	884.8	0
putative efflux protein, MATE family	Pgjcvi_00013	PG JCVI SC001	MATE efflux family protein	PG W83	PG0006	1, 442	99.3	853.2	0
putative efflux protein, MATE family	Pgjcvi_00013	PG JCVI SC001	putative Na+ driven multidrug efflux pump	PG TDC60	PGTDC60_0006	1, 459	99.3	880.9	0
Protein of unknown function (DUF1661).	Pgjcvi_00016	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2058	1, 43	65.1	53.9	5.80E-06
Protein of unknown function (DUF1661).	Pgjcvi_00016	PG JCVI SC001	hypothetical protein	PG W83	PG2064	1, 42	61.9	50.8	4.90E-05
Protein of unknown function (DUF1661).	Pgjcvi_00016	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0213	1, 64	46.9	52	2.20E-05
ATPases with chaperone activity, ATP-binding subunit	Pgjcvi_00017	PG JCVI SC001	ATP-dependent Clp protease ATP-binding subunit ClpC	PG ATCC 33277	PGN_0008	1, 859	99.5	1657.5	0
ATPases with chaperone activity, ATP-binding subunit	Pgjcvi_00017	PG JCVI SC001	ATP-dependent Clp protease, ATP-binding subunit ClpC	PG W83	PG0010	1, 859	99.5	1657.9	0
ATPases with chaperone activity, ATP-binding subunit	Pgjcvi_00017	PG JCVI SC001	ATP-dependent Clp protease, ATP-binding subunit ClpC	PG TDC60	PGTDC60_0010	1, 859	98.7	1647.5	0
Beta-glucosidase-related glycosidases	Pgjcvi_00018	PG JCVI SC001	glycosyl hydrolase family 3	PG ATCC 33277	PGN_0009	1, 1003	99.5	1978.4	0
Beta-glucosidase-related glycosidases	Pgjcvi_00018	PG JCVI SC001	glycosyl hydrolase, group 3 family protein	PG TDC60	PGTDC60_0011	1, 1003	99.5	1979.1	0
Beta-glucosidase-related glycosidases	Pgjcvi_00018	PG JCVI SC001	glycosyl hydrolase, family 3	PG W83	PG0011	1, 1003	99.2	1973.4	0
Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase	Pgjcvi_00019	PG JCVI SC001	L-threonine-O-3-phosphate decarboxylase, putative	PG W83	PG0012	1, 342	100	698	0
Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase	Pgjcvi_00019	PG JCVI SC001	L-threonine-O-3-phosphate decarboxylase	PG TDC60	PGTDC60_0012	1, 342	100	698	0
Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase	Pgjcvi_00019	PG JCVI SC001	probable L-threonine-O-3-phosphate decarboxylase	PG ATCC 33277	PGN_0010	1, 342	99.7	697.6	0
Phosphosulfolactate phosphohydrolase and related enzymes	Pgjcvi_00020	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0011	1, 256	98.8	508.4	0
Phosphosulfolactate phosphohydrolase and related enzymes	Pgjcvi_00020	PG JCVI SC001	hypothetical protein	PG W83	PG0013	1, 256	98.4	507.7	0
Phosphosulfolactate phosphohydrolase and related enzymes	Pgjcvi_00020	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0013	1, 256	98.4	509.2	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00021	PG JCVI SC001	two-component system response regulator	PG ATCC 33277	PGN_0012	1, 449	99.1	865.9	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00021	PG JCVI SC001	sigma-54 dependent DNA-binding response regulator	PG TDC60	PGTDC60_0014	1, 449	99.1	865.5	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00021	PG JCVI SC001	sigma-54 dependent DNA-binding response regulator	PG W83	PG0016	1, 449	98.2	857.4	0
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_00022	PG JCVI SC001	sensor histidine kinase	PG W83	PG0017	1, 445	99.8	862.1	0
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_00022	PG JCVI SC001	putative two-component system sensor histidine kinase	PG ATCC 33277	PGN_0013	1, 445	99.6	859	0

Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_00022	PG JCVI SC001	putative two-component system sensor histidine kinase	PG TDC60	PGTDC60_0015	1, 445	98.7	851.7	0
hypothetical protein	Pgjcvi_00023	PG JCVI SC001	hypothetical protein	PG W83	PG0018	1, 748	99.3	1515	0
hypothetical protein	Pgjcvi_00023	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0016	1, 726	98.5	1453.3	0
hypothetical protein	Pgjcvi_00023	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0014	1, 748	98.3	1498	0
Transcriptional regulators	Pgjcvi_00024	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_0015	1, 234	99.6	468	0
Transcriptional regulators	Pgjcvi_00024	PG JCVI SC001	transcriptional regulator, MarR family	PG W83	PG0020	1, 234	99.6	468	0
Transcriptional regulators	Pgjcvi_00024	PG JCVI SC001	MarR family transcriptional regulator	PG TDC60	PGTDC60_0017	1, 231	99.1	459.9	0
putative TIM-barrel protein, nifR3 family	Pgjcvi_00025	PG JCVI SC001	putative TIM-barrel protein	PG ATCC 33277	PGN_0016	1, 333	99.4	654.1	0
putative TIM-barrel protein, nifR3 family	Pgjcvi_00025	PG JCVI SC001	TIM-barrel protein, putative, NifR3 family	PG W83	PG0021	1, 333	99.4	654.1	0
putative TIM-barrel protein, nifR3 family	Pgjcvi_00025	PG JCVI SC001	NifR3 family TIM-barrel protein	PG TDC60	PGTDC60_0018	1, 333	99.4	654.8	0
high affinity sulphate transporter 1	Pgjcvi_00026	PG JCVI SC001	sulfate transporter permease	PG TDC60	PGTDC60_0019	1, 558	99.8	1073.9	0
high affinity sulphate transporter 1	Pgjcvi_00026	PG JCVI SC001	sulfate transporter permease	PG ATCC 33277	PGN_0017	1, 558	99.6	1072	0
high affinity sulphate transporter 1	Pgjcvi_00026	PG JCVI SC001	sulfate permease family protein	PG W83	PG0022	1, 558	99.6	1072	0
AT-rich DNA-binding protein	Pgjcvi_00027	PG JCVI SC001	probable DNA-binding protein	PG ATCC 33277	PGN_0020	1, 218	99.5	432.2	0
AT-rich DNA-binding protein	Pgjcvi_00027	PG JCVI SC001	redox-sensing transcriptional repressor Rex	PG TDC60	PGTDC60_0021	1, 218	99.5	432.2	0
AT-rich DNA-binding protein	Pgjcvi_00027	PG JCVI SC001	redox-sensing transcriptional repressor Rex	PG W83	PG0024	1, 218	99.1	429.9	0
2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Pgjcvi_00028	PG JCVI SC001	fumarylacetoacetate hydrolase family protein	PG W83	PG0025	1, 219	99.5	441	0
2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Pgjcvi_00028	PG JCVI SC001	probable hydrolase	PG ATCC 33277	PGN_0021	1, 219	99.1	438.7	0
2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Pgjcvi_00028	PG JCVI SC001	fumarylacetoacetate hydrolase family protein	PG TDC60	PGTDC60_0022	1, 219	99.1	438	0
Peptidase family C25.	Pgjcvi_00029	PG JCVI SC001	hypothetical protein	PG W83	PG0026	1, 1123	99.6	2249.2	0
Peptidase family C25.	Pgjcvi_00029	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0023	1, 1132	99.6	2272.7	0
Peptidase family C25.	Pgjcvi_00029	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0022	1, 1158	99.5	2311.6	0
hypothetical protein	Pgjcvi_00030	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0023	1, 391	100	784.6	0
hypothetical protein	Pgjcvi_00030	PG JCVI SC001	hypothetical protein	PG W83	PG0027	1, 391	100	784.6	0
hypothetical protein	Pgjcvi_00030	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0024	1, 391	99.5	781.9	0
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Pgjcvi_00031	PG JCVI SC001	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	PG W83	PG0028	1, 162	100	323.6	0
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Pgjcvi_00031	PG JCVI SC001	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	PG TDC60	PGTDC60_0025	1, 162	100	323.6	0
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Pgjcvi_00031	PG JCVI SC001	putative 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	PG ATCC 33277	PGN_0024	1, 162	99.4	322	0
rRNA methylases	Pgjcvi_00032	PG JCVI SC001	probable SpoU rRNA methylase family protein	PG ATCC 33277	PGN_0025	1, 180	98.9	357.5	0
rRNA methylases	Pgjcvi_00032	PG JCVI SC001	putative SpoU rRNA methylase family protein	PG TDC60	PGTDC60_0026	1, 180	98.9	357.5	0
rRNA methylases	Pgjcvi_00032	PG JCVI SC001	RNA methyltransferase, TrmH family	PG W83	PG1848	55, 241	28.1	67.4	7.00E-10
cytidine deaminase, homotetrameric	Pgjcvi_00034	PG JCVI SC001	putative cytidine deaminase	PG ATCC 33277	PGN_0026	1, 158	100	311.2	0
cytidine deaminase, homotetrameric	Pgjcvi_00034	PG JCVI SC001	cytidine deaminase	PG W83	PG0030	1, 158	100	311.2	0
cytidine deaminase, homotetrameric	Pgjcvi_00034	PG JCVI SC001	cytidine deaminase	PG TDC60	PGTDC60_0027	1, 158	100	311.2	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_00035	PG JCVI SC001	beta-mannosidase, putative	PG W83	PG0032	1, 861	98.8	1775.4	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_00035	PG JCVI SC001	beta-mannosidase	PG TDC60	PGTDC60_0031	1, 843	98.8	1743.4	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_00035	PG JCVI SC001	beta-mannosidase	PG ATCC 33277	PGN_0030	1, 848	98.3	1749.9	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00036	PG JCVI SC001	RmuC domain-containing protein	PG TDC60	PGTDC60_0032	1, 432	99.3	835.9	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00036	PG JCVI SC001	conserved hypothetical protein with RmuC domain	PG ATCC 33277	PGN_0031	1, 432	98.6	832	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00036	PG JCVI SC001	RmuC domain protein	PG W83	PG0033	1, 432	97.9	822.8	0
hypothetical protein	Pgjcvi_00037	PG JCVI SC001	hypothetical protein	PG W83	PG1715	1, 887	99.4	1767.3	0
hypothetical protein	Pgjcvi_00037	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0400	1, 926	99.2	1836.2	0
hypothetical protein	Pgjcvi_00037	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0586	1, 916	99.2	1815.8	0
hypothetical protein	Pgjcvi_00038	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0585	1, 31	83.9	59.3	3.30E-08
thioredoxin	Pgjcvi_00039	PG JCVI SC001	thioredoxin	PG ATCC 33277	PGN_0033	1, 104	100	213	0
thioredoxin	Pgjcvi_00039	PG JCVI SC001	thioredoxin	PG W83	PG0034	1, 104	100	213	0
thioredoxin	Pgjcvi_00039	PG JCVI SC001	thioredoxin	PG TDC60	PGTDC60_0034	1, 104	100	213	0
DNA-directed DNA polymerase III (polc)	Pgjcvi_00040	PG JCVI SC001	DNA polymerase III subunit alpha	PG TDC60	PGTDC60_0035	1, 1228	99.9	2457.2	0
DNA-directed DNA polymerase III (polc)	Pgjcvi_00040	PG JCVI SC001	DNA polymerase III alpha subunit	PG ATCC 33277	PGN_0034	1, 1228	99.8	2457.6	0
DNA-directed DNA polymerase III (polc)	Pgjcvi_00040	PG JCVI SC001	DNA polymerase III, alpha subunit	PG W83	PG0035	1, 1228	99.8	2452.9	0
ribosomal protein L19, bacterial type	Pgjcvi_00041	PG JCVI SC001	50S ribosomal protein L19	PG ATCC 33277	PGN_0035	1, 121	100	241.9	0
ribosomal protein L19, bacterial type	Pgjcvi_00041	PG JCVI SC001	50S ribosomal protein L19	PG W83	PG0037	1, 121	100	241.9	0
ribosomal protein L19, bacterial type	Pgjcvi_00041	PG JCVI SC001	50S ribosomal protein L19	PG TDC60	PGTDC60_0036	1, 121	100	241.9	0
Glycine/serine hydroxymethyltransferase	Pgjcvi_00043	PG JCVI SC001	serine hydroxymethyltransferase	PG ATCC 33277	PGN_0038	1, 426	100	852.8	0
Glycine/serine hydroxymethyltransferase	Pgjcvi_00043	PG JCVI SC001	serine hydroxymethyltransferase	PG W83	PG0042	1, 426	100	852.8	0
Glycine/serine hydroxymethyltransferase	Pgjcvi_00043	PG JCVI SC001	serine hydroxymethyltransferase	PG TDC60	PGTDC60_0039	1, 426	100	852.8	0
N-acetyl-beta-hexosaminidase	Pgjcvi_00044	PG JCVI SC001	beta-hexosaminidase	PG ATCC 33277	PGN_0039	3, 779	99.7	1581.6	0
N-acetyl-beta-hexosaminidase	Pgjcvi_00044	PG JCVI SC001	beta-hexosaminidase	PG W83	PG0043	1, 777	99.6	1579.7	0
N-acetyl-beta-hexosaminidase	Pgjcvi_00044	PG JCVI SC001	beta-hexosaminidase	PG TDC60	PGTDC60_0040	1, 777	99.6	1580.5	0
Molecular chaperone, HSP90 family	Pgjcvi_00047	PG JCVI SC001	heat shock protein 90	PG W83	PG0045	1, 684	99.6	1353.6	0
Molecular chaperone, HSP90 family	Pgjcvi_00047	PG JCVI SC001	heat shock protein 90	PG TDC60	PGTDC60_0042	1, 684	99.6	1357.4	0
Molecular chaperone, HSP90 family	Pgjcvi_00047	PG JCVI SC001	heat shock protein 90	PG ATCC 33277	PGN_0041	1, 684	99.4	1352.8	0
Predicted CDP-diglyceride synthetase/phosphatidate cytidylyltransferase	Pgjcvi_00048	PG JCVI SC001	probable phosphatidate cytidylyltransferase	PG ATCC 33277	PGN_0042	1, 284	100	560.8	0
Predicted CDP-diglyceride synthetase/phosphatidate cytidylyltransferase	Pgjcvi_00048	PG JCVI SC001	phosphatidate cytidylyltransferase	PG W83	PG0046	1, 284	100	560.8	0
Predicted CDP-diglyceride synthetase/phosphatidate cytidylyltransferase	Pgjcvi_00048	PG JCVI SC001	phosphatidate cytidylyltransferase	PG TDC60	PGTDC60_0043	1, 284	99.6	559.3	0
ATP-dependent metalloprotease FtsH	Pgjcvi_00049	PG JCVI SC001	putative transmembrane AAA-metalloprotease FtsH	PG ATCC 33277	PGN_0043	1, 673	100	1343.2	0
ATP-dependent metalloprotease FtsH	Pgjcvi_00049	PG JCVI SC001	cell division protein FtsH, putative	PG W83	PG0047	1, 673	99.9	1341.6	0
ATP-dependent metalloprotease FtsH	Pgjcvi_00049	PG JCVI SC001	transmembrane AAA-metalloprotease FtsH	PG TDC60	PGTDC60_0044	1, 673	99.9	1340.9	0
GTP-binding protein YchF	Pgjcvi_00050	PG JCVI SC001	conserved hypothetical protein TIGR00092	PG W83	PG0048	1, 367	100	719.5	0

GTP-binding protein YchF	Pgjcvi_00050	PG JCVI SC001	GTP-dependent nucleic acid-binding protein EngD	PG TDC60	PGTDC60_0045	1, 367	99.5	717.6	0
GTP-binding protein YchF	Pgjcvi_00050	PG JCVI SC001	GTP-binding protein	PG ATCC 33277	PGN_0044	1, 367	99.2	715.3	0
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1, 452	99.1	931.4	0
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1, 409	99	842	0
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1, 468	98.5	948.3	0
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2048, 2293	40.5	172.2	5.00E-41
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	680, 925	40.5	171	1.10E-40
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1136, 1381	40.5	171	1.10E-40
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1592, 1837	40.5	171	1.10E-40
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	621, 866	40.5	170.2	1.90E-40
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1073, 1318	40.5	170.2	1.90E-40
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	660, 905	40.5	169.9	2.50E-40
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1112, 1357	40.5	170.6	1.50E-40
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1564, 1809	40.5	166.8	2.10E-39
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1525, 1770	40.1	169.1	4.20E-40
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2260, 2546	39.3	191.8	0
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1737, 2023	38.7	192.2	0
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	833, 1083	38.6	162.2	5.20E-38
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1285, 1535	38.6	162.2	5.20E-38
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1776, 2079	38.2	195.7	0
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	872, 1122	38.2	160.6	1.50E-37
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1324, 1574	38.2	160.6	1.50E-37
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1348, 1602	38	159.8	2.60E-37
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1804, 2058	37.6	158.3	7.50E-37
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	892, 1146	37.4	159.8	2.60E-37
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	388, 670	37.4	176.8	2.00E-42
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	404, 690	36.9	172.9	2.90E-41
Domain of unknown function (DUF2436)./Cleaved Adhesin Domain.	Pgjcvi_00052	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	345, 631	36.6	171.4	8.50E-41
nucleoside transporter	Pgjcvi_00053	PG JCVI SC001	nucleoside permease NupG	PG W83	PG1836	2, 411	100	815.5	0
nucleoside transporter	Pgjcvi_00053	PG JCVI SC001	nucleoside permease NupG	PG TDC60	PGTDC60_0059	2, 411	100	815.5	0
nucleoside transporter	Pgjcvi_00053	PG JCVI SC001	nucleoside permease NupG	PG ATCC 33277	PGN_1734	1, 407	99.5	807	0
hypothetical protein	Pgjcvi_00054	PG JCVI SC001	lipoprotein, putative	PG W83	PG1835	12, 455	99.8	878.2	0
hypothetical protein	Pgjcvi_00054	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1735	12, 455	98.9	871.3	0
hypothetical protein	Pgjcvi_00054	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0060	1, 444	98.9	870.9	0
Glycogen synthase	Pgjcvi_00055	PG JCVI SC001	glycogen synthase-related protein	PG W83	PG1834	1, 271	99.3	541.6	0
Glycogen synthase	Pgjcvi_00055	PG JCVI SC001	putative glycogen synthase	PG ATCC 33277	PGN_1736	1, 271	98.5	537.3	0
Glycogen synthase	Pgjcvi_00055	PG JCVI SC001	glycogen synthase-like protein	PG TDC60	PGTDC60_0061	1, 271	97.8	536.6	0
ATP-dependent DNA helicase, RecQ family	Pgjcvi_00056	PG JCVI SC001	ATP-dependent DNA helicase RecQ	PG W83	PG1831	1, 655	99.5	1311.2	0
ATP-dependent DNA helicase, RecQ family	Pgjcvi_00056	PG JCVI SC001	ATP-dependent DNA helicase RecQ	PG TDC60	PGTDC60_0063	1, 707	99	1411.7	0
ATP-dependent DNA helicase, RecQ family	Pgjcvi_00056	PG JCVI SC001	ATP-dependent DNA helicase RecQ	PG ATCC 33277	PGN_1737	1, 707	98.7	1408.3	0
Long-chain acyl-CoA synthetases (AMP-forming)	Pgjcvi_00057	PG JCVI SC001	long-chain-fatty-acid--CoA ligase, putative	PG W83	PG1829	1, 557	99.3	1109	0
Long-chain acyl-CoA synthetases (AMP-forming)	Pgjcvi_00057	PG JCVI SC001	putative long-chain-fatty-acid-CoA ligase	PG TDC60	PGTDC60_0064	1, 557	99.3	1109	0
Long-chain acyl-CoA synthetases (AMP-forming)	Pgjcvi_00057	PG JCVI SC001	putative long-chain-fatty-acid-CoA ligase	PG ATCC 33277	PGN_1738	1, 557	99.1	1107.4	0
hypothetical protein	Pgjcvi_00058	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1739	1, 70	100	131.3	1.40E-29
hypothetical protein	Pgjcvi_00058	PG JCVI SC001	lipoprotein, putative	PG W83	PG1828	1, 70	100	131.3	1.40E-29
hypothetical protein	Pgjcvi_00058	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0065	1, 70	100	131.3	1.40E-29
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00059	PG JCVI SC001	putative RNA polymerase ECF-type sigma factor	PG ATCC 33277	PGN_1740	1, 167	100	333.6	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00059	PG JCVI SC001	RNA polymerase sigma-70 factor, ECF subfamily	PG W83	PG1827	47, 213	100	333.6	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00059	PG JCVI SC001	ECF subfamily RNA polymerase sigma factor	PG TDC60	PGTDC60_0066	1, 167	100	333.6	0
Uncharacterized conserved protein	Pgjcvi_00060	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1741	1, 139	97.8	268.5	0
Uncharacterized conserved protein	Pgjcvi_00060	PG JCVI SC001	hypothetical protein	PG W83	PG1826	1, 139	97.8	270.4	0
Uncharacterized conserved protein	Pgjcvi_00060	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0067	1, 139	97.8	268.9	0
phosphopyruvate hydratase	Pgjcvi_00061	PG JCVI SC001	phosphopyruvate hydratase	PG W83	PG1824	1, 425	99.8	840.5	0
phosphopyruvate hydratase	Pgjcvi_00061	PG JCVI SC001	phosphopyruvate hydratase	PG TDC60	PGTDC60_0069	1, 425	99.8	840.5	0
phosphopyruvate hydratase	Pgjcvi_00061	PG JCVI SC001	phosphopyruvate hydratase	PG ATCC 33277	PGN_1743	1, 425	99.5	839	0
hypothetical protein	Pgjcvi_00062	PG JCVI SC001	hypothetical protein	PG W83	PG1823	14, 217	100	402.1	0
hypothetical protein	Pgjcvi_00062	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0070	1, 204	100	402.1	0
hypothetical protein	Pgjcvi_00062	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1744	24, 227	99.5	400.6	0
cytochrome c nitrate reductase, small subunit	Pgjcvi_00064	PG JCVI SC001	putative NapC/NirT cytochrome c-type protein	PG ATCC 33277	PGN_1745	1, 203	99	426.4	0
cytochrome c nitrate reductase, small subunit	Pgjcvi_00064	PG JCVI SC001	cytochrome c nitrite reductase, small subunit NrfH	PG W83	PG1821	1, 203	99	426.4	0
cytochrome c nitrate reductase, small subunit	Pgjcvi_00064	PG JCVI SC001	cytochrome c nitrite reductase small subunit NrfH	PG TDC60	PGTDC60_0071	1, 203	99	426.4	0
Formate-dependent nitrite reductase, periplasmic cytochrome c552 subunit	Pgjcvi_00065	PG JCVI SC001	cytochrome c nitrite reductase catalytic subunit NrfA	PG ATCC 33277	PGN_1746	1, 379	100	793.9	0
Formate-dependent nitrite reductase, periplasmic cytochrome c552 subunit	Pgjcvi_00065	PG JCVI SC001	cytochrome c nitrite reductase, catalytic subunit NrfA	PG W83	PG1820	1, 498	100	1037.3	0
Formate-dependent nitrite reductase, periplasmic cytochrome c552 subunit	Pgjcvi_00065	PG JCVI SC001	cytochrome c552	PG TDC60	PGTDC60_0072	1, 498	99.8	1035.4	0
hypothetical protein	Pgjcvi_00066	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0073	1, 368	99.7	729.6	0
hypothetical protein	Pgjcvi_00066	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1747	1, 368	98.9	724.5	0
hypothetical protein	Pgjcvi_00066	PG JCVI SC001	hypothetical protein	PG W83	PG1819	1, 208	96.6	402.1	0
hypothetical protein	Pgjcvi_00067	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1747	386, 431	100	96.3	3.30E-19
hypothetical protein	Pgjcvi_00067	PG JCVI SC001	hypothetical protein	PG W83	PG1818	193, 238	100	96.3	3.30E-19
hypothetical protein	Pgjcvi_00067	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0073	386, 431	100	96.3	3.30E-19
ABC-type transport system involved in cytochrome c biogenesis, permease component	Pgjcvi_00068	PG JCVI SC001	hypothetical protein	PG W83	PG1817	1, 271	100	565.1	0
ABC-type transport system involved in cytochrome c biogenesis, permease component	Pgjcvi_00068	PG JCVI SC001	putative cytochrome c biogenesis protein CcsA	PG TDC60	PGTDC60_0074	1, 203	99	423.3	0

ABC-type transport system involved in cytochrome c biogenesis, permease component	Pgjcvi_00068	PG JCVI SC001	putative cytochrome c biogenesis protein CcsA	PG ATCC 33277	PGN_1748	1, 271	98.9	559.3	0
Putative NADPH-quinone reductase (modulator of drug activity B)	Pgjcvi_00069	PG JCVI SC001	probable NADPH-quinone reductase	PG ATCC 33277	PGN_1749	1, 173	100	366.3	0
Putative NADPH-quinone reductase (modulator of drug activity B)	Pgjcvi_00069	PG JCVI SC001	NAD(P)H dehydrogenase, quinone family, putative	PG W83	PG1816	1, 173	100	366.3	0
Putative NADPH-quinone reductase (modulator of drug activity B)	Pgjcvi_00069	PG JCVI SC001	quinone family NAD(P)H dehydrogenase	PG TDC60	PGTDC60_0075	1, 173	100	366.3	0
3-deoxy-D-manno-octulosonate cytidylyltransferase	Pgjcvi_00070	PG JCVI SC001	3-deoxy-manno-octulosonate cytidylyltransferase	PG W83	PG1815	1, 254	100	506.9	0
3-deoxy-D-manno-octulosonate cytidylyltransferase	Pgjcvi_00070	PG JCVI SC001	3-deoxy-manno-octulosonate cytidylyltransferase	PG TDC60	PGTDC60_0076	1, 254	100	506.9	0
3-deoxy-D-manno-octulosonate cytidylyltransferase	Pgjcvi_00070	PG JCVI SC001	putative 3-deoxy-D-manno-octulosonate cytidylyltransferase	PG ATCC 33277	PGN_1750	1, 254	98.8	502.7	0
DNA primase, catalytic core	Pgjcvi_00071	PG JCVI SC001	DNA primase	PG W83	PG1814	1, 673	99.9	1320.4	0
DNA primase, catalytic core	Pgjcvi_00071	PG JCVI SC001	DNA primase	PG TDC60	PGTDC60_0077	1, 673	99	1307.7	0
DNA primase, catalytic core	Pgjcvi_00071	PG JCVI SC001	DNA primase	PG ATCC 33277	PGN_1751	1, 673	98.5	1305	0
Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	Pgjcvi_00072	PG JCVI SC001	putative ferredoxin 4Fe-4S	PG ATCC 33277	PGN_1752	1, 75	100	166	5.60E-40
Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	Pgjcvi_00072	PG JCVI SC001	ferredoxin, 4Fe-4S	PG W83	PG1813	1, 75	100	166	5.60E-40
Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	Pgjcvi_00072	PG JCVI SC001	ferredoxin, 4Fe-4S	PG TDC60	PGTDC60_0078	1, 75	100	166	5.60E-40
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit	Pgjcvi_00073	PG JCVI SC001	putative 2-oxoglutarate oxidoreductase alpha subunit	PG ATCC 33277	PGN_1753	1, 360	99.7	716.8	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit	Pgjcvi_00073	PG JCVI SC001	2-oxoglutarate ferredoxin oxidoreductase	PG W83	PG1812	1, 353	99.7	704.1	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit	Pgjcvi_00073	PG JCVI SC001	2-ketoisovalerate ferredoxin reductase	PG TDC60	PGTDC60_0079	1, 360	98.9	712.6	0
hypothetical protein	Pgjcvi_00074	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1754	1, 59	98.3	115.9	5.20E-25
hypothetical protein	Pgjcvi_00074	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0080	1, 59	98.3	115.9	5.20E-25
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	Pgjcvi_00075	PG JCVI SC001	2-oxoglutarate oxidoreductase, beta subunit	PG W83	PG1810	1, 230	100	470.3	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	Pgjcvi_00075	PG JCVI SC001	putative 2-oxoglutarate oxidoreductase beta subunit	PG ATCC 33277	PGN_1755	1, 235	99.6	479.6	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	Pgjcvi_00075	PG JCVI SC001	2-oxoglutarate oxidoreductase subunit beta	PG TDC60	PGTDC60_0081	1, 254	99.6	516.9	0
2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-ketoisovalerate family	Pgjcvi_00076	PG JCVI SC001	2-oxoglutarate oxidoreductase, gamma subunit	PG W83	PG1809	1, 181	100	356.3	0
2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-ketoisovalerate family	Pgjcvi_00076	PG JCVI SC001	putative 2-oxoglutarate oxidoreductase gamma subunit	PG ATCC 33277	PGN_1756	1, 181	99.4	354.4	0
2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-ketoisovalerate family	Pgjcvi_00076	PG JCVI SC001	2-oxoglutarate oxidoreductase, gamma subunit	PG TDC60	PGTDC60_0082	1, 181	99.4	354.4	0
(p)ppGpp synthetase, RelA/SpoT family	Pgjcvi_00077	PG JCVI SC001	GTP pyrophosphokinase	PG ATCC 33277	PGN_1757	1, 762	100	1516.1	0
(p)ppGpp synthetase, RelA/SpoT family	Pgjcvi_00077	PG JCVI SC001	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	PG W83	PG1808	1, 762	99.9	1515.7	0
(p)ppGpp synthetase, RelA/SpoT family	Pgjcvi_00077	PG JCVI SC001	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	PG TDC60	PGTDC60_0083	1, 762	99.9	1515	0
ATP synthase subunit C.	Pgjcvi_00078	PG JCVI SC001	putative v-type ATPase subunit K	PG ATCC 33277	PGN_1758	1, 158	100	305.1	0
ATP synthase subunit C.	Pgjcvi_00078	PG JCVI SC001	v-type ATPase, subunit K	PG W83	PG1807	1, 158	100	305.1	0
ATP synthase subunit C.	Pgjcvi_00078	PG JCVI SC001	V-type ATPase, subunit K	PG TDC60	PGTDC60_0084	1, 158	100	305.1	0
Archaeal/vacuolar-type H+-ATPase subunit I	Pgjcvi_00079	PG JCVI SC001	v-type ATPase, subunit I	PG W83	PG1806	1, 604	99.7	1177.9	0
Archaeal/vacuolar-type H+-ATPase subunit I	Pgjcvi_00079	PG JCVI SC001	putative v-type ATPase subunit I	PG ATCC 33277	PGN_1759	1, 604	99.5	1176.8	0
Archaeal/vacuolar-type H+-ATPase subunit I	Pgjcvi_00079	PG JCVI SC001	V-type ATPase, subunit I	PG TDC60	PGTDC60_0085	1, 604	99	1173.3	0
Archaeal/vacuolar-type H+-ATPase subunit D	Pgjcvi_00080	PG JCVI SC001	putative v-type ATPase subunit D	PG ATCC 33277	PGN_1760	1, 204	100	395.2	0
Archaeal/vacuolar-type H+-ATPase subunit D	Pgjcvi_00080	PG JCVI SC001	V-type ATP synthase, subunit D	PG TDC60	PGTDC60_0086	1, 204	100	395.2	0
Archaeal/vacuolar-type H+-ATPase subunit D	Pgjcvi_00080	PG JCVI SC001	V-type ATP synthase subunit D	PG W83	PG1805	1, 204	99.5	393.3	0
Archaeal/vacuolar-type H+-ATPase subunit B	Pgjcvi_00081	PG JCVI SC001	V-type ATP synthase subunit B	PG W83	PG1804	1, 439	100	865.5	0
Archaeal/vacuolar-type H+-ATPase subunit B	Pgjcvi_00081	PG JCVI SC001	V-type ATP synthase, subunit B	PG TDC60	PGTDC60_0087	1, 439	100	865.5	0
Archaeal/vacuolar-type H+-ATPase subunit B	Pgjcvi_00081	PG JCVI SC001	v-type ATPase subunit B	PG ATCC 33277	PGN_1761	1, 439	99.8	865.1	0
Archaeal/vacuolar-type H+-ATPase subunit A	Pgjcvi_00082	PG JCVI SC001	v-type ATPase subunit A	PG ATCC 33277	PGN_1762	1, 584	99.8	1171	0
Archaeal/vacuolar-type H+-ATPase subunit A	Pgjcvi_00082	PG JCVI SC001	V-type ATP synthase subunit A	PG W83	PG1803	1, 584	99.8	1171	0
Archaeal/vacuolar-type H+-ATPase subunit A	Pgjcvi_00082	PG JCVI SC001	V-type ATP synthase, subunit A	PG TDC60	PGTDC60_0088	1, 584	99.8	1171	0
Protein of unknown function (DUF2764).	Pgjcvi_00083	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1763	1, 312	99.7	625.5	0
Protein of unknown function (DUF2764).	Pgjcvi_00083	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0089	1, 312	99.7	625.5	0
Protein of unknown function (DUF2764).	Pgjcvi_00083	PG JCVI SC001	hypothetical protein	PG W83	PG1802	1, 312	98.7	617.8	0
Archaeal/vacuolar-type H+-ATPase subunit E	Pgjcvi_00084	PG JCVI SC001	v-type ATPase, subunit E, putative	PG W83	PG1801	1, 196	98.5	371.3	0
Archaeal/vacuolar-type H+-ATPase subunit E	Pgjcvi_00084	PG JCVI SC001	V-type ATPase, subunit E	PG TDC60	PGTDC60_0090	1, 196	98.5	370.9	0
Archaeal/vacuolar-type H+-ATPase subunit E	Pgjcvi_00084	PG JCVI SC001	putative v-type ATPase subunit E	PG ATCC 33277	PGN_1764	1, 196	97.4	367.5	0
Por secretion system C-terminal sorting domain	Pgjcvi_00085	PG JCVI SC001	immunoreactive 46 kDa antigen	PG ATCC 33277	PGN_1767	19, 423	98.8	808.9	0
Por secretion system C-terminal sorting domain	Pgjcvi_00085	PG JCVI SC001	immunoreactive 46 kDa antigen PG99	PG TDC60	PGTDC60_0093	1, 405	98.8	809.7	0
Por secretion system C-terminal sorting domain	Pgjcvi_00085	PG JCVI SC001	immunoreactive 46 kDa antigen PG99	PG W83	PG1798	1, 405	98.3	806.6	0
Response regulator containing a CheY-like receiver domain and an HD-GYP domain	Pgjcvi_00086	PG JCVI SC001	DNA-binding response regulator/sensor histidine kinase	PG W83	PG1797	684, 961	99.6	546.2	0
Response regulator containing a CheY-like receiver domain and an HD-GYP domain	Pgjcvi_00086	PG JCVI SC001	putative DNA-binding response regulator/sensor histidine kinase	PG ATCC 33277	PGN_1768	684, 961	99.3	543.5	0
Response regulator containing a CheY-like receiver domain and an HD-GYP domain	Pgjcvi_00086	PG JCVI SC001	DNA-binding response regulator/sensor histidine kinase	PG TDC60	PGTDC60_0094	608, 885	99.3	543.9	0
His Kinase A (phosphoacceptor) domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_00087	PG JCVI SC001	DNA-binding response regulator/sensor histidine kinase	PG W83	PG1797	1, 651	99.8	1269.6	0
His Kinase A (phosphoacceptor) domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_00087	PG JCVI SC001	DNA-binding response regulator/sensor histidine kinase	PG TDC60	PGTDC60_0094	1, 575	99.5	1118.2	0
His Kinase A (phosphoacceptor) domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_00087	PG JCVI SC001	putative DNA-binding response regulator/sensor histidine kinase	PG ATCC 33277	PGN_1768	1, 651	99.2	1259.6	0

hypothetical protein	Pgjcvi_00088	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1770	1, 262	96.2	503.4	0
hypothetical protein	Pgjcvi_00088	PG JCVI SC001	hypothetical protein	PG W83	PG1795	1, 273	94.1	512.7	0
hypothetical protein	Pgjcvi_00088	PG JCVI SC001	arginine-specific cysteine proteinase RgpB	PG TDC60	PGTDC60_1623	563, 725	26.9	50.4	0.00012
DNA polymerase I	Pgjcvi_00089	PG JCVI SC001	DNA polymerase type I	PG W83	PG1794	1, 926	99.1	1807.3	0
DNA polymerase I	Pgjcvi_00089	PG JCVI SC001	DNA polymerase I	PG TDC60	PGTDC60_0100	1, 926	98.8	1801.2	0
DNA polymerase I	Pgjcvi_00089	PG JCVI SC001	DNA polymerase I	PG ATCC 33277	PGN_1771	1, 926	98.6	1794.6	0
1,4-alpha-glucan branching enzyme	Pgjcvi_00090	PG JCVI SC001	1,4-alpha-glucan branching enzyme	PG W83	PG1793	1, 668	98.7	1403.3	0
1,4-alpha-glucan branching enzyme	Pgjcvi_00090	PG JCVI SC001	1,4-alpha-glucan branching enzyme	PG TDC60	PGTDC60_0101	1, 668	98.4	1399	0
1,4-alpha-glucan branching enzyme	Pgjcvi_00090	PG JCVI SC001	1,4-alpha-glucan branching enzyme	PG ATCC 33277	PGN_1772	1, 668	98.2	1400.6	0
Kef-type K+ transport systems, membrane components	Pgjcvi_00091	PG JCVI SC001	sodium/hydrogen antiporter	PG W83	PG1792	1, 767	99.9	1488.4	0
Kef-type K+ transport systems, membrane components	Pgjcvi_00091	PG JCVI SC001	sodium/hydrogen antiporter	PG TDC60	PGTDC60_0102	1, 767	99.9	1488.4	0
Kef-type K+ transport systems, membrane components	Pgjcvi_00091	PG JCVI SC001	sodium/hydrogen antiporter	PG ATCC 33277	PGN_1773	1, 767	99.5	1483.4	0
7-keto-8-aminopelargonate synthetase and related enzymes	Pgjcvi_00093	PG JCVI SC001	8-amino-7-oxononanoate synthase	PG TDC60	PGTDC60_1168	1, 382	98.4	739.2	0
7-keto-8-aminopelargonate synthetase and related enzymes	Pgjcvi_00093	PG JCVI SC001	8-amino-7-oxononanoate synthase	PG W83	PG1195	1, 382	98.2	737.3	0
7-keto-8-aminopelargonate synthetase and related enzymes	Pgjcvi_00093	PG JCVI SC001	8-amino-7-oxononanoate synthase	PG ATCC 33277	PGN_0938	1, 382	97.1	731.1	0
hypothetical protein	Pgjcvi_00094	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1169	1, 139	99.3	289.7	0
hypothetical protein	Pgjcvi_00094	PG JCVI SC001	hypothetical protein	PG W83	PG1198	1, 79	98.7	164.1	3.90E-39
hypothetical protein	Pgjcvi_00094	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0939	1, 139	97.8	283.9	0
hypothetical protein	Pgjcvi_00095	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1170	1, 141	99.3	282.3	0
hypothetical protein	Pgjcvi_00095	PG JCVI SC001	hypothetical protein	PG W83	PG1199	1, 141	95.7	272.3	0
Protein involved in cell division	Pgjcvi_00097	PG JCVI SC001	cell filamentation protein (fic)	PG TDC60	PGTDC60_1175	7, 296	75.2	461.8	0
Predicted transcriptional regulators	Pgjcvi_00098	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0927	2, 59	86.2	95.9	6.40E-19
Predicted transcriptional regulators	Pgjcvi_00098	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_1176	1, 68	85.3	116.3	4.60E-25
Predicted transcriptional regulators	Pgjcvi_00098	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG1203	2, 63	77.4	99.4	5.80E-20
Relaxase/Mobilisation nuclease domain.	Pgjcvi_00100	PG JCVI SC001	mobilization protein	PG TDC60	PGTDC60_1944	1, 269	46.4	242.7	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_00100	PG JCVI SC001	putative mobilization protein	PG ATCC 33277	PGN_0925	1, 308	45.7	271.6	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_00100	PG JCVI SC001	hypothetical protein	PG W83	PG1489	1, 304	24.3	76.3	2.40E-12
Bacterial mobilisation protein (MobC).	Pgjcvi_00101	PG JCVI SC001	mobilization protein	PG W83	PG0869	8, 117	45.5	104	5.80E-21
Bacterial mobilisation protein (MobC).	Pgjcvi_00101	PG JCVI SC001	mobilization protein	PG ATCC 33277	PGN_0924	11, 116	44.3	100.5	6.40E-20
Bacterial mobilisation protein (MobC).	Pgjcvi_00101	PG JCVI SC001	mobilization protein	PG TDC60	PGTDC60_1943	6, 114	42.2	99	1.90E-19
DNA primase (bacterial type)	Pgjcvi_00102	PG JCVI SC001	putative DNA primase	PG ATCC 33277	PGN_0923	1, 294	47.1	296.6	0
DNA primase (bacterial type)	Pgjcvi_00102	PG JCVI SC001	mobilizable transposon, excision protein, putative	PG W83	PG0841	1, 278	37.4	191.4	0
DNA primase (bacterial type)	Pgjcvi_00102	PG JCVI SC001	CHC2 zinc finger containing protein	PG TDC60	PGTDC60_1942	1, 302	33.8	169.9	1.50E-40
Predicted P-loop ATPase and inactivated derivatives	Pgjcvi_00103	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0922	7, 401	78.3	637.9	0
hypothetical protein	Pgjcvi_00104	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0921	1, 53	67.9	79.7	8.30E-14
hypothetical protein	Pgjcvi_00104	PG JCVI SC001	mobilizable transposon, xis protein	PG W83	PG0872	1, 101	47.1	105.1	1.80E-21
hypothetical protein	Pgjcvi_00105	PG JCVI SC001	hypothetical protein	PG W83	PG1206	11, 73	65.1	89.4	2.20E-16
hypothetical protein	Pgjcvi_00105	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1178	11, 73	63.5	87	1.10E-15
Site-specific recombinase XerD	Pgjcvi_00106	PG JCVI SC001	tyrosine type site-specific recombinase	PG ATCC 33277	PGN_0917	1, 418	76.1	654.4	0
Site-specific recombinase XerD	Pgjcvi_00106	PG JCVI SC001	mobilizable transposon, int protein	PG W83	PG0874	40, 366	37.8	221.9	0
Site-specific recombinase XerD	Pgjcvi_00106	PG JCVI SC001	integrase	PG TDC60	PGTDC60_2028	2, 386	23.7	105.5	5.00E-21
NAD(P)H-nitrite reductase	Pgjcvi_00107	PG JCVI SC001	mobilizable transposon, tnpA protein	PG W83	PG0875	1, 176	30.6	93.6	8.70E-18
chaperone protein DnaK	Pgjcvi_00108	PG JCVI SC001	molecular chaperone DnaK	PG W83	PG1208	1, 640	100	1247.3	0
chaperone protein DnaK	Pgjcvi_00108	PG JCVI SC001	molecular chaperone DnaK	PG TDC60	PGTDC60_1180	1, 640	99.7	1243.8	0
chaperone protein DnaK	Pgjcvi_00108	PG JCVI SC001	molecular chaperone DnaK	PG ATCC 33277	PGN_0916	1, 640	99.5	1243	0
hypothetical protein	Pgjcvi_00109	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0104	1, 469	99.1	956.1	0
hypothetical protein	Pgjcvi_00109	PG JCVI SC001	hypothetical protein	PG W83	PG1790	1, 494	99	999.2	0
hypothetical protein	Pgjcvi_00109	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1775	1, 494	98.8	998	0
Zn-dependent oligopeptidases	Pgjcvi_00110	PG JCVI SC001	peptidyl-dipeptidase	PG TDC60	PGTDC60_0105	1, 678	99.6	1372.8	0
Zn-dependent oligopeptidases	Pgjcvi_00110	PG JCVI SC001	peptidyl-dipeptidase	PG ATCC 33277	PGN_1776	1, 678	99.3	1370.1	0
Zn-dependent oligopeptidases	Pgjcvi_00110	PG JCVI SC001	peptidyl-dipeptidase Dcp	PG W83	PG1789	1, 678	99.1	1369.4	0
Aminopeptidase C	Pgjcvi_00111	PG JCVI SC001	bleomycin hydrolase	PG ATCC 33277	PGN_1777	24, 423	99.8	814.7	0
Aminopeptidase C	Pgjcvi_00111	PG JCVI SC001	cysteine peptidase, putative	PG W83	PG1788	24, 423	99.5	812.4	0
Aminopeptidase C	Pgjcvi_00111	PG JCVI SC001	bleomycin hydrolase	PG TDC60	PGTDC60_0106	1, 400	99.5	811.6	0
endoribonuclease L-PSP, putative	Pgjcvi_00112	PG JCVI SC001	endoribonuclease L-PSP, putative	PG W83	PG1847	1, 126	100	248.1	0
endoribonuclease L-PSP, putative	Pgjcvi_00112	PG JCVI SC001	endoribonuclease L-PSP	PG TDC60	PGTDC60_0110	1, 126	99.2	246.1	0
endoribonuclease L-PSP, putative	Pgjcvi_00112	PG JCVI SC001	putative YjgF-like protein	PG ATCC 33277	PGN_1780	1, 126	97.6	243	0
rRNA methylase, putative, group 3	Pgjcvi_00113	PG JCVI SC001	RNA methyltransferase, TrmH family	PG W83	PG1848	1, 249	100	481.1	0
rRNA methylase, putative, group 3	Pgjcvi_00113	PG JCVI SC001	tRNA:rRNA methyltransferase	PG TDC60	PGTDC60_0111	1, 249	99.6	479.6	0
rRNA methylase, putative, group 3	Pgjcvi_00113	PG JCVI SC001	putative tRNA:rRNA methyltransferase	PG ATCC 33277	PGN_1781	1, 249	99.2	479.2	0
DNA repair protein RecN	Pgjcvi_00114	PG JCVI SC001	DNA repair protein RecN	PG W83	PG1849	1, 551	99.8	1065.8	0
DNA repair protein RecN	Pgjcvi_00114	PG JCVI SC001	DNA repair protein RecN	PG ATCC 33277	PGN_1782	1, 551	99.6	1064.7	0
DNA repair protein RecN	Pgjcvi_00114	PG JCVI SC001	DNA repair protein RecN	PG TDC60	PGTDC60_0112	1, 551	99.1	1058.9	0
hypothetical protein	Pgjcvi_00115	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1783	1, 302	100	607.1	0
hypothetical protein	Pgjcvi_00115	PG JCVI SC001	hypothetical protein	PG W83	PG1850	1, 302	100	607.1	0
hypothetical protein	Pgjcvi_00115	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0113	1, 298	99	596.7	0
phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase, prokaryotic	Pgjcvi_00116	PG JCVI SC001	DNA/pantothenate metabolism flavoprotein	PG ATCC 33277	PGN_1784	1, 403	99.8	785.8	0
phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase, prokaryotic	Pgjcvi_00116	PG JCVI SC001	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	PG W83	PG1851	1, 404	99.8	788.9	0
phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase, prokaryotic	Pgjcvi_00116	PG JCVI SC001	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	PG TDC60	PGTDC60_0114	1, 404	97.5	769.2	0

DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00117	PG JCVI SC001	exonuclease	PG W83	PG1852	1, 259	100	526.9	0
DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00117	PG JCVI SC001	putative DNA polymerase III epsilon chain	PG ATCC 33277	PGN_1785	1, 259	99.2	521.5	0
DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00117	PG JCVI SC001	putative DNA polymerase III epsilon chain	PG TDC60	PGTDC60_0115	1, 259	99.2	521.5	0
DNA polymerase III, beta subunit	Pgjcvi_00118	PG JCVI SC001	putative DNA polymerase III beta chain	PG ATCC 33277	PGN_1786	1, 377	99.5	726.1	0
DNA polymerase III, beta subunit	Pgjcvi_00118	PG JCVI SC001	DNA polymerase III, beta subunit	PG W83	PG1853	1, 377	98.7	723.8	0
DNA polymerase III, beta subunit	Pgjcvi_00118	PG JCVI SC001	DNA polymerase III subunit beta	PG TDC60	PGTDC60_0116	1, 377	98.7	723.8	0
5,10-methenyltetrahydrofolate synthetase	Pgjcvi_00119	PG JCVI SC001	probable 5-formyltetrahydrofolate cyclo-ligase	PG ATCC 33277	PGN_1787	2, 167	100	335.5	0
5,10-methenyltetrahydrofolate synthetase	Pgjcvi_00119	PG JCVI SC001	5-formyltetrahydrofolate cyclo-ligase family protein	PG TDC60	PGTDC60_0119	1, 185	99.5	369	0
5,10-methenyltetrahydrofolate synthetase	Pgjcvi_00119	PG JCVI SC001	5-formyltetrahydrofolate cyclo-ligase family protein	PG W83	PG1854	1, 185	98.9	367.5	0
C-terminal peptidase (prc)	Pgjcvi_00120	PG JCVI SC001	carboxyl-terminal protease	PG W83	PG1855	1, 544	100	1072	0
C-terminal peptidase (prc)	Pgjcvi_00120	PG JCVI SC001	carboxyl-terminal processing protease	PG ATCC 33277	PGN_1788	1, 544	99.8	1068.9	0
C-terminal peptidase (prc)	Pgjcvi_00120	PG JCVI SC001	carboxyl-terminal protease	PG TDC60	PGTDC60_0120	1, 544	98.9	1060.1	0
Deoxycytidylate deaminase	Pgjcvi_00121	PG JCVI SC001	putative deoxycytidylate deaminase	PG ATCC 33277	PGN_1789	3, 151	100	299.3	0
Deoxycytidylate deaminase	Pgjcvi_00121	PG JCVI SC001	cytidine/deoxycytidylate deaminase family protein	PG W83	PG1856	3, 151	100	299.3	0
Deoxycytidylate deaminase	Pgjcvi_00121	PG JCVI SC001	cytidine/deoxycytidylate deaminase family protein	PG TDC60	PGTDC60_0121	3, 151	100	299.3	0
Protein of unknown function (DUF2023).	Pgjcvi_00122	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1790	1, 117	100	243.4	0
Protein of unknown function (DUF2023).	Pgjcvi_00122	PG JCVI SC001	hypothetical protein	PG W83	PG1857	1, 117	100	243.4	0
Protein of unknown function (DUF2023).	Pgjcvi_00122	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0122	1, 117	100	243.4	0
flavodoxin, long chain	Pgjcvi_00123	PG JCVI SC001	putative flavodoxin	PG ATCC 33277	PGN_1791	1, 165	99.4	331.6	0
flavodoxin, long chain	Pgjcvi_00123	PG JCVI SC001	flavodoxin	PG W83	PG1858	1, 165	99.4	331.6	0
flavodoxin, long chain	Pgjcvi_00123	PG JCVI SC001	flavodoxin FldA	PG TDC60	PGTDC60_0123	1, 165	99.4	331.6	0
glycerate kinase	Pgjcvi_00124	PG JCVI SC001	glycerate kinase family protein	PG W83	PG1859	1, 386	99.2	753.8	0
glycerate kinase	Pgjcvi_00124	PG JCVI SC001	glycerate kinase family protein	PG TDC60	PGTDC60_0124	1, 386	99	751.9	0
glycerate kinase	Pgjcvi_00124	PG JCVI SC001	glycerate kinase	PG ATCC 33277	PGN_1792	1, 386	97.9	742.3	0
Predicted ATPase (AAA+ superfamily)	Pgjcvi_00125	PG JCVI SC001	hypothetical protein	PG W83	PG1860	1, 394	100	788.1	0
Predicted ATPase (AAA+ superfamily)	Pgjcvi_00125	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0125	1, 370	100	740.7	0
Predicted ATPase (AAA+ superfamily)	Pgjcvi_00125	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1793	1, 394	99.7	786.6	0
hypothetical protein	Pgjcvi_00126	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1795	1, 148	100	310.1	0
hypothetical protein	Pgjcvi_00126	PG JCVI SC001	hypothetical protein	PG W83	PG1862	1, 97	100	206.1	0
hypothetical protein	Pgjcvi_00126	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0127	1, 148	95.3	297	0
hypothetical protein	Pgjcvi_00127	PG JCVI SC001	leucine-rich protein	PG W83	PG1864	243, 1266	84.9	1698.3	0
hypothetical protein	Pgjcvi_00127	PG JCVI SC001	leucine-rich protein	PG TDC60	PGTDC60_0128	369, 1384	83.4	1661	0
hypothetical protein	Pgjcvi_00127	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1796	89, 1125	76.2	1526.9	0
hypothetical protein	Pgjcvi_00127	PG JCVI SC001	leucine-rich protein	PG W83	PG1864	35, 337	60.4	312.4	0
hypothetical protein	Pgjcvi_00127	PG JCVI SC001	leucine-rich protein	PG TDC60	PGTDC60_0128	1, 303	58.7	298.9	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00129	PG JCVI SC001	hypothetical protein	PG W83	PG1868	1, 173	99.4	349.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00129	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1797	1, 173	98.8	346.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00129	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0129	1, 173	98.8	346.3	0
hypothetical protein	Pgjcvi_00130	PG JCVI SC001	hypothetical protein	PG W83	PG1869	1, 55	87.3	101.3	1.20E-20
hypothetical protein	Pgjcvi_00130	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0130	1, 55	85.5	98.2	1.00E-19
Methylase involved in ubiquinone/menaquinone biosynthesis	Pgjcvi_00131	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1798	1, 221	99.5	461.1	0
Methylase involved in ubiquinone/menaquinone biosynthesis	Pgjcvi_00131	PG JCVI SC001	UbiE/COQ5 family methlytransferase	PG TDC60	PGTDC60_0131	1, 221	99.5	461.5	0
Methylase involved in ubiquinone/menaquinone biosynthesis	Pgjcvi_00131	PG JCVI SC001	methlytransferase, UbiE/COQ5 family	PG W83	PG1870	1, 219	98.2	450.7	0
urocanate hydratase	Pgjcvi_00132	PG JCVI SC001	urocanate hydratase	PG ATCC 33277	PGN_1800	1, 659	99.8	1345.9	0
urocanate hydratase	Pgjcvi_00132	PG JCVI SC001	urocanate hydratase	PG TDC60	PGTDC60_0133	1, 659	99.8	1345.9	0
urocanate hydratase	Pgjcvi_00132	PG JCVI SC001	urocanate hydratase	PG W83	PG1872	1, 659	99.7	1342.8	0
Predicted endonuclease distantly related to archaeal Holliday junction resolvase	Pgjcvi_00133	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1801	1, 135	100	266.5	0
Predicted endonuclease distantly related to archaeal Holliday junction resolvase	Pgjcvi_00133	PG JCVI SC001	hypothetical protein	PG W83	PG1874	1, 135	100	266.5	0
Predicted endonuclease distantly related to archaeal Holliday junction resolvase	Pgjcvi_00133	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0134	1, 135	100	266.5	0
hypothetical protein	Pgjcvi_00134	PG JCVI SC001	hemolysin	PG W83	PG1875	1, 324	100	651.4	0
hypothetical protein	Pgjcvi_00134	PG JCVI SC001	hemolysin	PG TDC60	PGTDC60_0135	1, 324	98.8	643.3	0
hypothetical protein	Pgjcvi_00134	PG JCVI SC001	hemolysin	PG ATCC 33277	PGN_1802	1, 324	98.5	640.6	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_00135	PG JCVI SC001	hypothetical protein	PG W83	PG1876	1, 275	100	559.3	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_00135	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0136	1, 275	99.6	556.2	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_00135	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1803	1, 275	99.3	555.4	0
Na+/H+ antiporter NhaA	Pgjcvi_00136	PG JCVI SC001	Na+/H+ antiporter	PG W83	PG1877	1, 452	100	875.5	0
Na+/H+ antiporter NhaA	Pgjcvi_00136	PG JCVI SC001	Na+/H+ antiporter	PG ATCC 33277	PGN_1804	1, 452	99.6	873.2	0
Na+/H+ antiporter NhaA	Pgjcvi_00136	PG JCVI SC001	Na+/H+ antiporter	PG TDC60	PGTDC60_0137	1, 452	99.3	871.7	0
cysteinyl-tRNA synthetase	Pgjcvi_00137	PG JCVI SC001	cysteinyl-tRNA synthetase	PG ATCC 33277	PGN_1805	1, 486	99.4	997.3	0
cysteinyl-tRNA synthetase	Pgjcvi_00137	PG JCVI SC001	cysteinyl-tRNA synthetase	PG W83	PG1878	1, 490	99.4	1001.1	0
cysteinyl-tRNA synthetase	Pgjcvi_00137	PG JCVI SC001	cysteinyl-tRNA synthetase	PG TDC60	PGTDC60_0138	1, 490	99.4	1006.1	0
Predicted esterase of the alpha-beta hydrolase superfamily	Pgjcvi_00138	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1806	1, 339	100	690.3	0
Predicted esterase of the alpha-beta hydrolase superfamily	Pgjcvi_00138	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0139	1, 339	100	690.3	0
Predicted esterase of the alpha-beta hydrolase superfamily	Pgjcvi_00138	PG JCVI SC001	hypothetical protein	PG W83	PG1879	1, 339	99.4	689.1	0
Predicted glycosyltransferases	Pgjcvi_00139	PG JCVI SC001	putative glycosyltransferase	PG ATCC 33277	PGN_1807	1, 336	98.8	672.9	0
Predicted glycosyltransferases	Pgjcvi_00139	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG1880	1, 336	97.6	663.7	0
Predicted glycosyltransferases	Pgjcvi_00139	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_0140	1, 338	97.3	662.9	0
hypothetical protein	Pgjcvi_00140	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0141	1, 480	98.8	943	0
hypothetical protein	Pgjcvi_00140	PG JCVI SC001	hypothetical protein	PG W83	PG1881	1, 480	98.3	940.6	0
hypothetical protein	Pgjcvi_00140	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1808	1, 480	98.1	940.3	0
hypothetical protein	Pgjcvi_00141	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0127	1, 57	78.5	101.7	1.40E-20
hypothetical protein	Pgjcvi_00141	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0228	1, 57	78.5	101.7	1.40E-20

Alpha-L-fucosidase	Pgjcvi_00142	PG JCVI SC001	alpha-L-fucosidase precursor, putative	PG W83	PG1884	1, 674	99.1	1375.1	0
Alpha-L-fucosidase	Pgjcvi_00142	PG JCVI SC001	putative alpha-L-fucosidase	PG ATCC 33277	PGN_1811	1, 697	98.6	1409.4	0
Alpha-L-fucosidase	Pgjcvi_00142	PG JCVI SC001	alpha-L-fucosidase precursor	PG TDC60	PGTDC60_0143	1, 698	96.6	1382.5	0
polyphosphate kinase 1	Pgjcvi_00143	PG JCVI SC001	polyphosphate kinase	PG W83	PG1885	1, 695	99.7	1379.4	0
polyphosphate kinase 1	Pgjcvi_00143	PG JCVI SC001	polyphosphate kinase	PG ATCC 33277	PGN_1812	1, 695	99.4	1376.3	0
polyphosphate kinase 1	Pgjcvi_00143	PG JCVI SC001	polyphosphate kinase	PG TDC60	PGTDC60_0144	1, 693	98.7	1361.7	0
GTP-binding protein HflX	Pgjcvi_00144	PG JCVI SC001	GTP-binding protein	PG ATCC 33277	PGN_1813	1, 406	100	792.3	0
GTP-binding protein HflX	Pgjcvi_00144	PG JCVI SC001	GTP-binding protein HflX	PG W83	PG1886	1, 406	100	792.3	0
GTP-binding protein HflX	Pgjcvi_00144	PG JCVI SC001	GTP-binding protein HflX	PG TDC60	PGTDC60_0145	1, 406	99.3	787.7	0
tRNA 2-selenouridine synthase	Pgjcvi_00145	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1814	1, 344	98.5	675.6	0
tRNA 2-selenouridine synthase	Pgjcvi_00145	PG JCVI SC001	rhodanese-like domain protein	PG W83	PG1887	1, 344	97.4	669.1	0
tRNA 2-selenouridine synthase	Pgjcvi_00145	PG JCVI SC001	tRNA 2-selenouridine synthase	PG TDC60	PGTDC60_0146	1, 344	97.4	668.7	0
selenium metabolism protein YedF	Pgjcvi_00146	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1815	1, 204	99.5	407.9	0
selenium metabolism protein YedF	Pgjcvi_00146	PG JCVI SC001	hypothetical protein	PG W83	PG1888	1, 204	98.5	403.7	0
selenium metabolism protein YedF	Pgjcvi_00146	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0147	1, 204	98.5	406.4	0
hypothetical protein	Pgjcvi_00147	PG JCVI SC001	hypothetical protein	PG W83	PG1889	1, 219	95	434.5	0
hypothetical protein	Pgjcvi_00147	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1816	1, 220	69.1	316.2	0
hypothetical protein	Pgjcvi_00147	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0148	1, 220	66.4	305.1	0
hypothetical protein	Pgjcvi_00148	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1248	2, 38	70.3	52.8	9.10E-06
hypothetical protein	Pgjcvi_00148	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1735	3, 71	62.3	75.9	1.00E-12
hypothetical protein	Pgjcvi_00149	PG JCVI SC001	lipoprotein, putative	PG W83	PG1890	3, 75	97.3	137.5	2.10E-31
hypothetical protein	Pgjcvi_00149	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0151	1, 63	87.3	105.5	8.70E-22
hypothetical protein	Pgjcvi_00149	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1817	1, 63	84.1	100.5	2.80E-20
hypothetical protein	Pgjcvi_00150	PG JCVI SC001	hypothetical protein	PG W83	PG1891	12, 169	98.1	317	0
hypothetical protein	Pgjcvi_00150	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1820	1, 121	93.4	233.4	0
hypothetical protein	Pgjcvi_00150	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0155	1, 158	89.9	290	0
hypothetical protein	Pgjcvi_00151	PG JCVI SC001	putative integrin subunit alpha	PG TDC60	PGTDC60_0156	1, 53	83	96.7	3.50E-19
hypothetical protein	Pgjcvi_00151	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1824	1, 53	81.1	94.4	1.70E-18
RHS repeat-associated core domain	Pgjcvi_00152	PG JCVI SC001	putative integrin subunit alpha	PG TDC60	PGTDC60_0156	86, 466	84.2	662.9	0
RHS repeat-associated core domain	Pgjcvi_00152	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1821	86, 296	47.1	164.9	6.20E-39
hypothetical protein	Pgjcvi_00154	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0163	1, 180	94.4	357.8	0
hypothetical protein	Pgjcvi_00154	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1819	1, 177	92.7	347.1	0
hypothetical protein	Pgjcvi_00156	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1826	1, 231	95.7	445.7	0
hypothetical protein	Pgjcvi_00156	PG JCVI SC001	hypothetical protein	PG W83	PG1895	1, 232	94.8	442.2	0
hypothetical protein	Pgjcvi_00156	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0162	1, 229	94.3	434.5	0
S-adenosylmethionine synthetase	Pgjcvi_00157	PG JCVI SC001	S-adenosylmethionine synthetase	PG TDC60	PGTDC60_0165	1, 429	99.5	848.2	0
S-adenosylmethionine synthetase	Pgjcvi_00157	PG JCVI SC001	S-adenosylmethionine synthetase	PG W83	PG1896	1, 429	99.3	847	0
S-adenosylmethionine synthetase	Pgjcvi_00157	PG JCVI SC001	S-adenosylmethionine synthase	PG ATCC 33277	PGN_1827	1, 429	98.4	840.1	0
thiamine pyrophosphokinase	Pgjcvi_00158	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1828	15, 239	100	456.4	0
thiamine pyrophosphokinase	Pgjcvi_00158	PG JCVI SC001	thiamin pyrophosphokinase catalytic domain protein	PG W83	PG1897	1, 225	100	456.4	0
thiamine pyrophosphokinase	Pgjcvi_00158	PG JCVI SC001	thiamin pyrophosphokinase catalytic subunit	PG TDC60	PGTDC60_0166	1, 225	100	456.4	0
nicotinamide mononucleotide transporter PnuC	Pgjcvi_00159	PG JCVI SC001	transporter, putative	PG W83	PG1898	1, 202	100	412.1	0
nicotinamide mononucleotide transporter PnuC	Pgjcvi_00159	PG JCVI SC001	transporter	PG TDC60	PGTDC60_0167	1, 202	100	412.1	0
nicotinamide mononucleotide transporter PnuC	Pgjcvi_00159	PG JCVI SC001	probable nicotinamide mononucleotide transporter	PG ATCC 33277	PGN_1829	1, 193	99	394	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00160	PG JCVI SC001	putative TonB-dependent receptor	PG ATCC 33277	PGN_1830	50, 794	99.5	1506.9	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00160	PG JCVI SC001	TonB-dependent receptor, putative	PG W83	PG1899	50, 794	99.5	1506.1	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00160	PG JCVI SC001	TonB-dependent receptor	PG TDC60	PGTDC60_0168	50, 794	99.2	1503	0
ribosome small subunit-dependent GTPase A	Pgjcvi_00162	PG JCVI SC001	putative GTPase	PG ATCC 33277	PGN_1831	1, 315	99.4	633.6	0
ribosome small subunit-dependent GTPase A	Pgjcvi_00162	PG JCVI SC001	ribosome-associated GTPase	PG W83	PG1900	1, 315	99.4	633.6	0
ribosome small subunit-dependent GTPase A	Pgjcvi_00162	PG JCVI SC001	ribosome-associated GTPase	PG TDC60	PGTDC60_0169	1, 315	99	632.5	0
ribosome recycling factor	Pgjcvi_00163	PG JCVI SC001	ribosome releasing factor	PG W83	PG1901	1, 173	100	339.3	0
ribosome recycling factor	Pgjcvi_00163	PG JCVI SC001	ribosome recycling factor	PG TDC60	PGTDC60_0170	1, 186	100	362.5	0
ribosome recycling factor	Pgjcvi_00163	PG JCVI SC001	putative ribosome recycling factor	PG ATCC 33277	PGN_1832	1, 186	99.5	360.1	0
uridylate kinase	Pgjcvi_00164	PG JCVI SC001	putative uridylate kinase	PG ATCC 33277	PGN_1833	1, 239	99.6	473	0
uridylate kinase	Pgjcvi_00164	PG JCVI SC001	uridylate kinase	PG W83	PG1902	1, 239	99.6	473	0
uridylate kinase	Pgjcvi_00164	PG JCVI SC001	uridylate kinase	PG TDC60	PGTDC60_0171	1, 239	99.2	470.3	0
hypothetical protein	Pgjcvi_00165	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1834	1, 663	99.8	1351.7	0
hypothetical protein	Pgjcvi_00165	PG JCVI SC001	hypothetical protein	PG W83	PG1903	1, 663	99.8	1351.7	0
hypothetical protein	Pgjcvi_00165	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0172	1, 663	99.8	1352.4	0
Protein of unknown function (DUF1661).	Pgjcvi_00166	PG JCVI SC001	hypothetical protein	PG W83	PG1904	22, 109	97.7	173.3	6.60E-42
Protein of unknown function (DUF1661).	Pgjcvi_00166	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1835	14, 101	96.6	170.6	4.30E-41
Protein of unknown function (DUF1661).	Pgjcvi_00166	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0173	14, 94	95.1	155.6	1.40E-36
ribosomal protein L17	Pgjcvi_00167	PG JCVI SC001	50S ribosomal protein L17	PG ATCC 33277	PGN_1840	1, 160	99.4	313.5	0
ribosomal protein L17	Pgjcvi_00167	PG JCVI SC001	ribosomal protein L17	PG W83	PG1910	1, 160	99.4	313.5	0
ribosomal protein L17	Pgjcvi_00167	PG JCVI SC001	50S ribosomal protein L17	PG TDC60	PGTDC60_0180	1, 159	98.1	305.4	0
DNA-directed RNA polymerase, alpha subunit, bacterial and chloroplast-type	Pgjcvi_00168	PG JCVI SC001	DNA-directed RNA polymerase alpha subunit	PG ATCC 33277	PGN_1841	1, 330	100	632.9	0
DNA-directed RNA polymerase, alpha subunit, bacterial and chloroplast-type	Pgjcvi_00168	PG JCVI SC001	DNA-directed RNA polymerase alpha subunit	PG W83	PG1911	1, 330	100	632.9	0
DNA-directed RNA polymerase, alpha subunit, bacterial and chloroplast-type	Pgjcvi_00168	PG JCVI SC001	DNA-directed RNA polymerase subunit alpha	PG TDC60	PGTDC60_0181	1, 330	99.7	631.3	0
ribosomal protein S4, bacterial/organelle type	Pgjcvi_00169	PG JCVI SC001	30S ribosomal protein S4	PG ATCC 33277	PGN_1842	1, 201	100	405.6	0
ribosomal protein S4, bacterial/organelle type	Pgjcvi_00169	PG JCVI SC001	30S ribosomal protein S4	PG W83	PG1912	1, 201	100	405.6	0
ribosomal protein S4, bacterial/organelle type	Pgjcvi_00169	PG JCVI SC001	30S ribosomal protein S4	PG TDC60	PGTDC60_0182	1, 201	100	405.6	0
30S ribosomal protein S11	Pgjcvi_00170	PG JCVI SC001	30S ribosomal protein S11	PG ATCC 33277	PGN_1843	1, 128	100	257.3	0

30S ribosomal protein S11	Pgjcvi_00170	PG JCVI SC001	30S ribosomal protein S11	PG W83	PG1913	1, 128	100	257.3	0
30S ribosomal protein S11	Pgjcvi_00170	PG JCVI SC001	30S ribosomal protein S11	PG TDC60	PGTDC60_0183	1, 128	100	257.3	0
30S ribosomal protein S13	Pgjcvi_00171	PG JCVI SC001	30S ribosomal protein S13	PG ATCC 33277	PGN_1844	1, 126	100	250.4	0
30S ribosomal protein S13	Pgjcvi_00171	PG JCVI SC001	30S ribosomal protein S13	PG W83	PG1914	1, 126	100	250.4	0
30S ribosomal protein S13	Pgjcvi_00171	PG JCVI SC001	30S ribosomal protein S13	PG TDC60	PGTDC60_0184	1, 126	99.2	247.3	0
ribosomal protein L36, bacterial type	Pgjcvi_00172	PG JCVI SC001	50S ribosomal protein L36	PG ATCC 33277	PGN_1845	1, 38	100	80.5	1.60E-14
ribosomal protein L36, bacterial type	Pgjcvi_00172	PG JCVI SC001	ribosomal protein L36	PG W83	PG1915	1, 38	100	80.5	1.60E-14
ribosomal protein L36, bacterial type	Pgjcvi_00172	PG JCVI SC001	50S ribosomal protein L36	PG TDC60	PGTDC60_0185	1, 38	100	80.5	1.60E-14
translation initiation factor IF-1	Pgjcvi_00173	PG JCVI SC001	translation initiation factor IF-1	PG ATCC 33277	PGN_1846	1, 72	100	145.2	9.80E-34
translation initiation factor IF-1	Pgjcvi_00173	PG JCVI SC001	translation initiation factor IF-1	PG W83	PG1916	1, 72	100	145.2	9.80E-34
translation initiation factor IF-1	Pgjcvi_00173	PG JCVI SC001	translation initiation factor IF-1	PG TDC60	PGTDC60_0186	1, 72	100	145.2	9.80E-34
methionine aminopeptidase, type I	Pgjcvi_00174	PG JCVI SC001	methionine aminopeptidase, type I	PG TDC60	PGTDC60_0187	1, 261	99.6	525.4	0
methionine aminopeptidase, type I	Pgjcvi_00174	PG JCVI SC001	putative methionine aminopeptidase type I	PG ATCC 33277	PGN_1847	1, 261	99.2	523.5	0
methionine aminopeptidase, type I	Pgjcvi_00174	PG JCVI SC001	methionine aminopeptidase, type I	PG W83	PG1917	1, 261	98.5	522.3	0
preprotein translocase, SecY subunit	Pgjcvi_00175	PG JCVI SC001	preprotein translocase SecY subunit	PG ATCC 33277	PGN_1848	1, 446	99.8	854	0
preprotein translocase, SecY subunit	Pgjcvi_00175	PG JCVI SC001	preprotein translocase SecY	PG W83	PG1918	1, 446	99.8	854	0
preprotein translocase, SecY subunit	Pgjcvi_00175	PG JCVI SC001	preprotein translocase subunit SecY	PG TDC60	PGTDC60_0188	1, 446	99.8	854	0
ribosomal protein L15, bacterial/organelle	Pgjcvi_00176	PG JCVI SC001	ribosomal protein L15	PG W83	PG1919	1, 148	99.3	281.2	0
ribosomal protein L15, bacterial/organelle	Pgjcvi_00176	PG JCVI SC001	50S ribosomal protein L15	PG TDC60	PGTDC60_0189	1, 148	99.3	281.2	0
ribosomal protein L15, bacterial/organelle	Pgjcvi_00176	PG JCVI SC001	50S ribosomal protein L15	PG ATCC 33277	PGN_1849	1, 148	98.6	279.6	0
ribosomal protein S5, bacterial/organelle type	Pgjcvi_00177	PG JCVI SC001	ribosomal protein S5	PG W83	PG1921	1, 172	100	334	0
ribosomal protein S5, bacterial/organelle type	Pgjcvi_00177	PG JCVI SC001	30S ribosomal protein S5	PG TDC60	PGTDC60_0191	1, 172	100	334	0
ribosomal protein S5, bacterial/organelle type	Pgjcvi_00177	PG JCVI SC001	30S ribosomal protein S5	PG ATCC 33277	PGN_1851	1, 172	99.4	332.8	0
ribosomal protein L18, bacterial type	Pgjcvi_00178	PG JCVI SC001	50S ribosomal protein L18	PG ATCC 33277	PGN_1852	1, 114	99.1	217.2	0
ribosomal protein L18, bacterial type	Pgjcvi_00178	PG JCVI SC001	50S ribosomal protein L18	PG TDC60	PGTDC60_0192	1, 114	99.1	217.2	0
ribosomal protein L18, bacterial type	Pgjcvi_00178	PG JCVI SC001	ribosomal protein L18	PG W83	PG1922	1, 114	98.2	216.1	0
ribosomal protein L6, bacterial type	Pgjcvi_00179	PG JCVI SC001	50S ribosomal protein L6	PG ATCC 33277	PGN_1853	1, 183	100	359.8	0
ribosomal protein L6, bacterial type	Pgjcvi_00179	PG JCVI SC001	50S ribosomal protein L6	PG W83	PG1923	1, 183	100	359.8	0
ribosomal protein L6, bacterial type	Pgjcvi_00179	PG JCVI SC001	50S ribosomal protein L6	PG TDC60	PGTDC60_0193	1, 183	100	359.8	0
Ribosomal protein S8	Pgjcvi_00180	PG JCVI SC001	30S ribosomal protein S8	PG ATCC 33277	PGN_1854	1, 131	100	261.2	0
Ribosomal protein S8	Pgjcvi_00180	PG JCVI SC001	ribosomal protein S8	PG W83	PG1924	1, 131	100	261.2	0
Ribosomal protein S8	Pgjcvi_00180	PG JCVI SC001	30S ribosomal protein S8	PG TDC60	PGTDC60_0194	1, 131	100	261.2	0
Ribosomal protein S14	Pgjcvi_00181	PG JCVI SC001	30S ribosomal protein S14	PG ATCC 33277	PGN_1855	1, 89	100	177.6	2.20E-43
Ribosomal protein S14	Pgjcvi_00181	PG JCVI SC001	ribosomal protein S14	PG W83	PG1925	1, 89	100	177.6	2.20E-43
Ribosomal protein S14	Pgjcvi_00181	PG JCVI SC001	30S ribosomal protein S14	PG TDC60	PGTDC60_0195	1, 89	100	177.6	2.20E-43
Ribosomal protein L5	Pgjcvi_00182	PG JCVI SC001	50S ribosomal protein L5	PG ATCC 33277	PGN_1856	1, 186	100	360.5	0
Ribosomal protein L5	Pgjcvi_00182	PG JCVI SC001	50S ribosomal protein L5	PG W83	PG1926	1, 186	100	360.5	0
Ribosomal protein L5	Pgjcvi_00182	PG JCVI SC001	50S ribosomal protein L5	PG TDC60	PGTDC60_0196	1, 186	100	360.5	0
ribosomal protein L24, bacterial/organelle	Pgjcvi_00183	PG JCVI SC001	50S ribosomal protein L24	PG ATCC 33277	PGN_1857	13, 106	100	186.4	0
ribosomal protein L24, bacterial/organelle	Pgjcvi_00183	PG JCVI SC001	50S ribosomal protein L24	PG W83	PG1927	13, 106	100	186.4	0
ribosomal protein L24, bacterial/organelle	Pgjcvi_00183	PG JCVI SC001	50S ribosomal protein L24	PG TDC60	PGTDC60_0197	13, 106	100	186.4	0
ribosomal protein L14, bacterial/organelle	Pgjcvi_00184	PG JCVI SC001	50S ribosomal protein L14	PG ATCC 33277	PGN_1858	1, 121	100	232.3	0
ribosomal protein L14, bacterial/organelle	Pgjcvi_00184	PG JCVI SC001	50S ribosomal protein L14	PG W83	PG1928	1, 121	100	232.3	0
ribosomal protein L14, bacterial/organelle	Pgjcvi_00184	PG JCVI SC001	50S ribosomal protein L14	PG TDC60	PGTDC60_0198	1, 121	100	232.3	0
30S ribosomal protein S17	Pgjcvi_00185	PG JCVI SC001	30S ribosomal protein S17	PG ATCC 33277	PGN_1859	1, 84	100	175.3	1.00E-42
30S ribosomal protein S17	Pgjcvi_00185	PG JCVI SC001	ribosomal protein S17	PG W83	PG1929	1, 84	100	175.3	1.00E-42
30S ribosomal protein S17	Pgjcvi_00185	PG JCVI SC001	30S ribosomal protein S17	PG TDC60	PGTDC60_0199	1, 84	100	175.3	1.00E-42
ribosomal protein L29	Pgjcvi_00186	PG JCVI SC001	50S ribosomal protein L29	PG ATCC 33277	PGN_1860	1, 64	100	125.2	9.30E-28
ribosomal protein L29	Pgjcvi_00186	PG JCVI SC001	50S ribosomal protein L29	PG W83	PG1930	1, 64	100	125.2	9.30E-28
ribosomal protein L29	Pgjcvi_00186	PG JCVI SC001	50S ribosomal protein L29	PG TDC60	PGTDC60_0200	1, 64	100	125.2	9.30E-28
ribosomal protein L16, bacterial/organelle	Pgjcvi_00187	PG JCVI SC001	50S ribosomal protein L16	PG ATCC 33277	PGN_1861	1, 144	100	291.2	0
ribosomal protein L16, bacterial/organelle	Pgjcvi_00187	PG JCVI SC001	50S ribosomal protein L16	PG W83	PG1931	1, 144	100	291.2	0
ribosomal protein L16, bacterial/organelle	Pgjcvi_00187	PG JCVI SC001	50S ribosomal protein L16	PG TDC60	PGTDC60_0201	1, 128	100	259.2	0
ribosomal protein S3, bacterial type	Pgjcvi_00188	PG JCVI SC001	30S ribosomal protein S3	PG ATCC 33277	PGN_1862	1, 246	100	483.4	0
ribosomal protein S3, bacterial type	Pgjcvi_00188	PG JCVI SC001	ribosomal protein S3	PG W83	PG1932	1, 246	100	483.4	0
ribosomal protein S3, bacterial type	Pgjcvi_00188	PG JCVI SC001	30S ribosomal protein S3	PG TDC60	PGTDC60_0202	1, 246	100	483.4	0
ribosomal protein L22, bacterial type	Pgjcvi_00189	PG JCVI SC001	50S ribosomal protein L22	PG ATCC 33277	PGN_1863	1, 134	100	265.8	0
ribosomal protein L22, bacterial type	Pgjcvi_00189	PG JCVI SC001	ribosomal protein L22	PG W83	PG1933	1, 116	100	231.5	0
ribosomal protein L22, bacterial type	Pgjcvi_00189	PG JCVI SC001	50S ribosomal protein L22	PG TDC60	PGTDC60_0203	1, 134	100	265.8	0
ribosomal protein S19, bacterial/organelle	Pgjcvi_00190	PG JCVI SC001	30S ribosomal protein S19	PG ATCC 33277	PGN_1864	1, 89	100	183.3	4.20E-45
ribosomal protein S19, bacterial/organelle	Pgjcvi_00190	PG JCVI SC001	30S ribosomal protein S19	PG W83	PG1934	1, 89	100	183.3	4.20E-45
ribosomal protein S19, bacterial/organelle	Pgjcvi_00190	PG JCVI SC001	30S ribosomal protein S19	PG TDC60	PGTDC60_0204	1, 89	100	183.3	4.20E-45
ribosomal protein L2, bacterial/organellar	Pgjcvi_00191	PG JCVI SC001	50S ribosomal protein L2	PG ATCC 33277	PGN_1865	1, 274	100	553.9	0
ribosomal protein L2, bacterial/organellar	Pgjcvi_00191	PG JCVI SC001	50S ribosomal protein L2	PG W83	PG1935	1, 274	100	553.9	0
ribosomal protein L2, bacterial/organellar	Pgjcvi_00191	PG JCVI SC001	50S ribosomal protein L2	PG TDC60	PGTDC60_0205	1, 274	100	553.9	0
Ribosomal protein L23	Pgjcvi_00192	PG JCVI SC001	50S ribosomal protein L23	PG ATCC 33277	PGN_1866	1, 97	100	191	0
Ribosomal protein L23	Pgjcvi_00192	PG JCVI SC001	ribosomal protein L23	PG W83	PG1936	1, 97	100	191	0
Ribosomal protein L23	Pgjcvi_00192	PG JCVI SC001	50S ribosomal protein L23	PG TDC60	PGTDC60_0206	1, 97	100	191	0
50S ribosomal protein L4, bacterial/organelle	Pgjcvi_00193	PG JCVI SC001	50S ribosomal protein L4	PG W83	PG1937	1, 209	99.5	403.7	0
50S ribosomal protein L4, bacterial/organelle	Pgjcvi_00193	PG JCVI SC001	50S ribosomal protein L4	PG TDC60	PGTDC60_0207	1, 209	99	401	0
50S ribosomal protein L4, bacterial/organelle	Pgjcvi_00193	PG JCVI SC001	50S ribosomal protein L4	PG ATCC 33277	PGN_1867	1, 209	98.6	399.8	0
50S ribosomal protein L3, bacterial	Pgjcvi_00194	PG JCVI SC001	50S ribosomal protein L3	PG ATCC 33277	PGN_1868	1, 205	100	415.2	0

50S ribosomal protein L3, bacterial	Pgjcvi_00194	PG JCVI SC001	50S ribosomal protein L3	PG W83	PG1938	1, 205	100	415.2	0
50S ribosomal protein L3, bacterial	Pgjcvi_00194	PG JCVI SC001	50S ribosomal protein L3	PG TDC60	PGTDC60_0208	1, 195	100	395.2	0
ribosomal protein S10, bacterial/organelle	Pgjcvi_00195	PG JCVI SC001	30S ribosomal protein S10	PG ATCC 33277	PGN_1869	1, 101	100	195.3	0
ribosomal protein S10, bacterial/organelle	Pgjcvi_00195	PG JCVI SC001	30S ribosomal protein S10	PG W83	PG1939	1, 101	100	195.3	0
ribosomal protein S10, bacterial/organelle	Pgjcvi_00195	PG JCVI SC001	30S ribosomal protein S10	PG TDC60	PGTDC60_0209	1, 101	100	195.3	0
translation elongation factor EF-G	Pgjcvi_00196	PG JCVI SC001	elongation factor G	PG TDC60	PGTDC60_0210	1, 707	100	1417.5	0
translation elongation factor EF-G	Pgjcvi_00196	PG JCVI SC001	elongation factor EF-2	PG W83	PG1940	1, 707	99.9	1415.6	0
translation elongation factor EF-G	Pgjcvi_00196	PG JCVI SC001	translation elongation factor G	PG ATCC 33277	PGN_1870	1, 707	99.7	1414.4	0
ribosomal protein S7, bacterial/organelle	Pgjcvi_00197	PG JCVI SC001	30S ribosomal protein S7	PG ATCC 33277	PGN_1871	1, 158	100	315.1	0
ribosomal protein S7, bacterial/organelle	Pgjcvi_00197	PG JCVI SC001	30S ribosomal protein S7	PG TDC60	PGTDC60_0211	1, 158	100	315.1	0
ribosomal protein S7, bacterial/organelle	Pgjcvi_00197	PG JCVI SC001	30S ribosomal protein S7	PG W83	PG1941	1, 158	99.4	312.4	0
ribosomal protein S12, bacterial/organelle	Pgjcvi_00198	PG JCVI SC001	30S ribosomal protein S12	PG W83	PG1942	1, 134	100	272.7	0
ribosomal protein S12, bacterial/organelle	Pgjcvi_00198	PG JCVI SC001	30S ribosomal protein S12	PG TDC60	PGTDC60_0212	1, 134	100	272.7	0
ribosomal protein S12, bacterial/organelle	Pgjcvi_00198	PG JCVI SC001	30S ribosomal protein S12	PG ATCC 33277	PGN_1872	1, 134	99.3	271.6	0
Protein of unknown function (DUF3667).	Pgjcvi_00199	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1873	1, 428	98.6	847	0
Protein of unknown function (DUF3667).	Pgjcvi_00199	PG JCVI SC001	hypothetical protein	PG W83	PG1943	1, 428	98.4	843.6	0
Protein of unknown function (DUF3667).	Pgjcvi_00199	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0214	1, 428	97.9	839	0
5-enolpyruvylshikimate-3-phosphate synthase	Pgjcvi_00200	PG JCVI SC001	putative 3-phosphoshikimate 1-carboxyvinyltransferase	PG ATCC 33277	PGN_1874	1, 419	98.8	824.7	0
5-enolpyruvylshikimate-3-phosphate synthase	Pgjcvi_00200	PG JCVI SC001	3-phosphoshikimate 1-carboxyvinyltransferase	PG W83	PG1944	1, 419	98.8	825.5	0
5-enolpyruvylshikimate-3-phosphate synthase	Pgjcvi_00200	PG JCVI SC001	3-phosphoshikimate 1-carboxyvinyltransferase	PG TDC60	PGTDC60_0215	1, 419	98.6	823.5	0
hypothetical protein	Pgjcvi_00201	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1875	1, 147	100	292.7	0
hypothetical protein	Pgjcvi_00201	PG JCVI SC001	hypothetical protein	PG W83	PG1945	1, 147	100	292.7	0
hypothetical protein	Pgjcvi_00201	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0216	1, 147	99.3	292.4	0
ABC-type Mn2+/Zn2+ transport systems, permease components	Pgjcvi_00202	PG JCVI SC001	ABC 3 transporter family protein	PG W83	PG1946	1, 268	100	506.5	0
ABC-type Mn2+/Zn2+ transport systems, permease components	Pgjcvi_00202	PG JCVI SC001	putative ABC transporter membrane protein	PG ATCC 33277	PGN_1876	1, 268	99.6	505.8	0
ABC-type Mn2+/Zn2+ transport systems, permease components	Pgjcvi_00202	PG JCVI SC001	ABC 3 transporter family protein	PG TDC60	PGTDC60_0217	1, 268	98.9	500.4	0
hypothetical protein	Pgjcvi_00203	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_1877	1, 1160	99.6	2289.2	0
hypothetical protein	Pgjcvi_00203	PG JCVI SC001	TPR domain protein	PG W83	PG1947	1, 1160	99.2	2279.6	0
hypothetical protein	Pgjcvi_00203	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0218	1, 1160	99	2275	0
Lysophospholipase	Pgjcvi_00204	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1878	1, 473	99.4	938.3	0
Lysophospholipase	Pgjcvi_00204	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0219	1, 473	99.2	935.6	0
Lysophospholipase	Pgjcvi_00204	PG JCVI SC001	lipoprotein, putative	PG W83	PG1948	1, 473	98.7	932.2	0
Malate/lactate dehydrogenases	Pgjcvi_00205	PG JCVI SC001	malate dehydrogenase	PG ATCC 33277	PGN_1880	1, 334	100	664.5	0
Malate/lactate dehydrogenases	Pgjcvi_00205	PG JCVI SC001	malate dehydrogenase	PG TDC60	PGTDC60_0221	1, 334	100	664.5	0
Malate/lactate dehydrogenases	Pgjcvi_00205	PG JCVI SC001	malate dehydrogenase	PG W83	PG1949	1, 334	99.7	662.1	0
Predicted permease	Pgjcvi_00206	PG JCVI SC001	probable permease	PG ATCC 33277	PGN_1882	1, 386	100	746.9	0
Predicted permease	Pgjcvi_00206	PG JCVI SC001	putative permease	PG TDC60	PGTDC60_0223	1, 386	100	746.9	0
Predicted permease	Pgjcvi_00206	PG JCVI SC001	hypothetical protein	PG W83	PG1950	1, 386	99.7	745.7	0
glutaminyl-tRNA synthetase	Pgjcvi_00207	PG JCVI SC001	glutaminyl-tRNA synthetase	PG W83	PG1951	1, 566	99.6	1163.3	0
glutaminyl-tRNA synthetase	Pgjcvi_00207	PG JCVI SC001	glutaminyl-tRNA synthetase	PG ATCC 33277	PGN_1883	1, 566	99.3	1159.4	0
glutaminyl-tRNA synthetase	Pgjcvi_00207	PG JCVI SC001	glutaminyl-tRNA synthetase	PG TDC60	PGTDC60_0224	1, 566	99.3	1159.4	0
Uncharacterized membrane-associated protein	Pgjcvi_00208	PG JCVI SC001	probable alkaline phosphatase	PG ATCC 33277	PGN_1884	1, 215	100	428.7	0
Uncharacterized membrane-associated protein	Pgjcvi_00208	PG JCVI SC001	DedA family protein	PG W83	PG1952	1, 215	100	428.7	0
Uncharacterized membrane-associated protein	Pgjcvi_00208	PG JCVI SC001	putative alkaline phosphatase	PG TDC60	PGTDC60_0225	1, 215	100	428.7	0
Uncharacterized conserved protein	Pgjcvi_00209	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1885	1, 311	100	599	0
Uncharacterized conserved protein	Pgjcvi_00209	PG JCVI SC001	YitT family protein	PG W83	PG1953	1, 311	100	599	0
Uncharacterized conserved protein	Pgjcvi_00209	PG JCVI SC001	YitT family protein	PG TDC60	PGTDC60_0226	1, 311	99.7	596.7	0
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_00210	PG JCVI SC001	NAD dependent epimerase/reductase-like protein	PG TDC60	PGTDC60_0227	1, 339	99.1	683.7	0
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_00210	PG JCVI SC001	putative NAD dependent epimerase	PG ATCC 33277	PGN_1886	1, 339	98.8	682.9	0
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_00210	PG JCVI SC001	NAD dependent epimerase/reductase-related protein	PG W83	PG1954	1, 339	98.8	681	0
hypothetical protein	Pgjcvi_00211	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0127	1, 57	91.2	108.6	1.00E-22
hypothetical protein	Pgjcvi_00211	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0228	1, 57	91.2	108.6	1.00E-22
Acetyl-CoA hydrolase	Pgjcvi_00212	PG JCVI SC001	4-hydroxybutyrate CoA-transferase	PG TDC60	PGTDC60_0229	1, 431	99.8	866.7	0
Acetyl-CoA hydrolase	Pgjcvi_00212	PG JCVI SC001	4-hydroxybutyrate CoA-transferase	PG ATCC 33277	PGN_1888	1, 431	99.3	863.2	0
Acetyl-CoA hydrolase	Pgjcvi_00212	PG JCVI SC001	4-hydroxybutyrate CoA-transferase	PG W83	PG1956	1, 431	99.3	864	0
hypothetical protein	Pgjcvi_00215	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1889	1, 49	100	100.9	1.40E-20
hypothetical protein	Pgjcvi_00215	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0230	1, 49	100	100.9	1.40E-20
ribosomal protein L33, bacterial type	Pgjcvi_00216	PG JCVI SC001	50S ribosomal protein L33	PG ATCC 33277	PGN_1890	1, 62	100	127.5	1.80E-28
ribosomal protein L33, bacterial type	Pgjcvi_00216	PG JCVI SC001	ribosomal protein L33	PG W83	PG1959	1, 62	100	127.5	1.80E-28
ribosomal protein L33, bacterial type	Pgjcvi_00216	PG JCVI SC001	50S ribosomal protein L33	PG TDC60	PGTDC60_0231	1, 62	100	127.5	1.80E-28
ribosomal protein L28	Pgjcvi_00217	PG JCVI SC001	50S ribosomal protein L28	PG ATCC 33277	PGN_1891	1, 79	100	161	1.90E-38
ribosomal protein L28	Pgjcvi_00217	PG JCVI SC001	ribosomal protein L28	PG W83	PG1960	1, 79	100	161	1.90E-38
ribosomal protein L28	Pgjcvi_00217	PG JCVI SC001	50S ribosomal protein L28	PG TDC60	PGTDC60_0232	1, 79	100	161	1.90E-38
Phosphate/sulphate permeases	Pgjcvi_00218	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0233	1, 755	100	1466.8	0
Phosphate/sulphate permeases	Pgjcvi_00218	PG JCVI SC001	hypothetical protein	PG W83	PG1961	1, 755	99.9	1464.1	0
Phosphate/sulphate permeases	Pgjcvi_00218	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1892	1, 755	99.7	1461	0
DNA-binding protein, histone-like, putative	Pgjcvi_00219	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1893	1, 203	99	392.9	0
DNA-binding protein, histone-like, putative	Pgjcvi_00219	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0234	6, 207	99	389	0
Uncharacterized conserved protein	Pgjcvi_00220	PG JCVI SC001	putative Fic family protein	PG ATCC 33277	PGN_0590	33, 276	23.3	56.6	3.00E-06
Sua5/YciO/YrdC/YwlC family protein	Pgjcvi_00221	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1895	1, 191	100	371.7	0
Sua5/YciO/YrdC/YwlC family protein	Pgjcvi_00221	PG JCVI SC001	Sua5/YciO/YrdC/YwlC family protein	PG TDC60	PGTDC60_0236	1, 191	99.5	370.2	0
Sua5/YciO/YrdC/YwlC family protein	Pgjcvi_00221	PG JCVI SC001	Sua5/YciO/YrdC/YwlC family protein	PG W83	PG1963	1, 191	99	368.6	0

exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase	Pgjcvi_00222	PG JCVI SC001	bacterial sugar transferase	PG W83	PG1964	1, 468	99.4	933.7	0
exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase	Pgjcvi_00222	PG JCVI SC001	sugar transferase	PG TDC60	PGTDC60_0237	1, 468	99.1	929.9	0
exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase	Pgjcvi_00222	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1896	1, 468	98.9	928.3	0
Chloride channel protein EriC	Pgjcvi_00223	PG JCVI SC001	putative transport related membrane protein	PG TDC60	PGTDC60_0238	1, 598	100	1179.5	0
Chloride channel protein EriC	Pgjcvi_00223	PG JCVI SC001	putative transport related membrane protein	PG ATCC 33277	PGN_1897	1, 598	99.8	1178.3	0
Small-conductance mechanosensitive channel	Pgjcvi_00224	PG JCVI SC001	probable transport protein	PG ATCC 33277	PGN_1898	1, 332	99.1	646.4	0
Small-conductance mechanosensitive channel	Pgjcvi_00224	PG JCVI SC001	putative transport protein	PG TDC60	PGTDC60_0239	1, 354	98.6	682.2	0
Small-conductance mechanosensitive channel	Pgjcvi_00224	PG JCVI SC001	hypothetical protein	PG W83	PG1966	1, 268	98.5	522.7	0
Tetratricopeptide repeat.	Pgjcvi_00225	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0240	1, 295	98.6	565.1	0
Tetratricopeptide repeat.	Pgjcvi_00225	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1899	1, 294	98	564.7	0
Tetratricopeptide repeat.	Pgjcvi_00225	PG JCVI SC001	TPR domain protein	PG W83	PG1967	1, 295	98	562	0
Por secretion system C-terminal sorting domain	Pgjcvi_00226	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0242	1, 300	99.7	611.7	0
Por secretion system C-terminal sorting domain	Pgjcvi_00226	PG JCVI SC001	hypothetical protein	PG W83	PG1969	1, 300	97.7	602.8	0
hypothetical protein	Pgjcvi_00227	PG JCVI SC001	hemagglutinin protein HagB	PG ATCC 33277	PGN_1904	1, 27	100	58.2	1.20E-07
hypothetical protein	Pgjcvi_00227	PG JCVI SC001	hemagglutinin protein HagB	PG W83	PG1972	24, 50	100	58.2	1.20E-07
hypothetical protein	Pgjcvi_00227	PG JCVI SC001	hemagglutinin protein HagB	PG TDC60	PGTDC60_0245	1, 27	100	58.2	1.20E-07
hypothetical protein	Pgjcvi_00228	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0246	1, 180	100	359.4	0
hypothetical protein	Pgjcvi_00229	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1905	35, 354	100	628.6	0
hypothetical protein	Pgjcvi_00229	PG JCVI SC001	hypothetical protein	PG W83	PG1974	44, 363	100	628.6	0
hypothetical protein	Pgjcvi_00229	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0247	1, 320	100	628.6	0
hypothetical protein	Pgjcvi_00231	PG JCVI SC001	hypothetical protein	PG W83	PG1977	1, 668	97.8	1335.5	0
hypothetical protein	Pgjcvi_00231	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0249	1, 667	96.6	1326.6	0
hypothetical protein	Pgjcvi_00231	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1907	1, 668	95.8	1304.7	0
hypothetical protein	Pgjcvi_00232	PG JCVI SC001	hypothetical protein	PG W83	PG1978	9, 204	99	382.1	0
hypothetical protein	Pgjcvi_00232	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0250	1, 196	99	381.7	0
hypothetical protein	Pgjcvi_00232	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1908	1, 37	73	49.7	0.00015
glucose-inhibited division protein A	Pgjcvi_00235	PG JCVI SC001	glucose-inhibited division protein A	PG ATCC 33277	PGN_1937	1, 625	99.4	1243.4	0
glucose-inhibited division protein A	Pgjcvi_00235	PG JCVI SC001	glucose-inhibited division protein A	PG W83	PG1992	1, 625	99.4	1242.3	0
glucose-inhibited division protein A	Pgjcvi_00235	PG JCVI SC001	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	PG TDC60	PGTDC60_0265	1, 625	98.6	1229.9	0
excinuclease ABC, C subunit	Pgjcvi_00236	PG JCVI SC001	excinuclease ABC C subunit	PG ATCC 33277	PGN_1938	1, 600	99.3	1193.7	0
excinuclease ABC, C subunit	Pgjcvi_00236	PG JCVI SC001	excinuclease ABC, C subunit	PG TDC60	PGTDC60_0266	1, 600	99.2	1191.4	0
excinuclease ABC, C subunit	Pgjcvi_00236	PG JCVI SC001	excinuclease ABC, C subunit	PG W83	PG1993	1, 599	98.8	1184.9	0
D-tyrosyl-tRNA(Tyr) deacylase	Pgjcvi_00237	PG JCVI SC001	putative D-tyrosyl-tRNA deacylase	PG ATCC 33277	PGN_1939	1, 150	100	288.9	0
D-tyrosyl-tRNA(Tyr) deacylase	Pgjcvi_00237	PG JCVI SC001	D-tyrosyl-tRNA deacylase	PG W83	PG1994	1, 150	100	288.9	0
D-tyrosyl-tRNA(Tyr) deacylase	Pgjcvi_00237	PG JCVI SC001	D-tyrosyl-tRNA(Tyr) deacylase	PG TDC60	PGTDC60_0267	1, 150	99.3	287	0
Predicted pyrophosphatase	Pgjcvi_00238	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1940	1, 116	100	232.6	0
Predicted pyrophosphatase	Pgjcvi_00238	PG JCVI SC001	hypothetical protein	PG W83	PG1995	1, 116	99.1	231.1	0
Predicted pyrophosphatase	Pgjcvi_00238	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0268	1, 116	99.1	231.5	0
deoxyribose-phosphate aldolase	Pgjcvi_00239	PG JCVI SC001	deoxyribose-phosphate aldolase	PG W83	PG1996	1, 289	99	560.1	0
deoxyribose-phosphate aldolase	Pgjcvi_00239	PG JCVI SC001	deoxyribose-phosphate aldolase	PG TDC60	PGTDC60_0269	1, 289	98.6	560.8	0
deoxyribose-phosphate aldolase	Pgjcvi_00239	PG JCVI SC001	putative deoxyribose-phosphate aldolase	PG ATCC 33277	PGN_1941	21, 309	97.2	550.8	0
hypothetical protein	Pgjcvi_00240	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1942	1, 53	94.3	107.8	1.30E-22
hypothetical protein	Pgjcvi_00240	PG JCVI SC001	hypothetical protein	PG W83	PG1997	1, 53	94.3	109.4	4.40E-23
hypothetical protein	Pgjcvi_00240	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0270	1, 53	92.5	107.1	2.20E-22
Geranylgeranyl pyrophosphate synthase	Pgjcvi_00241	PG JCVI SC001	polyprenyl synthetase	PG W83	PG1998	1, 292	99.7	558.5	0
Geranylgeranyl pyrophosphate synthase	Pgjcvi_00241	PG JCVI SC001	putative polyprenyl synthetase	PG ATCC 33277	PGN_1943	1, 324	98.8	622.1	0
Geranylgeranyl pyrophosphate synthase	Pgjcvi_00241	PG JCVI SC001	putative polyprenyl synthetase	PG TDC60	PGTDC60_0271	1, 324	98.8	622.1	0
WbqC-like protein family.	Pgjcvi_00242	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1944	1, 212	100	446.8	0
WbqC-like protein family.	Pgjcvi_00242	PG JCVI SC001	hypothetical protein	PG W83	PG1999	1, 212	99.1	441.8	0
WbqC-like protein family.	Pgjcvi_00242	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0272	1, 212	99.1	440.3	0
signal peptidase I, bacterial type	Pgjcvi_00243	PG JCVI SC001	probable signal peptidase-related protein	PG ATCC 33277	PGN_1945	1, 208	99.5	411.4	0
signal peptidase I, bacterial type	Pgjcvi_00243	PG JCVI SC001	signal peptidase-related protein	PG W83	PG2000	1, 208	99.5	414.5	0
signal peptidase I, bacterial type	Pgjcvi_00243	PG JCVI SC001	signal peptidase-like protein	PG TDC60	PGTDC60_0273	1, 167	99.4	339	0
signal peptidase I, bacterial type	Pgjcvi_00244	PG JCVI SC001	signal peptidase I	PG TDC60	PGTDC60_0274	1, 465	100	968.8	0
signal peptidase I, bacterial type	Pgjcvi_00244	PG JCVI SC001	signal peptidase I	PG W83	PG2001	1, 465	99.8	966.5	0
signal peptidase I, bacterial type	Pgjcvi_00244	PG JCVI SC001	signal peptidase I	PG ATCC 33277	PGN_1946	1, 465	99.6	964.9	0
dihydrodipicolinate reductase	Pgjcvi_00245	PG JCVI SC001	putative dihydrodipicolinate reductase	PG ATCC 33277	PGN_1947	1, 238	100	483.8	0
dihydrodipicolinate reductase	Pgjcvi_00245	PG JCVI SC001	dihydrodipicolinate reductase	PG W83	PG2002	1, 238	100	483.8	0
dihydrodipicolinate reductase	Pgjcvi_00245	PG JCVI SC001	dihydrodipicolinate reductase	PG TDC60	PGTDC60_0275	1, 238	99.2	479.6	0
deoxyguanosinetriphosphate triphosphohydrolase, putative	Pgjcvi_00246	PG JCVI SC001	deoxyguanosinetriphosphate triphosphohydrolase	PG W83	PG2003	3, 447	99.6	901.7	0
deoxyguanosinetriphosphate triphosphohydrolase, putative	Pgjcvi_00246	PG JCVI SC001	deoxyguanosinetriphosphate triphosphohydrolase	PG TDC60	PGTDC60_0276	3, 447	99.6	900.2	0
deoxyguanosinetriphosphate triphosphohydrolase, putative	Pgjcvi_00246	PG JCVI SC001	deoxyguanosinetriphosphate triphosphohydrolase	PG ATCC 33277	PGN_1948	3, 447	99.3	899	0
Predicted membrane protein	Pgjcvi_00247	PG JCVI SC001	hypothetical protein	PG W83	PG2004	1, 330	99.7	637.1	0
Predicted membrane protein	Pgjcvi_00247	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0277	1, 282	99.6	541.6	0
Predicted membrane protein	Pgjcvi_00247	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1949	1, 330	99.4	635.6	0
hypothetical protein	Pgjcvi_00248	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1951	1, 119	99.2	241.9	0
hypothetical protein	Pgjcvi_00248	PG JCVI SC001	hypothetical protein	PG W83	PG2006	1, 119	99.2	241.9	0
hypothetical protein	Pgjcvi_00248	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0279	1, 119	99.2	241.9	0
hypothetical protein	Pgjcvi_00249	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1952	1, 39	94.9	81.6	1.10E-14
hypothetical protein	Pgjcvi_00249	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0280	1, 39	94.9	81.6	1.10E-14
Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_00250	PG JCVI SC001	TonB-dependent outer membrane receptor	PG ATCC 33277	PGN_1953	1, 833	99.8	1679.5	0
Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_00250	PG JCVI SC001	TonB-dependent receptor, putative	PG W83	PG2008	1, 833	99.6	1678.3	0

Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_00250	PG JCVI SC001	TonB-dependent receptor	PG TDC60	PGTDC60_0281	1, 833	99.6	1677.5	0
Recombinational DNA repair protein (RecF pathway)	Pgjcvi_00251	PG JCVI SC001	DNA repair protein RecO, putative	PG W83	PG2009	1, 245	99.6	492.7	0
Recombinational DNA repair protein (RecF pathway)	Pgjcvi_00251	PG JCVI SC001	probable DNA repair protein RecO	PG ATCC 33277	PGN_1954	1, 245	99.2	490.7	0
Recombinational DNA repair protein (RecF pathway)	Pgjcvi_00251	PG JCVI SC001	DNA repair protein RecO	PG TDC60	PGTDC60_0282	1, 245	99.2	490.7	0
Phosphomannomutase	Pgjcvi_00252	PG JCVI SC001	phosphomannomutase, putative	PG W83	PG2010	1, 550	99.8	1097	0
Phosphomannomutase	Pgjcvi_00252	PG JCVI SC001	phosphomannomutase	PG ATCC 33277	PGN_1955	1, 582	99.3	1154	0
Phosphomannomutase	Pgjcvi_00252	PG JCVI SC001	phosphomannomutase	PG TDC60	PGTDC60_0283	1, 582	99	1148.3	0
Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	Pgjcvi_00253	PG JCVI SC001	hypothetical protein	PG W83	PG2021	1, 643	98.4	1286.6	0
Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	Pgjcvi_00253	PG JCVI SC001	putative sulfatase	PG ATCC 33277	PGN_1967	1, 640	97.8	1273.5	0
Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	Pgjcvi_00253	PG JCVI SC001	putative sulfatase	PG TDC60	PGTDC60_0297	1, 643	97.7	1275.4	0
hypothetical protein	Pgjcvi_00254	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0298	1, 847	99.3	1682.5	0
hypothetical protein	Pgjcvi_00254	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1968	1, 847	98.9	1679.1	0
hypothetical protein	Pgjcvi_00254	PG JCVI SC001	hypothetical protein	PG W83	PG2022	1, 847	98.8	1677.1	0
methionyl-tRNA formyltransferase	Pgjcvi_00255	PG JCVI SC001	putative methionyl-tRNA formyltransferase	PG ATCC 33277	PGN_1969	11, 323	99.7	632.9	0
methionyl-tRNA formyltransferase	Pgjcvi_00255	PG JCVI SC001	methionyl-tRNA formyltransferase	PG TDC60	PGTDC60_0299	11, 323	99.7	632.1	0
methionyl-tRNA formyltransferase	Pgjcvi_00255	PG JCVI SC001	methionyl-tRNA formyltransferase	PG W83	PG2023	11, 323	99	627.1	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	540, 919	99.5	770	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	537, 916	99.2	768.5	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	521, 900	98.9	766.5	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1272, 1377	53.4	108.2	7.20E-22
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	1249, 1354	53.4	108.2	7.20E-22
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	1269, 1372	52.6	106.3	2.80E-21
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	912, 955	48.9	45.8	0.0044
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	893, 936	48.9	45.8	0.0044
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	1365, 1638	47.5	254.6	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	1346, 1618	46.6	251.5	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1369, 1641	46.4	251.5	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25.	Pgjcvi_00257	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	885, 952	37.8	47	0.002
Peptidase family C25.	Pgjcvi_00258	PG JCVI SC001	arginine-specific cysteine proteinase	PG W83	PG0506	269, 569	94.4	588.2	0
Peptidase family C25.	Pgjcvi_00258	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	264, 564	93.4	582.4	0
Peptidase family C25.	Pgjcvi_00258	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	248, 548	93.4	583.6	0
Peptidase family C25./Propeptide_C25.	Pgjcvi_00259	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1, 270	100	535.4	0
Peptidase family C25./Propeptide_C25.	Pgjcvi_00259	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	1, 251	100	499.2	0
Peptidase family C25./Propeptide_C25.	Pgjcvi_00259	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	1, 267	99.6	528.5	0
Fructose-2,6-bisphosphatase	Pgjcvi_00260	PG JCVI SC001	probable phosphoglycerate mutase	PG ATCC 33277	PGN_1973	1, 172	99.4	354.4	0
Fructose-2,6-bisphosphatase	Pgjcvi_00260	PG JCVI SC001	phosphoglycerate mutase family protein	PG W83	PG2026	1, 177	98.9	362.5	0
Fructose-2,6-bisphosphatase	Pgjcvi_00260	PG JCVI SC001	phosphoglycerate mutase family protein	PG TDC60	PGTDC60_0303	1, 177	98.9	363.6	0
hypothetical protein	Pgjcvi_00261	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0304	1, 153	96.7	310.5	0
hypothetical protein	Pgjcvi_00261	PG JCVI SC001	hypothetical protein	PG W83	PG2027	2, 174	96.5	344	0
hypothetical protein	Pgjcvi_00261	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1974	2, 174	95.4	339	0
ybaK/ebsC protein	Pgjcvi_00262	PG JCVI SC001	putative regulatory protein	PG ATCC 33277	PGN_1975	1, 169	100	340.1	0
ybaK/ebsC protein	Pgjcvi_00262	PG JCVI SC001	ebsC protein	PG TDC60	PGTDC60_0305	5, 173	99.4	337	0
ybaK/ebsC protein	Pgjcvi_00262	PG JCVI SC001	ebsC protein	PG W83	PG2028	1, 169	98.8	336.7	0
Matrixin.	Pgjcvi_00263	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1976	1, 859	99.9	1729.1	0
Matrixin.	Pgjcvi_00263	PG JCVI SC001	hypothetical protein	PG W83	PG2029	1, 859	99.8	1727.2	0
Matrixin.	Pgjcvi_00263	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0306	1, 850	99.8	1708	0
hypothetical protein	Pgjcvi_00264	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1977	1, 211	99.5	424.9	0
hypothetical protein	Pgjcvi_00264	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0308	1, 177	98.9	357.8	0
hypothetical protein	Pgjcvi_00264	PG JCVI SC001	hypothetical protein	PG W83	PG2030	1, 193	97.9	386.7	0
Uncharacterized conserved protein	Pgjcvi_00265	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1978	1, 131	100	276.6	0
Uncharacterized conserved protein	Pgjcvi_00265	PG JCVI SC001	hypothetical protein	PG W83	PG2031	12, 150	100	292.4	0
Uncharacterized conserved protein	Pgjcvi_00265	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0309	1, 131	99.2	276.2	0
primosomal protein N''	Pgjcvi_00266	PG JCVI SC001	primosomal protein N	PG ATCC 33277	PGN_1979	1, 837	100	1647.1	0
primosomal protein N''	Pgjcvi_00266	PG JCVI SC001	primosomal protein N'	PG TDC60	PGTDC60_0310	1, 837	99.3	1637.5	0
primosomal protein N''	Pgjcvi_00266	PG JCVI SC001	primosomal protein N'	PG W83	PG2032	1, 837	99.2	1633.2	0
glutamate synthase (NADPH), homotetrameric	Pgjcvi_00267	PG JCVI SC001	glutamate synthase, small subunit	PG W83	PG2033	1, 462	100	911.4	0
glutamate synthase (NADPH), homotetrameric	Pgjcvi_00267	PG JCVI SC001	putative NADPH-dependent glutamate synthase	PG ATCC 33277	PGN_1980	1, 462	99.8	908.7	0
glutamate synthase (NADPH), homotetrameric	Pgjcvi_00267	PG JCVI SC001	glutamate synthase, small subunit	PG TDC60	PGTDC60_0311	1, 490	99.6	960.7	0
2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	Pgjcvi_00268	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1981	1, 263	100	512.7	0
2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	Pgjcvi_00268	PG JCVI SC001	oxidoreductase, FAD-binding, putative	PG W83	PG2034	1, 263	100	512.7	0

2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	Pgjcvi_00268	PG JCVI SC001	ferredoxin-NADP(+) reductase alpha subunit	PG TDC60	PGTDC60_0312	1, 263	99.6	510.8	0
tRNA (guanine-N1)-methyltransferase	Pgjcvi_00269	PG JCVI SC001	tRNA (guanine-N(1)-)-methyltransferase	PG W83	PG2035	1, 225	99.6	451.8	0
tRNA (guanine-N1)-methyltransferase	Pgjcvi_00269	PG JCVI SC001	tRNA (guanine-N(1)-)-methyltransferase	PG TDC60	PGTDC60_0313	1, 225	99.1	450.3	0
tRNA (guanine-N1)-methyltransferase	Pgjcvi_00269	PG JCVI SC001	putative tRNA guanine 1-methyltransferase	PG ATCC 33277	PGN_1982	1, 225	98.7	451.1	0
Kef-type K+ transport systems, predicted NAD-binding component	Pgjcvi_00270	PG JCVI SC001	putative ion transporter	PG ATCC 33277	PGN_1983	1, 303	99.7	604	0
Kef-type K+ transport systems, predicted NAD-binding component	Pgjcvi_00270	PG JCVI SC001	ion transporter	PG TDC60	PGTDC60_0314	1, 303	99.7	600.9	0
Kef-type K+ transport systems, predicted NAD-binding component	Pgjcvi_00270	PG JCVI SC001	ion transporter	PG W83	PG2036	1, 303	99	600.1	0
hypothetical protein	Pgjcvi_00271	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1984	1, 73	97.3	147.9	1.50E-34
hypothetical protein	Pgjcvi_00271	PG JCVI SC001	hypothetical protein	PG W83	PG2037	1, 73	97.3	147.9	1.50E-34
hypothetical protein	Pgjcvi_00271	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0315	1, 73	97.3	147.9	1.50E-34
Negative regulator of beta-lactamase expression	Pgjcvi_00272	PG JCVI SC001	N-acetylmuramoyl-L-alanine amidase	PG TDC60	PGTDC60_0316	1, 149	99.3	316.2	0
Negative regulator of beta-lactamase expression	Pgjcvi_00272	PG JCVI SC001	N-acetylmuramoyl-L-alanine amidase, putative	PG W83	PG2038	1, 132	99.2	282	0
Negative regulator of beta-lactamase expression	Pgjcvi_00272	PG JCVI SC001	probable N-acetylmuramoyl-L-alanine amidase	PG ATCC 33277	PGN_1985	1, 149	98.7	313.9	0
DNA-binding protein, histone-like, putative	Pgjcvi_00273	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG2040	1, 158	100	309.3	0
DNA-binding protein, histone-like, putative	Pgjcvi_00273	PG JCVI SC001	histone-like family DNA-binding protein	PG TDC60	PGTDC60_0317	1, 158	100	309.3	0
DNA-binding protein, histone-like, putative	Pgjcvi_00273	PG JCVI SC001	DNA-binding protein, histone-like family	PG ATCC 33277	PGN_1986	1, 158	99.4	305.8	0
hypothetical protein	Pgjcvi_00274	PG JCVI SC001	hypothetical protein	PG W83	PG2041	1, 243	99.6	498.8	0
hypothetical protein	Pgjcvi_00274	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0318	1, 243	98.8	494.2	0
hypothetical protein	Pgjcvi_00274	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1987	1, 243	97.9	489.2	0
Thiol-disulfide isomerase and thioredoxins	Pgjcvi_00275	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1988	1, 505	99.6	1018.5	0
Thiol-disulfide isomerase and thioredoxins	Pgjcvi_00275	PG JCVI SC001	thioredoxin family protein	PG W83	PG2042	1, 336	98.8	676.4	0
Protein of unknown function (DUF3575).	Pgjcvi_00276	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1255	1, 197	100	420.6	0
Protein of unknown function (DUF3575).	Pgjcvi_00276	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0129	1, 197	99.5	419.5	0
Protein of unknown function (DUF3575).	Pgjcvi_00276	PG JCVI SC001	hypothetical protein	PG W83	PG2168	1, 189	98.9	401.7	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00277	PG JCVI SC001	immunoreactive 53 kDa antigen PG123	PG TDC60	PGTDC60_1256	11, 489	99.6	929.9	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00277	PG JCVI SC001	immunoreactive 53 kDa antigen PG123	PG W83	PG2167	1, 479	99.2	926	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00277	PG JCVI SC001	immunoreactive 53 kDa antigen	PG ATCC 33277	PGN_0128	1, 479	98.1	916.8	0
glycyl-tRNA synthetase, dimeric type	Pgjcvi_00279	PG JCVI SC001	glycyl-tRNA synthetase	PG W83	PG2165	1, 515	100	1045.8	0
glycyl-tRNA synthetase, dimeric type	Pgjcvi_00279	PG JCVI SC001	glycyl-tRNA synthetase	PG ATCC 33277	PGN_0209	1, 515	99.8	1044.3	0
glycyl-tRNA synthetase, dimeric type	Pgjcvi_00279	PG JCVI SC001	glycyl-tRNA synthetase	PG TDC60	PGTDC60_1258	1, 515	99.6	1042.3	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_00280	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0208	1, 185	98.4	369	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_00280	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, FKBP-type	PG W83	PG2164	1, 185	97.3	364.4	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_00280	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, FKBP-type	PG TDC60	PGTDC60_1259	1, 185	96.8	362.1	0
5''/3''-nucleotidase SurE	Pgjcvi_00281	PG JCVI SC001	probable stationary-phase survival protein	PG ATCC 33277	PGN_0207	1, 256	100	516.5	0
5''/3''-nucleotidase SurE	Pgjcvi_00281	PG JCVI SC001	acid phosphatase	PG W83	PG2163	1, 256	100	516.5	0
5''/3''-nucleotidase SurE	Pgjcvi_00281	PG JCVI SC001	stationary phase survival protein SurE	PG TDC60	PGTDC60_1260	1, 256	99.6	515.4	0
lipid-A-disaccharide synthase	Pgjcvi_00282	PG JCVI SC001	lipid A disaccharide synthase	PG W83	PG2162	1, 383	99.2	766.5	0
lipid-A-disaccharide synthase	Pgjcvi_00282	PG JCVI SC001	lipid A disaccharide synthase	PG TDC60	PGTDC60_1261	1, 383	99.2	765.4	0
lipid-A-disaccharide synthase	Pgjcvi_00282	PG JCVI SC001	putative lipid A disaccharide synthase	PG ATCC 33277	PGN_0206	1, 383	99	765	0
AraC-type DNA-binding domain-containing proteins	Pgjcvi_00283	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0205	1, 299	99.3	611.7	0
AraC-type DNA-binding domain-containing proteins	Pgjcvi_00283	PG JCVI SC001	AraC family transcriptional regulator	PG TDC60	PGTDC60_1262	1, 299	99	609	0
AraC-type DNA-binding domain-containing proteins	Pgjcvi_00283	PG JCVI SC001	transcriptional regulator, AraC family	PG W83	PG2161	1, 299	98.3	605.9	0
dinuclear metal center protein, YbgI/SA1388 family	Pgjcvi_00284	PG JCVI SC001	conserved hypothetical protein TIGR00486	PG W83	PG2043	1, 364	99.2	726.1	0
dinuclear metal center protein, YbgI/SA1388 family	Pgjcvi_00284	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0320	1, 364	98.9	723.4	0
dinuclear metal center protein, YbgI/SA1388 family	Pgjcvi_00284	PG JCVI SC001	conserved hypothetical protein with NIF3 domain	PG ATCC 33277	PGN_1989	21, 384	98.4	718.4	0
Zn-ribbon protein, possibly nucleic acid-binding	Pgjcvi_00285	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1990	1, 251	99.2	479.6	0
Zn-ribbon protein, possibly nucleic acid-binding	Pgjcvi_00285	PG JCVI SC001	hypothetical protein	PG W83	PG2044	1, 251	99.2	479.9	0
Zn-ribbon protein, possibly nucleic acid-binding	Pgjcvi_00285	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0321	1, 251	99.2	479.9	0
tRNA(Ile)-lysidine synthetase, N-terminal domain/tRNA(Ile)-lysidine synthetase, C-terminal domain	Pgjcvi_00286	PG JCVI SC001	hypothetical protein	PG W83	PG2046	1, 454	98.9	899	0
tRNA(Ile)-lysidine synthetase, N-terminal domain/tRNA(Ile)-lysidine synthetase, C-terminal domain	Pgjcvi_00286	PG JCVI SC001	putative cell-cycle protein	PG TDC60	PGTDC60_0322	1, 454	98.9	899	0
tRNA(Ile)-lysidine synthetase, N-terminal domain/tRNA(Ile)-lysidine synthetase, C-terminal domain	Pgjcvi_00286	PG JCVI SC001	putative cell-cycle protein	PG ATCC 33277	PGN_1991	1, 454	98.5	897.1	0
PIF1 helicase.	Pgjcvi_00287	PG JCVI SC001	putative helicase	PG ATCC 33277	PGN_1992	1, 761	98.8	1493.4	0
PIF1 helicase.	Pgjcvi_00287	PG JCVI SC001	helicase	PG TDC60	PGTDC60_0323	1, 761	98.7	1491.1	0
PIF1 helicase.	Pgjcvi_00287	PG JCVI SC001	helicase, putative	PG W83	PG2047	1, 761	98.3	1487.2	0
hypothetical protein	Pgjcvi_00288	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1993	1, 126	99.2	253.4	0
hypothetical protein	Pgjcvi_00288	PG JCVI SC001	hypothetical protein	PG W83	PG2048	1, 126	99.2	253.4	0
hypothetical protein	Pgjcvi_00288	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0324	1, 126	99.2	253.4	0
hypothetical protein	Pgjcvi_00289	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1994	1, 125	100	243.8	0
hypothetical protein	Pgjcvi_00289	PG JCVI SC001	hypothetical protein	PG W83	PG2049	1, 125	99.2	241.1	0
hypothetical protein	Pgjcvi_00289	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0325	1, 125	97.6	238.4	0
hypothetical protein	Pgjcvi_00290	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1995	1, 91	100	180.6	2.70E-44
hypothetical protein	Pgjcvi_00290	PG JCVI SC001	hypothetical protein	PG W83	PG2050	1, 91	100	180.6	2.70E-44
hypothetical protein	Pgjcvi_00290	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0326	1, 91	100	180.6	2.70E-44
dihydrodipicolinate synthase	Pgjcvi_00291	PG JCVI SC001	dihydrodipicolinate synthase	PG TDC60	PGTDC60_0327	1, 297	99.3	577.4	0
dihydrodipicolinate synthase	Pgjcvi_00291	PG JCVI SC001	putative dihydrodipicolinate synthase	PG ATCC 33277	PGN_1996	1, 297	99	575.9	0
dihydrodipicolinate synthase	Pgjcvi_00291	PG JCVI SC001	dihydrodipicolinate synthase	PG W83	PG2052	1, 289	98.6	559.7	0
dethiobiotin synthase	Pgjcvi_00292	PG JCVI SC001	dithiobiotin synthetase	PG W83	PG2053	1, 217	99.5	439.1	0
dethiobiotin synthase	Pgjcvi_00292	PG JCVI SC001	putative dethiobiotin synthase	PG ATCC 33277	PGN_1997	1, 217	99.1	436	0
dethiobiotin synthase	Pgjcvi_00292	PG JCVI SC001	dithiobiotin synthetase	PG TDC60	PGTDC60_0328	1, 217	98.6	436.4	0

Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00293	PG JCVI SC001	immunoreactive 23 kDa antigen	PG ATCC 33277	PGN_1998	1, 223	100	429.1	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00293	PG JCVI SC001	immunoreactive 23 kDa antigen PG3	PG TDC60	PGTDC60_0329	1, 223	100	429.1	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00293	PG JCVI SC001	lipoprotein PG3	PG W83	PG2054	1, 223	99.6	427.6	0
Dihydroorotate dehydrogenase	Pgjcvi_00294	PG JCVI SC001	dihydroorotate dehydrogenase	PG W83	PG2055	1, 326	100	629	0
Dihydroorotate dehydrogenase	Pgjcvi_00294	PG JCVI SC001	dihydroorotate dehydrogenase 2	PG TDC60	PGTDC60_0330	1, 326	100	629	0
Dihydroorotate dehydrogenase	Pgjcvi_00294	PG JCVI SC001	putative dihydroorotate dehydrogenase	PG ATCC 33277	PGN_1999	1, 326	99.7	627.1	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1706, 2104	61.6	488.4	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	1334, 1732	61.6	490	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2229, 2627	61.3	486.1	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	802, 1075	61.3	343.2	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1254, 1527	61.3	343.2	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	415, 682	60.8	334.7	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	861, 1138	60.8	343.2	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	356, 623	60.8	335.5	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1317, 1594	60.1	339.3	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1773, 2050	59.7	337.8	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	880, 1155	50.5	271.2	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2054, 2286	43.2	185.7	4.20E-45
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	1159, 1391	43.2	186	4.20E-45
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	686, 918	42.8	183	2.90E-44
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1142, 1374	42.8	183	2.90E-44
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1598, 1830	42.8	183	2.90E-44
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	627, 859	42.8	183.7	1.70E-44
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1079, 1311	42.8	184.1	1.40E-44
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1531, 1763	42.8	183.7	1.70E-44
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	145, 432	38.2	192.6	0
Cleaved Adhesin Domain./Propeptide_C25.	Pgjcvi_00295	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	204, 491	37.5	185.3	5.60E-45
Signal transduction histidine kinase	Pgjcvi_00298	PG JCVI SC001	sensor histidine kinase	PG TDC60	PGTDC60_0334	1, 395	99.5	770	0
Signal transduction histidine kinase	Pgjcvi_00298	PG JCVI SC001	putative sensor histidine kinase	PG ATCC 33277	PGN_2001	1, 395	99.2	768.5	0
Signal transduction histidine kinase	Pgjcvi_00298	PG JCVI SC001	sensor histidine kinase	PG W83	PG0052	1, 395	99.2	769.6	0
single-stranded-DNA-specific exonuclease RecJ	Pgjcvi_00299	PG JCVI SC001	single-stranded-DNA-specific exonuclease RecJ	PG W83	PG0054	1, 584	99.8	1166	0
single-stranded-DNA-specific exonuclease RecJ	Pgjcvi_00299	PG JCVI SC001	single-stranded-DNA-specific exonuclease RecJ	PG TDC60	PGTDC60_0336	1, 584	99.8	1166	0
single-stranded-DNA-specific exonuclease RecJ	Pgjcvi_00299	PG JCVI SC001	single-stranded-DNA-specific exonuclease	PG ATCC 33277	PGN_2003	1, 584	99.7	1164.1	0
Putative stress-responsive transcriptional regulator	Pgjcvi_00300	PG JCVI SC001	hypothetical protein	PG W83	PG0055	1, 351	99.4	698.4	0
Putative stress-responsive transcriptional regulator	Pgjcvi_00300	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0337	1, 351	99.4	698.4	0
Putative stress-responsive transcriptional regulator	Pgjcvi_00300	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2004	1, 351	99.1	698	0
hypothetical protein	Pgjcvi_00301	PG JCVI SC001	hypothetical protein	PG W83	PG0056	1, 566	98.9	1097.8	0
hypothetical protein	Pgjcvi_00301	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0338	1, 510	98.4	971.8	0
hypothetical protein	Pgjcvi_00301	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2005	1, 560	97.9	1069.7	0
nicotinate phosphoribosyltransferase	Pgjcvi_00302	PG JCVI SC001	nicotinate phosphoribosyltransferase	PG W83	PG0057	1, 394	100	804.3	0
nicotinate phosphoribosyltransferase	Pgjcvi_00302	PG JCVI SC001	nicotinate phosphoribosyltransferase	PG ATCC 33277	PGN_2006	1, 394	99.5	801.2	0
nicotinate phosphoribosyltransferase	Pgjcvi_00302	PG JCVI SC001	nicotinate phosphoribosyltransferase	PG TDC60	PGTDC60_0339	1, 394	99.5	801.2	0
nicotinate (nicotinamide) nucleotide adenylyltransferase	Pgjcvi_00303	PG JCVI SC001	probable nicotinamide-nucleotide adenylyltransferase	PG ATCC 33277	PGN_2007	1, 197	99	406.8	0
nicotinate (nicotinamide) nucleotide adenylyltransferase	Pgjcvi_00303	PG JCVI SC001	nicotinic acid mononucleotide adenyltransferase	PG W83	PG0058	1, 197	99	406	0
nicotinate (nicotinamide) nucleotide adenylyltransferase	Pgjcvi_00303	PG JCVI SC001	nicotinic acid mononucleotide adenylyltransferase	PG TDC60	PGTDC60_0340	1, 197	99	406.8	0
hypothetical protein	Pgjcvi_00304	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2008	1, 127	100	248.1	0
hypothetical protein	Pgjcvi_00304	PG JCVI SC001	hypothetical protein	PG W83	PG0059	1, 127	100	248.1	0
hypothetical protein	Pgjcvi_00304	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0341	1, 127	100	248.1	0
hypothetical protein	Pgjcvi_00305	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2009	1, 60	100	120.9	1.60E-26
hypothetical protein	Pgjcvi_00305	PG JCVI SC001	hypothetical protein	PG W83	PG0060	1, 60	100	120.9	1.60E-26
hypothetical protein	Pgjcvi_00305	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0342	1, 60	100	120.9	1.60E-26
Uncharacterized protein conserved in bacteria	Pgjcvi_00306	PG JCVI SC001	yngK protein	PG TDC60	PGTDC60_0343	1, 493	99.2	1037.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00306	PG JCVI SC001	putative secreted protein	PG ATCC 33277	PGN_2010	1, 493	99	1035.4	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00306	PG JCVI SC001	yngK protein	PG W83	PG0061	1, 512	98.8	1072.8	0
PIF1 helicase./Helicase.	Pgjcvi_00307	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0344	1, 680	99.4	1336.2	0
PIF1 helicase./Helicase.	Pgjcvi_00307	PG JCVI SC001	TPR domain protein	PG W83	PG0062	1, 680	99.3	1333.5	0
PIF1 helicase./Helicase.	Pgjcvi_00307	PG JCVI SC001	putative helicase	PG ATCC 33277	PGN_2011	1, 680	99.1	1330.5	0
Outer membrane protein	Pgjcvi_00308	PG JCVI SC001	outer membrane efflux protein	PG ATCC 33277	PGN_2012	1, 392	99.5	755	0
Outer membrane protein	Pgjcvi_00308	PG JCVI SC001	outer membrane efflux protein	PG W83	PG0063	1, 392	99	751.5	0
Outer membrane protein	Pgjcvi_00308	PG JCVI SC001	outer membrane efflux protein	PG TDC60	PGTDC60_0345	1, 392	99	753.4	0
heavy metal efflux pump (cobalt-zinc-cadmium)	Pgjcvi_00309	PG JCVI SC001	cation efflux system protein	PG ATCC 33277	PGN_2013	1, 1039	99.5	1963.3	0
heavy metal efflux pump (cobalt-zinc-cadmium)	Pgjcvi_00309	PG JCVI SC001	heavy metal efflux pump, CzcA family	PG W83	PG0064	1, 1039	99.4	1961	0
heavy metal efflux pump (cobalt-zinc-cadmium)	Pgjcvi_00309	PG JCVI SC001	CzcA family heavy metal efflux protein	PG TDC60	PGTDC60_0346	1, 1039	99.2	1955.3	0
RND family efflux transporter, MFP subunit	Pgjcvi_00310	PG JCVI SC001	cation efflux system protein	PG TDC60	PGTDC60_0347	1, 392	99.7	764.6	0
RND family efflux transporter, MFP subunit	Pgjcvi_00310	PG JCVI SC001	cation efflux system protein	PG ATCC 33277	PGN_2014	1, 392	99.5	761.5	0
RND family efflux transporter, MFP subunit	Pgjcvi_00310	PG JCVI SC001	efflux transporter, RND family, MFP subunit	PG W83	PG0065	1, 324	99.1	626.7	0
hypothetical protein	Pgjcvi_00312	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2016	1, 139	98.6	295	0
hypothetical protein	Pgjcvi_00312	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0348	1, 139	97.8	293.9	0
yjeF C-terminal region, hydroxyethylthiazole kinase-related/yjeF N-terminal region	Pgjcvi_00313	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2017	1, 504	99.6	1006.5	0
yjeF C-terminal region, hydroxyethylthiazole kinase-related/yjeF N-terminal region	Pgjcvi_00313	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0349	1, 504	99.6	1005.4	0
yjeF C-terminal region, hydroxyethylthiazole kinase-related/yjeF N-terminal region	Pgjcvi_00313	PG JCVI SC001	hypothetical protein	PG W83	PG0069	1, 504	99.4	1006.1	0
acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	Pgjcvi_00314	PG JCVI SC001	putative UDP-N-acetylglucosamine acyltransferase	PG ATCC 33277	PGN_2018	1, 263	99.6	530.4	0

acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	Pgjcvi_00314	PG JCVI SC001	UDP-N-acetylglucosamine acyltransferase	PG TDC60	PGTDC60_0350	2, 264	99.6	530.4	0
acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	Pgjcvi_00314	PG JCVI SC001	UDP-N-acetylglucosamine acyltransferase	PG W83	PG0070	2, 264	99.2	530	0
beta-hydroxyacyl-[acyl carrier protein] dehydratase FabZ	Pgjcvi_00315	PG JCVI SC001	bifunctional UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase/(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase	PG TDC60	PGTDC60_0351	1, 462	100	914.8	0
beta-hydroxyacyl-[acyl carrier protein] dehydratase FabZ	Pgjcvi_00315	PG JCVI SC001	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	PG ATCC 33277	PGN_2019	1, 462	99.8	912.1	0
beta-hydroxyacyl-[acyl carrier protein] dehydratase FabZ	Pgjcvi_00315	PG JCVI SC001	UDP-3-O-acyl-GlcNAc deacetylase/beta-hydroxyacyl-[acyl carrier protein] dehydratase FabZ	PG W83	PG0071	1, 462	99.8	912.1	0
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	Pgjcvi_00316	PG JCVI SC001	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	PG ATCC 33277	PGN_2020	1, 349	100	704.1	0
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	Pgjcvi_00316	PG JCVI SC001	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	PG W83	PG0072	1, 349	99.4	701.4	0
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	Pgjcvi_00316	PG JCVI SC001	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	PG TDC60	PGTDC60_0352	1, 349	99.4	699.9	0
orotidine 5''-phosphate decarboxylase, subfamily 2	Pgjcvi_00317	PG JCVI SC001	orotidine 5'-phosphate decarboxylase	PG ATCC 33277	PGN_2021	1, 276	99.3	546.6	0
orotidine 5''-phosphate decarboxylase, subfamily 2	Pgjcvi_00317	PG JCVI SC001	orotidine 5'-phosphate decarboxylase	PG TDC60	PGTDC60_0353	1, 276	99.3	546.6	0
orotidine 5''-phosphate decarboxylase, subfamily 2	Pgjcvi_00317	PG JCVI SC001	orotidine 5'-monophosphate decarboxylase	PG W83	PG0073	1, 276	98.9	544.3	0
peptide chain release factor 1	Pgjcvi_00318	PG JCVI SC001	peptide chain release factor 1	PG TDC60	PGTDC60_0354	1, 361	100	705.3	0
peptide chain release factor 1	Pgjcvi_00318	PG JCVI SC001	peptide chain release factor 1	PG W83	PG0074	1, 361	99.7	703.7	0
peptide chain release factor 1	Pgjcvi_00318	PG JCVI SC001	peptide chain release factor 1	PG ATCC 33277	PGN_2022	1, 352	99.4	685.6	0
Phosphoribosylaminoimidazole (AIR) synthetase	Pgjcvi_00319	PG JCVI SC001	putative phosphoribosylformylglycinamidine cyclo-ligase	PG ATCC 33277	PGN_2023	1, 388	99.7	773.9	0
Phosphoribosylaminoimidazole (AIR) synthetase	Pgjcvi_00319	PG JCVI SC001	phosphoribosylformylglycinamidine cyclo-ligase, putative	PG W83	PG0075	26, 413	99.2	769.6	0
Phosphoribosylaminoimidazole (AIR) synthetase	Pgjcvi_00319	PG JCVI SC001	phosphoribosylformylglycinamidine cyclo-ligase	PG TDC60	PGTDC60_0355	1, 388	98.7	766.1	0
Muramidase (flagellum-specific)	Pgjcvi_00320	PG JCVI SC001	putative hemagglutinin	PG ATCC 33277	PGN_2024	1, 313	100	643.3	0
Muramidase (flagellum-specific)	Pgjcvi_00320	PG JCVI SC001	N-acetylmuramoyl-L-alanine amidase, family 4	PG W83	PG0076	1, 313	100	643.3	0
Muramidase (flagellum-specific)	Pgjcvi_00320	PG JCVI SC001	N-acetylmuramoyl-L-alanine amidase	PG TDC60	PGTDC60_0356	1, 313	99	639.8	0
hypothetical protein	Pgjcvi_00321	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2025	1, 232	97.9	469.2	0
hypothetical protein	Pgjcvi_00321	PG JCVI SC001	hypothetical protein	PG W83	PG0078	1, 232	97.4	467.6	0
hypothetical protein	Pgjcvi_00321	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0357	1, 64	90.6	125.2	3.40E-27
hypothetical protein	Pgjcvi_00322	PG JCVI SC001	putative abortive infection protein	PG ATCC 33277	PGN_2026	1, 433	99.1	860.5	0
hypothetical protein	Pgjcvi_00322	PG JCVI SC001	abortive infection protein, putative	PG W83	PG0079	1, 433	98.6	856.3	0
hypothetical protein	Pgjcvi_00323	PG JCVI SC001	hypothetical protein	PG W83	PG0081	1, 725	100	1448.7	0
hypothetical protein	Pgjcvi_00323	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0359	1, 639	100	1277.7	0
hypothetical protein	Pgjcvi_00323	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2028	1, 661	98.9	1307.7	0
hypothetical protein	Pgjcvi_00324	PG JCVI SC001	hypothetical protein	PG W83	PG0082	1, 300	99.7	604.7	0
hypothetical protein	Pgjcvi_00324	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0360	1, 300	99.7	604.7	0
hypothetical protein	Pgjcvi_00324	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2029	1, 300	98.7	600.1	0
hypothetical protein	Pgjcvi_00325	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0361	1, 221	99.5	446.4	0
hypothetical protein	Pgjcvi_00325	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2030	1, 261	99.2	526.9	0
hypothetical protein	Pgjcvi_00325	PG JCVI SC001	hypothetical protein	PG W83	PG0083	1, 261	99.2	526.2	0
L-serine dehydratase, iron-sulfur-dependent, single chain form	Pgjcvi_00326	PG JCVI SC001	L-serine dehydratase	PG ATCC 33277	PGN_2031	1, 399	99.5	798.1	0
L-serine dehydratase, iron-sulfur-dependent, single chain form	Pgjcvi_00326	PG JCVI SC001	L-serine dehydratase, iron-sulfur-dependent, single chain form	PG W83	PG0084	1, 399	99.5	798.9	0
L-serine dehydratase, iron-sulfur-dependent, single chain form	Pgjcvi_00326	PG JCVI SC001	L-serine dehydratase, iron-sulfur-dependent, single chain form	PG TDC60	PGTDC60_0362	1, 399	98.7	792.3	0
Melibiase.	Pgjcvi_00327	PG JCVI SC001	putative alpha-galactosidase	PG ATCC 33277	PGN_2032	1, 481	99.4	979.9	0
Melibiase.	Pgjcvi_00327	PG JCVI SC001	alpha-galactosidase	PG TDC60	PGTDC60_0363	1, 434	98.8	882.5	0
Melibiase.	Pgjcvi_00327	PG JCVI SC001	alpha-galactosidase	PG W83	PG0085	1, 434	98.4	879.8	0
Superfamily II DNA and RNA helicases	Pgjcvi_00328	PG JCVI SC001	ATP-dependent RNA helicase, DEAD/DEAH box family	PG W83	PG0086	1, 604	99.5	1190.6	0
Superfamily II DNA and RNA helicases	Pgjcvi_00328	PG JCVI SC001	ATP-dependent RNA helicase	PG ATCC 33277	PGN_2033	1, 604	99.2	1186.4	0
Superfamily II DNA and RNA helicases	Pgjcvi_00328	PG JCVI SC001	DEAD-box ATP dependent DNA helicase	PG TDC60	PGTDC60_0365	1, 376	98.4	728	0
Predicted sugar phosphate isomerase involved in capsule formation	Pgjcvi_00329	PG JCVI SC001	SIS domain protein	PG W83	PG0087	1, 206	100	409.5	0
Predicted sugar phosphate isomerase involved in capsule formation	Pgjcvi_00329	PG JCVI SC001	SIS domain-containing protein	PG TDC60	PGTDC60_0366	1, 206	100	409.5	0
Predicted sugar phosphate isomerase involved in capsule formation	Pgjcvi_00329	PG JCVI SC001	probable sugar isomerase	PG ATCC 33277	PGN_2034	1, 213	99.1	418.3	0
Predicted Zn-dependent peptidases	Pgjcvi_00330	PG JCVI SC001	peptidase, M16 family	PG W83	PG0088	1, 405	99.3	817.4	0
Predicted Zn-dependent peptidases	Pgjcvi_00330	PG JCVI SC001	M16 family peptidase	PG TDC60	PGTDC60_0367	1, 405	99.3	818.9	0
Predicted Zn-dependent peptidases	Pgjcvi_00330	PG JCVI SC001	putative peptidase	PG ATCC 33277	PGN_2035	1, 405	99	817.8	0
DNA-binding ferritin-like protein (oxidative damage protectant)	Pgjcvi_00331	PG JCVI SC001	DNA-binding protein from starved cells Dps	PG ATCC 33277	PGN_2037	1, 159	99.4	311.2	0
DNA-binding ferritin-like protein (oxidative damage protectant)	Pgjcvi_00331	PG JCVI SC001	Dps family protein	PG W83	PG0090	1, 159	99.4	309.7	0
DNA-binding ferritin-like protein (oxidative damage protectant)	Pgjcvi_00331	PG JCVI SC001	DNA-binding protein from starved cells Dps	PG TDC60	PGTDC60_0370	1, 159	98.7	309.7	0
ABC-type multidrug transport system, permease component	Pgjcvi_00332	PG JCVI SC001	transporter, putative	PG W83	PG0091	1, 405	99.8	805.8	0
ABC-type multidrug transport system, permease component	Pgjcvi_00332	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2038	1, 424	99.5	840.9	0
ABC-type multidrug transport system, permease component	Pgjcvi_00332	PG JCVI SC001	transporter	PG TDC60	PGTDC60_0371	1, 386	99.2	760	0
ABC-type multidrug transport system, permease component	Pgjcvi_00333	PG JCVI SC001	transporter, putative	PG W83	PG0092	1, 379	99.2	746.9	0
ABC-type multidrug transport system, permease component	Pgjcvi_00333	PG JCVI SC001	transporter	PG TDC60	PGTDC60_0372	1, 393	99	774.2	0
ABC-type multidrug transport system, permease component	Pgjcvi_00333	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2039	1, 393	98.7	770.4	0
Multidrug resistance efflux pump	Pgjcvi_00334	PG JCVI SC001	HlyD family secretion protein	PG W83	PG0093	1, 331	99.7	630.9	0
Multidrug resistance efflux pump	Pgjcvi_00334	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2040	1, 331	99.4	629	0
Multidrug resistance efflux pump	Pgjcvi_00334	PG JCVI SC001	HlyD family secretion protein	PG TDC60	PGTDC60_0373	1, 331	99.4	628.2	0
Outer membrane protein	Pgjcvi_00335	PG JCVI SC001	putative alkaline protease AprF	PG TDC60	PGTDC60_0374	1, 501	99.2	969.1	0
Outer membrane protein	Pgjcvi_00335	PG JCVI SC001	putative alkaline protease AprF	PG ATCC 33277	PGN_2041	1, 501	99	966.8	0
Outer membrane protein	Pgjcvi_00335	PG JCVI SC001	outer membrane efflux protein, putative	PG W83	PG0094	1, 501	98.6	964.1	0
DNA mismatch repair protein MutS	Pgjcvi_00336	PG JCVI SC001	DNA mismatch repair protein MutS	PG TDC60	PGTDC60_0375	1, 881	99.7	1726.8	0
DNA mismatch repair protein MutS	Pgjcvi_00336	PG JCVI SC001	DNA mismatch repair protein	PG W83	PG0095	1, 891	99.6	1744.9	0
DNA mismatch repair protein MutS	Pgjcvi_00336	PG JCVI SC001	DNA mismatch repair protein MutS	PG ATCC 33277	PGN_2042	1, 882	99	1721.1	0
DNA-binding regulatory protein, YebC/PmpR family	Pgjcvi_00337	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2043	1, 230	100	462.6	0
DNA-binding regulatory protein, YebC/PmpR family	Pgjcvi_00337	PG JCVI SC001	hypothetical protein	PG W83	PG0097	1, 230	100	462.6	0
DNA-binding regulatory protein, YebC/PmpR family	Pgjcvi_00337	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0376	1, 242	100	486.5	0

phenylalanyl-tRNA synthetase, beta subunit, non-spirochete bacterial	Pgjcvi_00338	PG JCVI SC001	phenylalanyl-tRNA synthetase beta subunit	PG ATCC 33277	PGN_2045	1, 819	99.1	1622.8	0
phenylalanyl-tRNA synthetase, beta subunit, non-spirochete bacterial	Pgjcvi_00338	PG JCVI SC001	phenylalanyl-tRNA synthetase beta subunit	PG W83	PG0099	1, 819	97.9	1600.9	0
phenylalanyl-tRNA synthetase, beta subunit, non-spirochete bacterial	Pgjcvi_00338	PG JCVI SC001	phenylalanyl-tRNA synthetase subunit beta	PG TDC60	PGTDC60_0377	343, 955	97.1	1181.8	0
phenylalanyl-tRNA synthetase, beta subunit, non-spirochete bacterial	Pgjcvi_00338	PG JCVI SC001	phenylalanyl-tRNA synthetase subunit beta	PG TDC60	PGTDC60_0377	1, 449	53.3	416.4	0
DNA topoisomerase III, bacteria and conjugative plasmid	Pgjcvi_00341	PG JCVI SC001	DNA topoisomerase III	PG W83	PG0104	1, 675	99.6	1350.9	0
DNA topoisomerase III, bacteria and conjugative plasmid	Pgjcvi_00341	PG JCVI SC001	DNA topoisomerase III	PG TDC60	PGTDC60_0383	1, 690	99.4	1377.8	0
DNA topoisomerase III, bacteria and conjugative plasmid	Pgjcvi_00341	PG JCVI SC001	DNA topoisomerase III	PG ATCC 33277	PGN_0221	21, 710	99.3	1376.3	0
UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	Pgjcvi_00342	PG JCVI SC001	glycosyl transferase, group 4 family protein	PG W83	PG0106	21, 229	99.5	397.5	0
UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	Pgjcvi_00342	PG JCVI SC001	glycosyl transferase, group 4 family protein	PG TDC60	PGTDC60_0386	21, 229	99	397.1	0
UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	Pgjcvi_00342	PG JCVI SC001	glycosyl transferase family 4	PG ATCC 33277	PGN_0223	11, 219	98.6	394.4	0
hypothetical protein	Pgjcvi_00343	PG JCVI SC001	glycosyl transferase family 4	PG ATCC 33277	PGN_0223	236, 368	98.5	259.6	0
hypothetical protein	Pgjcvi_00343	PG JCVI SC001	glycosyl transferase, group 4 family protein	PG W83	PG0106	246, 378	98.5	259.6	0
hypothetical protein	Pgjcvi_00343	PG JCVI SC001	glycosyl transferase, group 4 family protein	PG TDC60	PGTDC60_0386	246, 378	98.5	259.6	0
nucleotide sugar dehydrogenase	Pgjcvi_00344	PG JCVI SC001	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	PG W83	PG0108	1, 402	98.5	798.5	0
nucleotide sugar dehydrogenase	Pgjcvi_00344	PG JCVI SC001	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	PG TDC60	PGTDC60_0387	1, 402	98.3	798.1	0
nucleotide sugar dehydrogenase	Pgjcvi_00344	PG JCVI SC001	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	PG ATCC 33277	PGN_0224	1, 402	96.8	786.2	0
hypothetical protein	Pgjcvi_00347	PG JCVI SC001	exopolysaccharide synthesis-like protein	PG TDC60	PGTDC60_1070	27, 344	24.4	65.1	6.20E-09
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_00348	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG0118	16, 116	34.9	57.8	7.70E-07
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_00348	PG JCVI SC001	putative glycosyltransferase	PG TDC60	PGTDC60_0388	4, 216	29	76.3	2.10E-12
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_00348	PG JCVI SC001	probable glycosyltransferase	PG ATCC 33277	PGN_0225	4, 216	28.6	74.7	6.10E-12
UDP-N-acetylglucosamine 2-epimerase	Pgjcvi_00350	PG JCVI SC001	UDP-N-acetylglucosamine 2-epimerase	PG ATCC 33277	PGN_0234	5, 386	99.2	751.5	0
UDP-N-acetylglucosamine 2-epimerase	Pgjcvi_00350	PG JCVI SC001	UDP-N-acetylglucosamine 2-epimerase	PG W83	PG0120	5, 386	99	751.5	0
UDP-N-acetylglucosamine 2-epimerase	Pgjcvi_00350	PG JCVI SC001	UDP-N-acetylglucosamine 2-epimerase	PG TDC60	PGTDC60_0397	5, 386	98.4	748.8	0
Bacterial nucleoid DNA-binding protein	Pgjcvi_00351	PG JCVI SC001	DNA-binding protein HU	PG ATCC 33277	PGN_0235	1, 88	100	169.1	7.70E-41
Bacterial nucleoid DNA-binding protein	Pgjcvi_00351	PG JCVI SC001	DNA-binding protein HU	PG W83	PG0121	1, 88	100	169.1	7.70E-41
Bacterial nucleoid DNA-binding protein	Pgjcvi_00351	PG JCVI SC001	DNA-binding protein HU	PG TDC60	PGTDC60_0398	1, 88	100	169.1	7.70E-41
hypothetical protein	Pgjcvi_00352	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0236	1, 189	98.9	394.8	0
hypothetical protein	Pgjcvi_00352	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0399	3, 191	98.9	392.1	0
hypothetical protein	Pgjcvi_00352	PG JCVI SC001	hypothetical protein	PG W83	PG0123	1, 172	97.1	356.7	0
Uncharacterized conserved protein	Pgjcvi_00353	PG JCVI SC001	hypothetical protein	PG W83	PG0124	1, 206	99.5	400.6	0
Uncharacterized conserved protein	Pgjcvi_00353	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0237	1, 206	99	399.1	0
Uncharacterized conserved protein	Pgjcvi_00353	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0400	1, 206	98.5	396.4	0
hypothetical protein	Pgjcvi_00354	PG JCVI SC001	hypothetical protein	PG W83	PG0125	1, 182	100	350.9	0
hypothetical protein	Pgjcvi_00354	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0238	1, 182	98.4	345.9	0
hypothetical protein	Pgjcvi_00354	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0401	1, 182	98.4	346.7	0
Uncharacterized proteins of the AP superfamily	Pgjcvi_00355	PG JCVI SC001	type I phosphodiesterase/nucleotide pyrophosphatase family protein	PG TDC60	PGTDC60_0402	1, 370	99.7	767.3	0
Uncharacterized proteins of the AP superfamily	Pgjcvi_00355	PG JCVI SC001	type I phosphodiesterase/nucleotide pyrophosphatase family protein	PG W83	PG0126	1, 411	99.5	842.8	0
Uncharacterized proteins of the AP superfamily	Pgjcvi_00355	PG JCVI SC001	putative type I phosphodiesterase-nucleotide pyrophosphatase	PG ATCC 33277	PGN_0239	1, 411	99	840.5	0
ferrochelatase	Pgjcvi_00356	PG JCVI SC001	ferrochelatase	PG W83	PG0127	1, 345	100	703.7	0
ferrochelatase	Pgjcvi_00356	PG JCVI SC001	ferrochelatase	PG TDC60	PGTDC60_0404	1, 345	99.1	696	0
ferrochelatase	Pgjcvi_00356	PG JCVI SC001	putative ferrochelatase	PG ATCC 33277	PGN_0240	1, 345	98.6	693	0
Mn2+-dependent serine/threonine protein kinase	Pgjcvi_00357	PG JCVI SC001	hypothetical protein	PG W83	PG0128	1, 324	98.8	639	0
Mn2+-dependent serine/threonine protein kinase	Pgjcvi_00357	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0405	1, 324	98.8	638.6	0
Mn2+-dependent serine/threonine protein kinase	Pgjcvi_00357	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0241	1, 324	98.1	636	0
Glycosyltransferase	Pgjcvi_00358	PG JCVI SC001	mannosyltransferase	PG W83	PG0129	1, 374	98.1	739.6	0
Glycosyltransferase	Pgjcvi_00358	PG JCVI SC001	probable glycosyl transferase family 1	PG ATCC 33277	PGN_0242	1, 382	97.9	753.1	0
Glycosyltransferase	Pgjcvi_00358	PG JCVI SC001	putative glycosyl transferase family 1	PG TDC60	PGTDC60_0406	1, 382	97.4	744.2	0
phosphoglycerate mutase, BPG-dependent, family 1	Pgjcvi_00359	PG JCVI SC001	phosphoglycerate mutase	PG ATCC 33277	PGN_0243	1, 248	100	511.5	0
phosphoglycerate mutase, BPG-dependent, family 1	Pgjcvi_00359	PG JCVI SC001	phosphoglyceromutase	PG W83	PG0130	1, 248	100	511.5	0
phosphoglycerate mutase, BPG-dependent, family 1	Pgjcvi_00359	PG JCVI SC001	phosphoglyceromutase	PG TDC60	PGTDC60_0407	1, 248	99.6	510	0
CDP-Glycerol:Poly(glycerophosphate) glycerophosphotransferase.	Pgjcvi_00360	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0409	1, 436	98.4	877.1	0
CDP-Glycerol:Poly(glycerophosphate) glycerophosphotransferase.	Pgjcvi_00360	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0245	1, 436	98.2	874.4	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_00361	PG JCVI SC001	hypothetical protein	PG W83	PG0133	1, 501	100	975.3	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_00361	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0246	1, 501	99.6	972.2	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_00361	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0410	1, 501	99.6	972.2	0
Mg2+ transporter (mgtE)	Pgjcvi_00362	PG JCVI SC001	putative magnesium transporter	PG ATCC 33277	PGN_0247	1, 450	100	863.2	0
Mg2+ transporter (mgtE)	Pgjcvi_00362	PG JCVI SC001	magnesium transporter	PG W83	PG0134	1, 450	99.8	862.4	0
Mg2+ transporter (mgtE)	Pgjcvi_00362	PG JCVI SC001	magnesium transporter	PG TDC60	PGTDC60_0411	1, 450	99.6	862.1	0
dimethyladenosine transferase	Pgjcvi_00363	PG JCVI SC001	putative dimethyladenosine transferase	PG ATCC 33277	PGN_0248	2, 258	100	514.6	0
dimethyladenosine transferase	Pgjcvi_00363	PG JCVI SC001	dimethyladenosine transferase	PG W83	PG0135	2, 258	100	514.6	0
dimethyladenosine transferase	Pgjcvi_00363	PG JCVI SC001	dimethyladenosine transferase	PG TDC60	PGTDC60_0412	2, 258	99.6	512.3	0
Predicted integral membrane protein	Pgjcvi_00364	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0249	10, 349	99.7	684.9	0
Predicted integral membrane protein	Pgjcvi_00364	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0413	10, 349	99.7	684.9	0
Predicted integral membrane protein	Pgjcvi_00364	PG JCVI SC001	hypothetical protein	PG W83	PG0136	10, 349	99.1	681.8	0
Xaa-His dipeptidase	Pgjcvi_00365	PG JCVI SC001	aminoacyl-histidine dipeptidase	PG ATCC 33277	PGN_0250	1, 484	99.8	966.5	0
Xaa-His dipeptidase	Pgjcvi_00365	PG JCVI SC001	aminoacyl-histidine dipeptidase	PG TDC60	PGTDC60_0414	1, 484	99.4	963.8	0
Xaa-His dipeptidase	Pgjcvi_00365	PG JCVI SC001	aminoacyl-histidine dipeptidase	PG W83	PG0137	1, 484	99.2	960.7	0
malonyl CoA-acyl carrier protein transacylase	Pgjcvi_00366	PG JCVI SC001	malonyl CoA-acyl carrier protein transacylase	PG W83	PG0138	1, 293	100	577	0
malonyl CoA-acyl carrier protein transacylase	Pgjcvi_00366	PG JCVI SC001	malonyl CoA-acyl carrier protein transacylase	PG ATCC 33277	PGN_0251	1, 293	99.7	575.5	0

malonyl CoA-acyl carrier protein transacylase	Pgjcvi_00366	PG JCVI SC001	malonyl CoA-acyl carrier protein transacylase	PG TDC60	PGTDC60_0415	1, 293	99.3	571.2	0
Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	Pgjcvi_00367	PG JCVI SC001	putative membrane-bound lytic murein transglycosylase D	PG ATCC 33277	PGN_0252	1, 448	99.6	892.5	0
Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	Pgjcvi_00367	PG JCVI SC001	membrane-bound lytic murein transglycosylase D, putative	PG W83	PG0139	1, 451	99.6	899.8	0
Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	Pgjcvi_00367	PG JCVI SC001	membrane-bound lytic murein transglycosylase D	PG TDC60	PGTDC60_0416	1, 451	99.6	899	0
hypothetical protein	Pgjcvi_00368	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0417	1, 235	98.7	481.9	0
hypothetical protein	Pgjcvi_00368	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0253	1, 235	98.3	479.9	0
hypothetical protein	Pgjcvi_00368	PG JCVI SC001	hypothetical protein	PG W83	PG0140	1, 235	97.9	476.9	0
ParB-like partition proteins	Pgjcvi_00369	PG JCVI SC001	putative ParB chromosome partitioning protein	PG ATCC 33277	PGN_0254	1, 289	100	556.6	0
ParB-like partition proteins	Pgjcvi_00369	PG JCVI SC001	spoOJ protein	PG W83	PG0141	1, 289	100	556.6	0
ParB-like partition proteins	Pgjcvi_00369	PG JCVI SC001	putative ParB chromosome partitioning protein	PG TDC60	PGTDC60_0418	1, 289	100	556.6	0
ATPases involved in chromosome partitioning	Pgjcvi_00370	PG JCVI SC001	putative ParA chromosome partitioning protein	PG TDC60	PGTDC60_0419	1, 258	99.6	499.6	0
ATPases involved in chromosome partitioning	Pgjcvi_00370	PG JCVI SC001	putative ParA chromosome partitioning protein	PG ATCC 33277	PGN_0255	1, 258	99.2	497.3	0
ATPases involved in chromosome partitioning	Pgjcvi_00370	PG JCVI SC001	SpoOJ regulator protein	PG W83	PG0142	1, 258	99.2	496.9	0
Predicted amidohydrolase	Pgjcvi_00371	PG JCVI SC001	carbon-nitrogen family hydrolase	PG TDC60	PGTDC60_0420	1, 292	99.7	594.3	0
Predicted amidohydrolase	Pgjcvi_00371	PG JCVI SC001	hydrolase, carbon-nitrogen family	PG W83	PG0143	1, 292	99.3	594	0
Predicted amidohydrolase	Pgjcvi_00371	PG JCVI SC001	hydrolase	PG ATCC 33277	PGN_0256	1, 292	98.6	590.5	0
Peptidylarginine deiminase and related enzymes	Pgjcvi_00372	PG JCVI SC001	putative arginine deiminase	PG TDC60	PGTDC60_0421	1, 312	100	636	0
Peptidylarginine deiminase and related enzymes	Pgjcvi_00372	PG JCVI SC001	hypothetical protein	PG W83	PG0144	1, 341	99.7	699.5	0
Peptidylarginine deiminase and related enzymes	Pgjcvi_00372	PG JCVI SC001	putative arginine deiminase	PG ATCC 33277	PGN_0257	1, 341	99.4	696.4	0
protein translocase, SecG subunit	Pgjcvi_00373	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0258	1, 128	100	247.3	0
protein translocase, SecG subunit	Pgjcvi_00373	PG JCVI SC001	preprotein translocase subunit SecG	PG TDC60	PGTDC60_0422	1, 128	100	247.3	0
hypothetical protein	Pgjcvi_00374	PG JCVI SC001	hypothetical protein	PG W83	PG0146	1, 235	98.7	463	0
hypothetical protein	Pgjcvi_00374	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0259	1, 235	98.3	461.1	0
hypothetical protein	Pgjcvi_00374	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0423	1, 235	97.9	458.8	0
hypothetical protein	Pgjcvi_00375	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0260	1, 179	99.4	356.3	0
hypothetical protein	Pgjcvi_00375	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0424	1, 179	99.4	356.3	0
hypothetical protein	Pgjcvi_00375	PG JCVI SC001	hypothetical protein	PG W83	PG0147	1, 179	98.9	354.4	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00376	PG JCVI SC001	sigma-54-dependent transcriptional regulator	PG W83	PG0148	1, 417	100	830.9	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00376	PG JCVI SC001	sigma-54-dependent transcriptional regulator	PG ATCC 33277	PGN_0261	1, 417	99.8	828.6	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00376	PG JCVI SC001	sigma-54-dependent transcriptional regulator	PG TDC60	PGTDC60_0425	3, 419	99.5	826.6	0
hypothetical protein	Pgjcvi_00377	PG JCVI SC001	hypothetical protein	PG W83	PG0149	1, 422	98.6	819.3	0
hypothetical protein	Pgjcvi_00377	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0426	1, 422	98.6	819.3	0
hypothetical protein	Pgjcvi_00377	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0262	1, 422	98.1	817	0
ribosomal protein S12 methylthiotransferase RimO	Pgjcvi_00378	PG JCVI SC001	putative Fe-S oxidoreductase	PG ATCC 33277	PGN_0263	1, 434	99.3	872.1	0
ribosomal protein S12 methylthiotransferase RimO	Pgjcvi_00378	PG JCVI SC001	conserved hypothetical protein TIGR01125	PG W83	PG0150	1, 434	99.1	871.3	0
ribosomal protein S12 methylthiotransferase RimO	Pgjcvi_00378	PG JCVI SC001	putative Fe-S oxidoreductase	PG TDC60	PGTDC60_0427	1, 434	98.8	868.6	0
signal recognition particle-docking protein FtsY	Pgjcvi_00379	PG JCVI SC001	signal recognition particle-docking protein	PG ATCC 33277	PGN_0264	1, 317	100	607.1	0
signal recognition particle-docking protein FtsY	Pgjcvi_00379	PG JCVI SC001	signal recognition particle-docking protein FtsY	PG W83	PG0151	1, 317	100	607.1	0
signal recognition particle-docking protein FtsY	Pgjcvi_00379	PG JCVI SC001	signal recognition particle-docking protein FtsY	PG TDC60	PGTDC60_0428	1, 317	100	607.1	0
carboxynorspermidine decarboxylase	Pgjcvi_00380	PG JCVI SC001	carboxynorspermidine decarboxylase	PG TDC60	PGTDC60_0429	1, 378	99.7	776.9	0
carboxynorspermidine decarboxylase	Pgjcvi_00380	PG JCVI SC001	carboxynorspermidine decarboxylase	PG ATCC 33277	PGN_0265	1, 378	99.5	775.4	0
carboxynorspermidine decarboxylase	Pgjcvi_00380	PG JCVI SC001	carboxynorspermidine decarboxylase	PG W83	PG0152	1, 378	98.7	771.9	0
aspartyl-tRNA synthetase, bacterial type	Pgjcvi_00381	PG JCVI SC001	aspartyl-tRNA synthetase	PG W83	PG0153	1, 582	98.1	1162.1	0
aspartyl-tRNA synthetase, bacterial type	Pgjcvi_00381	PG JCVI SC001	aspartyl-tRNA synthetase	PG TDC60	PGTDC60_0430	1, 582	98.1	1162.1	0
aspartyl-tRNA synthetase, bacterial type	Pgjcvi_00381	PG JCVI SC001	aspartyl-tRNA synthetase	PG ATCC 33277	PGN_0266	1, 582	97.9	1159.4	0
riboflavin biosynthesis protein RibD	Pgjcvi_00383	PG JCVI SC001	putative riboflavin biosynthesis protein	PG ATCC 33277	PGN_0267	1, 330	99.1	661	0
riboflavin biosynthesis protein RibD	Pgjcvi_00383	PG JCVI SC001	riboflavin biosynthesis protein RibD	PG W83	PG0155	1, 330	98.8	660.2	0
riboflavin biosynthesis protein RibD	Pgjcvi_00383	PG JCVI SC001	riboflavin biosynthesis protein RibD	PG TDC60	PGTDC60_0431	1, 330	98.8	659.1	0
protein-(glutamine-N5) methyltransferase, release factor-specific	Pgjcvi_00384	PG JCVI SC001	protoporphyrinogen oxidase	PG ATCC 33277	PGN_0268	1, 293	99.3	576.2	0
protein-(glutamine-N5) methyltransferase, release factor-specific	Pgjcvi_00384	PG JCVI SC001	modification methylase, HemK family	PG W83	PG0156	1, 293	99.3	577	0
protein-(glutamine-N5) methyltransferase, release factor-specific	Pgjcvi_00384	PG JCVI SC001	HemK family modification methylase	PG TDC60	PGTDC60_0432	1, 293	99.3	578.2	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00385	PG JCVI SC001	regulatory protein RecX	PG W83	PG0157	1, 161	100	323.6	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00385	PG JCVI SC001	putative transcriptional regulatory protein	PG ATCC 33277	PGN_0269	1, 161	98.1	316.6	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00385	PG JCVI SC001	regulatory protein RecX	PG TDC60	PGTDC60_0433	1, 161	97.5	311.2	0
Predicted amidophosphoribosyltransferases	Pgjcvi_00386	PG JCVI SC001	competence protein F-related protein	PG W83	PG0158	1, 246	99.6	493.4	0
Predicted amidophosphoribosyltransferases	Pgjcvi_00386	PG JCVI SC001	competence protein F-like protein	PG TDC60	PGTDC60_0434	1, 246	99.6	493.4	0
Predicted amidophosphoribosyltransferases	Pgjcvi_00386	PG JCVI SC001	probable amidophosphoribosyl-transferase	PG ATCC 33277	PGN_0270	1, 246	99.2	491.9	0
Predicted metalloendopeptidase	Pgjcvi_00387	PG JCVI SC001	endopeptidase PepO	PG ATCC 33277	PGN_0271	1, 689	99.6	1405.2	0
Predicted metalloendopeptidase	Pgjcvi_00387	PG JCVI SC001	endopeptidase PepO	PG W83	PG0159	1, 689	99.6	1403.3	0
Predicted metalloendopeptidase	Pgjcvi_00387	PG JCVI SC001	endopeptidase PepO	PG TDC60	PGTDC60_0435	1, 671	99.6	1370.1	0
hypothetical protein	Pgjcvi_00388	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0272	1, 300	99.3	609.4	0
hypothetical protein	Pgjcvi_00388	PG JCVI SC001	hypothetical protein	PG W83	PG0160	1, 300	99.3	608.6	0
hypothetical protein	Pgjcvi_00388	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0436	1, 300	99.3	608.6	0
hypothetical protein	Pgjcvi_00389	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0273	1, 44	100	89.7	3.10E-17
hypothetical protein	Pgjcvi_00389	PG JCVI SC001	hypothetical protein	PG W83	PG0161	4, 49	97.8	91.3	1.10E-17
hypothetical protein	Pgjcvi_00389	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0437	4, 49	97.8	91.3	1.10E-17

RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00390	PG JCVI SC001	putative RNA polymerase sigma-70 factor ECF subfamily	PG ATCC 33277	PGN_0274	1, 193	100	382.1	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00390	PG JCVI SC001	RNA polymerase sigma-70 factor, ECF subfamily	PG W83	PG0162	1, 193	100	382.1	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00390	PG JCVI SC001	putative RNA polymerase sigma-70 factor ECFsubfamily	PG TDC60	PGTDC60_0438	1, 193	100	382.1	0
diphosphate--fructose-6-phosphate 1-phosphotransferase	Pgjcvi_00391	PG JCVI SC001	diphosphate--fructose-6-phosphate 1-phosphotransferase	PG W83	PG0163	1, 549	100	1103.2	0
diphosphate--fructose-6-phosphate 1-phosphotransferase	Pgjcvi_00391	PG JCVI SC001	phosphofructokinase	PG ATCC 33277	PGN_0275	1, 549	99.8	1101.7	0
diphosphate--fructose-6-phosphate 1-phosphotransferase	Pgjcvi_00391	PG JCVI SC001	diphosphate--fructose-6-phosphate 1-phosphotransferase	PG TDC60	PGTDC60_0439	1, 549	99.8	1100.9	0
Domain of unknown function (DUF1905).	Pgjcvi_00392	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0440	1, 104	98.1	209.1	0
Domain of unknown function (DUF1905).	Pgjcvi_00392	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0276	1, 104	97.1	207.6	0
Domain of unknown function (DUF1905).	Pgjcvi_00392	PG JCVI SC001	hypothetical protein	PG W83	PG0164	1, 104	97.1	207.2	0
Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	Pgjcvi_00393	PG JCVI SC001	heat shock protein 15	PG W83	PG0165	1, 145	99.3	295	0
Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	Pgjcvi_00393	PG JCVI SC001	putative heat shock protein 15	PG ATCC 33277	PGN_0277	1, 144	98.6	292.4	0
Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	Pgjcvi_00393	PG JCVI SC001	heat shock protein 15	PG TDC60	PGTDC60_0441	1, 145	98.6	294.7	0
peptidyl-tRNA hydrolase	Pgjcvi_00394	PG JCVI SC001	peptidyl-tRNA hydrolase	PG W83	PG0166	1, 185	100	372.9	0
peptidyl-tRNA hydrolase	Pgjcvi_00394	PG JCVI SC001	peptidyl-tRNA hydrolase	PG TDC60	PGTDC60_0442	1, 185	100	372.9	0
peptidyl-tRNA hydrolase	Pgjcvi_00394	PG JCVI SC001	putative peptidyl-tRNA hydrolase	PG ATCC 33277	PGN_0278	1, 185	99.5	370.9	0
ribosomal protein L25, Ctc-form	Pgjcvi_00395	PG JCVI SC001	putative 50S ribosomal protein L25	PG ATCC 33277	PGN_0279	1, 192	99.5	372.5	0
ribosomal protein L25, Ctc-form	Pgjcvi_00395	PG JCVI SC001	ribosomal protein L25	PG W83	PG0167	1, 192	99.5	372.5	0
ribosomal protein L25, Ctc-form	Pgjcvi_00395	PG JCVI SC001	50S ribosomal protein L25/general stress protein Ctc	PG TDC60	PGTDC60_0443	1, 192	99.5	370.2	0
methionyl-tRNA synthetase/methionyl-tRNA synthetase C-terminal region/beta chain	Pgjcvi_00396	PG JCVI SC001	methionyl-tRNA synthetase	PG ATCC 33277	PGN_0281	1, 680	99.7	1389.4	0
methionyl-tRNA synthetase/methionyl-tRNA synthetase C-terminal region/beta chain	Pgjcvi_00396	PG JCVI SC001	methionyl-tRNA synthetase	PG W83	PG0170	1, 680	99.6	1385.5	0
methionyl-tRNA synthetase/methionyl-tRNA synthetase C-terminal region/beta chain	Pgjcvi_00396	PG JCVI SC001	methionyl-tRNA synthetase	PG TDC60	PGTDC60_0445	1, 680	99.4	1383.6	0
5''-nucleotidase/2'',3''-cyclic phosphodiesterase and related esterases	Pgjcvi_00397	PG JCVI SC001	2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor	PG ATCC 33277	PGN_0282	4, 593	99.3	1187.9	0
5''-nucleotidase/2'',3''-cyclic phosphodiesterase and related esterases	Pgjcvi_00397	PG JCVI SC001	5'-nucleotidase family protein	PG W83	PG0171	1, 590	99.2	1184.5	0
5''-nucleotidase/2'',3''-cyclic phosphodiesterase and related esterases	Pgjcvi_00397	PG JCVI SC001	2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor	PG TDC60	PGTDC60_0446	1, 533	98.7	1065.8	0
DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00398	PG JCVI SC001	probable exonuclease	PG ATCC 33277	PGN_0283	1, 260	99.2	529.6	0
DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00398	PG JCVI SC001	exonuclease	PG W83	PG0172	1, 260	99.2	530	0
DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00398	PG JCVI SC001	putative exonuclease	PG TDC60	PGTDC60_0447	1, 260	98.1	523.5	0
Transcriptional regulators	Pgjcvi_00399	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_0284	1, 117	100	229.2	0
Transcriptional regulators	Pgjcvi_00399	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_0448	1, 126	99.2	248.1	0
Transcriptional regulators	Pgjcvi_00399	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG0173	1, 117	99.1	227.3	0
Uncharacterized NAD(FAD)-dependent dehydrogenases	Pgjcvi_00400	PG JCVI SC001	pyridine nucleotide-disulphide oxidoreductase family protein	PG W83	PG0174	126, 938	99.3	1607	0
Uncharacterized NAD(FAD)-dependent dehydrogenases	Pgjcvi_00400	PG JCVI SC001	pyridine nucleotide-disulfide oxidoreductase family protein	PG TDC60	PGTDC60_0449	1, 813	98.9	1601.3	0
Uncharacterized NAD(FAD)-dependent dehydrogenases	Pgjcvi_00400	PG JCVI SC001	pyridine nucleotide-disulphide oxidoreductase	PG ATCC 33277	PGN_0285	14, 826	98.8	1599.3	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_00401	PG JCVI SC001	Mfa1 fimbrilin	PG ATCC 33277	PGN_0287	1, 562	36	301.2	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_00401	PG JCVI SC001	Mfa1 fimbrilin	PG TDC60	PGTDC60_0450	1, 564	35.4	289.7	0
Protein of unknown function (DUF1812).	Pgjcvi_00402	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0451	1, 305	85.2	561.2	0
Protein of unknown function (DUF1812).	Pgjcvi_00402	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0288	7, 324	84.3	583.2	0
Protein of unknown function (DUF1812).	Pgjcvi_00402	PG JCVI SC001	hypothetical protein	PG W83	PG0179	7, 324	84.3	583.2	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_00403	PG JCVI SC001	lipoprotein, putative	PG W83	PG0180	1, 446	66.4	636.3	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_00403	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0289	1, 446	66.1	632.5	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_00403	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0452	1, 392	65.3	560.1	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_00404	PG JCVI SC001	immunoreactive 32 kDa antigen	PG ATCC 33277	PGN_0290	1, 333	73.4	508.8	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_00404	PG JCVI SC001	immunoreactive 32 kDa antigen PG49	PG W83	PG0181	1, 333	73.4	509.6	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_00404	PG JCVI SC001	immunoreactive 32 kDa antigen PG49	PG TDC60	PGTDC60_0453	1, 332	72.5	499.6	0
Mg-chelatase subunit ChlD	Pgjcvi_00405	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0291	2, 769	99.3	1543.9	0
Mg-chelatase subunit ChlD	Pgjcvi_00405	PG JCVI SC001	von Willebrand factor type A domain protein	PG W83	PG0182	2, 769	99.3	1544.3	0
Mg-chelatase subunit ChlD	Pgjcvi_00405	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0454	525, 912	34.6	166.8	3.50E-39
hypothetical protein	Pgjcvi_00406	PG JCVI SC001	lipoprotein, putative	PG W83	PG0183	1772, 2071	97.7	612.5	0
hypothetical protein	Pgjcvi_00406	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0291	796, 1095	96.7	605.1	0
hypothetical protein	Pgjcvi_00406	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0454	907, 1206	96.7	605.5	0
hypothetical protein	Pgjcvi_00407	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0291	1073, 1228	95.5	297.4	0
hypothetical protein	Pgjcvi_00407	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0454	1184, 1339	95.5	297	0
hypothetical protein	Pgjcvi_00407	PG JCVI SC001	lipoprotein, putative	PG W83	PG0183	2049, 2204	94.2	296.6	0
TonB-linked outer membrane protein, SusC/RagA family	Pgjcvi_00408	PG JCVI SC001	receptor antigen A	PG ATCC 33277	PGN_0293	1, 1036	72.6	1503.8	0
TonB-linked outer membrane protein, SusC/RagA family	Pgjcvi_00408	PG JCVI SC001	receptor antigen A	PG TDC60	PGTDC60_0456	1, 1018	72.3	1470.3	0
TonB-linked outer membrane protein, SusC/RagA family	Pgjcvi_00408	PG JCVI SC001	ragA protein	PG W83	PG0185	1, 1017	70.7	1464.9	0
SusD family.	Pgjcvi_00409	PG JCVI SC001	lipoprotein RagB	PG W83	PG0186	1, 499	56.8	577.8	0
SusD family.	Pgjcvi_00409	PG JCVI SC001	receptor antigen B	PG ATCC 33277	PGN_0294	1, 501	49	481.9	0
SusD family.	Pgjcvi_00409	PG JCVI SC001	receptor antigen B	PG TDC60	PGTDC60_0457	1, 501	49	481.9	0
hypothetical protein	Pgjcvi_00410	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0459	1, 456	98.9	929.9	0
hypothetical protein	Pgjcvi_00410	PG JCVI SC001	lipoprotein, putative	PG W83	PG0188	1, 456	96.1	911	0
hypothetical protein	Pgjcvi_00410	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0296	1, 386	94.8	758.8	0
hypothetical protein	Pgjcvi_00411	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0297	1, 235	98.3	473.4	0
hypothetical protein	Pgjcvi_00411	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0460	1, 235	97.9	472.2	0
hypothetical protein	Pgjcvi_00411	PG JCVI SC001	hypothetical protein	PG W83	PG0189	1, 235	97.4	470.7	0
undecaprenyl diphosphate synthase	Pgjcvi_00412	PG JCVI SC001	undecaprenyl diphosphate synthase	PG W83	PG0190	1, 254	99.6	506.9	0
undecaprenyl diphosphate synthase	Pgjcvi_00412	PG JCVI SC001	putative undecaprenyl diphosphate synthase	PG ATCC 33277	PGN_0298	1, 254	98.8	503.8	0
undecaprenyl diphosphate synthase	Pgjcvi_00412	PG JCVI SC001	undecaprenyl pyrophosphate synthase	PG TDC60	PGTDC60_0461	1, 254	98.8	505.8	0
Outer membrane protein/protective antigen OMA87	Pgjcvi_00413	PG JCVI SC001	outer membrane protein, putative	PG W83	PG0191	1, 891	100	1805.8	0

Outer membrane protein/protective antigen OMA87	Pgjcvi_00413	PG JCVI SC001	putative outer membrane protein	PG ATCC 33277	PGN_0299	1, 891	99.9	1804.6	0
Outer membrane protein/protective antigen OMA87	Pgjcvi_00413	PG JCVI SC001	putative outer membrane protein	PG TDC60	PGTDC60_0462	1, 891	99.9	1804.6	0
Outer membrane protein	Pgjcvi_00414	PG JCVI SC001	cationic outer membrane protein OmpH	PG W83	PG0192	5, 174	99.4	330.9	0
Outer membrane protein	Pgjcvi_00414	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0300	5, 174	98.8	330.9	0
Outer membrane protein	Pgjcvi_00414	PG JCVI SC001	cationic outer membrane protein OmpH	PG TDC60	PGTDC60_0463	5, 174	98.8	330.9	0
Outer membrane protein	Pgjcvi_00415	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0301	1, 163	100	313.2	0
Outer membrane protein	Pgjcvi_00415	PG JCVI SC001	cationic outer membrane protein OmpH	PG W83	PG0193	1, 163	100	313.2	0
Outer membrane protein	Pgjcvi_00415	PG JCVI SC001	cationic outer membrane protein OmpH	PG TDC60	PGTDC60_0464	1, 163	100	313.2	0
Rubrerythrin	Pgjcvi_00416	PG JCVI SC001	rubrerythrin	PG ATCC 33277	PGN_0302	1, 192	99.5	387.1	0
Rubrerythrin	Pgjcvi_00416	PG JCVI SC001	rubrerythrin	PG TDC60	PGTDC60_0465	1, 192	99.5	387.1	0
Rubrerythrin	Pgjcvi_00416	PG JCVI SC001	rubrerythrin	PG W83	PG0195	1, 192	99	385.6	0
Predicted Zn-dependent peptidases	Pgjcvi_00417	PG JCVI SC001	putative zinc protease	PG ATCC 33277	PGN_0303	1, 941	99.6	1855.5	0
Predicted Zn-dependent peptidases	Pgjcvi_00417	PG JCVI SC001	peptidase, M16 family	PG W83	PG0196	1, 941	99.4	1852.4	0
Predicted Zn-dependent peptidases	Pgjcvi_00417	PG JCVI SC001	M16 family peptidase	PG TDC60	PGTDC60_0466	1, 941	99.4	1852.4	0
Predicted membrane protein	Pgjcvi_00418	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0306	71, 280	100	420.2	0
Predicted membrane protein	Pgjcvi_00418	PG JCVI SC001	hypothetical protein	PG W83	PG0198	1, 179	99.4	356.7	0
Predicted membrane protein	Pgjcvi_00418	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0472	1, 179	99.4	356.7	0
Mg-dependent DNase	Pgjcvi_00419	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0307	5, 241	99.6	483.8	0
Mg-dependent DNase	Pgjcvi_00419	PG JCVI SC001	TatD family protein	PG TDC60	PGTDC60_0473	1, 237	98.7	478.4	0
Mg-dependent DNase	Pgjcvi_00419	PG JCVI SC001	TatD family protein	PG W83	PG0199	1, 237	98.3	475.7	0
conserved hypothetical protein YidD	Pgjcvi_00420	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0308	1, 76	100	162.2	8.20E-39
conserved hypothetical protein YidD	Pgjcvi_00420	PG JCVI SC001	hypothetical protein	PG W83	PG0200	1, 76	100	162.2	8.20E-39
conserved hypothetical protein YidD	Pgjcvi_00420	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0474	1, 76	100	162.2	8.20E-39
ribonuclease P protein component, eubacterial	Pgjcvi_00421	PG JCVI SC001	probable ribonuclease P protein component	PG ATCC 33277	PGN_0309	1, 137	99.3	263.5	0
ribonuclease P protein component, eubacterial	Pgjcvi_00421	PG JCVI SC001	ribonuclease P	PG TDC60	PGTDC60_0475	1, 137	98.5	261.9	0
ribonuclease P protein component, eubacterial	Pgjcvi_00421	PG JCVI SC001	ribonuclease P	PG W83	PG0201	1, 137	97.8	260	0
Uroporphyrinogen-III synthase	Pgjcvi_00422	PG JCVI SC001	putative uroporphyrinogen-III synthase	PG ATCC 33277	PGN_0310	1, 248	100	495.4	0
Uroporphyrinogen-III synthase	Pgjcvi_00422	PG JCVI SC001	uroporphyrinogen-III synthase HemD, putative	PG W83	PG0202	1, 248	100	495.4	0
Uroporphyrinogen-III synthase	Pgjcvi_00422	PG JCVI SC001	uroporphyrinogen-III synthase HemD	PG TDC60	PGTDC60_0476	1, 248	100	495.4	0
hypothetical protein	Pgjcvi_00423	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0477	1, 235	99.1	486.5	0
hypothetical protein	Pgjcvi_00423	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0311	1, 235	98.7	485.3	0
hypothetical protein	Pgjcvi_00423	PG JCVI SC001	hypothetical protein	PG W83	PG0203	1, 235	98.7	485	0
hypothetical protein	Pgjcvi_00424	PG JCVI SC001	hypothetical protein	PG W83	PG0204	10, 81	98.6	139	7.00E-32
hypothetical protein	Pgjcvi_00424	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0478	1, 72	97.2	137.5	2.00E-31
hypothetical protein	Pgjcvi_00424	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0312	10, 81	95.8	136	5.90E-31
peptide chain release factor 3	Pgjcvi_00425	PG JCVI SC001	peptide chain release factor 3	PG W83	PG0205	1, 526	99.2	1053.5	0
peptide chain release factor 3	Pgjcvi_00425	PG JCVI SC001	peptide chain release factor 3	PG ATCC 33277	PGN_0313	1, 526	98.9	1049.7	0
peptide chain release factor 3	Pgjcvi_00425	PG JCVI SC001	peptide chain release factor 3	PG TDC60	PGTDC60_0479	1, 526	98.7	1049.3	0
formate/nitrite transporter	Pgjcvi_00427	PG JCVI SC001	probable formate/nitrite transporter	PG ATCC 33277	PGN_0314	1, 261	98.9	530	0
formate/nitrite transporter	Pgjcvi_00427	PG JCVI SC001	formate/nitrite transporter	PG W83	PG0209	1, 261	98.5	528.1	0
formate/nitrite transporter	Pgjcvi_00427	PG JCVI SC001	formate/nitrite transporter	PG TDC60	PGTDC60_0482	1, 261	98.5	527.3	0
Cobalamin biosynthesis protein CbiD	Pgjcvi_00428	PG JCVI SC001	precorrin-6x reductase/cobalamin biosynthetic protein CbiD	PG ATCC 33277	PGN_0315	1, 602	99.5	1176	0
Cobalamin biosynthesis protein CbiD	Pgjcvi_00428	PG JCVI SC001	precorrin-6x reductase/cobalamin biosynthetic protein CbiD	PG W83	PG0210	1, 602	98.8	1167.1	0
Cobalamin biosynthesis protein CbiD	Pgjcvi_00428	PG JCVI SC001	precorrin-6x reductase/cobalamin biosynthetic protein CbiD	PG TDC60	PGTDC60_0483	1, 602	98.8	1167.1	0
precorrin-4 C11-methyltransferase	Pgjcvi_00429	PG JCVI SC001	cobalamin biosynthesis protein CbiG/precorrin-4 C11-methyltransferase	PG TDC60	PGTDC60_0484	1, 614	99	1204.5	0
precorrin-4 C11-methyltransferase	Pgjcvi_00429	PG JCVI SC001	cobalamin biosynthesis protein CbiG/precorrin-4 C11-methyltransferase	PG W83	PG0211	1, 614	98.2	1199.1	0
precorrin-4 C11-methyltransferase	Pgjcvi_00429	PG JCVI SC001	precorrin-4 C11-methyltransferase	PG ATCC 33277	PGN_0316	1, 614	98	1194.5	0
hypothetical protein	Pgjcvi_00430	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0485	1, 203	90.1	380.9	0
hypothetical protein	Pgjcvi_00431	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0486	1, 72	91.7	131.7	1.10E-29
precorrin-6y C5,15-methyltransferase (decarboxylating), CbiE subunit/precorrin-6Y C5,15-methyltransferase (decarboxylating), CbiT subunit	Pgjcvi_00432	PG JCVI SC001	decarboxylating precorrin-6Y C5,15-methyltransferase	PG ATCC 33277	PGN_0317	1, 412	98.1	817.8	0
precorrin-6y C5,15-methyltransferase (decarboxylating), CbiE subunit/precorrin-6Y C5,15-methyltransferase (decarboxylating), CbiT subunit	Pgjcvi_00432	PG JCVI SC001	precorrin-6Y C5,15-methyltransferase, decarboxylating	PG TDC60	PGTDC60_0487	1, 413	98.1	820.5	0
precorrin-6y C5,15-methyltransferase (decarboxylating), CbiE subunit/precorrin-6Y C5,15-methyltransferase (decarboxylating), CbiT subunit	Pgjcvi_00432	PG JCVI SC001	precorrin-6Y C5,15-methyltransferase, decarboxylating	PG W83	PG0212	1, 412	97.8	818.1	0
precorrin-3B C17-methyltransferase	Pgjcvi_00433	PG JCVI SC001	precorrin-3B C17-methyltransferase	PG ATCC 33277	PGN_0318	1, 468	99.4	927.5	0
precorrin-3B C17-methyltransferase	Pgjcvi_00433	PG JCVI SC001	precorrin-3 methylase/precorrin-8X methylmutase	PG W83	PG0213	1, 468	99.4	928.7	0
precorrin-3B C17-methyltransferase	Pgjcvi_00433	PG JCVI SC001	precorrin-3 methylase/precorrin-8X methylmutase	PG TDC60	PGTDC60_0488	1, 506	98.8	997.3	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00434	PG JCVI SC001	RNA polymerase sigma-70 factor, ECF subfamily	PG W83	PG0214	1, 166	100	318.5	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00434	PG JCVI SC001	ECF subfamily RNA polymerase sigma factor	PG TDC60	PGTDC60_0490	1, 166	100	318.5	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00434	PG JCVI SC001	probable RNA polymerase sigma-70 factor ECF subfamily	PG ATCC 33277	PGN_0319	1, 177	98.3	335.1	0
hypothetical protein	Pgjcvi_00435	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0320	1, 161	98.8	315.1	0
hypothetical protein	Pgjcvi_00435	PG JCVI SC001	hypothetical protein	PG W83	PG0215	2, 162	98.8	313.9	0
hypothetical protein	Pgjcvi_00435	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0491	1, 161	98.1	314.7	0
hypothetical protein	Pgjcvi_00436	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0321	17, 166	99.3	298.1	0
hypothetical protein	Pgjcvi_00436	PG JCVI SC001	hypothetical protein	PG W83	PG0216	17, 166	99.3	298.1	0
hypothetical protein	Pgjcvi_00436	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0492	1, 150	99.3	298.1	0
hypothetical protein	Pgjcvi_00437	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0322	1, 297	99.3	592.4	0
hypothetical protein	Pgjcvi_00437	PG JCVI SC001	hypothetical protein	PG W83	PG0217	1, 297	99	590.1	0
hypothetical protein	Pgjcvi_00437	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0493	1, 297	99	590.1	0
hypothetical protein	Pgjcvi_00438	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0323	1, 285	99.6	565.8	0
hypothetical protein	Pgjcvi_00438	PG JCVI SC001	hypothetical protein	PG W83	PG0218	35, 319	99.3	562.8	0

hypothetical protein	Pgjcvi_00438	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0494	1, 285	97.5	553.5	0
DNA-binding protein, histone-like, putative	Pgjcvi_00441	PG JCVI SC001	DNA-binding protein histone-like family	PG ATCC 33277	PGN_0460	1, 145	98.6	282	0
DNA-binding protein, histone-like, putative	Pgjcvi_00441	PG JCVI SC001	histone-like family DNA-binding protein	PG TDC60	PGTDC60_0498	1, 155	98.1	298.5	0
DNA-binding protein, histone-like, putative	Pgjcvi_00441	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG0222	1, 155	92.9	287	0
DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00442	PG JCVI SC001	exonuclease	PG W83	PG0223	1, 163	98.8	336.3	0
DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00442	PG JCVI SC001	putative DNA polymerase III epsilon chain	PG TDC60	PGTDC60_0502	1, 163	98.8	337	0
DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases	Pgjcvi_00442	PG JCVI SC001	putative DNA polymerase III epsilon chain	PG ATCC 33277	PGN_0327	1, 163	98.2	335.1	0
Multiple antibiotic transporter	Pgjcvi_00443	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0503	1, 212	100	404.4	0
Multiple antibiotic transporter	Pgjcvi_00443	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0328	1, 212	99.5	402.1	0
Multiple antibiotic transporter	Pgjcvi_00443	PG JCVI SC001	hypothetical protein	PG W83	PG0224	1, 212	99.5	404.1	0
Transglutaminase-like enzymes, putative cysteine proteases	Pgjcvi_00444	PG JCVI SC001	transglutaminase-like protein	PG TDC60	PGTDC60_0504	1, 897	99.6	1785	0
Transglutaminase-like enzymes, putative cysteine proteases	Pgjcvi_00444	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0329	1, 897	99.4	1782.7	0
Transglutaminase-like enzymes, putative cysteine proteases	Pgjcvi_00444	PG JCVI SC001	transglutaminase-related protein	PG W83	PG0226	1, 897	99.2	1779.2	0
DNA repair protein RadA	Pgjcvi_00445	PG JCVI SC001	DNA repair protein	PG ATCC 33277	PGN_0330	1, 461	99.8	905.2	0
DNA repair protein RadA	Pgjcvi_00445	PG JCVI SC001	DNA repair protein RadA	PG TDC60	PGTDC60_0505	1, 461	99.8	905.2	0
DNA repair protein RadA	Pgjcvi_00445	PG JCVI SC001	DNA repair protein RadA	PG W83	PG0227	1, 461	99.6	902.5	0
N-Dimethylarginine dimethylaminohydrolase	Pgjcvi_00446	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0331	1, 294	99.7	592	0
N-Dimethylarginine dimethylaminohydrolase	Pgjcvi_00446	PG JCVI SC001	DdaH family protein	PG TDC60	PGTDC60_0506	1, 308	99.7	620.5	0
N-Dimethylarginine dimethylaminohydrolase	Pgjcvi_00446	PG JCVI SC001	DdaH family protein	PG W83	PG0228	1, 308	99	614.4	0
TonB dependent receptor.	Pgjcvi_00447	PG JCVI SC001	hypothetical protein	PG W83	PG0441	9, 409	31.4	181.8	1.20E-43
TonB dependent receptor.	Pgjcvi_00447	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1561	9, 424	31.3	183.7	3.10E-44
TonB dependent receptor.	Pgjcvi_00447	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1520	8, 423	30.8	179.9	4.50E-43
Protein of unknown function (Porph_ging).	Pgjcvi_00448	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1560	130, 233	37.3	70.5	1.20E-10
Protein of unknown function (Porph_ging).	Pgjcvi_00448	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1521	5, 254	25.1	73.9	1.10E-11
Protein of unknown function (Porph_ging).	Pgjcvi_00448	PG JCVI SC001	hypothetical protein	PG W83	PG0439	5, 254	24.7	71.2	7.10E-11
Protein of unknown function (DUF1661).	Pgjcvi_00449	PG JCVI SC001	hypothetical protein	PG W83	PG2064	2, 45	54.5	48.9	0.00024
Protein of unknown function (DUF1661).	Pgjcvi_00449	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0280	28, 86	50.8	47.8	0.00054
Protein of unknown function (DUF1661).	Pgjcvi_00449	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0444	37, 95	50.8	47.8	0.00054
fructose-6-phosphate aldolase, TalC/MipB family	Pgjcvi_00450	PG JCVI SC001	putative transaldolase	PG ATCC 33277	PGN_0333	1, 220	100	439.1	0
fructose-6-phosphate aldolase, TalC/MipB family	Pgjcvi_00450	PG JCVI SC001	transaldolase	PG W83	PG0230	1, 220	100	439.1	0
fructose-6-phosphate aldolase, TalC/MipB family	Pgjcvi_00450	PG JCVI SC001	putative translaldolase	PG TDC60	PGTDC60_0508	1, 220	99.5	438.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00451	PG JCVI SC001	conserved hypothetical protein with DUF1343 domain	PG ATCC 33277	PGN_0334	1, 432	99.3	868.6	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00451	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0509	2, 383	99	768.5	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00451	PG JCVI SC001	hypothetical protein	PG W83	PG0231	1, 432	98.4	860.1	0
Por secretion system C-terminal sorting domain	Pgjcvi_00452	PG JCVI SC001	conserved hypothetical protein with Zinc carboxypeptidase domain	PG ATCC 33277	PGN_0335	1, 821	99.6	1655.2	0
Por secretion system C-terminal sorting domain	Pgjcvi_00452	PG JCVI SC001	zinc carboxypeptidase, putative	PG W83	PG0232	1, 821	99.5	1651.7	0
Por secretion system C-terminal sorting domain	Pgjcvi_00452	PG JCVI SC001	zinc carboxypeptidase	PG TDC60	PGTDC60_0510	1, 821	99.3	1651	0
hypothetical protein	Pgjcvi_00453	PG JCVI SC001	immunoreactive 23 kDa antigen	PG ATCC 33277	PGN_0336	1, 207	100	425.2	0
hypothetical protein	Pgjcvi_00453	PG JCVI SC001	immunoreactive 23 kDa antigen PG66	PG W83	PG0234	1, 207	100	425.2	0
hypothetical protein	Pgjcvi_00453	PG JCVI SC001	immunoreactive 23 kDa antigen PG66	PG TDC60	PGTDC60_0513	1, 204	100	419.5	0
C-terminal peptidase (prc)	Pgjcvi_00455	PG JCVI SC001	carboxyl-terminal processing protease	PG ATCC 33277	PGN_0340	1, 533	99.1	1038.9	0
C-terminal peptidase (prc)	Pgjcvi_00455	PG JCVI SC001	carboxyl-terminal protease	PG W83	PG0235	1, 507	99	996.1	0
C-terminal peptidase (prc)	Pgjcvi_00455	PG JCVI SC001	carboxyl-terminal protease	PG TDC60	PGTDC60_0515	1, 507	98.6	990.7	0
hypothetical protein	Pgjcvi_00456	PG JCVI SC001	hypothetical protein	PG W83	PG0236	1, 506	99.2	997.3	0
hypothetical protein	Pgjcvi_00456	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0341	1, 506	98.4	989.9	0
hypothetical protein	Pgjcvi_00456	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0516	1, 506	98	981.1	0
uracil-DNA glycosylase	Pgjcvi_00457	PG JCVI SC001	putative uracil-DNA glycosylase	PG ATCC 33277	PGN_0342	1, 222	98.6	460.7	0
uracil-DNA glycosylase	Pgjcvi_00457	PG JCVI SC001	uracil-DNA glycosylase	PG W83	PG0237	1, 222	98.6	459.1	0
uracil-DNA glycosylase	Pgjcvi_00457	PG JCVI SC001	uracil-DNA glycosylase	PG TDC60	PGTDC60_0517	1, 222	98.6	459.1	0
hypothetical protein	Pgjcvi_00458	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0518	1, 57	96.5	114	1.90E-24
hypothetical protein	Pgjcvi_00458	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1887	1, 57	94.7	110.5	2.10E-23
HAD superfamily (subfamily IA) hydrolase, TIGR02254	Pgjcvi_00459	PG JCVI SC001	putative haloacid dehalogenase-like hydrolase	PG TDC60	PGTDC60_0520	1, 271	99.3	546.6	0
HAD superfamily (subfamily IA) hydrolase, TIGR02254	Pgjcvi_00459	PG JCVI SC001	hydrolase, haloacid dehalogenase-like family	PG W83	PG0240	1, 232	99.1	477.2	0
HAD superfamily (subfamily IA) hydrolase, TIGR02254	Pgjcvi_00459	PG JCVI SC001	probable haloacid dehalogenase-like hydrolase	PG ATCC 33277	PGN_0344	1, 271	97.4	536.6	0
hypothetical protein	Pgjcvi_00460	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0345	1, 284	100	545	0
hypothetical protein	Pgjcvi_00460	PG JCVI SC001	lipoprotein, putative	PG W83	PG0241	1, 284	100	545	0
hypothetical protein	Pgjcvi_00460	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0521	1, 295	100	568.5	0
probable S-adenosylmethionine-dependent methyltransferase, YraL family	Pgjcvi_00461	PG JCVI SC001	putative methyltransferase	PG ATCC 33277	PGN_0346	1, 233	99.6	462.2	0
probable S-adenosylmethionine-dependent methyltransferase, YraL family	Pgjcvi_00461	PG JCVI SC001	conserved hypothetical protein TIGR00096	PG W83	PG0242	1, 233	99.6	462.2	0
probable S-adenosylmethionine-dependent methyltransferase, YraL family	Pgjcvi_00461	PG JCVI SC001	putative methyltransferase	PG TDC60	PGTDC60_0522	1, 233	99.6	462.2	0
hypothetical protein	Pgjcvi_00462	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0347	1, 158	100	314.3	0
hypothetical protein	Pgjcvi_00462	PG JCVI SC001	hypothetical protein	PG W83	PG0243	1, 158	100	314.3	0
hypothetical protein	Pgjcvi_00462	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0523	1, 158	100	314.3	0
Universal stress protein UspA and related nucleotide-binding proteins	Pgjcvi_00464	PG JCVI SC001	putative universal stress protein UspA	PG ATCC 33277	PGN_0348	1, 370	100	728.4	0
Universal stress protein UspA and related nucleotide-binding proteins	Pgjcvi_00464	PG JCVI SC001	universal stress protein family	PG W83	PG0245	1, 370	100	728.4	0
Universal stress protein UspA and related nucleotide-binding proteins	Pgjcvi_00464	PG JCVI SC001	universal stress protein UspA	PG TDC60	PGTDC60_0524	1, 370	100	728.4	0
hypothetical protein	Pgjcvi_00465	PG JCVI SC001	upregulated in stationary phase protein A	PG ATCC 33277	PGN_0349	1, 84	100	169.1	7.40E-41
hypothetical protein	Pgjcvi_00465	PG JCVI SC001	hypothetical protein	PG W83	PG0246	1, 63	100	128.3	1.40E-28
hypothetical protein	Pgjcvi_00465	PG JCVI SC001	upregulated in stationary phase protein A	PG TDC60	PGTDC60_0525	1, 84	100	169.1	7.40E-41
Translation initiation factor 1 (eIF-1/SUI1) and related proteins	Pgjcvi_00466	PG JCVI SC001	translation initation factor SUI1, putative	PG W83	PG0248	1, 110	100	223	0
Translation initiation factor 1 (eIF-1/SUI1) and related proteins	Pgjcvi_00466	PG JCVI SC001	translation initation factor SUI1	PG TDC60	PGTDC60_0526	1, 110	100	223	0
Translation initiation factor 1 (eIF-1/SUI1) and related proteins	Pgjcvi_00466	PG JCVI SC001	probable translation initation factor SUI1	PG ATCC 33277	PGN_0350	1, 110	99.1	220.7	0

Pyruvate/oxaloacetate carboxyltransferase	Pgjcvi_00467	PG JCVI SC001	oxaloacetate decarboxylase, putative	PG W83	PG0249	1, 619	99.8	1260.4	0
Pyruvate/oxaloacetate carboxyltransferase	Pgjcvi_00467	PG JCVI SC001	oxaloacetate decarboxylase	PG TDC60	PGTDC60_0527	1, 619	99.7	1257.3	0
Pyruvate/oxaloacetate carboxyltransferase	Pgjcvi_00467	PG JCVI SC001	pyruvate carboxylase subunit B	PG ATCC 33277	PGN_0351	1, 619	99.5	1256.9	0
hypothetical protein	Pgjcvi_00468	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0352	1, 58	100	120.9	2.90E-26
hypothetical protein	Pgjcvi_00468	PG JCVI SC001	hypothetical protein	PG W83	PG0250	1, 58	100	120.9	2.90E-26
hypothetical protein	Pgjcvi_00468	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0528	1, 58	98.3	119.4	8.60E-26
Uncharacterized protein conserved in bacteria	Pgjcvi_00469	PG JCVI SC001	hypothetical protein	PG W83	PG0253	1, 152	96.1	287	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00469	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0533	1, 152	96.1	287.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00469	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0353	1, 152	95.4	286.2	0
transcription termination factor NusA	Pgjcvi_00470	PG JCVI SC001	putative nitrogen utilization substance protein A	PG ATCC 33277	PGN_0354	1, 444	99.8	864	0
transcription termination factor NusA	Pgjcvi_00470	PG JCVI SC001	transcription elongation factor NusA	PG W83	PG0254	1, 444	99.8	864	0
transcription termination factor NusA	Pgjcvi_00470	PG JCVI SC001	transcription elongation factor NusA	PG TDC60	PGTDC60_0534	1, 444	99.5	862.8	0
translation initiation factor IF-2	Pgjcvi_00471	PG JCVI SC001	translation initiation factor IF-2	PG ATCC 33277	PGN_0355	1, 979	99.4	1886.3	0
translation initiation factor IF-2	Pgjcvi_00471	PG JCVI SC001	translation initiation factor IF-2	PG W83	PG0255	1, 979	99.3	1883.2	0
translation initiation factor IF-2	Pgjcvi_00471	PG JCVI SC001	translation initiation factor IF-2	PG TDC60	PGTDC60_0535	1, 979	99.3	1881.3	0
Uncharacterized membrane protein, required for colicin V production	Pgjcvi_00472	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0356	1, 163	99.4	317	0
Uncharacterized membrane protein, required for colicin V production	Pgjcvi_00472	PG JCVI SC001	CvpA family protein	PG W83	PG0256	1, 163	99.4	317	0
Uncharacterized membrane protein, required for colicin V production	Pgjcvi_00472	PG JCVI SC001	CvpA family protein	PG TDC60	PGTDC60_0536	1, 163	98.8	314.7	0
FeS assembly protein SufB	Pgjcvi_00473	PG JCVI SC001	ABC transporter membrane protein	PG ATCC 33277	PGN_0357	1, 481	100	966.8	0
FeS assembly protein SufB	Pgjcvi_00473	PG JCVI SC001	hypothetical protein	PG W83	PG0257	1, 481	99.8	963	0
FeS assembly protein SufB	Pgjcvi_00473	PG JCVI SC001	cysteine desulfurase activator complex subunit SufB	PG TDC60	PGTDC60_0537	1, 483	99.6	962.6	0
FeS assembly ATPase SufC	Pgjcvi_00474	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0358	1, 250	100	489.6	0
FeS assembly ATPase SufC	Pgjcvi_00474	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_0538	1, 250	100	489.6	0
FeS assembly ATPase SufC	Pgjcvi_00474	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG0258	1, 250	99.6	487.6	0
FeS assembly protein SufD	Pgjcvi_00475	PG JCVI SC001	hypothetical protein	PG W83	PG0259	1, 447	99.6	897.9	0
FeS assembly protein SufD	Pgjcvi_00475	PG JCVI SC001	putative ABC transporter permease protein	PG TDC60	PGTDC60_0539	1, 447	99.3	895.6	0
FeS assembly protein SufD	Pgjcvi_00475	PG JCVI SC001	putative ABC transporter permease protein	PG ATCC 33277	PGN_0359	1, 447	99.1	892.1	0
tyrosyl-tRNA synthetase	Pgjcvi_00476	PG JCVI SC001	tyrosyl-tRNA synthetase	PG TDC60	PGTDC60_0542	1, 430	99.8	859.8	0
tyrosyl-tRNA synthetase	Pgjcvi_00476	PG JCVI SC001	tyrosyl-tRNA synthetase	PG ATCC 33277	PGN_0360	1, 430	99.5	860.5	0
tyrosyl-tRNA synthetase	Pgjcvi_00476	PG JCVI SC001	tyrosyl-tRNA synthetase	PG W83	PG0263	1, 430	99.3	859	0
Predicted glycosyltransferases	Pgjcvi_00477	PG JCVI SC001	putative glycosyl transferase family 2	PG ATCC 33277	PGN_0361	1, 355	100	718.8	0
Predicted glycosyltransferases	Pgjcvi_00477	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG0264	1, 355	100	718.8	0
Predicted glycosyltransferases	Pgjcvi_00477	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_0543	1, 355	99.7	716.8	0
hypothetical protein	Pgjcvi_00478	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0108	1, 61	98.4	128.3	1.50E-28
hypothetical protein	Pgjcvi_00478	PG JCVI SC001	hypothetical protein	PG W83	PG0197	52, 84	93.9	64.3	2.70E-09
arginyl-tRNA synthetase	Pgjcvi_00479	PG JCVI SC001	arginyl-tRNA synthetase	PG W83	PG0267	1, 597	99.8	1182.9	0
arginyl-tRNA synthetase	Pgjcvi_00479	PG JCVI SC001	arginyl-tRNA synthetase	PG TDC60	PGTDC60_0547	1, 597	99.5	1178.3	0
arginyl-tRNA synthetase	Pgjcvi_00479	PG JCVI SC001	arginyl-tRNA synthetase	PG ATCC 33277	PGN_0365	1, 597	99.3	1176	0
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Pgjcvi_00480	PG JCVI SC001	putative tRNA 5-methylaminomethyl-2-thiouridylate 5-methyltransferase	PG ATCC 33277	PGN_0366	1, 361	98.6	740.7	0
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Pgjcvi_00480	PG JCVI SC001	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	PG W83	PG0268	1, 361	98.6	740.7	0
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Pgjcvi_00480	PG JCVI SC001	tRNA-specific 2-thiouridylase MnmA	PG TDC60	PGTDC60_0548	1, 361	98.1	736.9	0
exodeoxyribonuclease III	Pgjcvi_00481	PG JCVI SC001	exodeoxyribonuclease III	PG W83	PG0269	1, 254	99.6	533.1	0
exodeoxyribonuclease III	Pgjcvi_00481	PG JCVI SC001	exodeoxyribonuclease III	PG ATCC 33277	PGN_0367	1, 254	99.2	529.6	0
exodeoxyribonuclease III	Pgjcvi_00481	PG JCVI SC001	exodeoxyribonuclease III	PG TDC60	PGTDC60_0549	1, 254	99.2	531.6	0
Transcriptional regulator	Pgjcvi_00482	PG JCVI SC001	redox-sensitive transcriptional activator OxyR	PG TDC60	PGTDC60_0550	1, 308	100	606.7	0
Transcriptional regulator	Pgjcvi_00482	PG JCVI SC001	redox-sensitive transcriptional activator OxyR	PG ATCC 33277	PGN_0368	1, 308	99.4	602.8	0
Transcriptional regulator	Pgjcvi_00482	PG JCVI SC001	redox-sensitive transcriptional activator OxyR	PG W83	PG0270	1, 308	99.4	602.8	0
single stranded DNA-binding protein (ssb)	Pgjcvi_00483	PG JCVI SC001	probable single-stranded binding protein	PG ATCC 33277	PGN_0369	1, 156	100	308.5	0
single stranded DNA-binding protein (ssb)	Pgjcvi_00483	PG JCVI SC001	single-stranded binding protein	PG TDC60	PGTDC60_0551	1, 156	100	308.5	0
single stranded DNA-binding protein (ssb)	Pgjcvi_00483	PG JCVI SC001	single-stranded binding protein	PG W83	PG0271	1, 156	98.7	304.3	0
gliding motility-associated protein GldE	Pgjcvi_00484	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0370	1, 442	99.8	869.8	0
gliding motility-associated protein GldE	Pgjcvi_00484	PG JCVI SC001	CBS domain protein	PG W83	PG0272	1, 419	99.8	824.7	0
gliding motility-associated protein GldE	Pgjcvi_00484	PG JCVI SC001	CBS domain-containing protein	PG TDC60	PGTDC60_0552	1, 442	99.8	869.8	0
Phosphopantetheinyl transferase	Pgjcvi_00485	PG JCVI SC001	4'-phosphopantetheinyl transferase family protein	PG W83	PG0273	1, 198	98	396	0
Phosphopantetheinyl transferase	Pgjcvi_00485	PG JCVI SC001	4'-phosphopantetheinyl transferase family protein	PG TDC60	PGTDC60_0553	1, 198	98	397.1	0
Phosphopantetheinyl transferase	Pgjcvi_00485	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0371	1, 198	97.5	392.9	0
Thioredoxin domain-containing protein	Pgjcvi_00486	PG JCVI SC001	putative thioredoxin	PG ATCC 33277	PGN_0373	1, 169	98.8	339.3	0
Thioredoxin domain-containing protein	Pgjcvi_00486	PG JCVI SC001	thioredoxin family protein	PG W83	PG0275	1, 169	98.8	338.6	0
Thioredoxin domain-containing protein	Pgjcvi_00486	PG JCVI SC001	putative thioredoxin	PG TDC60	PGTDC60_0555	1, 169	98.2	337	0
hypothetical protein	Pgjcvi_00487	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0374	1, 375	100	766.1	0
hypothetical protein	Pgjcvi_00487	PG JCVI SC001	hypothetical protein	PG W83	PG0276	21, 395	100	766.1	0
hypothetical protein	Pgjcvi_00487	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0556	1, 375	100	766.1	0
Uridine kinase	Pgjcvi_00488	PG JCVI SC001	phosphoribulokinase family protein	PG W83	PG1745	1, 529	99.8	1062	0
Uridine kinase	Pgjcvi_00488	PG JCVI SC001	phosphoribulose/uridine kinase	PG TDC60	PGTDC60_0557	1, 554	99.8	1115.1	0
Uridine kinase	Pgjcvi_00488	PG JCVI SC001	phosphoribulose/uridine kinase	PG ATCC 33277	PGN_0375	1, 554	99.5	1112.1	0
3-deoxy-8-phosphooctulonate synthase	Pgjcvi_00489	PG JCVI SC001	2-dehydro-3-deoxyphosphooctonate aldolase	PG TDC60	PGTDC60_0559	1, 272	98.9	525	0
3-deoxy-8-phosphooctulonate synthase	Pgjcvi_00489	PG JCVI SC001	2-dehydro-3-deoxyphosphooctonate aldolase	PG ATCC 33277	PGN_0376	1, 272	98.5	523.5	0
3-deoxy-8-phosphooctulonate synthase	Pgjcvi_00489	PG JCVI SC001	2-dehydro-3-deoxyphosphooctonate aldolase	PG W83	PG1743	1, 272	98.5	522.7	0
Aspartate ammonia-lyase	Pgjcvi_00490	PG JCVI SC001	aspartate ammonia-lyase	PG ATCC 33277	PGN_0377	1, 475	100	958.7	0
Aspartate ammonia-lyase	Pgjcvi_00490	PG JCVI SC001	aspartate ammonia-lyase	PG W83	PG1741	1, 475	100	958.7	0
Aspartate ammonia-lyase	Pgjcvi_00490	PG JCVI SC001	aspartate ammonia-lyase	PG TDC60	PGTDC60_0561	1, 475	100	958.7	0
Exopolyphosphatase	Pgjcvi_00491	PG JCVI SC001	putative exopolyphosphatase	PG TDC60	PGTDC60_0562	1, 302	100	589.7	0

Exopolyphosphatase	Pgjcvi_00491	PG JCVI SC001	putative exopolyphosphatase	PG ATCC 33277	PGN_0378	1, 302	99.7	588.2	0
Exopolyphosphatase	Pgjcvi_00491	PG JCVI SC001	hypothetical protein	PG W83	PG1739	1, 151	98	292.7	0
Exopolyphosphatase	Pgjcvi_00491	PG JCVI SC001	hypothetical protein	PG W83	PG1739	148, 193	93.5	86.7	1.70E-15
PAP2 superfamily.	Pgjcvi_00492	PG JCVI SC001	hypothetical protein	PG W83	PG1738	1, 344	100	696.4	0
PAP2 superfamily.	Pgjcvi_00492	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0563	1, 344	100	696.4	0
PAP2 superfamily.	Pgjcvi_00492	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0379	1, 310	99.7	634.4	0
Transcriptional regulator/sugar kinase	Pgjcvi_00493	PG JCVI SC001	glucose kinase	PG TDC60	PGTDC60_0564	1, 319	99.1	632.5	0
Transcriptional regulator/sugar kinase	Pgjcvi_00493	PG JCVI SC001	partial ROK family transcriptional repressor with glucose kinase domain	PG ATCC 33277	PGN_0380	1, 223	97.3	440.7	0
ADP-ribose pyrophosphatase	Pgjcvi_00494	PG JCVI SC001	MutT/nudix family protein	PG W83	PG1735	1, 184	98.9	374	0
ADP-ribose pyrophosphatase	Pgjcvi_00494	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0382	1, 184	98.4	370.2	0
ADP-ribose pyrophosphatase	Pgjcvi_00494	PG JCVI SC001	MutT/nudix family protein	PG TDC60	PGTDC60_0565	1, 145	97.9	284.6	0
Predicted Na+-dependent transporter	Pgjcvi_00495	PG JCVI SC001	transporter, putative	PG W83	PG1734	11, 313	99.7	597.8	0
Predicted Na+-dependent transporter	Pgjcvi_00495	PG JCVI SC001	transporter	PG TDC60	PGTDC60_0566	1, 303	99.7	597.8	0
Predicted Na+-dependent transporter	Pgjcvi_00495	PG JCVI SC001	probable transporter	PG ATCC 33277	PGN_0383	1, 303	99	595.1	0
Family of unknown function (DUF695).	Pgjcvi_00496	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0384	1, 145	99.3	293.9	0
Family of unknown function (DUF695).	Pgjcvi_00496	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0567	1, 145	98.6	292.4	0
Family of unknown function (DUF695).	Pgjcvi_00496	PG JCVI SC001	hypothetical protein	PG W83	PG1733	1, 145	97.9	290.4	0
Site-specific recombinase XerD	Pgjcvi_00497	PG JCVI SC001	putative integrase/recombinase XerD	PG ATCC 33277	PGN_0385	1, 308	99.4	596.7	0
Site-specific recombinase XerD	Pgjcvi_00497	PG JCVI SC001	integrase/recombinase XerD	PG W83	PG1732	1, 308	99	595.5	0
Site-specific recombinase XerD	Pgjcvi_00497	PG JCVI SC001	integrase/recombinase XerD	PG TDC60	PGTDC60_0568	1, 308	98.7	595.1	0
3-dehydroquinate dehydratase II	Pgjcvi_00498	PG JCVI SC001	3-dehydroquinate dehydratase	PG TDC60	PGTDC60_0569	1, 141	98.6	275.8	0
3-dehydroquinate dehydratase II	Pgjcvi_00498	PG JCVI SC001	probable 3-dehydroquinate dehydratase type II	PG ATCC 33277	PGN_0386	1, 141	97.9	273.9	0
3-dehydroquinate dehydratase II	Pgjcvi_00498	PG JCVI SC001	3-dehydroquinate dehydratase	PG W83	PG1731	1, 141	97.2	272.3	0
Predicted O-methyltransferase	Pgjcvi_00499	PG JCVI SC001	O-methyltransferase family protein	PG W83	PG1730	7, 216	99	420.2	0
Predicted O-methyltransferase	Pgjcvi_00499	PG JCVI SC001	putative O-methyltransferase	PG ATCC 33277	PGN_0387	7, 216	98.6	418.3	0
Predicted O-methyltransferase	Pgjcvi_00499	PG JCVI SC001	putative O-methyltransferase	PG TDC60	PGTDC60_0570	5, 214	98.6	419.9	0
Peroxiredoxin	Pgjcvi_00500	PG JCVI SC001	thiol peroxidase	PG W83	PG1729	1, 179	99.4	347.8	0
Peroxiredoxin	Pgjcvi_00500	PG JCVI SC001	thiol peroxidase	PG TDC60	PGTDC60_0571	4, 182	99.4	347.8	0
Peroxiredoxin	Pgjcvi_00500	PG JCVI SC001	putative thiol peroxidase	PG ATCC 33277	PGN_0388	1, 179	98.9	346.7	0
Cytosine/adenosine deaminases	Pgjcvi_00501	PG JCVI SC001	cytidine/deoxycytidylate deaminase family protein	PG TDC60	PGTDC60_0572	1, 163	100	342.8	0
Cytosine/adenosine deaminases	Pgjcvi_00501	PG JCVI SC001	putative cytidine/deoxycytidylate deaminase	PG ATCC 33277	PGN_0389	1, 159	99.4	332	0
Cytosine/adenosine deaminases	Pgjcvi_00501	PG JCVI SC001	cytidine/deoxycytidylate deaminase family protein	PG W83	PG1728	1, 150	99.3	312.8	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00502	PG JCVI SC001	yitL protein	PG TDC60	PGTDC60_0573	1, 285	99.3	567.4	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00502	PG JCVI SC001	yitL protein	PG W83	PG1727	1, 285	98.6	564.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00502	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0390	1, 285	98.2	560.8	0
Periplasmic protease	Pgjcvi_00503	PG JCVI SC001	PDZ domain protein	PG W83	PG1726	1, 472	99.6	936.4	0
Periplasmic protease	Pgjcvi_00503	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0391	1, 472	99.4	934.9	0
Periplasmic protease	Pgjcvi_00503	PG JCVI SC001	PDZ domain-containing protein	PG TDC60	PGTDC60_0574	1, 472	99.2	935.3	0
competence/damage-inducible protein CinA C-terminal domain	Pgjcvi_00504	PG JCVI SC001	competence/damage inducible protein CinA	PG TDC60	PGTDC60_0575	1, 160	100	316.2	0
competence/damage-inducible protein CinA C-terminal domain	Pgjcvi_00504	PG JCVI SC001	conserved hypothetical protein with competence-damaged protein domain	PG ATCC 33277	PGN_0392	1, 160	99.4	312.8	0
competence/damage-inducible protein CinA C-terminal domain	Pgjcvi_00504	PG JCVI SC001	competence/damage-inducible protein CinA domain protein	PG W83	PG1725	1, 160	98.1	308.5	0
putative glycoprotease GCP	Pgjcvi_00505	PG JCVI SC001	O-sialoglycoprotein endopeptidase	PG W83	PG1724	1, 341	99.7	678.3	0
putative glycoprotease GCP	Pgjcvi_00505	PG JCVI SC001	putative DNA-binding/iron metalloprotein/AP endonuclease	PG TDC60	PGTDC60_0576	1, 341	99.7	676.4	0
putative glycoprotease GCP	Pgjcvi_00505	PG JCVI SC001	putative O-sialoglycoprotein endopeptidase	PG ATCC 33277	PGN_0393	1, 341	99.1	674.1	0
ribosomal protein S20	Pgjcvi_00507	PG JCVI SC001	probable 30S ribosomal protein S20	PG ATCC 33277	PGN_0394	1, 83	100	163.3	4.10E-39
ribosomal protein S20	Pgjcvi_00507	PG JCVI SC001	ribosomal protein S20	PG W83	PG1723	1, 83	100	163.3	4.10E-39
ribosomal protein S20	Pgjcvi_00507	PG JCVI SC001	30S ribosomal protein S20	PG TDC60	PGTDC60_0577	1, 83	100	163.3	4.10E-39
ribonuclease R	Pgjcvi_00509	PG JCVI SC001	ribonuclease R	PG TDC60	PGTDC60_0582	1, 731	99.7	1454.9	0
ribonuclease R	Pgjcvi_00509	PG JCVI SC001	ribonuclease R	PG ATCC 33277	PGN_0396	1, 731	99.6	1454.1	0
ribonuclease R	Pgjcvi_00509	PG JCVI SC001	ribonuclease R	PG W83	PG1721	1, 702	99.6	1397.9	0
GH3 auxin-responsive promoter.	Pgjcvi_00510	PG JCVI SC001	hypothetical protein	PG W83	PG1720	7, 509	99	1005	0
GH3 auxin-responsive promoter.	Pgjcvi_00510	PG JCVI SC001	putative auxin-regulated protein	PG TDC60	PGTDC60_0583	1, 503	98.8	1000.7	0
GH3 auxin-responsive promoter.	Pgjcvi_00510	PG JCVI SC001	putative auxin-regulated protein	PG ATCC 33277	PGN_0397	7, 509	98.6	1002.3	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_00511	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_0584	1, 616	99.5	1208.7	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_00511	PG JCVI SC001	ABC transporter ATP-binding protein MsbA family	PG ATCC 33277	PGN_0398	1, 605	99.2	1183.7	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_00511	PG JCVI SC001	ABC transporter, ATP-binding protein, MsbA family	PG W83	PG1719	1, 616	99.2	1206	0
pyridoxamine-phosphate oxidase	Pgjcvi_00512	PG JCVI SC001	putative pyridoxamine-phosphate oxidase	PG ATCC 33277	PGN_0403	1, 214	100	444.1	0
pyridoxamine-phosphate oxidase	Pgjcvi_00512	PG JCVI SC001	pyridoxamine-phosphate oxidase	PG W83	PG1714	1, 214	99.5	443.4	0
pyridoxamine-phosphate oxidase	Pgjcvi_00512	PG JCVI SC001	pyridoxamine-phosphate oxidase	PG TDC60	PGTDC60_0590	1, 214	99.5	443.4	0
Rhodanese-related sulfurtransferase	Pgjcvi_00513	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0591	1, 134	100	268.9	0
Rhodanese-related sulfurtransferase	Pgjcvi_00513	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0404	1, 134	98.5	265.4	0
Rhodanese-related sulfurtransferase	Pgjcvi_00513	PG JCVI SC001	lipoprotein, putative	PG W83	PG1713	1, 134	98.5	265.8	0
alpha-1,2-mannosidase, putative	Pgjcvi_00514	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG TDC60	PGTDC60_0592	6, 786	98.6	1621.3	0
alpha-1,2-mannosidase, putative	Pgjcvi_00514	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG ATCC 33277	PGN_0405	1, 781	98.1	1613.2	0
alpha-1,2-mannosidase, putative	Pgjcvi_00514	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG W83	PG1712	1, 781	97.4	1602	0
alpha-1,2-mannosidase, putative	Pgjcvi_00515	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG TDC60	PGTDC60_0593	1, 753	99.5	1556.2	0
alpha-1,2-mannosidase, putative	Pgjcvi_00515	PG JCVI SC001	conserved hypothetical protein with glycosyl hydrolase family 92 domain	PG ATCC 33277	PGN_0406	1, 767	99.2	1578.5	0
alpha-1,2-mannosidase, putative	Pgjcvi_00515	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG W83	PG1711	1, 753	99.2	1553.9	0
Septum formation initiator	Pgjcvi_00516	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0408	1, 117	100	237.3	0
Septum formation initiator	Pgjcvi_00516	PG JCVI SC001	hypothetical protein	PG W83	PG1707	5, 121	100	237.3	0
Septum formation initiator	Pgjcvi_00516	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0595	1, 117	100	237.3	0
hypothetical protein	Pgjcvi_00517	PG JCVI SC001	hypothetical protein	PG W83	PG1706	1, 120	100	233	0

hypothetical protein	Pgjcvi_00517	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0596	1, 120	100	233	0
hypothetical protein	Pgjcvi_00517	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0409	1, 120	99.2	231.5	0
Pseudouridylate synthases, 23S RNA-specific	Pgjcvi_00518	PG JCVI SC001	probable RNA pseudouridylate synthase	PG ATCC 33277	PGN_0410	1, 324	99.7	641	0
Pseudouridylate synthases, 23S RNA-specific	Pgjcvi_00518	PG JCVI SC001	putative RNA pseudouridylate synthase	PG TDC60	PGTDC60_0597	1, 324	99.7	641	0
Thiol:disulfide interchange protein	Pgjcvi_00519	PG JCVI SC001	thiol-disulfide interchange protein	PG ATCC 33277	PGN_0411	1, 682	100	1372.8	0
Thiol:disulfide interchange protein	Pgjcvi_00519	PG JCVI SC001	thiol:disulfide interchange protein dsbD, putative	PG W83	PG1704	1, 682	100	1372.8	0
Thiol:disulfide interchange protein	Pgjcvi_00519	PG JCVI SC001	thiol:disulfide interchange protein dsbD	PG TDC60	PGTDC60_0598	1, 682	99.9	1371.3	0
MazG family protein	Pgjcvi_00520	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0412	1, 260	100	526.2	0
MazG family protein	Pgjcvi_00520	PG JCVI SC001	MazG family protein	PG W83	PG1703	1, 261	100	527.7	0
MazG family protein	Pgjcvi_00520	PG JCVI SC001	nucleoside triphosphate pyrophosphohydrolase	PG TDC60	PGTDC60_0599	1, 261	100	527.7	0
DNA gyrase, B subunit	Pgjcvi_00521	PG JCVI SC001	DNA gyrase B subunit	PG ATCC 33277	PGN_0413	1, 654	100	1293.1	0
DNA gyrase, B subunit	Pgjcvi_00521	PG JCVI SC001	DNA gyrase, B subunit	PG W83	PG1702	1, 654	100	1293.1	0
DNA gyrase, B subunit	Pgjcvi_00521	PG JCVI SC001	DNA gyrase, B subunit	PG TDC60	PGTDC60_0600	1, 654	100	1293.1	0
Zn-dependent dipeptidase, microsomal dipeptidase homolog	Pgjcvi_00522	PG JCVI SC001	glutamine amidotransferase, class II/dipeptidase	PG TDC60	PGTDC60_0601	1, 602	98.3	1186.8	0
Zn-dependent dipeptidase, microsomal dipeptidase homolog	Pgjcvi_00522	PG JCVI SC001	probable membrane-bound dipeptidase	PG ATCC 33277	PGN_0414	1, 602	97.8	1182.5	0
Zn-dependent dipeptidase, microsomal dipeptidase homolog	Pgjcvi_00522	PG JCVI SC001	glutamine amidotransferase, class II/dipeptidase	PG W83	PG1701	1, 602	97.8	1182.2	0
DNA or RNA helicases of superfamily II	Pgjcvi_00523	PG JCVI SC001	type II restriction endonuclease, putative	PG W83	PG1697	1, 1324	99.6	2682.1	0
DNA or RNA helicases of superfamily II	Pgjcvi_00523	PG JCVI SC001	restriction endonuclease	PG ATCC 33277	PGN_0415	1, 1324	99.5	2679.4	0
DNA or RNA helicases of superfamily II	Pgjcvi_00523	PG JCVI SC001	type II restriction endonuclease	PG TDC60	PGTDC60_0604	1, 1324	99.5	2677.9	0
hypothetical protein	Pgjcvi_00524	PG JCVI SC001	putative type II DNA modification methyltransferase	PG ATCC 33277	PGN_0416	4, 337	99.4	694.9	0
hypothetical protein	Pgjcvi_00524	PG JCVI SC001	type II DNA modification methyltransferase, putative	PG W83	PG1696	12, 345	99.4	694.9	0
hypothetical protein	Pgjcvi_00524	PG JCVI SC001	type II DNA modification methyltransferase	PG TDC60	PGTDC60_0605	4, 337	99.4	694.9	0
conserved hypothetical protein, YceG family	Pgjcvi_00525	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0607	1, 324	99.1	647.5	0
conserved hypothetical protein, YceG family	Pgjcvi_00525	PG JCVI SC001	conserved hypothetical protein with aminodeoxychorismate lyase domain	PG ATCC 33277	PGN_0418	1, 364	98.6	719.2	0
conserved hypothetical protein, YceG family	Pgjcvi_00525	PG JCVI SC001	hypothetical protein	PG W83	PG1694	1, 364	98.6	719.2	0
Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 1	Pgjcvi_00526	PG JCVI SC001	putative dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis	PG ATCC 33277	PGN_0419	1, 249	98	471.9	0
Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 1	Pgjcvi_00526	PG JCVI SC001	HesA/MoeB/ThiF family protein	PG W83	PG1693	1, 249	98	471.9	0
Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 1	Pgjcvi_00526	PG JCVI SC001	HesA/MoeB/ThiF family protein	PG TDC60	PGTDC60_0608	1, 249	98	471.1	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_00527	PG JCVI SC001	putative lipoprotein releasing system ATP-binding protein	PG ATCC 33277	PGN_0420	1, 219	99.1	421	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_00527	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG1692	1, 219	99.1	421	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_00527	PG JCVI SC001	putative lipoprotein releasing system ATP-binding protein	PG TDC60	PGTDC60_0609	1, 219	99.1	421	0
hypothetical protein	Pgjcvi_00528	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0421	1, 234	98.7	464.5	0
hypothetical protein	Pgjcvi_00528	PG JCVI SC001	hypothetical protein	PG W83	PG1691	1, 234	98.7	464.5	0
hypothetical protein	Pgjcvi_00528	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0610	1, 234	98.3	460.7	0
Sua5/YciO/YrdC/YwlC family protein	Pgjcvi_00529	PG JCVI SC001	Sua5/YciO/YrdC/YwlC family protein	PG W83	PG1690	1, 200	99.5	402.9	0
Sua5/YciO/YrdC/YwlC family protein	Pgjcvi_00529	PG JCVI SC001	Sua5/YciO/YrdC/YwlC family protein	PG TDC60	PGTDC60_0611	1, 200	99.5	402.9	0
Sua5/YciO/YrdC/YwlC family protein	Pgjcvi_00529	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0422	1, 200	99	401.7	0
transcription elongation factor GreA	Pgjcvi_00530	PG JCVI SC001	putative transcription elongation factor	PG ATCC 33277	PGN_0423	1, 156	100	294.3	0
transcription elongation factor GreA	Pgjcvi_00530	PG JCVI SC001	transcription elongation factor GreA	PG W83	PG1688	1, 156	100	294.3	0
transcription elongation factor GreA	Pgjcvi_00530	PG JCVI SC001	transcription elongation factor GreA	PG TDC60	PGTDC60_0612	1, 156	100	294.3	0
Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	Pgjcvi_00531	PG JCVI SC001	putative HIT family protein	PG ATCC 33277	PGN_0424	1, 129	99.2	257.3	0
Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	Pgjcvi_00531	PG JCVI SC001	HIT family protein	PG W83	PG1687	1, 129	99.2	256.5	0
Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	Pgjcvi_00531	PG JCVI SC001	HIT family protein	PG TDC60	PGTDC60_0613	1, 129	98.4	255	0
Protein of unknown function, DUF481.	Pgjcvi_00533	PG JCVI SC001	hypothetical protein	PG W83	PG1685	1, 260	100	528.1	0
hypothetical protein	Pgjcvi_00535	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0426	1, 158	100	315.8	0
hypothetical protein	Pgjcvi_00535	PG JCVI SC001	hypothetical protein	PG W83	PG1684	1, 158	100	315.8	0
hypothetical protein	Pgjcvi_00535	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0616	1, 158	100	315.8	0
Alpha-amylase/alpha-mannosidase	Pgjcvi_00536	PG JCVI SC001	putative glycosyl hydrolase	PG TDC60	PGTDC60_0617	1, 428	99.5	873.2	0
Alpha-amylase/alpha-mannosidase	Pgjcvi_00536	PG JCVI SC001	hypothetical protein	PG W83	PG1683	1, 428	99.3	869.8	0
Alpha-amylase/alpha-mannosidase	Pgjcvi_00536	PG JCVI SC001	putative glycosyl hydrolase	PG ATCC 33277	PGN_0427	1, 428	99.1	870.5	0
Glycosyltransferase	Pgjcvi_00537	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG TDC60	PGTDC60_0618	1, 416	99.3	845.5	0
Glycosyltransferase	Pgjcvi_00537	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG W83	PG1682	5, 420	99	843.2	0
Glycosyltransferase	Pgjcvi_00537	PG JCVI SC001	putative glycosyl transferase family 1	PG ATCC 33277	PGN_0428	5, 420	98.8	841.3	0
Glycogen debranching enzyme	Pgjcvi_00538	PG JCVI SC001	glycogen debranching protein	PG TDC60	PGTDC60_0619	1, 658	99.8	1354.3	0
Glycogen debranching enzyme	Pgjcvi_00538	PG JCVI SC001	putative 4-alpha-glucanotransferase	PG ATCC 33277	PGN_0429	1, 658	99.7	1352.4	0
Glycogen debranching enzyme	Pgjcvi_00538	PG JCVI SC001	glycogen debranching enzyme, archaeal type, putative	PG W83	PG1681	1, 658	99.7	1353.6	0
ABC-type multidrug transport system, ATPase component	Pgjcvi_00540	PG JCVI SC001	putative ATP-binding component of ABC transporter protein	PG ATCC 33277	PGN_0430	1, 233	99.6	458.8	0
ABC-type multidrug transport system, ATPase component	Pgjcvi_00540	PG JCVI SC001	putative ATP-binding component of ABC transporter protein	PG TDC60	PGTDC60_0621	1, 233	99.6	459.1	0
ABC-type multidrug transport system, ATPase component	Pgjcvi_00540	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG0628	8, 232	24.7	77	1.10E-12
hypothetical protein	Pgjcvi_00541	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0622	1, 490	99.6	957.6	0
hypothetical protein	Pgjcvi_00541	PG JCVI SC001	hypothetical protein	PG W83	PG1679	1, 464	98.3	898.3	0
hypothetical protein	Pgjcvi_00541	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0431	1, 452	98.2	870.9	0
3-phosphoglycerate kinase	Pgjcvi_00542	PG JCVI SC001	phosphoglycerate kinase	PG W83	PG1677	1, 418	99.3	817.4	0
3-phosphoglycerate kinase	Pgjcvi_00542	PG JCVI SC001	phosphoglycerate kinase	PG ATCC 33277	PGN_0433	1, 418	99	815.8	0
3-phosphoglycerate kinase	Pgjcvi_00542	PG JCVI SC001	phosphoglycerate kinase	PG TDC60	PGTDC60_0623	1, 418	98.8	813.5	0
phosphoenolpyruvate carboxykinase (ATP)	Pgjcvi_00543	PG JCVI SC001	phosphoenolpyruvate carboxykinase	PG W83	PG1676	1, 535	99.8	1080.1	0
phosphoenolpyruvate carboxykinase (ATP)	Pgjcvi_00543	PG JCVI SC001	phosphoenolpyruvate carboxykinase	PG TDC60	PGTDC60_0624	1, 535	99.8	1080.1	0
phosphoenolpyruvate carboxykinase (ATP)	Pgjcvi_00543	PG JCVI SC001	phosphoenolpyruvate carboxykinase	PG ATCC 33277	PGN_0434	1, 535	99.6	1077.8	0
hypothetical protein	Pgjcvi_00544	PG JCVI SC001	probable partial hemagglutinin-related protein	PG ATCC 33277	PGN_0435	1, 70	94.3	137.1	3.30E-31

hypothetical protein	Pgjcvi_00544	PG JCVI SC001	putative partial hemagglutinin-like protein	PG TDC60	PGTDC60_0625	1, 70	94.3	139.8	5.00E-32
hypothetical protein	Pgjcvi_00544	PG JCVI SC001	hemagglutinin-related protein	PG W83	PG0443	113, 191	47.1	84.3	2.50E-15
hypothetical protein	Pgjcvi_00545	PG JCVI SC001	probable partial hemagglutinin-related protein	PG ATCC 33277	PGN_0436	1, 120	98.3	236.5	0
hypothetical protein	Pgjcvi_00545	PG JCVI SC001	putative partial hemagglutinin-like protein	PG TDC60	PGTDC60_0626	1, 120	95.8	231.5	0
hypothetical protein	Pgjcvi_00545	PG JCVI SC001	hemagglutinin-related protein	PG W83	PG0443	10, 99	60	108.2	2.20E-22
hypothetical protein	Pgjcvi_00546	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0441	1, 33	93.9	70.1	2.40E-11
Outer membrane protein	Pgjcvi_00548	PG JCVI SC001	probable outer membrane efflux protein	PG ATCC 33277	PGN_0444	1, 455	98.9	859.4	0
Outer membrane protein	Pgjcvi_00548	PG JCVI SC001	outer membrane efflux protein	PG W83	PG1667	1, 455	98.9	859.4	0
Outer membrane protein	Pgjcvi_00548	PG JCVI SC001	immunoreactive 51 kDa antigen PG52	PG TDC60	PGTDC60_0631	1, 455	98.7	856.7	0
RND family efflux transporter, MFP subunit	Pgjcvi_00549	PG JCVI SC001	efflux transporter, MFP component, RND family	PG W83	PG1666	1, 368	99.7	701.4	0
RND family efflux transporter, MFP subunit	Pgjcvi_00549	PG JCVI SC001	RND family efflux transporter MFP subunit	PG TDC60	PGTDC60_0632	1, 368	99.7	701.4	0
RND family efflux transporter, MFP subunit	Pgjcvi_00549	PG JCVI SC001	membrane fusion efflux protein	PG ATCC 33277	PGN_0445	1, 368	99.5	698.7	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_00550	PG JCVI SC001	ABC transporter, permease protein, putative	PG W83	PG1665	1, 420	99.8	820.1	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_00550	PG JCVI SC001	ABC transporter permease	PG TDC60	PGTDC60_0633	1, 420	99.8	820.5	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_00550	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0446	1, 420	99.5	818.5	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_00551	PG JCVI SC001	putative ABC transporter permease protein	PG ATCC 33277	PGN_0447	1, 424	99.8	841.3	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_00551	PG JCVI SC001	ABC transporter permease	PG TDC60	PGTDC60_0634	1, 424	99.8	841.3	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_00551	PG JCVI SC001	ABC transporter, permease protein, putative	PG W83	PG1664	1, 424	98.6	833.6	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_00552	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0448	1, 219	99.5	425.6	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_00552	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG1663	1, 219	99.5	425.6	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_00552	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_0635	1, 219	99.5	425.6	0
hypothetical protein	Pgjcvi_00553	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0449	1, 135	77	201.8	0
hypothetical protein	Pgjcvi_00553	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0636	1, 135	77	201.4	0
hypothetical protein	Pgjcvi_00553	PG JCVI SC001	hypothetical protein	PG W83	PG1662	1, 124	75	183	8.40E-45
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00554	PG JCVI SC001	putative RNA polymerase sigma-70 factor ECF subfamily	PG ATCC 33277	PGN_0450	1, 174	98.9	342	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00554	PG JCVI SC001	putative RNA polymerase sigma-70 factor ECFsubfamily	PG TDC60	PGTDC60_0638	7, 180	98.9	340.1	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00554	PG JCVI SC001	RNA polymerase sigma-70 factor, ECF subfamily	PG W83	PG1660	1, 174	97.7	337.8	0
hypothetical protein	Pgjcvi_00555	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0639	1, 130	97.7	251.5	0
hypothetical protein	Pgjcvi_00555	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0451	1, 130	96.2	244.2	0
hypothetical protein	Pgjcvi_00555	PG JCVI SC001	hypothetical protein	PG W83	PG1659	1, 130	96.2	244.2	0
hypothetical protein	Pgjcvi_00556	PG JCVI SC001	partial transposase Orf1 in ISPg5	PG ATCC 33277	PGN_0455	1, 45	100	94.4	3.30E-18
hypothetical protein	Pgjcvi_00556	PG JCVI SC001	ISPg5, transposase Orf1	PG W83	PG0459	6, 125	63.6	147.9	2.50E-34
hypothetical protein	Pgjcvi_00557	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0497	27, 72	97.8	91.7	9.60E-18
hypothetical protein	Pgjcvi_00557	PG JCVI SC001	hypothetical protein	PG W83	PG0221	27, 72	95.7	90.5	2.10E-17
D-alanyl-D-alanine dipeptidase	Pgjcvi_00561	PG JCVI SC001	probable D-alanyl-D-alanine dipeptidase	PG ATCC 33277	PGN_0461	1, 207	98.6	417.2	0
D-alanyl-D-alanine dipeptidase	Pgjcvi_00561	PG JCVI SC001	D-alanyl-D-alanine dipeptidase	PG TDC60	PGTDC60_0646	1, 223	98.2	446.4	0
D-alanyl-D-alanine dipeptidase	Pgjcvi_00561	PG JCVI SC001	D-alanyl-D-alanine dipeptidase	PG W83	PG1654	1, 207	98.1	416.4	0
HAD-superfamily hydrolase, subfamily IIB	Pgjcvi_00562	PG JCVI SC001	putative haloacid dehalogenase-like hydrolase	PG TDC60	PGTDC60_0647	1, 407	99.8	796.6	0
HAD-superfamily hydrolase, subfamily IIB	Pgjcvi_00562	PG JCVI SC001	hypothetical protein	PG W83	PG1653	1, 407	99.5	796.2	0
HAD-superfamily hydrolase, subfamily IIB	Pgjcvi_00562	PG JCVI SC001	probable haloacid dehalogenase-like hydrolase	PG ATCC 33277	PGN_0462	1, 407	99.3	795	0
hypothetical protein	Pgjcvi_00563	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0463	5, 593	99.3	1196.8	0
hypothetical protein	Pgjcvi_00563	PG JCVI SC001	hypothetical protein	PG W83	PG1652	8, 596	99.3	1196.4	0
hypothetical protein	Pgjcvi_00563	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0648	5, 593	99.3	1196.4	0
hypothetical protein	Pgjcvi_00564	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0464	1, 995	99.4	1922.9	0
hypothetical protein	Pgjcvi_00564	PG JCVI SC001	TPR domain protein	PG W83	PG1651	1, 995	99.2	1917.1	0
hypothetical protein	Pgjcvi_00564	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0649	1, 995	99	1914.8	0
Guanosine polyphosphate pyrophosphohydrolases/synthetases	Pgjcvi_00565	PG JCVI SC001	GTP pyrophosphokinase	PG ATCC 33277	PGN_0465	1, 746	99.7	1470.3	0
Guanosine polyphosphate pyrophosphohydrolases/synthetases	Pgjcvi_00565	PG JCVI SC001	RelA/SpoT family protein	PG TDC60	PGTDC60_0650	1, 746	99.7	1467.2	0
Guanosine polyphosphate pyrophosphohydrolases/synthetases	Pgjcvi_00565	PG JCVI SC001	RelA/SpoT family protein	PG W83	PG1648	1, 746	99.6	1467.2	0
Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	Pgjcvi_00566	PG JCVI SC001	putative cardiolipin synthetase	PG ATCC 33277	PGN_0466	12, 473	99.8	924.9	0
Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	Pgjcvi_00566	PG JCVI SC001	cardiolipin synthetase	PG W83	PG1647	12, 473	99.4	921.4	0
Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	Pgjcvi_00566	PG JCVI SC001	cardiolipin synthetase	PG TDC60	PGTDC60_0651	12, 473	99.4	921.4	0
Protein of unknown function (DUF1661).	Pgjcvi_00567	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0467	1, 58	98.3	119.4	9.30E-26
Protein of unknown function (DUF1661).	Pgjcvi_00567	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0652	1, 81	96.3	162.2	1.20E-38
Protein of unknown function (DUF1661).	Pgjcvi_00567	PG JCVI SC001	hypothetical protein	PG W83	PG1980	1, 35	74.3	53.5	6.20E-06
Uncharacterized protein conserved in bacteria	Pgjcvi_00568	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0653	23, 250	99.6	475.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00568	PG JCVI SC001	hypothetical protein	PG W83	PG1618	1, 228	98.2	468.8	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00568	PG JCVI SC001	conserved hypothetical protein with DUF452 domain	PG ATCC 33277	PGN_0468	23, 250	97.8	468.4	0
biotin biosynthesis protein BioC	Pgjcvi_00569	PG JCVI SC001	putative biotin synthesis protein BioC	PG TDC60	PGTDC60_0654	1, 255	99.6	523.5	0
biotin biosynthesis protein BioC	Pgjcvi_00569	PG JCVI SC001	biotin synthesis protein BioC, putative	PG W83	PG1619	1, 255	98.8	521.5	0
biotin biosynthesis protein BioC	Pgjcvi_00569	PG JCVI SC001	probable biotin synthesis protein	PG ATCC 33277	PGN_0469	1, 251	98.4	510.4	0
Periplasmic protease	Pgjcvi_00570	PG JCVI SC001	carboxyl-terminal protease-related protein	PG W83	PG1620	6, 358	99.2	727.2	0
Periplasmic protease	Pgjcvi_00570	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0470	6, 358	98.9	724.5	0
Periplasmic protease	Pgjcvi_00570	PG JCVI SC001	carboxyl-terminal protease-like protein	PG TDC60	PGTDC60_0655	6, 358	98	718.8	0
Protein of unknown function (DUF3316).	Pgjcvi_00571	PG JCVI SC001	hypothetical protein	PG W83	PG1621	1, 315	98.7	642.5	0
Protein of unknown function (DUF3316).	Pgjcvi_00571	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0471	1, 315	98.4	639	0
Protein of unknown function (DUF3316).	Pgjcvi_00571	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0656	1, 315	98.4	637.1	0
Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	Pgjcvi_00572	PG JCVI SC001	DNA topoisomerase IV A subunit	PG ATCC 33277	PGN_0472	1, 898	99.8	1795	0
Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	Pgjcvi_00572	PG JCVI SC001	DNA topoisomerase IV subunit A	PG W83	PG1622	1, 898	99.7	1794.6	0

Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	Pgjcvi_00572	PG JCVI SC001	DNA topoisomerase IV, subunit A	PG TDC60	PGTDC60_0657	1, 898	99.7	1792.3	0
FMN-binding domain.	Pgjcvi_00573	PG JCVI SC001	membrane bound regulatory protein, putative	PG W83	PG1623	1, 396	98.7	781.6	0
FMN-binding domain.	Pgjcvi_00573	PG JCVI SC001	membrane bound regulatory protein	PG TDC60	PGTDC60_0658	1, 396	98.7	781.6	0
FMN-binding domain.	Pgjcvi_00573	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0473	1, 397	97.7	774.2	0
hypothetical protein	Pgjcvi_00574	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0475	70, 136	100	136	6.00E-31
hypothetical protein	Pgjcvi_00575	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0476	1, 399	98.8	853.2	0
hypothetical protein	Pgjcvi_00575	PG JCVI SC001	hypothetical protein	PG W83	PG1625	3, 400	98.5	852.4	0
hypothetical protein	Pgjcvi_00575	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0661	3, 400	98.5	853.2	0
hypothetical protein	Pgjcvi_00576	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0662	1, 554	99.5	1120.5	0
hypothetical protein	Pgjcvi_00576	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0477	1, 554	99.1	1114.4	0
hypothetical protein	Pgjcvi_00576	PG JCVI SC001	hypothetical protein	PG W83	PG1626	1, 554	99.1	1115.1	0
hypothetical protein	Pgjcvi_00577	PG JCVI SC001	partial transposase in ISPg4	PG ATCC 33277	PGN_0480	63, 147	97.6	175.6	8.00E-43
hypothetical protein	Pgjcvi_00577	PG JCVI SC001	ISPg4, transposase	PG W83	PG0970	212, 271	56.7	74.7	1.90E-12
hypothetical protein	Pgjcvi_00578	PG JCVI SC001	hypothetical protein	PG W83	PG1630	1, 96	100	197.6	0
hypothetical protein	Pgjcvi_00578	PG JCVI SC001	putative immunoreactive 23 kDa antigen	PG TDC60	PGTDC60_0669	1, 209	79.4	343.6	0
hypothetical protein	Pgjcvi_00578	PG JCVI SC001	probable immunoreactive 23 kDa antigen	PG ATCC 33277	PGN_0482	1, 209	78.9	341.3	0
Galactose mutarotase and related enzymes	Pgjcvi_00579	PG JCVI SC001	putative aldose 1-epimerase	PG ATCC 33277	PGN_0483	1, 355	98.9	731.5	0
Galactose mutarotase and related enzymes	Pgjcvi_00579	PG JCVI SC001	aldose 1-epimerase	PG TDC60	PGTDC60_0670	1, 355	98.9	728.8	0
Galactose mutarotase and related enzymes	Pgjcvi_00579	PG JCVI SC001	aldose 1-epimerase	PG W83	PG1632	1, 355	98.6	730.3	0
galactokinase	Pgjcvi_00580	PG JCVI SC001	putative galactokinase	PG ATCC 33277	PGN_0484	1, 384	99.5	775.8	0
galactokinase	Pgjcvi_00580	PG JCVI SC001	galactokinase	PG W83	PG1633	1, 384	99.5	776.9	0
galactokinase	Pgjcvi_00580	PG JCVI SC001	galactokinase	PG TDC60	PGTDC60_0671	1, 384	99.5	776.5	0
hypothetical protein	Pgjcvi_00581	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0672	1, 141	100	282.7	0
hypothetical protein	Pgjcvi_00581	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0485	1, 141	96.5	274.2	0
hypothetical protein	Pgjcvi_00581	PG JCVI SC001	hypothetical protein	PG W83	PG1634	1, 141	96.5	274.2	0
hypothetical protein	Pgjcvi_00582	PG JCVI SC001	hypothetical protein	PG W83	PG1635	1, 215	99.5	417.5	0
hypothetical protein	Pgjcvi_00582	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0673	1, 206	99	396.7	0
hypothetical protein	Pgjcvi_00582	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0486	1, 215	98.6	412.5	0
DNA segregation ATPase FtsK/SpoIIIE and related proteins	Pgjcvi_00583	PG JCVI SC001	FtsK/SpoIIIE family protein	PG W83	PG1636	1, 861	99.7	1698.7	0
DNA segregation ATPase FtsK/SpoIIIE and related proteins	Pgjcvi_00583	PG JCVI SC001	FtsK/SpoIIIE family cell division protein	PG TDC60	PGTDC60_0674	1, 826	99.6	1623.2	0
DNA segregation ATPase FtsK/SpoIIIE and related proteins	Pgjcvi_00583	PG JCVI SC001	FtsK/SpoIIIE family cell division protein	PG ATCC 33277	PGN_0487	1, 861	99.3	1696.8	0
Thiol-disulfide isomerase and thioredoxins	Pgjcvi_00584	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0488	1, 370	99.5	738.8	0
Thiol-disulfide isomerase and thioredoxins	Pgjcvi_00584	PG JCVI SC001	thioredoxin family protein	PG TDC60	PGTDC60_0675	1, 361	99.4	723.8	0
Thiol-disulfide isomerase and thioredoxins	Pgjcvi_00584	PG JCVI SC001	thioredoxin family protein	PG W83	PG1638	1, 328	98.5	656	0
putative efflux protein, MATE family	Pgjcvi_00585	PG JCVI SC001	putative DNA-damage-inducible protein F	PG ATCC 33277	PGN_0490	1, 436	100	840.1	0
putative efflux protein, MATE family	Pgjcvi_00585	PG JCVI SC001	DNA-damage-inducible protein F	PG TDC60	PGTDC60_0677	1, 444	99.5	852	0
putative efflux protein, MATE family	Pgjcvi_00585	PG JCVI SC001	DNA-damage-inducible protein F	PG W83	PG1640	1, 436	99.3	834.7	0
Protein-tyrosine-phosphatase	Pgjcvi_00586	PG JCVI SC001	phosphotyrosine protein phosphatase	PG W83	PG1641	1, 167	99.4	342	0
Protein-tyrosine-phosphatase	Pgjcvi_00586	PG JCVI SC001	phosphotyrosine protein phosphatase	PG TDC60	PGTDC60_0678	1, 167	99.4	343.2	0
Protein-tyrosine-phosphatase	Pgjcvi_00586	PG JCVI SC001	probable phosphotyrosine protein phosphatase	PG ATCC 33277	PGN_0491	1, 167	98.8	340.9	0
copper-(or silver)-translocating P-type ATPase	Pgjcvi_00587	PG JCVI SC001	cation-transporting ATPase	PG ATCC 33277	PGN_0492	1, 735	99.3	1406	0
copper-(or silver)-translocating P-type ATPase	Pgjcvi_00587	PG JCVI SC001	cation-transporting ATPase	PG TDC60	PGTDC60_0679	1, 735	99.2	1404.8	0
copper-(or silver)-translocating P-type ATPase	Pgjcvi_00587	PG JCVI SC001	calcium-transporting ATPase	PG W83	PG0938	724, 843	30.8	63.5	3.80E-08
copper-(or silver)-translocating P-type ATPase	Pgjcvi_00587	PG JCVI SC001	calcium-transporting ATPase	PG W83	PG0938	273, 639	24.4	79.3	6.70E-13
Copper chaperone	Pgjcvi_00588	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0493	19, 87	98.6	136.7	3.30E-31
Copper chaperone	Pgjcvi_00588	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0680	19, 87	95.7	132.5	6.30E-30
succinate dehydrogenase (or fumarate reductase) cytochrome b subunit, b558 family	Pgjcvi_00589	PG JCVI SC001	hypothetical protein	PG W83	PG1616	1, 230	100	468.8	0
succinate dehydrogenase (or fumarate reductase) cytochrome b subunit, b558 family	Pgjcvi_00589	PG JCVI SC001	putative cytochrome B subunit	PG ATCC 33277	PGN_0496	1, 230	99.6	467.6	0
succinate dehydrogenase (or fumarate reductase) cytochrome b subunit, b558 family	Pgjcvi_00589	PG JCVI SC001	putative cytochrome B subunit	PG TDC60	PGTDC60_0683	1, 217	99.5	443.4	0
succinate dehydrogenase or fumarate reductase, flavoprotein subunit, Bacillus subtilis subgroup	Pgjcvi_00590	PG JCVI SC001	fumarate reductase flavoprotein subunit	PG ATCC 33277	PGN_0497	1, 647	100	1314.3	0
succinate dehydrogenase or fumarate reductase, flavoprotein subunit, Bacillus subtilis subgroup	Pgjcvi_00590	PG JCVI SC001	succinate dehydrogenase	PG W83	PG1615	1, 647	99.8	1313.9	0
succinate dehydrogenase or fumarate reductase, flavoprotein subunit, Bacillus subtilis subgroup	Pgjcvi_00590	PG JCVI SC001	succinate dehydrogenase flavoprotein subunit	PG TDC60	PGTDC60_0684	1, 647	99.8	1312.7	0
Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	Pgjcvi_00591	PG JCVI SC001	succinate dehydrogenase	PG W83	PG1614	1, 251	100	516.2	0
Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	Pgjcvi_00591	PG JCVI SC001	succinate dehydrogenase/fumarate reductase iron-sulfur subunit	PG TDC60	PGTDC60_0685	1, 251	100	516.2	0
Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	Pgjcvi_00591	PG JCVI SC001	fumarate reductase iron-sulfur protein	PG ATCC 33277	PGN_0498	1, 251	99.6	512.3	0
methylmalonyl-CoA epimerase	Pgjcvi_00592	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0499	1, 134	100	270	0
methylmalonyl-CoA epimerase	Pgjcvi_00592	PG JCVI SC001	glyoxalase family protein	PG W83	PG1613	1, 134	100	270	0
methylmalonyl-CoA epimerase	Pgjcvi_00592	PG JCVI SC001	glyoxalase family protein	PG TDC60	PGTDC60_0686	1, 134	100	270	0
Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)	Pgjcvi_00593	PG JCVI SC001	methylmalonyl-CoA decarboxylase alpha subunit	PG ATCC 33277	PGN_0500	1, 517	99.8	1025.4	0
Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)	Pgjcvi_00593	PG JCVI SC001	methylmalonyl-CoA decarboxylase, alpha subunit	PG W83	PG1612	1, 517	99.8	1025.4	0
Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)	Pgjcvi_00593	PG JCVI SC001	methylmalonyl-CoA decarboxylase subunit alpha	PG TDC60	PGTDC60_0687	1, 517	99.8	1025.4	0
Oxaloacetate decarboxylase, gamma chain.	Pgjcvi_00594	PG JCVI SC001	hypothetical protein	PG W83	PG1611	1, 313	99.7	623.6	0
Oxaloacetate decarboxylase, gamma chain.	Pgjcvi_00594	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0688	1, 313	99.7	623.6	0
Oxaloacetate decarboxylase, gamma chain.	Pgjcvi_00594	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0501	1, 313	99.4	622.1	0
hypothetical protein	Pgjcvi_00595	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0502	1, 78	97.4	154.8	1.30E-36
hypothetical protein	Pgjcvi_00595	PG JCVI SC001	hypothetical protein	PG W83	PG1610	1, 78	96.2	154.1	2.30E-36
hypothetical protein	Pgjcvi_00595	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0689	1, 78	94.9	151.4	1.50E-35
Acetyl/propionyl-CoA carboxylase, alpha subunit	Pgjcvi_00596	PG JCVI SC001	methylmalonyl-CoA decarboxylase, gamma subunit	PG W83	PG1609	1, 144	98.6	278.9	0
Acetyl/propionyl-CoA carboxylase, alpha subunit	Pgjcvi_00596	PG JCVI SC001	methylmalonyl-CoA decarboxylase, gamma subunit	PG TDC60	PGTDC60_0690	1, 144	97.9	277.3	0

Acetyl/propionyl-CoA carboxylase, alpha subunit	Pgjcvi_00596	PG JCVI SC001	putative biotin carboxyl carrier protein	PG ATCC 33277	PGN_0503	1, 148	96.6	275.8	0
sodium ion-translocating decarboxylase, beta subunit	Pgjcvi_00597	PG JCVI SC001	methylmalonyl-CoA decarboxylase beta subunit	PG ATCC 33277	PGN_0504	1, 383	100	740.7	0
sodium ion-translocating decarboxylase, beta subunit	Pgjcvi_00597	PG JCVI SC001	methylmalonyl-CoA decarboxylase, beta subunit	PG W83	PG1608	1, 383	99.7	740	0
sodium ion-translocating decarboxylase, beta subunit	Pgjcvi_00597	PG JCVI SC001	methylmalonyl-CoA decarboxylase subunit beta	PG TDC60	PGTDC60_0691	1, 383	99.7	738.4	0
hypothetical protein	Pgjcvi_00598	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0694	1, 56	98.2	117.1	2.20E-25
hypothetical protein	Pgjcvi_00599	PG JCVI SC001	metal dependent phosphohydrolase	PG TDC60	PGTDC60_0695	1, 47	95.7	100.1	2.80E-20
HD superfamily phosphohydrolases	Pgjcvi_00600	PG JCVI SC001	metal dependent phosphohydrolase	PG TDC60	PGTDC60_0695	51, 912	99.2	1703.7	0
Aminopeptidase C	Pgjcvi_00601	PG JCVI SC001	aminopeptidase C	PG TDC60	PGTDC60_0696	1, 467	99.8	945.7	0
Aminopeptidase C	Pgjcvi_00601	PG JCVI SC001	putative aminopeptidase	PG ATCC 33277	PGN_0508	1, 467	99.4	944.9	0
Aminopeptidase C	Pgjcvi_00601	PG JCVI SC001	aminopeptidase C	PG W83	PG1605	1, 447	99.3	911	0
hypothetical protein	Pgjcvi_00602	PG JCVI SC001	immunoreactive 84 kDa antigen PG93	PG TDC60	PGTDC60_0697	9, 776	99.7	1526.5	0
hypothetical protein	Pgjcvi_00602	PG JCVI SC001	immunoreactive 84 kDa antigen	PG ATCC 33277	PGN_0509	1, 768	99.6	1525.8	0
hypothetical protein	Pgjcvi_00602	PG JCVI SC001	immunoreactive 84 kDa antigen PG93	PG W83	PG1604	9, 776	99.1	1519.6	0
non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family	Pgjcvi_00603	PG JCVI SC001	putative deoxyribonucleoside-triphosphatase	PG TDC60	PGTDC60_0698	1, 194	100	395.6	0
non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family	Pgjcvi_00603	PG JCVI SC001	probable xanthosine triphosphate pyrophosphatase	PG ATCC 33277	PGN_0510	1, 194	99.5	392.5	0
non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family	Pgjcvi_00603	PG JCVI SC001	HAM1 protein	PG W83	PG1603	1, 194	99	389.4	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00604	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0699	1, 126	99.2	253.8	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00604	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0511	1, 126	98.4	252.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_00604	PG JCVI SC001	hypothetical protein	PG W83	PG1602	1, 126	97.6	250.8	0
birA, biotin-[acetyl-CoA-carboxylase] ligase region	Pgjcvi_00605	PG JCVI SC001	probable biotin--acetyl-CoA-carboxylase ligase	PG ATCC 33277	PGN_0512	1, 257	98.1	509.6	0
birA, biotin-[acetyl-CoA-carboxylase] ligase region	Pgjcvi_00605	PG JCVI SC001	biotin--acetyl-CoA-carboxylase ligase	PG TDC60	PGTDC60_0700	1, 257	98.1	514.2	0
birA, biotin-[acetyl-CoA-carboxylase] ligase region	Pgjcvi_00605	PG JCVI SC001	biotin--acetyl-CoA-carboxylase ligase	PG W83	PG1601	1, 257	96.9	504.2	0
Fucose 4-O-acetylase and related acetyltransferases	Pgjcvi_00606	PG JCVI SC001	hypothetical protein	PG W83	PG1600	1, 341	99.7	689.5	0
Fucose 4-O-acetylase and related acetyltransferases	Pgjcvi_00606	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0513	1, 341	99.1	684.1	0
Fucose 4-O-acetylase and related acetyltransferases	Pgjcvi_00606	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0701	1, 341	99.1	684.1	0
hypothetical protein	Pgjcvi_00607	PG JCVI SC001	hypothetical protein	PG W83	PG1599	1, 262	99.6	523.1	0
hypothetical protein	Pgjcvi_00607	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0514	1, 262	98.5	516.5	0
hypothetical protein	Pgjcvi_00607	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0702	1, 262	97.7	513.8	0
Lipoprotein signal peptidase	Pgjcvi_00608	PG JCVI SC001	probable lipoprotein signal peptidase	PG ATCC 33277	PGN_0515	1, 226	100	459.9	0
Lipoprotein signal peptidase	Pgjcvi_00608	PG JCVI SC001	lipoprotein signal peptidase, putative	PG W83	PG1598	1, 226	100	459.9	0
Lipoprotein signal peptidase	Pgjcvi_00608	PG JCVI SC001	lipoprotein signal peptidase	PG TDC60	PGTDC60_0703	1, 226	100	459.9	0
DnaK suppressor protein	Pgjcvi_00609	PG JCVI SC001	putative DnaK suppressor protein	PG ATCC 33277	PGN_0516	1, 126	100	245	0
DnaK suppressor protein	Pgjcvi_00609	PG JCVI SC001	DnaK suppressor protein, putative	PG W83	PG1597	1, 126	100	245	0
DnaK suppressor protein	Pgjcvi_00609	PG JCVI SC001	putative DnaK suppressor protein	PG TDC60	PGTDC60_0704	1, 126	100	245	0
isoleucyl-tRNA synthetase	Pgjcvi_00610	PG JCVI SC001	isoleucyl-tRNA synthetase	PG TDC60	PGTDC60_0705	1, 1137	99.9	2323.9	0
isoleucyl-tRNA synthetase	Pgjcvi_00610	PG JCVI SC001	isoleucyl-tRNA synthetase, putative	PG W83	PG1596	1, 1137	99.8	2321.2	0
isoleucyl-tRNA synthetase	Pgjcvi_00610	PG JCVI SC001	isoleucyl-tRNA synthetase	PG ATCC 33277	PGN_0517	1, 1137	99.5	2313.9	0
ribulose-phosphate 3-epimerase	Pgjcvi_00611	PG JCVI SC001	putative ribulose-phosphate 3-epimerase	PG ATCC 33277	PGN_0518	1, 218	100	430.6	0
ribulose-phosphate 3-epimerase	Pgjcvi_00611	PG JCVI SC001	ribulose-phosphate 3-epimerase	PG W83	PG1595	1, 218	100	430.6	0
ribulose-phosphate 3-epimerase	Pgjcvi_00611	PG JCVI SC001	ribulose-phosphate 3-epimerase	PG TDC60	PGTDC60_0706	1, 218	100	430.6	0
ComEC/Rec2-related protein	Pgjcvi_00612	PG JCVI SC001	ComEC/Rec2-like protein	PG TDC60	PGTDC60_0707	1, 511	97.8	991.5	0
ComEC/Rec2-related protein	Pgjcvi_00612	PG JCVI SC001	probable competence protein	PG ATCC 33277	PGN_0519	1, 494	97.6	946	0
ComEC/Rec2-related protein	Pgjcvi_00612	PG JCVI SC001	ComEC/Rec2-related protein	PG W83	PG1594	1, 511	97.1	981.5	0
Shikimate kinase	Pgjcvi_00613	PG JCVI SC001	probable shikimate kinase	PG ATCC 33277	PGN_0520	1, 186	100	369	0
Shikimate kinase	Pgjcvi_00613	PG JCVI SC001	shikimate kinase	PG W83	PG1593	1, 186	100	369	0
Shikimate kinase	Pgjcvi_00613	PG JCVI SC001	shikimate kinase	PG TDC60	PGTDC60_0708	1, 186	100	369	0
uncharacterized domain HDIG	Pgjcvi_00614	PG JCVI SC001	HDIG domain protein	PG W83	PG1592	1, 690	100	1363.2	0
uncharacterized domain HDIG	Pgjcvi_00614	PG JCVI SC001	HDIG domain-containing protein	PG TDC60	PGTDC60_0709	1, 694	99.9	1369.4	0
uncharacterized domain HDIG	Pgjcvi_00614	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0521	1, 690	99.7	1357.8	0
hypothetical protein	Pgjcvi_00616	PG JCVI SC001	hypothetical protein	PG W83	PG1591	317, 365	95.9	90.5	2.30E-17
Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen	Pgjcvi_00618	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_0933	1, 485	86.5	855.9	0
Uncharacterized conserved protein	Pgjcvi_00621	PG JCVI SC001	hypothetical protein	PG W83	PG1591	1, 350	93.1	642.1	0
dihydropteroate synthase	Pgjcvi_00622	PG JCVI SC001	putative dihydropteroate synthase	PG ATCC 33277	PGN_0522	1, 281	99.3	546.2	0
dihydropteroate synthase	Pgjcvi_00622	PG JCVI SC001	dihydropteroate synthase	PG W83	PG1589	1, 281	99.3	546.2	0
dihydropteroate synthase	Pgjcvi_00622	PG JCVI SC001	dihydropteroate synthase	PG TDC60	PGTDC60_0710	1, 281	98.9	544.3	0
TIGR00159 family protein	Pgjcvi_00623	PG JCVI SC001	hypothetical protein	PG W83	PG1588	1, 255	100	493.8	0
TIGR00159 family protein	Pgjcvi_00623	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0523	1, 255	99.6	492.3	0
TIGR00159 family protein	Pgjcvi_00623	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0711	1, 255	99.6	492.3	0
PAP2 superfamily.	Pgjcvi_00624	PG JCVI SC001	PAP2 superfamily protein	PG W83	PG1587	1, 238	100	488.8	0
PAP2 superfamily.	Pgjcvi_00624	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0524	1, 236	99.6	483.8	0
PAP2 superfamily.	Pgjcvi_00624	PG JCVI SC001	PAP2 superfamily protein	PG TDC60	PGTDC60_0712	1, 238	99.6	487.6	0
DNA uptake lipoprotein	Pgjcvi_00625	PG JCVI SC001	probable aerotolerance-related exported protein BatE	PG ATCC 33277	PGN_0525	1, 302	99	586.3	0
DNA uptake lipoprotein	Pgjcvi_00625	PG JCVI SC001	batE protein	PG W83	PG1586	1, 302	99	584.3	0
DNA uptake lipoprotein	Pgjcvi_00625	PG JCVI SC001	aerotolerance-related exported protein BatE	PG TDC60	PGTDC60_0713	1, 302	98	581.6	0
hypothetical protein	Pgjcvi_00626	PG JCVI SC001	aerotolerance-related exported protein BatD	PG TDC60	PGTDC60_0714	1, 566	99.5	1098.6	0
hypothetical protein	Pgjcvi_00626	PG JCVI SC001	aerotolerance-related exported protein BatD	PG ATCC 33277	PGN_0526	1, 600	99	1161.4	0
hypothetical protein	Pgjcvi_00626	PG JCVI SC001	batD protein	PG W83	PG1585	1, 600	98.8	1160.2	0
Tetratricopeptide repeat.	Pgjcvi_00627	PG JCVI SC001	batC protein	PG W83	PG1584	1, 247	100	499.2	0
Tetratricopeptide repeat.	Pgjcvi_00627	PG JCVI SC001	probable aerotolerance-related exported protein BatC	PG ATCC 33277	PGN_0527	1, 248	98.8	490.3	0
Tetratricopeptide repeat.	Pgjcvi_00627	PG JCVI SC001	aerotolerance-related exported protein BatC	PG TDC60	PGTDC60_0715	1, 247	98.4	490.7	0
Mg-chelatase subunit ChlD	Pgjcvi_00628	PG JCVI SC001	aerotolerance-related exported protein BatB	PG TDC60	PGTDC60_0716	1, 339	99.4	655.6	0

Mg-chelatase subunit ChlD	Pgjcvi_00628	PG JCVI SC001	putative aerotolerance-related exported protein BatB	PG ATCC 33277	PGN_0528	1, 339	98.8	652.5	0
Mg-chelatase subunit ChlD	Pgjcvi_00628	PG JCVI SC001	batB protein	PG W83	PG1583	1, 339	98.5	649	0
Mg-chelatase subunit ChlD	Pgjcvi_00629	PG JCVI SC001	aerotolerance-related membrane protein BatA	PG ATCC 33277	PGN_0529	1, 327	100	641.3	0
Mg-chelatase subunit ChlD	Pgjcvi_00629	PG JCVI SC001	batA protein	PG W83	PG1582	1, 327	99.7	639	0
Mg-chelatase subunit ChlD	Pgjcvi_00629	PG JCVI SC001	aerotolerance-related membrane protein BatA	PG TDC60	PGTDC60_0717	1, 327	99.7	639	0
hypothetical protein	Pgjcvi_00630	PG JCVI SC001	hypothetical protein	PG W83	PG1581	1, 318	99.1	614	0
hypothetical protein	Pgjcvi_00630	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0718	1, 318	99.1	614	0
hypothetical protein	Pgjcvi_00630	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0530	1, 318	96.5	596.7	0
Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)	Pgjcvi_00631	PG JCVI SC001	putative von Willebrand factor type A	PG TDC60	PGTDC60_0719	38, 290	100	495.4	0
Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)	Pgjcvi_00631	PG JCVI SC001	hypothetical protein	PG W83	PG1580	38, 290	99.6	493.8	0
Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)	Pgjcvi_00631	PG JCVI SC001	putative von Willebrand factor type A	PG ATCC 33277	PGN_0531	38, 290	98.8	490.7	0
MoxR-like ATPases	Pgjcvi_00632	PG JCVI SC001	MoxR family ATPase	PG TDC60	PGTDC60_0720	1, 331	99.4	637.1	0
MoxR-like ATPases	Pgjcvi_00632	PG JCVI SC001	magnesium chelatase subunit I	PG ATCC 33277	PGN_0532	1, 331	99.1	635.2	0
MoxR-like ATPases	Pgjcvi_00632	PG JCVI SC001	ATPase, MoxR family	PG W83	PG1579	1, 331	99.1	637.1	0
quinolinate synthetase complex, A subunit	Pgjcvi_00633	PG JCVI SC001	quinolinate synthetase	PG TDC60	PGTDC60_0721	1, 308	99.7	617.1	0
quinolinate synthetase complex, A subunit	Pgjcvi_00633	PG JCVI SC001	putative quinolinate synthetase complex subunit A	PG ATCC 33277	PGN_0533	1, 308	99.4	615.9	0
quinolinate synthetase complex, A subunit	Pgjcvi_00633	PG JCVI SC001	quinolinate synthetase	PG W83	PG1578	1, 308	99.4	615.9	0
nicotinate-nucleotide pyrophosphorylase	Pgjcvi_00634	PG JCVI SC001	putative nicotinate-nucleotide pyrophosphorylase	PG ATCC 33277	PGN_0534	1, 280	100	538.1	0
nicotinate-nucleotide pyrophosphorylase	Pgjcvi_00634	PG JCVI SC001	nicotinate-nucleotide pyrophosphorylase	PG W83	PG1577	1, 275	99.6	524.6	0
nicotinate-nucleotide pyrophosphorylase	Pgjcvi_00634	PG JCVI SC001	nicotinate-nucleotide pyrophosphorylase	PG TDC60	PGTDC60_0722	1, 280	99.3	534.3	0
L-aspartate oxidase	Pgjcvi_00635	PG JCVI SC001	L-aspartate oxidase	PG ATCC 33277	PGN_0535	1, 518	100	1049.3	0
L-aspartate oxidase	Pgjcvi_00635	PG JCVI SC001	L-aspartate oxidase	PG W83	PG1576	1, 518	99.8	1045	0
L-aspartate oxidase	Pgjcvi_00635	PG JCVI SC001	L-aspartate oxidase	PG TDC60	PGTDC60_0723	1, 518	99.8	1046.2	0
Transposase and inactivated derivatives	Pgjcvi_00638	PG JCVI SC001	ISPg5 transposase Orf2	PG W83	PG0008	64, 276	41.9	151.8	5.80E-35
cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Pgjcvi_00640	PG JCVI SC001	Crp family transcriptional regulator	PG TDC60	PGTDC60_0725	1, 239	100	467.2	0
cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Pgjcvi_00640	PG JCVI SC001	probable transcriptional regulator Crp family	PG ATCC 33277	PGN_0537	1, 207	99.5	400.2	0
cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Pgjcvi_00640	PG JCVI SC001	transcriptional regulator, Crp family	PG W83	PG1573	51, 283	91.8	407.1	0
Predicted permeases	Pgjcvi_00641	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0726	1, 268	100	514.2	0
Predicted permeases	Pgjcvi_00641	PG JCVI SC001	hypothetical protein	PG W83	PG1572	1, 268	99.3	507.3	0
Predicted permeases	Pgjcvi_00641	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0538	1, 268	98.9	505	0
Zn-dependent hydrolases, including glyoxylases	Pgjcvi_00642	PG JCVI SC001	metallo-beta-lactamase superfamily protein	PG TDC60	PGTDC60_0727	1, 471	100	948.7	0
Zn-dependent hydrolases, including glyoxylases	Pgjcvi_00642	PG JCVI SC001	metallo-beta-lactamase superfamily protein	PG W83	PG1571	1, 471	99.8	948.3	0
Zn-dependent hydrolases, including glyoxylases	Pgjcvi_00642	PG JCVI SC001	metallo-beta-lactamase superfamily protein	PG ATCC 33277	PGN_0539	1, 471	98.9	938.7	0
Rhodanese-related sulfurtransferase	Pgjcvi_00643	PG JCVI SC001	rhodanese-like domain protein	PG W83	PG1570	1, 127	100	244.6	0
Rhodanese-related sulfurtransferase	Pgjcvi_00643	PG JCVI SC001	rhodanese-like domain-containing protein	PG TDC60	PGTDC60_0728	1, 106	100	209.1	0
Rhodanese-related sulfurtransferase	Pgjcvi_00643	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0540	1, 127	99.2	243	0
hypothetical protein	Pgjcvi_00644	PG JCVI SC001	partial transposase in ISPg2	PG ATCC 33277	PGN_0542	7, 78	100	147.5	2.30E-34
hypothetical protein	Pgjcvi_00644	PG JCVI SC001	ISPg2, transposase	PG W83	PG1350	1, 65	69.7	88.6	1.30E-16
glutamyl-tRNA synthetase, bacterial family	Pgjcvi_00645	PG JCVI SC001	glutamyl-tRNA synthetase	PG TDC60	PGTDC60_0732	1, 571	100	1162.1	0
glutamyl-tRNA synthetase, bacterial family	Pgjcvi_00645	PG JCVI SC001	glutamyl-tRNA synthetase	PG ATCC 33277	PGN_0543	1, 507	99.6	1025	0
glutamyl-tRNA synthetase, bacterial family	Pgjcvi_00645	PG JCVI SC001	glutamyl-tRNA synthetase	PG W83	PG1566	2, 505	99.4	1019.2	0
3-deoxy-D-manno-octulosonic-acid transferase	Pgjcvi_00646	PG JCVI SC001	3-deoxy-D-manno-octulosonic-acid transferase	PG TDC60	PGTDC60_0733	1, 412	99.8	830.5	0
3-deoxy-D-manno-octulosonic-acid transferase	Pgjcvi_00646	PG JCVI SC001	3-deoxy-D-manno-octulosonic-acid transferase	PG ATCC 33277	PGN_0544	1, 412	99	823.9	0
3-deoxy-D-manno-octulosonic-acid transferase	Pgjcvi_00646	PG JCVI SC001	3-deoxy-D-manno-octulosonic-acid transferase, putative	PG W83	PG1565	1, 412	98.8	820.5	0
Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	Pgjcvi_00647	PG JCVI SC001	putative sulfatase	PG TDC60	PGTDC60_0734	1, 651	99.4	1323.9	0
Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	Pgjcvi_00647	PG JCVI SC001	putative sulfatase	PG ATCC 33277	PGN_0545	1, 651	98.8	1318.5	0
Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	Pgjcvi_00647	PG JCVI SC001	hypothetical protein	PG W83	PG1564	1, 651	98.8	1315.8	0
glucose-1-phosphate thymidylyltransferase, short form	Pgjcvi_00648	PG JCVI SC001	glucose-1-phosphate thymidylyltransferase	PG ATCC 33277	PGN_0546	1, 289	100	577	0
glucose-1-phosphate thymidylyltransferase, short form	Pgjcvi_00648	PG JCVI SC001	glucose-1-phosphate thymidylyltransferase	PG W83	PG1563	1, 289	100	577	0
glucose-1-phosphate thymidylyltransferase, short form	Pgjcvi_00648	PG JCVI SC001	glucose-1-phosphate thymidylyltransferase	PG TDC60	PGTDC60_0735	1, 289	100	577	0
dTDP-4-dehydrorhamnose 3,5-epimerase	Pgjcvi_00649	PG JCVI SC001	dTDP-4-dehydrorhamnose 3,5-epimerase	PG TDC60	PGTDC60_0736	1, 196	100	405.2	0
dTDP-4-dehydrorhamnose 3,5-epimerase	Pgjcvi_00649	PG JCVI SC001	dTDP-4-dehydrorhamnose 3,5-epimerase	PG ATCC 33277	PGN_0547	1, 196	99.5	403.7	0
dTDP-4-dehydrorhamnose 3,5-epimerase	Pgjcvi_00649	PG JCVI SC001	dTDP-4-dehydrorhamnose 3,5-epimerase	PG W83	PG1562	1, 196	99	401.7	0
dTDP-4-dehydrorhamnose reductase	Pgjcvi_00650	PG JCVI SC001	putative dTDP-4-dehydrorhamnose reductase	PG ATCC 33277	PGN_0548	1, 285	98.9	569.3	0
dTDP-4-dehydrorhamnose reductase	Pgjcvi_00650	PG JCVI SC001	dTDP-4-dehydrorhamnose reductase	PG W83	PG1561	1, 285	98.9	569.3	0
dTDP-4-dehydrorhamnose reductase	Pgjcvi_00650	PG JCVI SC001	dTDP-4-dehydrorhamnose reductase	PG TDC60	PGTDC60_0737	1, 285	98.9	569.3	0
dTDP-glucose 4,6-dehydratase	Pgjcvi_00651	PG JCVI SC001	dTDP-glucose 4,6-dehydratase	PG ATCC 33277	PGN_0549	1, 354	99.7	733	0
dTDP-glucose 4,6-dehydratase	Pgjcvi_00651	PG JCVI SC001	dTDP-glucose 4,6-dehydratase	PG W83	PG1560	1, 354	99.7	733	0
dTDP-glucose 4,6-dehydratase	Pgjcvi_00651	PG JCVI SC001	dTDP-glucose 4,6-dehydratase	PG TDC60	PGTDC60_0738	1, 354	99.4	731.5	0
glycine cleavage system T protein	Pgjcvi_00652	PG JCVI SC001	aminomethyltransferase	PG ATCC 33277	PGN_0550	1, 362	99.7	744.6	0
glycine cleavage system T protein	Pgjcvi_00652	PG JCVI SC001	aminomethyltransferase	PG W83	PG1559	1, 362	99.7	744.6	0
glycine cleavage system T protein	Pgjcvi_00652	PG JCVI SC001	glycine cleavage system aminomethyltransferaseT	PG TDC60	PGTDC60_0739	1, 362	99.7	744.6	0
hypothetical protein	Pgjcvi_00653	PG JCVI SC001	putative mobilization protein TraG family	PG ATCC 33277	PGN_0076	511, 669	98.7	302.8	0
hypothetical protein	Pgjcvi_00653	PG JCVI SC001	TraG family protein	PG TDC60	PGTDC60_1006	512, 670	96.2	294.7	0
hypothetical protein	Pgjcvi_00653	PG JCVI SC001	TraG family protein	PG W83	PG1490	512, 665	69.5	219.2	0
B-box zinc finger.	Pgjcvi_00654	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0078	1, 70	97.1	145.6	1.50E-33

B-box zinc finger.	Pgjcvi_00654	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1004	1, 67	83.6	125.2	2.10E-27
Uncharacterized conserved protein	Pgjcvi_00655	PG JCVI SC001	conserved hypothetical protein with DUF1016 domain	PG ATCC 33277	PGN_0079	3, 345	99.4	678.3	0
Uncharacterized conserved protein	Pgjcvi_00655	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1947	5, 101	32.7	59.7	2.60E-07
Uncharacterized conserved protein	Pgjcvi_00655	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1947	128, 422	29	164.5	7.40E-39
RteC protein.	Pgjcvi_00656	PG JCVI SC001	probable tetracycline resistance element mobilization regulatory protein RteC	PG ATCC 33277	PGN_0080	1, 108	92.6	206.8	0
RteC protein.	Pgjcvi_00656	PG JCVI SC001	RteC protein	PG TDC60	PGTDC60_0796	4, 124	88.4	220.3	0
hypothetical protein	Pgjcvi_00660	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0948	33, 425	45.3	343.2	0
hypothetical protein	Pgjcvi_00660	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1153	33, 425	45	341.7	0
hypothetical protein	Pgjcvi_00660	PG JCVI SC001	hypothetical protein	PG W83	PG1178	33, 425	44.8	341.3	0
Protein of unknown function (DUF1329).	Pgjcvi_00661	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0947	6, 261	60.5	325.5	0
Protein of unknown function (DUF1329).	Pgjcvi_00661	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1154	6, 261	60.5	325.5	0
Protein of unknown function (DUF1329).	Pgjcvi_00661	PG JCVI SC001	hypothetical protein	PG W83	PG1179	6, 261	60.1	325.1	0
Predicted exporters of the RND superfamily	Pgjcvi_00662	PG JCVI SC001	hypothetical protein	PG W83	PG1180	1, 780	48.6	779.6	0
Predicted exporters of the RND superfamily	Pgjcvi_00662	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1920	1, 780	48.5	776.9	0
Predicted exporters of the RND superfamily	Pgjcvi_00662	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1155	1, 780	48.3	775.4	0
hypothetical protein	Pgjcvi_00664	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0083	1, 318	96.5	616.3	0
hypothetical protein	Pgjcvi_00664	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0995	1, 318	93.1	592.8	0
hypothetical protein	Pgjcvi_00664	PG JCVI SC001	hypothetical protein	PG W83	PG1494	2, 288	46.2	259.6	0
hypothetical protein	Pgjcvi_00664	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0995	343, 416	28.9	45.4	0.0055
hypothetical protein	Pgjcvi_00665	PG JCVI SC001	hypothetical protein	PG W83	PG0854	13, 272	100	518.8	0
tRNA modification GTPase TrmE	Pgjcvi_00666	PG JCVI SC001	tRNA modification GTPase	PG W83	PG0876	45, 518	98.9	909.4	0
tRNA modification GTPase TrmE	Pgjcvi_00666	PG JCVI SC001	tRNA modification GTPase TrmE	PG TDC60	PGTDC60_0803	1, 474	98.1	901.4	0
tRNA modification GTPase TrmE	Pgjcvi_00666	PG JCVI SC001	tRNA modification GTPase	PG ATCC 33277	PGN_1062	45, 518	97.5	897.1	0
hypothetical protein	Pgjcvi_00667	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1061	1, 303	99	606.3	0
hypothetical protein	Pgjcvi_00667	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0804	1, 303	98.7	605.1	0
hypothetical protein	Pgjcvi_00667	PG JCVI SC001	hypothetical protein	PG W83	PG0877	1, 235	97	468	0
Homologues of TraJ from Bacteroides conjugative transposon.	Pgjcvi_00669	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1059	1, 81	88.9	150.6	4.40E-35
Homologues of TraJ from Bacteroides conjugative transposon.	Pgjcvi_00669	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0807	43, 159	78.9	188.7	0
Homologues of TraJ from Bacteroides conjugative transposon.	Pgjcvi_00669	PG JCVI SC001	hypothetical protein	PG W83	PG0879	43, 160	67.7	157.5	3.60E-37
Peroxiredoxin	Pgjcvi_00670	PG JCVI SC001	putative bacterioferritin comigratory protein	PG ATCC 33277	PGN_1058	1, 151	99.3	308.9	0
Peroxiredoxin	Pgjcvi_00670	PG JCVI SC001	bacterioferritin comigratory protein	PG TDC60	PGTDC60_0808	1, 151	99.3	308.9	0
Peroxiredoxin	Pgjcvi_00670	PG JCVI SC001	bacterioferritin comigratory protein	PG W83	PG0880	1, 167	98.2	336.3	0
protein RecA	Pgjcvi_00671	PG JCVI SC001	recombinase A	PG ATCC 33277	PGN_1057	1, 340	100	659.8	0
protein RecA	Pgjcvi_00671	PG JCVI SC001	recombinase A	PG W83	PG0881	1, 340	100	659.8	0
protein RecA	Pgjcvi_00671	PG JCVI SC001	recombinase A	PG TDC60	PGTDC60_0809	1, 340	100	659.8	0
hypothetical protein	Pgjcvi_00672	PG JCVI SC001	virulence modulating gene A	PG ATCC 33277	PGN_1056	13, 321	98.4	635.2	0
hypothetical protein	Pgjcvi_00672	PG JCVI SC001	virulence modulating gene A	PG TDC60	PGTDC60_0810	1, 309	98.4	635.2	0
hypothetical protein	Pgjcvi_00672	PG JCVI SC001	hypothetical protein	PG W83	PG0882	1, 309	98.1	636	0
hypothetical protein	Pgjcvi_00673	PG JCVI SC001	hypothetical protein	PG W83	PG0883	1, 453	100	927.2	0
hypothetical protein	Pgjcvi_00673	PG JCVI SC001	virulence modulating gene E	PG TDC60	PGTDC60_0811	1, 453	99.8	923.3	0
hypothetical protein	Pgjcvi_00673	PG JCVI SC001	virulence modulating gene E	PG ATCC 33277	PGN_1055	1, 453	99.3	916.4	0
Glycosyltransferase	Pgjcvi_00674	PG JCVI SC001	hypothetical protein	PG W83	PG0884	1, 416	100	843.6	0
Glycosyltransferase	Pgjcvi_00674	PG JCVI SC001	virulence modulating gene F	PG ATCC 33277	PGN_1054	1, 416	98.1	828.2	0
Glycosyltransferase	Pgjcvi_00674	PG JCVI SC001	virulence modulating gene F	PG TDC60	PGTDC60_0812	1, 416	98.1	828.9	0
3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	Pgjcvi_00675	PG JCVI SC001	putative phospho-2-dehydro-3-deoxyheptonate aldolase/chorismate mutase	PG ATCC 33277	PGN_1053	1, 366	100	733.8	0
3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	Pgjcvi_00675	PG JCVI SC001	phospho-2-dehydro-3-deoxyheptonate aldolase/chorismate mutase	PG W83	PG0885	1, 366	100	733.8	0
3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	Pgjcvi_00675	PG JCVI SC001	putative phospho-2-dehydro-3-deoxyheptonate aldolase/chorismate mutase	PG TDC60	PGTDC60_0813	1, 366	100	733.8	0
7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	Pgjcvi_00676	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1052	1, 254	99.6	518.5	0
7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	Pgjcvi_00676	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0814	1, 254	99.6	518.5	0
7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	Pgjcvi_00676	PG JCVI SC001	hypothetical protein	PG W83	PG0886	1, 254	98.8	511.9	0
Xaa-Pro aminopeptidase	Pgjcvi_00677	PG JCVI SC001	peptidase, M24 family	PG W83	PG0889	1, 398	99.7	785	0
Xaa-Pro aminopeptidase	Pgjcvi_00677	PG JCVI SC001	M24 family peptidase	PG TDC60	PGTDC60_0816	1, 398	99.7	785	0
Xaa-Pro aminopeptidase	Pgjcvi_00677	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1050	1, 398	99.2	783.5	0
Alkaline phosphatase	Pgjcvi_00678	PG JCVI SC001	alkaline phosphatase, putative	PG W83	PG0890	1, 563	99.5	1132.5	0
Alkaline phosphatase	Pgjcvi_00678	PG JCVI SC001	alkaline phosphatase	PG TDC60	PGTDC60_0817	1, 563	99.5	1131.3	0
Alkaline phosphatase	Pgjcvi_00678	PG JCVI SC001	putative alkaline phosphatase	PG ATCC 33277	PGN_1049	1, 563	99.1	1128.2	0
hydroxylamine reductase	Pgjcvi_00679	PG JCVI SC001	hydroxylamine reductase	PG ATCC 33277	PGN_1047	5, 550	99.5	1082.8	0
hydroxylamine reductase	Pgjcvi_00679	PG JCVI SC001	hydroxylamine reductase	PG W83	PG0893	5, 550	99.5	1083.9	0
hydroxylamine reductase	Pgjcvi_00679	PG JCVI SC001	hydroxylamine reductase	PG TDC60	PGTDC60_0821	5, 550	99.5	1082.8	0
DNA repair protein radc	Pgjcvi_00680	PG JCVI SC001	putative DNA repair protein	PG ATCC 33277	PGN_1046	1, 230	100	446.8	0
DNA repair protein radc	Pgjcvi_00680	PG JCVI SC001	DNA repair protein RadC	PG W83	PG0894	1, 227	99.6	439.5	0
DNA repair protein radc	Pgjcvi_00680	PG JCVI SC001	DNA repair protein RadC	PG TDC60	PGTDC60_0822	1, 230	99.6	445.3	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_00682	PG JCVI SC001	beta-galactosidase	PG ATCC 33277	PGN_1045	1, 1068	99.4	2212.2	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_00682	PG JCVI SC001	beta-galactosidase	PG TDC60	PGTDC60_0824	1, 1017	99.4	2116.7	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_00682	PG JCVI SC001	beta-galactosidase	PG W83	PG0896	1, 1017	99.3	2114	0
Glycosidases	Pgjcvi_00683	PG JCVI SC001	alpha-amylase family protein	PG W83	PG0897	1, 534	99.4	1101.7	0
Glycosidases	Pgjcvi_00683	PG JCVI SC001	alpha-amylase	PG ATCC 33277	PGN_1044	7, 564	98.6	1142.9	0
Glycosidases	Pgjcvi_00683	PG JCVI SC001	alpha-amylase	PG TDC60	PGTDC60_0825	7, 564	98.4	1140.2	0
Predicted esterase of the alpha-beta hydrolase superfamily	Pgjcvi_00684	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0826	1, 263	100	528.9	0
Predicted esterase of the alpha-beta hydrolase superfamily	Pgjcvi_00684	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1043	1, 263	99.6	526.9	0
Predicted esterase of the alpha-beta hydrolase superfamily	Pgjcvi_00684	PG JCVI SC001	hypothetical protein	PG W83	PG0898	1, 263	99.2	522.7	0
Cytochrome bd-type quinol oxidase, subunit 2	Pgjcvi_00685	PG JCVI SC001	cytochrome d ubiquinol oxidase, subunit II	PG W83	PG0899	1, 387	99.2	775.8	0

Cytochrome bd-type quinol oxidase, subunit 2	Pgjcvi_00685	PG JCVI SC001	cytochrome d ubiquinol oxidase subunit II	PG ATCC 33277	PGN_1042	1, 387	99	775.4	0
Cytochrome bd-type quinol oxidase, subunit 2	Pgjcvi_00685	PG JCVI SC001	cytochrome d ubiquinol oxidase, subunit II	PG TDC60	PGTDC60_0827	1, 387	99	773.9	0
Cytochrome bd-type quinol oxidase, subunit 1	Pgjcvi_00686	PG JCVI SC001	cytochrome d ubiquinol oxidase, subunit I	PG W83	PG0900	1, 527	100	1064.7	0
Cytochrome bd-type quinol oxidase, subunit 1	Pgjcvi_00686	PG JCVI SC001	cytochrome d ubiquinol oxidase subunit I	PG ATCC 33277	PGN_1041	1, 529	99.6	1066.2	0
Cytochrome bd-type quinol oxidase, subunit 1	Pgjcvi_00686	PG JCVI SC001	cytochrome d ubiquinol oxidase subunit I	PG TDC60	PGTDC60_0828	1, 529	99.4	1063.1	0
hypothetical protein	Pgjcvi_00687	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1040	1, 82	100	164.1	2.30E-39
hypothetical protein	Pgjcvi_00687	PG JCVI SC001	hypothetical protein	PG W83	PG0901	1, 82	100	164.1	2.30E-39
hypothetical protein	Pgjcvi_00687	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0829	1, 82	96.3	159.1	7.50E-38
alpha-1,2-mannosidase, putative	Pgjcvi_00688	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG TDC60	PGTDC60_0830	1, 741	99.2	1523.8	0
alpha-1,2-mannosidase, putative	Pgjcvi_00688	PG JCVI SC001	putative alpha-1,2-mannosidase precursor	PG ATCC 33277	PGN_1039	15, 755	98.9	1523.5	0
alpha-1,2-mannosidase, putative	Pgjcvi_00688	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG W83	PG0902	1, 741	98.7	1517.3	0
Uncharacterized conserved protein	Pgjcvi_00689	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1038	1, 180	100	364.8	0
Uncharacterized conserved protein	Pgjcvi_00689	PG JCVI SC001	hypothetical protein	PG W83	PG0903	1, 180	100	364.8	0
Uncharacterized conserved protein	Pgjcvi_00689	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0831	1, 180	100	364.8	0
Uncharacterized lipoprotein NlpE involved in copper resistance	Pgjcvi_00690	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1037	1, 150	98.7	285	0
Uncharacterized lipoprotein NlpE involved in copper resistance	Pgjcvi_00690	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0832	1, 150	98.7	285.4	0
Uncharacterized lipoprotein NlpE involved in copper resistance	Pgjcvi_00690	PG JCVI SC001	lipoprotein, putative	PG W83	PG0906	1, 150	98	283.1	0
G:T/U mismatch-specific DNA glycosylase	Pgjcvi_00692	PG JCVI SC001	G/U mismatch-specific DNA glycosylase, putative	PG W83	PG0908	1, 163	100	336.3	0
G:T/U mismatch-specific DNA glycosylase	Pgjcvi_00692	PG JCVI SC001	G/U mismatch-specific DNA glycosylase	PG TDC60	PGTDC60_0833	1, 163	98.8	332	0
G:T/U mismatch-specific DNA glycosylase	Pgjcvi_00692	PG JCVI SC001	putative G/U mismatch-specific DNA glycosylase	PG ATCC 33277	PGN_1036	1, 160	95.6	321.6	0
Uncharacterized conserved protein	Pgjcvi_00693	PG JCVI SC001	hypothetical protein	PG W83	PG0909	1, 433	100	833.9	0
Uncharacterized conserved protein	Pgjcvi_00693	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0834	1, 433	99.5	831.2	0
Uncharacterized conserved protein	Pgjcvi_00693	PG JCVI SC001	conserved hypothetical protein with DUF1063 domain	PG ATCC 33277	PGN_1035	1, 433	98.8	825.1	0
FHA domain.	Pgjcvi_00694	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1034	1, 190	98.4	385.2	0
FHA domain.	Pgjcvi_00694	PG JCVI SC001	FHA domain protein	PG W83	PG0910	1, 190	98.4	385.2	0
FHA domain.	Pgjcvi_00694	PG JCVI SC001	FHA domain-containing protein	PG TDC60	PGTDC60_0835	1, 151	96.7	300.1	0
hypothetical protein	Pgjcvi_00695	PG JCVI SC001	polysaccharide transport protein, putative	PG W83	PG0912	1, 521	99.6	1025.4	0
hypothetical protein	Pgjcvi_00695	PG JCVI SC001	putative polysaccharide transport protein	PG ATCC 33277	PGN_1033	1, 521	99.4	1022.3	0
hypothetical protein	Pgjcvi_00695	PG JCVI SC001	putative polysaccharide transport protein	PG TDC60	PGTDC60_0836	1, 521	99.4	1023.1	0
hypothetical protein	Pgjcvi_00696	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1032	1, 237	100	468.4	0
hypothetical protein	Pgjcvi_00696	PG JCVI SC001	hypothetical protein	PG W83	PG0914	1, 237	100	468.4	0
hypothetical protein	Pgjcvi_00696	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0837	1, 237	100	468.4	0
hypothetical protein	Pgjcvi_00697	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1031	5, 110	98.1	211.5	0
hypothetical protein	Pgjcvi_00697	PG JCVI SC001	hypothetical protein	PG W83	PG0915	5, 130	97.6	249.6	0
hypothetical protein	Pgjcvi_00697	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0838	5, 110	97.2	211.8	0
hypothetical protein	Pgjcvi_00698	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1030	20, 61	88.1	82.8	3.50E-15
Predicted membrane protein	Pgjcvi_00700	PG JCVI SC001	GtrA family protein	PG TDC60	PGTDC60_0841	1, 131	100	270.4	0
Predicted membrane protein	Pgjcvi_00700	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1029	1, 131	98.5	268.1	0
Predicted membrane protein	Pgjcvi_00700	PG JCVI SC001	GtrA family protein	PG W83	PG0917	1, 131	98.5	268.1	0
hypothetical protein	Pgjcvi_00701	PG JCVI SC001	hypothetical protein	PG W83	PG0918	1, 251	100	495.4	0
hypothetical protein	Pgjcvi_00701	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0842	1, 251	100	495.4	0
hypothetical protein	Pgjcvi_00701	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1028	1, 220	99.5	433.3	0
Dihydroorotase and related cyclic amidohydrolases	Pgjcvi_00702	PG JCVI SC001	dihydroorotase	PG ATCC 33277	PGN_1027	1, 449	99.1	904	0
Dihydroorotase and related cyclic amidohydrolases	Pgjcvi_00702	PG JCVI SC001	dihydroorotase	PG W83	PG0919	1, 449	98.9	901.7	0
Dihydroorotase and related cyclic amidohydrolases	Pgjcvi_00702	PG JCVI SC001	dihydroorotase	PG TDC60	PGTDC60_0843	1, 449	98.4	900.6	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_00703	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_0844	1, 245	100	503.4	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_00703	PG JCVI SC001	glycosyl transferase family 2	PG ATCC 33277	PGN_1026	1, 245	99.6	501.5	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_00703	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG0920	1, 226	99.6	465.3	0
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_00704	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1025	1, 407	98.3	760.8	0
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_00704	PG JCVI SC001	hypothetical protein	PG W83	PG0922	1, 407	98.3	765	0
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_00704	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0845	1, 407	98.3	762.7	0
ribosome-binding factor A	Pgjcvi_00705	PG JCVI SC001	putative ribosome-binding factor A	PG ATCC 33277	PGN_1024	1, 111	99.1	213.4	0
ribosome-binding factor A	Pgjcvi_00705	PG JCVI SC001	ribosome-binding factor A	PG W83	PG0923	1, 111	99.1	213.4	0
ribosome-binding factor A	Pgjcvi_00705	PG JCVI SC001	ribosome-binding factor A	PG TDC60	PGTDC60_0846	1, 111	99.1	213.4	0
5''-nucleotidase, lipoprotein e(P4) family	Pgjcvi_00706	PG JCVI SC001	acid phosphatase OlpA	PG ATCC 33277	PGN_1023	1, 271	99.6	560.1	0
5''-nucleotidase, lipoprotein e(P4) family	Pgjcvi_00706	PG JCVI SC001	5'-nucleotidase, lipoprotein e(P4) family	PG W83	PG0924	1, 271	98.5	553.1	0
5''-nucleotidase, lipoprotein e(P4) family	Pgjcvi_00706	PG JCVI SC001	5'-nucleotidase	PG TDC60	PGTDC60_0847	1, 271	97.8	548.5	0
Thymidine kinase	Pgjcvi_00707	PG JCVI SC001	thymidine kinase	PG W83	PG0925	1, 204	100	408.3	0
Thymidine kinase	Pgjcvi_00707	PG JCVI SC001	thymidine kinase	PG TDC60	PGTDC60_0848	1, 204	100	408.3	0
Thymidine kinase	Pgjcvi_00707	PG JCVI SC001	putative thymidine kinase	PG ATCC 33277	PGN_1022	1, 204	99.5	406.4	0
hypothetical protein	Pgjcvi_00708	PG JCVI SC001	hypothetical protein	PG W83	PG0926	1, 75	100	148.7	9.20E-35
hypothetical protein	Pgjcvi_00708	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0849	1, 75	100	148.7	9.20E-35
hypothetical protein	Pgjcvi_00708	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1021	1, 75	98.7	146.7	3.50E-34
ATPase, YjeE family	Pgjcvi_00709	PG JCVI SC001	conserved hypothetical protein TIGR00150	PG W83	PG0927	1, 138	100	283.5	0
ATPase, YjeE family	Pgjcvi_00709	PG JCVI SC001	putative ATP/GTP-binding transmembrane protein	PG TDC60	PGTDC60_0850	1, 138	100	283.5	0
ATPase, YjeE family	Pgjcvi_00709	PG JCVI SC001	probable ATP/GTP-binding transmembrane protein	PG ATCC 33277	PGN_1020	1, 138	99.3	281.6	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00710	PG JCVI SC001	response regulator	PG ATCC 33277	PGN_1019	5, 518	99.6	1035.4	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00710	PG JCVI SC001	response regulator	PG W83	PG0928	5, 518	99.6	1035	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_00710	PG JCVI SC001	response regulator	PG TDC60	PGTDC60_0851	5, 518	99.4	1034.2	0

hypothetical protein	Pgjcvi_00711	PG JCVI SC001	hypothetical protein	PG W83	PG0929	19, 160	93.7	253.8	0
hypothetical protein	Pgjcvi_00712	PG JCVI SC001	hypothetical protein	PG W83	PG0930	1, 129	97.7	270.4	0
hypothetical protein	Pgjcvi_00712	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0853	1, 107	97.2	226.1	0
hypothetical protein	Pgjcvi_00712	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1017	1, 129	93.8	258.5	0
DNA-binding protein, histone-like, putative	Pgjcvi_00713	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0854	1, 213	99.1	420.2	0
DNA-binding protein, histone-like, putative	Pgjcvi_00713	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1016	1, 204	99	403.3	0
DNA polymerase III, delta'' subunit	Pgjcvi_00714	PG JCVI SC001	DNA polymerase III, delta prime subunit, putative	PG W83	PG0932	1, 416	99.5	828.2	0
DNA polymerase III, delta'' subunit	Pgjcvi_00714	PG JCVI SC001	DNA polymerase III, delta prime subunit	PG TDC60	PGTDC60_0855	1, 381	99	754.2	0
DNA polymerase III, delta'' subunit	Pgjcvi_00714	PG JCVI SC001	putative DNA polymerase III delta prime subunit	PG ATCC 33277	PGN_1015	1, 416	98.8	824.3	0
small GTP-binding protein domain	Pgjcvi_00715	PG JCVI SC001	elongation factor G	PG ATCC 33277	PGN_1014	1, 719	100	1429.8	0
small GTP-binding protein domain	Pgjcvi_00715	PG JCVI SC001	translation elongation factor G, putative	PG W83	PG0933	1, 719	99.9	1427.5	0
small GTP-binding protein domain	Pgjcvi_00715	PG JCVI SC001	elongation factor G	PG TDC60	PGTDC60_0856	1, 719	99.6	1425.6	0
uncharacterized radical SAM protein YgiQ	Pgjcvi_00716	PG JCVI SC001	hypothetical protein	PG W83	PG0934	18, 634	99.2	1250.7	0
uncharacterized radical SAM protein YgiQ	Pgjcvi_00716	PG JCVI SC001	putative Fe-S oxidoreductase	PG ATCC 33277	PGN_1013	18, 634	98.7	1247.6	0
uncharacterized radical SAM protein YgiQ	Pgjcvi_00716	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0857	1, 617	98.7	1245.7	0
4-diphosphocytidyl-2C-methyl-D-erythritol kinase	Pgjcvi_00717	PG JCVI SC001	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	PG W83	PG0935	1, 274	96	526.9	0
4-diphosphocytidyl-2C-methyl-D-erythritol kinase	Pgjcvi_00717	PG JCVI SC001	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	PG TDC60	PGTDC60_0858	1, 274	96	528.5	0
4-diphosphocytidyl-2C-methyl-D-erythritol kinase	Pgjcvi_00717	PG JCVI SC001	putative 4-diphosphocytidyl-2C-methyl-D- erythritol kinase	PG ATCC 33277	PGN_1012	1, 274	94.9	523.1	0
Permeases	Pgjcvi_00718	PG JCVI SC001	xanthine/uracil permease family protein	PG W83	PG0936	1, 433	99.8	820.8	0
Permeases	Pgjcvi_00718	PG JCVI SC001	xanthine/uracil permease family protein	PG TDC60	PGTDC60_0859	1, 433	99.8	821.6	0
Permeases	Pgjcvi_00718	PG JCVI SC001	xanthine/uracil/vitamin C permease	PG ATCC 33277	PGN_1011	1, 433	99.3	817.8	0
hypothetical protein	Pgjcvi_00719	PG JCVI SC001	hypothetical protein	PG W83	PG0937	1, 240	100	511.1	0
hypothetical protein	Pgjcvi_00719	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1010	1, 240	98.3	502.3	0
hypothetical protein	Pgjcvi_00719	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0860	1, 240	97.1	498.4	0
plasma-membrane calcium-translocating P-type ATPase	Pgjcvi_00720	PG JCVI SC001	calcium-transporting ATPase	PG TDC60	PGTDC60_0861	1, 918	99.1	1800.4	0
plasma-membrane calcium-translocating P-type ATPase	Pgjcvi_00720	PG JCVI SC001	calcium-transporting ATPase	PG ATCC 33277	PGN_1009	1, 941	98.8	1841.6	0
plasma-membrane calcium-translocating P-type ATPase	Pgjcvi_00720	PG JCVI SC001	calcium-transporting ATPase	PG W83	PG0938	123, 1063	98.7	1840.9	0
hypothetical protein	Pgjcvi_00721	PG JCVI SC001	probable ABC transporter permease protein	PG ATCC 33277	PGN_1005	1, 442	100	865.5	0
hypothetical protein	Pgjcvi_00721	PG JCVI SC001	putative ABC transporter permease protein	PG TDC60	PGTDC60_0867	1, 442	100	865.5	0
hypothetical protein	Pgjcvi_00721	PG JCVI SC001	ABC transporter, permease protein, putative	PG W83	PG0945	1, 442	99.8	863.6	0
ABC-type uncharacterized transport system, ATPase component	Pgjcvi_00722	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG0946	1, 319	99.4	638.3	0
ABC-type uncharacterized transport system, ATPase component	Pgjcvi_00722	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_1004	1, 319	99.1	634.4	0
ABC-type uncharacterized transport system, ATPase component	Pgjcvi_00722	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_0868	1, 325	98.8	647.5	0
hypothetical protein	Pgjcvi_00723	PG JCVI SC001	hypothetical protein	PG W83	PG0947	1, 157	98.1	318.9	0
hypothetical protein	Pgjcvi_00723	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0869	1, 157	97.5	315.5	0
hypothetical protein	Pgjcvi_00723	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1003	1, 157	96.8	314.3	0
AMP nucleosidase, putative	Pgjcvi_00724	PG JCVI SC001	AMP nucleosidase	PG ATCC 33277	PGN_1002	1, 258	98.8	518.1	0
AMP nucleosidase, putative	Pgjcvi_00724	PG JCVI SC001	AMP nucleosidase	PG W83	PG0948	1, 258	98.8	518.1	0
AMP nucleosidase, putative	Pgjcvi_00724	PG JCVI SC001	AMP nucleosidase	PG TDC60	PGTDC60_0870	1, 258	98.1	515.8	0
DNA polymerase III, delta subunit	Pgjcvi_00725	PG JCVI SC001	hypothetical protein	PG W83	PG0949	1, 335	100	665.2	0
DNA polymerase III, delta subunit	Pgjcvi_00725	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0871	1, 335	99.4	660.2	0
DNA polymerase III, delta subunit	Pgjcvi_00725	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1001	1, 335	99.1	659.8	0
glycine cleavage system H protein	Pgjcvi_00726	PG JCVI SC001	putative glycine cleavage system H protein	PG ATCC 33277	PGN_1000	1, 126	100	251.9	0
glycine cleavage system H protein	Pgjcvi_00726	PG JCVI SC001	glycine cleavage system protein H	PG W83	PG0950	1, 126	100	251.9	0
glycine cleavage system H protein	Pgjcvi_00726	PG JCVI SC001	glycine cleavage system protein H	PG TDC60	PGTDC60_0872	1, 126	100	251.9	0
phosphoribosylaminoimidazole carboxylase, PurE protein	Pgjcvi_00727	PG JCVI SC001	putative phosphoribosylaminoimidazole carboxylase	PG ATCC 33277	PGN_0999	1, 168	100	321.2	0
phosphoribosylaminoimidazole carboxylase, PurE protein	Pgjcvi_00727	PG JCVI SC001	phosphoribosylaminoimidazole carboxylase, PurE protein	PG W83	PG0951	1, 168	100	321.2	0
phosphoribosylaminoimidazole carboxylase, PurE protein	Pgjcvi_00727	PG JCVI SC001	phosphoribosylaminoimidazole carboxylase subunit PurE	PG TDC60	PGTDC60_0873	1, 168	100	321.2	0
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	Pgjcvi_00728	PG JCVI SC001	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	PG ATCC 33277	PGN_0998	1, 581	99.5	1155.6	0
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	Pgjcvi_00728	PG JCVI SC001	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	PG W83	PG0952	1, 581	99.5	1155.6	0
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	Pgjcvi_00728	PG JCVI SC001	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	PG TDC60	PGTDC60_0874	1, 581	99.3	1154.8	0
deoxyuridine 5''-triphosphate nucleotidohydrolase (dut)	Pgjcvi_00729	PG JCVI SC001	putative deoxyuridine 5'-triphosphate nucleotidohydrolase	PG ATCC 33277	PGN_0997	1, 144	100	289.7	0
deoxyuridine 5''-triphosphate nucleotidohydrolase (dut)	Pgjcvi_00729	PG JCVI SC001	deoxyuridine 5'-triphosphate nucleotidohydrolase	PG TDC60	PGTDC60_0875	1, 144	100	289.7	0
deoxyuridine 5''-triphosphate nucleotidohydrolase (dut)	Pgjcvi_00729	PG JCVI SC001	deoxyuridine 5'-triphosphate nucleotidohydrolase	PG W83	PG0953	1, 144	99.3	288.1	0
Tetratricopeptide repeat.	Pgjcvi_00730	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_0996	1, 384	99.7	762.3	0
Tetratricopeptide repeat.	Pgjcvi_00730	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0876	1, 579	99	1143.3	0
Tetratricopeptide repeat.	Pgjcvi_00730	PG JCVI SC001	TPR domain protein	PG W83	PG0954	1, 579	98.8	1142.9	0
hypothetical protein	Pgjcvi_00731	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0877	1, 286	98.3	548.1	0
hypothetical protein	Pgjcvi_00731	PG JCVI SC001	hypothetical protein	PG W83	PG0955	31, 317	97.2	548.1	0
hypothetical protein	Pgjcvi_00731	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0994	1, 287	96.9	545	0
Membrane-bound metallopeptidase	Pgjcvi_00732	PG JCVI SC001	peptidase, M23/M37 family, putative	PG W83	PG0956	1, 431	97.4	811.6	0
Membrane-bound metallopeptidase	Pgjcvi_00732	PG JCVI SC001	M24/M37 family peptidase	PG TDC60	PGTDC60_0878	1, 431	97.4	813.9	0
Membrane-bound metallopeptidase	Pgjcvi_00732	PG JCVI SC001	putative peptidase M23/M37 family	PG ATCC 33277	PGN_0993	1, 431	97.2	812.8	0
riboflavin kinase/FMN adenylyltransferase	Pgjcvi_00733	PG JCVI SC001	riboflavin biosynthesis protein RibF	PG W83	PG0957	1, 323	100	643.7	0
riboflavin kinase/FMN adenylyltransferase	Pgjcvi_00733	PG JCVI SC001	riboflavin biosynthesis protein RibF	PG TDC60	PGTDC60_0879	1, 323	99.4	640.6	0
riboflavin kinase/FMN adenylyltransferase	Pgjcvi_00733	PG JCVI SC001	putative riboflavin biosynthesis protein	PG ATCC 33277	PGN_0992	1, 323	99.1	638.3	0
Predicted membrane protein	Pgjcvi_00734	PG JCVI SC001	putative ribonuclease BN	PG ATCC 33277	PGN_0991	1, 475	99.8	936.4	0
Predicted membrane protein	Pgjcvi_00734	PG JCVI SC001	ribonuclease BN, putative	PG W83	PG0958	1, 411	99.8	805.8	0
Predicted membrane protein	Pgjcvi_00734	PG JCVI SC001	putative ribonuclease BN	PG TDC60	PGTDC60_0880	1, 434	99.8	850.9	0
ATPases involved in chromosome partitioning	Pgjcvi_00736	PG JCVI SC001	ATP-binding protein Mrp/Nbp35 family	PG ATCC 33277	PGN_0990	1, 372	100	733	0
ATPases involved in chromosome partitioning	Pgjcvi_00736	PG JCVI SC001	ATP-binding protein, Mrp/Nbp35 family	PG W83	PG0959	1, 372	99.7	731.1	0
ATPases involved in chromosome partitioning	Pgjcvi_00736	PG JCVI SC001	ATP-binding protein Mrp/Nbp35 family	PG TDC60	PGTDC60_0881	1, 372	99.7	731.5	0

Predicted S-adenosylmethionine-dependent methyltransferase	Pgjcvi_00737	PG JCVI SC001	putative methyltransferase	PG ATCC 33277	PGN_0989	1, 255	98.4	520	0
Predicted S-adenosylmethionine-dependent methyltransferase	Pgjcvi_00737	PG JCVI SC001	tRNA (guanine-N(7)-)-methyltransferase	PG TDC60	PGTDC60_0882	1, 255	98.4	520.4	0
Predicted S-adenosylmethionine-dependent methyltransferase	Pgjcvi_00737	PG JCVI SC001	tRNA (guanine-N(7)-)-methyltransferase	PG W83	PG0960	1, 244	98	497.7	0
hypothetical protein	Pgjcvi_00738	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0988	1, 109	100	218.8	0
hypothetical protein	Pgjcvi_00738	PG JCVI SC001	hypothetical protein	PG W83	PG0961	1, 109	100	218.8	0
hypothetical protein	Pgjcvi_00738	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0883	1, 109	99.1	217.2	0
prolyl-tRNA synthetase, family I	Pgjcvi_00739	PG JCVI SC001	prolyl-tRNA synthetase	PG ATCC 33277	PGN_0987	1, 493	100	999.6	0
prolyl-tRNA synthetase, family I	Pgjcvi_00739	PG JCVI SC001	prolyl-tRNA synthetase	PG TDC60	PGTDC60_0884	1, 493	99.8	999.2	0
prolyl-tRNA synthetase, family I	Pgjcvi_00739	PG JCVI SC001	prolyl-tRNA synthetase	PG W83	PG0962	1, 493	99.4	996.9	0
hypothetical protein	Pgjcvi_00740	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0986	1, 81	100	164.9	1.30E-39
hypothetical protein	Pgjcvi_00740	PG JCVI SC001	hypothetical protein	PG W83	PG0963	1, 81	100	164.9	1.30E-39
hypothetical protein	Pgjcvi_00740	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0885	1, 81	100	164.9	1.30E-39
CDP-diacylglycerol--serine O-phosphatidyltransferase	Pgjcvi_00741	PG JCVI SC001	putative phosphatidylserine synthase	PG TDC60	PGTDC60_0886	1, 236	100	460.7	0
CDP-diacylglycerol--serine O-phosphatidyltransferase	Pgjcvi_00741	PG JCVI SC001	probable phosphatidylserine synthase	PG ATCC 33277	PGN_0985	1, 236	97.9	448.7	0
phosphatidylserine decarboxylase precursor-related protein	Pgjcvi_00742	PG JCVI SC001	probable phosphatidylserine decarboxylase proenzyme	PG ATCC 33277	PGN_0984	1, 221	100	438.7	0
phosphatidylserine decarboxylase precursor-related protein	Pgjcvi_00742	PG JCVI SC001	phosphatidylserine decarboxylase	PG W83	PG0965	1, 221	100	438.7	0
phosphatidylserine decarboxylase precursor-related protein	Pgjcvi_00742	PG JCVI SC001	phosphatidylserine decarboxylase	PG TDC60	PGTDC60_0887	1, 221	100	438.7	0
Restriction endonuclease	Pgjcvi_00743	PG JCVI SC001	Mrr restriction system protein	PG TDC60	PGTDC60_0890	1, 305	100	605.9	0
Restriction endonuclease	Pgjcvi_00743	PG JCVI SC001	Mrr restriction system protein	PG W83	PG0968	1, 305	99.7	604.4	0
Restriction endonuclease	Pgjcvi_00743	PG JCVI SC001	putative Mrr restriction system protein	PG ATCC 33277	PGN_0982	1, 305	99.3	602.4	0
S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)	Pgjcvi_00745	PG JCVI SC001	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	PG TDC60	PGTDC60_0891	1, 405	98.5	804.3	0
S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)	Pgjcvi_00745	PG JCVI SC001	S-adenosylmethionine:tRNA ribosyltransferase-isomerase, putative	PG W83	PG0969	1, 405	98.3	802.4	0
S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)	Pgjcvi_00745	PG JCVI SC001	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	PG ATCC 33277	PGN_0981	1, 405	96.8	792.7	0
alpha-1,2-mannosidase, putative	Pgjcvi_00746	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG W83	PG0973	1, 771	99.2	1592.4	0
alpha-1,2-mannosidase, putative	Pgjcvi_00746	PG JCVI SC001	putative alpha-1,2-mannosidase family protein	PG ATCC 33277	PGN_0980	1, 771	98.4	1575.1	0
alpha-1,2-mannosidase, putative	Pgjcvi_00746	PG JCVI SC001	alpha-1,2-mannosidase family protein	PG TDC60	PGTDC60_0892	1, 771	98.1	1566.2	0
Phosphate starvation-inducible protein PhoH, predicted ATPase	Pgjcvi_00747	PG JCVI SC001	PhoH family protein	PG W83	PG0975	1, 330	99.4	635.6	0
Phosphate starvation-inducible protein PhoH, predicted ATPase	Pgjcvi_00747	PG JCVI SC001	PhoH family protein	PG TDC60	PGTDC60_0895	1, 330	99.1	635.2	0
Phosphate starvation-inducible protein PhoH, predicted ATPase	Pgjcvi_00747	PG JCVI SC001	phosphate starvation-inducible PhoH-like protein	PG ATCC 33277	PGN_0977	1, 330	98.5	629.8	0
Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	Pgjcvi_00748	PG JCVI SC001	phosphoribosylaminoimidazole- succinocarboxamidesynthase	PG TDC60	PGTDC60_0896	1, 313	100	636.3	0
Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	Pgjcvi_00748	PG JCVI SC001	phosphoribosylaminoimidazole-succinocarboxamide synthase	PG ATCC 33277	PGN_0976	1, 313	99.7	635.2	0
Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	Pgjcvi_00748	PG JCVI SC001	phosphoribosylaminoimidazole-succinocarboxamide synthase	PG W83	PG0976	1, 313	99.7	634.8	0
ubiquinone/menaquinone biosynthesis methyltransferases	Pgjcvi_00749	PG JCVI SC001	ubiquinone/menaquinone biosynthesis methyltransferase	PG W83	PG0977	1, 245	99.6	497.3	0
ubiquinone/menaquinone biosynthesis methyltransferases	Pgjcvi_00749	PG JCVI SC001	ubiquinone/menaquinone biosynthesis methyltransferase	PG TDC60	PGTDC60_0897	1, 245	99.6	497.3	0
ubiquinone/menaquinone biosynthesis methyltransferases	Pgjcvi_00749	PG JCVI SC001	putative ubiquinone/menaquinone biosynthesis methyltransferase	PG ATCC 33277	PGN_0975	1, 245	99.2	496.1	0
Shikimate 5-dehydrogenase	Pgjcvi_00750	PG JCVI SC001	shikimate 5-dehydrogenase	PG W83	PG0978	1, 249	99.2	499.6	0
Shikimate 5-dehydrogenase	Pgjcvi_00750	PG JCVI SC001	putative shikimate 5-dehydrogenase	PG ATCC 33277	PGN_0974	1, 249	98.8	495.7	0
Shikimate 5-dehydrogenase	Pgjcvi_00750	PG JCVI SC001	shikimate 5-dehydrogenase	PG TDC60	PGTDC60_0898	1, 249	98.8	495.7	0
Outer membrane protein/protective antigen OMA87	Pgjcvi_00751	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0900	1, 756	99.3	1517.3	0
Outer membrane protein/protective antigen OMA87	Pgjcvi_00751	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0973	1, 774	99.2	1550	0
Outer membrane protein/protective antigen OMA87	Pgjcvi_00751	PG JCVI SC001	hypothetical protein	PG W83	PG0980	1, 745	99.1	1493	0
Site-specific recombinase XerD	Pgjcvi_00753	PG JCVI SC001	integrase	PG TDC60	PGTDC60_2028	5, 397	39.3	286.2	0
Site-specific recombinase XerD	Pgjcvi_00753	PG JCVI SC001	integrase	PG W83	PG1435	5, 348	37.9	240	0
Site-specific recombinase XerD	Pgjcvi_00753	PG JCVI SC001	tyrosine type site-specific recombinase	PG ATCC 33277	PGN_0917	161, 411	28	89.7	2.80E-16
hypothetical protein	Pgjcvi_00754	PG JCVI SC001	histone-like family DNA-binding protein	PG TDC60	PGTDC60_1669	1, 75	73.3	112.5	1.20E-23
hypothetical protein	Pgjcvi_00754	PG JCVI SC001	putative partial DNA-binding protein histone-like family	PG ATCC 33277	PGN_1422	1, 85	72.9	125.6	1.40E-27
hypothetical protein	Pgjcvi_00754	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG1205	1, 88	72.7	128.6	1.60E-28
hypothetical protein	Pgjcvi_00757	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0795	2, 118	82.1	192.6	0
hypothetical protein	Pgjcvi_00757	PG JCVI SC001	hypothetical protein	PG W83	PG0829	21, 157	74.5	203	0
hypothetical protein	Pgjcvi_00757	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0074	1, 137	70.1	189.9	0
hypothetical protein	Pgjcvi_00759	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1012	1, 40	77.5	62	8.20E-09
hypothetical protein	Pgjcvi_00759	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0071	1, 40	75	62	8.20E-09
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00770	PG JCVI SC001	RNA polymerase sigma-70 factor, ECF subfamily	PG W83	PG0985	1, 168	98.8	330.5	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00770	PG JCVI SC001	ECF subfamily RNA polymerase sigma factor	PG TDC60	PGTDC60_0901	1, 144	97.9	281.2	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_00770	PG JCVI SC001	putative RNA polymerase sigma-70 factor ECF subfamily	PG ATCC 33277	PGN_0970	1, 168	97	322.4	0
hypothetical protein	Pgjcvi_00771	PG JCVI SC001	hypothetical protein	PG W83	PG0986	2, 186	100	365.2	0
hypothetical protein	Pgjcvi_00771	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0969	2, 186	99.5	363.6	0
hypothetical protein	Pgjcvi_00771	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0902	2, 186	99.5	362.1	0
hypothetical protein	Pgjcvi_00772	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0968	1, 258	98.4	501.9	0
hypothetical protein	Pgjcvi_00772	PG JCVI SC001	hypothetical protein	PG W83	PG0987	1, 258	98.1	502.7	0
hypothetical protein	Pgjcvi_00772	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0903	1, 258	97.7	498	0
Transposase and inactivated derivatives	Pgjcvi_00774	PG JCVI SC001	partial transposase in ISPg1	PG ATCC 33277	PGN_0219	24, 189	98.2	322.4	0
Transposase and inactivated derivatives	Pgjcvi_00774	PG JCVI SC001	ISPg1, transposase	PG W83	PG0825	27, 182	62.4	199.1	0
Transposase and inactivated derivatives	Pgjcvi_00774	PG JCVI SC001	transposase in ISPg1	PG TDC60	PGTDC60_1413	27, 182	61.8	198.4	0
ribosomal protein L20	Pgjcvi_00775	PG JCVI SC001	putative 50S ribosomal protein L20	PG ATCC 33277	PGN_0965	1, 115	99.1	231.9	0
ribosomal protein L20	Pgjcvi_00775	PG JCVI SC001	50S ribosomal protein L20	PG TDC60	PGTDC60_0906	1, 115	99.1	231.9	0
ribosomal protein L20	Pgjcvi_00775	PG JCVI SC001	50S ribosomal protein L20	PG W83	PG0989	1, 115	98.3	229.9	0
ribosomal protein L35	Pgjcvi_00776	PG JCVI SC001	probable 50S ribosomal protein L35	PG ATCC 33277	PGN_0964	1, 65	100	132.9	4.50E-30
ribosomal protein L35	Pgjcvi_00776	PG JCVI SC001	ribosomal protein L35	PG W83	PG0990	1, 65	100	132.9	4.50E-30
ribosomal protein L35	Pgjcvi_00776	PG JCVI SC001	50S ribosomal protein L35	PG TDC60	PGTDC60_0907	1, 65	100	132.9	4.50E-30
translation initiation factor IF-3	Pgjcvi_00777	PG JCVI SC001	translation initiation factor IF-3	PG ATCC 33277	PGN_0963	1, 201	99.5	395.2	0
translation initiation factor IF-3	Pgjcvi_00777	PG JCVI SC001	translation initiation factor IF-3	PG W83	PG0991	1, 201	99.5	395.2	0

translation initiation factor IF-3	Pgjcvi_00777	PG JCVI SC001	translation initiation factor IF-3	PG TDC60	PGTDC60_0908	1, 201	99.5	395.2	0
threonyl-tRNA synthetase	Pgjcvi_00778	PG JCVI SC001	threonyl-tRNA synthetase	PG ATCC 33277	PGN_0962	1, 653	100	1337	0
threonyl-tRNA synthetase	Pgjcvi_00778	PG JCVI SC001	threonyl-tRNA synthetase	PG W83	PG0992	1, 653	99.8	1333.9	0
threonyl-tRNA synthetase	Pgjcvi_00778	PG JCVI SC001	threonyl-tRNA synthetase	PG TDC60	PGTDC60_0909	1, 653	99.8	1335.9	0
hypothetical protein	Pgjcvi_00779	PG JCVI SC001	transposase in ISPg2	PG TDC60	PGTDC60_1232	1, 66	97	138.7	1.50E-31
hypothetical protein	Pgjcvi_00779	PG JCVI SC001	ISPg2, transposase	PG W83	PG0865	4, 99	39.6	73.9	4.50E-12
hypothetical protein	Pgjcvi_00779	PG JCVI SC001	transposase in ISPg2	PG ATCC 33277	PGN_1160	30, 105	39.5	60.8	4.00E-08
Helix-turn-helix.	Pgjcvi_00780	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG0997	1, 88	98.9	169.5	7.00E-41
Helix-turn-helix.	Pgjcvi_00780	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_0959	4, 107	94.2	189.1	0
Helix-turn-helix.	Pgjcvi_00780	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_0918	3, 94	93.5	165.2	1.30E-39
DNA alkylation repair enzyme.	Pgjcvi_00782	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0921	6, 210	97.1	404.1	0
DNA alkylation repair enzyme.	Pgjcvi_00782	PG JCVI SC001	hypothetical protein	PG W83	PG1000	6, 210	96.6	401.7	0
DNA alkylation repair enzyme.	Pgjcvi_00782	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1353	1, 138	96.4	280	0
Uncharacterized conserved protein	Pgjcvi_00783	PG JCVI SC001	conserved hypothetical protein with DUF1706 domain	PG ATCC 33277	PGN_1352	1, 178	98.9	371.7	0
Uncharacterized conserved protein	Pgjcvi_00783	PG JCVI SC001	hypothetical protein	PG W83	PG1001	1, 178	98.9	370.2	0
Uncharacterized conserved protein	Pgjcvi_00783	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0922	1, 178	97.2	364.8	0
hypothetical protein	Pgjcvi_00784	PG JCVI SC001	hypothetical protein	PG W83	PG1002	3, 37	94.3	74.7	1.30E-12
hypothetical protein	Pgjcvi_00784	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0923	3, 54	82.7	87.8	1.40E-16
hypothetical protein	Pgjcvi_00785	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1351	12, 94	96.4	153.3	4.10E-36
hypothetical protein	Pgjcvi_00785	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0924	1, 83	94	151.4	1.60E-35
hypothetical protein	Pgjcvi_00785	PG JCVI SC001	hypothetical protein	PG W83	PG1002	56, 128	83.1	125.2	1.20E-27
Nitroreductase family.	Pgjcvi_00786	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1350	1, 330	98.2	653.7	0
Nitroreductase family.	Pgjcvi_00786	PG JCVI SC001	hypothetical protein	PG W83	PG1003	1, 330	98.2	653.3	0
Nitroreductase family.	Pgjcvi_00786	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0925	1, 330	97.3	649	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_00787	PG JCVI SC001	putative dipeptidyl anminopeptidase	PG TDC60	PGTDC60_0926	1, 744	99.9	1501.9	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_00787	PG JCVI SC001	probable dipeptidyl anminopeptidase	PG ATCC 33277	PGN_1349	1, 759	99.7	1526.9	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_00787	PG JCVI SC001	prolyl oligopeptidase family protein	PG W83	PG1004	1, 759	99.7	1527.3	0
Protein of unknown function (DUF2807).	Pgjcvi_00788	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0927	1, 246	100	479.2	0
Protein of unknown function (DUF2807).	Pgjcvi_00788	PG JCVI SC001	lipoprotein, putative	PG W83	PG1005	1, 246	99.6	478.8	0
Protein of unknown function (DUF2807).	Pgjcvi_00788	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1348	1, 246	98.8	476.1	0
hypothetical protein	Pgjcvi_00789	PG JCVI SC001	putative TonB-dependent receptor exported protein	PG ATCC 33277	PGN_1347	750, 834	100	172.2	8.80E-42
hypothetical protein	Pgjcvi_00789	PG JCVI SC001	putative TonB-dependent receptor exported protein	PG TDC60	PGTDC60_0928	732, 816	100	172.2	8.80E-42
hypothetical protein	Pgjcvi_00789	PG JCVI SC001	hypothetical protein	PG W83	PG1006	810, 894	98.8	171	2.00E-41
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00790	PG JCVI SC001	hypothetical protein	PG W83	PG1006	61, 808	98.9	1500	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00790	PG JCVI SC001	putative TonB-dependent receptor exported protein	PG TDC60	PGTDC60_0928	1, 730	98.8	1469.5	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00790	PG JCVI SC001	putative TonB-dependent receptor exported protein	PG ATCC 33277	PGN_1347	1, 748	98.5	1496.5	0
Predicted transcriptional regulators	Pgjcvi_00792	PG JCVI SC001	transcriptional regulator, GntR family	PG W83	PG1007	1, 123	100	238.4	0
Predicted transcriptional regulators	Pgjcvi_00792	PG JCVI SC001	putative transcriptional regulator	PG TDC60	PGTDC60_0930	1, 123	99.2	236.9	0
Predicted transcriptional regulators	Pgjcvi_00792	PG JCVI SC001	putative transcriptional regulator	PG ATCC 33277	PGN_1346	1, 123	98.4	235.7	0
hypothetical protein	Pgjcvi_00793	PG JCVI SC001	hypothetical protein	PG W83	PG1008	1, 252	100	499.2	0
hypothetical protein	Pgjcvi_00793	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1345	1, 252	99.2	496.1	0
hypothetical protein	Pgjcvi_00793	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0931	1, 252	99.2	496.1	0
hypothetical protein	Pgjcvi_00794	PG JCVI SC001	hypothetical protein	PG W83	PG1009	1, 284	99.3	551.2	0
hypothetical protein	Pgjcvi_00794	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0932	1, 284	99.3	551.2	0
hypothetical protein	Pgjcvi_00794	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1344	1, 284	98.9	550.8	0
ABC-type multidrug transport system, ATPase component	Pgjcvi_00795	PG JCVI SC001	probable ABC transporter ATP-binding protein	PG ATCC 33277	PGN_1343	1, 275	98.9	537.3	0
ABC-type multidrug transport system, ATPase component	Pgjcvi_00795	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG1010	1, 275	98.9	537.3	0
ABC-type multidrug transport system, ATPase component	Pgjcvi_00795	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_0933	1, 275	98.9	535.8	0
tRNA-N(6)-(isopentenyl)adenosine-37 thiotransferase enzyme MiaB	Pgjcvi_00797	PG JCVI SC001	tRNA-i(6)A37 modification enzyme MiaB	PG W83	PG1012	1, 463	99.4	915.2	0
tRNA-N(6)-(isopentenyl)adenosine-37 thiotransferase enzyme MiaB	Pgjcvi_00797	PG JCVI SC001	putative SAM/TRAM family methylase protein	PG ATCC 33277	PGN_1342	1, 463	98.9	908.7	0
tRNA-N(6)-(isopentenyl)adenosine-37 thiotransferase enzyme MiaB	Pgjcvi_00797	PG JCVI SC001	(dimethylallyl)adenosine tRNA methylthiotransferase	PG TDC60	PGTDC60_0934	1, 463	98.9	912.5	0
succinate CoA transferases	Pgjcvi_00798	PG JCVI SC001	putative CoA transferase	PG ATCC 33277	PGN_1341	1, 498	100	1003.4	0
succinate CoA transferases	Pgjcvi_00798	PG JCVI SC001	acetyl-CoA hydrolase/transferase family protein	PG TDC60	PGTDC60_0935	1, 498	100	1003.4	0
succinate CoA transferases	Pgjcvi_00798	PG JCVI SC001	acetyl-CoA hydrolase/transferase family protein	PG W83	PG1013	1, 498	99.8	1001.1	0
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1340	1, 463	94.8	904.8	0
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0936	1, 443	66.3	601.7	0
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	TPR domain protein	PG W83	PG1014	6, 460	65.9	615.9	0
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1340	685, 777	65.6	133.3	2.60E-29
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	TPR domain protein	PG W83	PG1014	446, 565	54.8	134.8	9.10E-30
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0936	429, 548	54	133.7	2.00E-29
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1340	764, 883	53.2	125.2	7.20E-27
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1340	434, 568	51.1	133.7	2.00E-29
hypothetical protein	Pgjcvi_00799	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1340	549, 673	50.4	123.2	2.70E-26
Tfp pilus assembly protein PilF	Pgjcvi_00800	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1340	622, 987	80.9	611.3	0
Tfp pilus assembly protein PilF	Pgjcvi_00800	PG JCVI SC001	TPR domain protein	PG W83	PG1014	367, 669	79.2	492.3	0
Tfp pilus assembly protein PilF	Pgjcvi_00800	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0936	350, 652	78.5	493	0
Tfp pilus assembly protein PilF	Pgjcvi_00800	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1340	283, 558	37.6	151	9.10E-35
hypothetical protein	Pgjcvi_00801	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1339	1, 46	93.5	97.4	1.50E-19
hypothetical protein	Pgjcvi_00801	PG JCVI SC001	hypothetical protein	PG W83	PG1015	1, 47	91.5	97.8	1.20E-19
hypothetical protein	Pgjcvi_00801	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0937	1, 47	91.5	98.6	6.90E-20
pyruvate, phosphate dikinase	Pgjcvi_00802	PG JCVI SC001	pyruvate phosphate dikinase	PG TDC60	PGTDC60_0938	1, 908	99.9	1804.6	0
pyruvate, phosphate dikinase	Pgjcvi_00802	PG JCVI SC001	pyruvate phosphate dikinase	PG W83	PG1017	1, 908	99.7	1801.2	0

pyruvate, phosphate dikinase	Pgjcvi_00802	PG JCVI SC001	pyruvate phosphate dikinase	PG ATCC 33277	PGN_1338	1, 908	99.4	1798.1	0
hypothetical protein	Pgjcvi_00803	PG JCVI SC001	lipoprotein, putative	PG W83	PG1019	1, 393	99.7	786.2	0
hypothetical protein	Pgjcvi_00803	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0940	1, 378	99.5	758.8	0
hypothetical protein	Pgjcvi_00803	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1336	1, 393	99.2	784.6	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00804	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0941	1, 936	99.5	1885.2	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00804	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1335	1, 936	99.4	1881.3	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_00804	PG JCVI SC001	hypothetical protein	PG W83	PG1020	1, 936	99.1	1880.1	0
hypothetical protein	Pgjcvi_00805	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0942	1, 547	98.7	1104	0
hypothetical protein	Pgjcvi_00805	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1334	1, 493	98.4	996.5	0
hypothetical protein	Pgjcvi_00805	PG JCVI SC001	hypothetical protein	PG W83	PG1022	1, 493	98.4	995.7	0
Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	Pgjcvi_00806	PG JCVI SC001	probable para-aminobenzoate synthase component I	PG ATCC 33277	PGN_1333	1, 199	99	397.1	0
Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	Pgjcvi_00806	PG JCVI SC001	putative para-aminobenzoate synthase componentI	PG TDC60	PGTDC60_0943	1, 199	98.5	394	0
Anthranilate/para-aminobenzoate synthases component I	Pgjcvi_00807	PG JCVI SC001	putative para-aminobenzoate synthase component I	PG ATCC 33277	PGN_1332	1, 325	98.8	641.3	0
Anthranilate/para-aminobenzoate synthases component I	Pgjcvi_00807	PG JCVI SC001	para-aminobenzoate synthase component I	PG TDC60	PGTDC60_0944	1, 298	98.3	585.5	0
Protein of unknown function (DUF1661).	Pgjcvi_00808	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0945	1, 70	95.7	142.1	1.20E-32
Protein of unknown function (DUF1661).	Pgjcvi_00808	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1331	2, 102	95	200.3	0
Protein of unknown function (DUF1661).	Pgjcvi_00808	PG JCVI SC001	hypothetical protein	PG W83	PG1655	9, 63	58.2	62.8	9.10E-09
Predicted ATPase	Pgjcvi_00809	PG JCVI SC001	hypothetical protein	PG W83	PG1025	1, 362	100	731.5	0
hypothetical protein	Pgjcvi_00810	PG JCVI SC001	hypothetical protein	PG W83	PG1026	10, 243	100	469.9	0
hypothetical protein	Pgjcvi_00811	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_1323	1, 564	99.8	1095.1	0
hypothetical protein	Pgjcvi_00811	PG JCVI SC001	TPR domain protein	PG W83	PG1028	1, 448	99.8	867.5	0
hypothetical protein	Pgjcvi_00811	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_0952	1, 565	99.6	1094.3	0
Por secretion system C-terminal sorting domain	Pgjcvi_00812	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0954	1, 446	99.1	893.3	0
Por secretion system C-terminal sorting domain	Pgjcvi_00812	PG JCVI SC001	hypothetical protein	PG W83	PG1030	1, 446	98.4	887.5	0
Por secretion system C-terminal sorting domain	Pgjcvi_00812	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1321	1, 446	98.2	890.2	0
ABC-type transport system involved in resistance to organic solvents, permease component	Pgjcvi_00814	PG JCVI SC001	hypothetical protein	PG W83	PG1033	1, 248	100	477.6	0
ABC-type transport system involved in resistance to organic solvents, permease component	Pgjcvi_00814	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0955	1, 248	100	477.6	0
ABC-type transport system involved in resistance to organic solvents, permease component	Pgjcvi_00814	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1320	1, 212	99.5	411.8	0
ABC-type transport system involved in resistance to organic solvents, ATPase component	Pgjcvi_00815	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_1318	1, 244	99.6	481.1	0
ABC-type transport system involved in resistance to organic solvents, ATPase component	Pgjcvi_00815	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG1034	1, 244	99.2	479.6	0
ABC-type transport system involved in resistance to organic solvents, ATPase component	Pgjcvi_00815	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_0956	1, 244	99.2	478	0
gliding motility-associated C-terminal domain	Pgjcvi_00816	PG JCVI SC001	hypothetical protein	PG W83	PG1035	40, 496	99.6	924.5	0
gliding motility-associated C-terminal domain	Pgjcvi_00816	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0957	1, 457	99.6	925.6	0
gliding motility-associated C-terminal domain	Pgjcvi_00816	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1317	40, 496	98.7	919.8	0
excinuclease ABC, A subunit	Pgjcvi_00817	PG JCVI SC001	excinuclease ABC, A subunit	PG TDC60	PGTDC60_0958	1, 967	99.9	1925.2	0
excinuclease ABC, A subunit	Pgjcvi_00817	PG JCVI SC001	excinuclease ABC, A subunit	PG W83	PG1036	1, 967	99.5	1919.1	0
excinuclease ABC, A subunit	Pgjcvi_00817	PG JCVI SC001	excinuclease ABC A subunit	PG ATCC 33277	PGN_1316	1, 967	99.3	1913.3	0
hypothetical protein	Pgjcvi_00818	PG JCVI SC001	hypothetical protein	PG W83	PG1037	1, 459	100	945.7	0
hypothetical protein	Pgjcvi_00818	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0959	1, 459	100	945.7	0
hypothetical protein	Pgjcvi_00818	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1315	1, 459	99.8	944.1	0
Superfamily I DNA and RNA helicases	Pgjcvi_00819	PG JCVI SC001	ATP-dependent DNA helicase UvrD/PcrA/Rep Family	PG W83	PG1038	1, 765	99.7	1496.9	0
Superfamily I DNA and RNA helicases	Pgjcvi_00819	PG JCVI SC001	ATP-dependent DNA helicase UvrD/PcrA/Rep family	PG TDC60	PGTDC60_0960	1, 765	99.6	1496.1	0
Superfamily I DNA and RNA helicases	Pgjcvi_00819	PG JCVI SC001	ATP-dependent DNA helicase	PG ATCC 33277	PGN_1314	1, 765	99.1	1486.1	0
Predicted membrane-associated, metal-dependent hydrolase	Pgjcvi_00820	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1313	1, 575	99.7	1150.6	0
Predicted membrane-associated, metal-dependent hydrolase	Pgjcvi_00820	PG JCVI SC001	integral membrane protein	PG TDC60	PGTDC60_0961	1, 345	99.7	693.7	0
Predicted membrane-associated, metal-dependent hydrolase	Pgjcvi_00820	PG JCVI SC001	integral membrane protein	PG W83	PG1039	1, 575	99.3	1147.5	0
Arginine repressor	Pgjcvi_00821	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG1040	1, 154	95.5	282	0
Arginine repressor	Pgjcvi_00821	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_0962	1, 154	95.5	282.3	0
Arginine repressor	Pgjcvi_00821	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_1312	1, 154	94.8	280.4	0
K+-dependent Na+/Ca+ exchanger related-protein	Pgjcvi_00822	PG JCVI SC001	putative K+-dependent Na+/Ca+ exchanger related-protein	PG ATCC 33277	PGN_1311	1, 317	97.2	579.7	0
K+-dependent Na+/Ca+ exchanger related-protein	Pgjcvi_00822	PG JCVI SC001	K+-dependent Na+/Ca+ exchanger related-protein	PG W83	PG1041	1, 317	97.2	579.7	0
K+-dependent Na+/Ca+ exchanger related-protein	Pgjcvi_00822	PG JCVI SC001	K+-dependent Na+/Ca+ exchanger related-protein	PG TDC60	PGTDC60_0963	1, 317	97.2	579.7	0
Glycosyltransferase	Pgjcvi_00823	PG JCVI SC001	glycogen synthase, putative	PG W83	PG1042	1, 548	98.2	1109.4	0
Glycosyltransferase	Pgjcvi_00823	PG JCVI SC001	glycogen synthase	PG ATCC 33277	PGN_1310	1, 548	97.6	1105.5	0
Glycosyltransferase	Pgjcvi_00823	PG JCVI SC001	glycogen synthase	PG TDC60	PGTDC60_0964	1, 548	97.4	1100.5	0
ferrous iron transporter FeoB	Pgjcvi_00824	PG JCVI SC001	ferrous iron transport protein B	PG ATCC 33277	PGN_1309	25, 724	99.6	1388.2	0
ferrous iron transporter FeoB	Pgjcvi_00824	PG JCVI SC001	ferrous iron transport protein B	PG W83	PG1043	26, 725	99.6	1388.2	0
ferrous iron transporter FeoB	Pgjcvi_00824	PG JCVI SC001	ferrous iron transport protein B	PG TDC60	PGTDC60_0965	1, 700	99.6	1384.8	0
Mn-dependent transcriptional regulator	Pgjcvi_00825	PG JCVI SC001	iron dependent repressor	PG TDC60	PGTDC60_0966	1, 310	99.4	621.7	0
Mn-dependent transcriptional regulator	Pgjcvi_00825	PG JCVI SC001	iron dependent repressor, putative	PG W83	PG1044	1, 310	99	619.8	0
Mn-dependent transcriptional regulator	Pgjcvi_00825	PG JCVI SC001	probable iron dependent repressor	PG ATCC 33277	PGN_1308	1, 310	98.7	614.8	0
N-acetylmuramoyl-L-alanine amidase	Pgjcvi_00827	PG JCVI SC001	putative N-acetylmuramoyl-L-alanine amidase	PG ATCC 33277	PGN_1305	1, 396	99.7	782.3	0
N-acetylmuramoyl-L-alanine amidase	Pgjcvi_00827	PG JCVI SC001	N-acetylmuramoyl-L-alanine amidase, family 3	PG W83	PG1048	1, 396	99.7	783.1	0
N-acetylmuramoyl-L-alanine amidase	Pgjcvi_00827	PG JCVI SC001	N-acetylmuramoyl-L-alanine amidase	PG TDC60	PGTDC60_0969	1, 383	99.7	753.1	0
ABC-type transport system involved in resistance to organic solvents, periplasmic component	Pgjcvi_00828	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1304	1, 292	100	562.4	0

ABC-type transport system involved in resistance to organic solvents, periplasmic component	Pgjcvi_00828	PG JCVI SC001	hypothetical protein	PG W83	PG1049	1, 292	100	562.4	0
ABC-type transport system involved in resistance to organic solvents, periplasmic component	Pgjcvi_00828	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0970	1, 292	99.7	560.8	0
hypothetical protein	Pgjcvi_00829	PG JCVI SC001	hypothetical protein	PG W83	PG1050	14, 298	98.6	548.1	0
hypothetical protein	Pgjcvi_00829	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0971	1, 285	97.9	543.9	0
hypothetical protein	Pgjcvi_00829	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1303	11, 295	97.5	544.3	0
O-Antigen ligase.	Pgjcvi_00830	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0972	1, 455	96.7	876.7	0
O-Antigen ligase.	Pgjcvi_00830	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1302	1, 471	96.4	902.1	0
O-Antigen ligase.	Pgjcvi_00830	PG JCVI SC001	hypothetical protein	PG W83	PG1051	1, 471	96.4	901	0
Predicted transcriptional regulators	Pgjcvi_00831	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG1052	1, 118	100	241.1	0
Predicted transcriptional regulators	Pgjcvi_00831	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_0973	1, 118	99.2	240	0
Predicted transcriptional regulators	Pgjcvi_00831	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_1301	1, 118	98.3	235.7	0
Cyclic nucleotide-binding domain./Bacterial regulatory proteins, gntR family.	Pgjcvi_00832	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_0974	1, 228	99.1	438.7	0
Cyclic nucleotide-binding domain./Bacterial regulatory proteins, gntR family.	Pgjcvi_00832	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_1300	1, 228	98.7	434.5	0
Cyclic nucleotide-binding domain./Bacterial regulatory proteins, gntR family.	Pgjcvi_00832	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG1053	1, 228	98.7	434.5	0
Calpain family cysteine protease.	Pgjcvi_00833	PG JCVI SC001	thiol protease	PG W83	PG1055	1, 481	85.9	820.1	0
Calpain family cysteine protease.	Pgjcvi_00833	PG JCVI SC001	thiol protease	PG TDC60	PGTDC60_0975	1, 251	80.9	416	0
6-pyruvoyl-tetrahydropterin synthase	Pgjcvi_00834	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1298	1, 139	98.6	294.7	0
6-pyruvoyl-tetrahydropterin synthase	Pgjcvi_00834	PG JCVI SC001	hypothetical protein	PG W83	PG1056	1, 139	98.6	294.7	0
6-pyruvoyl-tetrahydropterin synthase	Pgjcvi_00834	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0978	1, 139	98.6	294.7	0
Organic radical activating enzymes	Pgjcvi_00835	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1297	1, 197	99	411.4	0
Organic radical activating enzymes	Pgjcvi_00835	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0979	1, 197	98.5	405.2	0
Organic radical activating enzymes	Pgjcvi_00835	PG JCVI SC001	hypothetical protein	PG W83	PG1057	1, 197	98	403.7	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00836	PG JCVI SC001	OmpA family protein	PG W83	PG1058	1, 672	99.7	1362.1	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00836	PG JCVI SC001	putative OmpA family protein	PG TDC60	PGTDC60_0980	1, 672	99.7	1364.7	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_00836	PG JCVI SC001	putative OmpA family protein	PG ATCC 33277	PGN_1296	1, 672	99.6	1359.7	0
Transposase and inactivated derivatives	Pgjcvi_00837	PG JCVI SC001	ISPg5, transposase Orf2	PG W83	PG0591	51, 312	98.5	533.9	0
Transposase and inactivated derivatives	Pgjcvi_00837	PG JCVI SC001	partial transposase Orf2 in ISPg5	PG ATCC 33277	PGN_1063	21, 63	69.8	66.6	1.60E-09
Uncharacterized protein, possibly involved in aromatic compounds catabolism	Pgjcvi_00838	PG JCVI SC001	probable thioesterase superfamily protein	PG ATCC 33277	PGN_1271	1, 157	100	330.1	0
Uncharacterized protein, possibly involved in aromatic compounds catabolism	Pgjcvi_00838	PG JCVI SC001	thioesterase family protein	PG W83	PG1174	9, 165	100	330.1	0
Uncharacterized protein, possibly involved in aromatic compounds catabolism	Pgjcvi_00838	PG JCVI SC001	thioesterase family protein	PG TDC60	PGTDC60_0981	1, 157	100	330.1	0
Uncharacterized conserved protein	Pgjcvi_00839	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1270	1, 194	100	391.3	0
Uncharacterized conserved protein	Pgjcvi_00839	PG JCVI SC001	YkgG family protein	PG W83	PG1173	11, 204	99.5	391	0
Uncharacterized conserved protein	Pgjcvi_00839	PG JCVI SC001	YkgG family protein	PG TDC60	PGTDC60_0982	1, 194	99.5	389	0
Uncharacterized conserved protein containing a ferredoxin-like domain	Pgjcvi_00840	PG JCVI SC001	iron-sulfur cluster binding protein, putative	PG W83	PG1172	1, 428	99.8	886.7	0
Uncharacterized conserved protein containing a ferredoxin-like domain	Pgjcvi_00840	PG JCVI SC001	iron-sulfur cluster binding protein	PG TDC60	PGTDC60_0983	1, 455	99.8	943.7	0
Uncharacterized conserved protein containing a ferredoxin-like domain	Pgjcvi_00840	PG JCVI SC001	putative electron transport protein	PG ATCC 33277	PGN_1269	1, 455	99.6	940.6	0
Fe-S oxidoreductase	Pgjcvi_00841	PG JCVI SC001	oxidoreductase, putative	PG W83	PG1171	1, 246	100	510	0
Fe-S oxidoreductase	Pgjcvi_00841	PG JCVI SC001	putative oxidoreductase	PG TDC60	PGTDC60_0984	1, 273	99.6	560.1	0
Fe-S oxidoreductase	Pgjcvi_00841	PG JCVI SC001	putative oxidoreductase	PG ATCC 33277	PGN_1268	1, 273	99.3	556.2	0
phosphoserine phosphatase SerB	Pgjcvi_00842	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1267	1, 290	99	561.6	0
phosphoserine phosphatase SerB	Pgjcvi_00842	PG JCVI SC001	SerB family protein	PG W83	PG1170	1, 290	98.6	557	0
phosphoserine phosphatase SerB	Pgjcvi_00842	PG JCVI SC001	SerB family protein	PG TDC60	PGTDC60_1040	1, 290	97.2	552	0
hypothetical protein	Pgjcvi_00843	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1266	1, 42	95.2	85.9	4.10E-16
hypothetical protein	Pgjcvi_00843	PG JCVI SC001	hypothetical protein	PG W83	PG1169	1, 32	93.8	65.5	5.80E-10
Site-specific recombinase XerD	Pgjcvi_00844	PG JCVI SC001	putative bacteriophage integrase	PG TDC60	PGTDC60_0986	104, 411	100	627.5	0
Site-specific recombinase XerD	Pgjcvi_00844	PG JCVI SC001	putative bacteriophage integrase	PG ATCC 33277	PGN_0094	104, 411	92.9	586.6	0
Site-specific recombinase XerD	Pgjcvi_00844	PG JCVI SC001	integrase	PG W83	PG1113	106, 398	41.9	231.5	0
hypothetical protein	Pgjcvi_00845	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0987	1, 120	100	246.9	0
hypothetical protein	Pgjcvi_00845	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0093	1, 121	86	216.9	0
hypothetical protein	Pgjcvi_00845	PG JCVI SC001	lipoprotein, putative	PG W83	PG0821	1, 120	64.2	156.4	7.10E-37
Predicted site-specific integrase-resolvase	Pgjcvi_00846	PG JCVI SC001	DNA binding domain, excisionase family	PG TDC60	PGTDC60_0988	1, 100	100	206.8	0
Predicted site-specific integrase-resolvase	Pgjcvi_00846	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0092	4, 103	91	190.3	0
Predicted site-specific integrase-resolvase	Pgjcvi_00846	PG JCVI SC001	hypothetical protein	PG W83	PG0546	15, 64	54	60.5	4.40E-08
hypothetical protein	Pgjcvi_00847	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0989	1, 92	100	189.1	0
hypothetical protein	Pgjcvi_00847	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0091	1, 92	95.7	180.6	2.70E-44
hypothetical protein	Pgjcvi_00848	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0990	1, 117	100	234.6	0
hypothetical protein	Pgjcvi_00848	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0090	1, 117	88	213.4	0
Helicase conserved C-terminal domain./SNF2 family N-terminal domain.	Pgjcvi_00850	PG JCVI SC001	DNA methylase	PG TDC60	PGTDC60_0992	1113, 1830	100	1408.3	0
Helicase conserved C-terminal domain./SNF2 family N-terminal domain.	Pgjcvi_00850	PG JCVI SC001	putative DNA methylase	PG ATCC 33277	PGN_0086	1111, 1828	91.5	1292.7	0
Helicase conserved C-terminal domain./SNF2 family N-terminal domain.	Pgjcvi_00850	PG JCVI SC001	hypothetical protein	PG W83	PG1500	70, 715	69.9	902.5	0
N-6 DNA Methylase.	Pgjcvi_00851	PG JCVI SC001	DNA methylase	PG TDC60	PGTDC60_0992	1, 1111	94.5	2093.5	0
N-6 DNA Methylase.	Pgjcvi_00851	PG JCVI SC001	putative DNA methylase	PG ATCC 33277	PGN_0086	1, 1109	94.3	2097.8	0
N-6 DNA Methylase.	Pgjcvi_00851	PG JCVI SC001	hypothetical protein	PG W83	PG1500	8, 67	63.3	75.5	1.50E-11
Domain of unknown function (DUF1896).	Pgjcvi_00852	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0993	1, 143	97.2	275.8	0
Domain of unknown function (DUF1896).	Pgjcvi_00852	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0085	1, 143	94.4	269.2	0
Domain of unknown function (DUF1896).	Pgjcvi_00852	PG JCVI SC001	hypothetical protein	PG W83	PG0816	10, 145	40.7	100.1	7.20E-20
Topoisomerase IA	Pgjcvi_00853	PG JCVI SC001	DNA topoisomerase III	PG TDC60	PGTDC60_0994	1, 709	96.8	1370.9	0
Topoisomerase IA	Pgjcvi_00853	PG JCVI SC001	DNA topoisomerase I	PG ATCC 33277	PGN_0084	1, 709	92.8	1334.3	0
Topoisomerase IA	Pgjcvi_00853	PG JCVI SC001	DNA topoisomerase III	PG W83	PG1495	1, 695	48.8	646.7	0
hypothetical protein	Pgjcvi_00854	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0995	300, 464	98.8	328.2	0

hypothetical protein	Pgjcvi_00854	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0083	300, 464	95.2	316.6	0
hypothetical protein	Pgjcvi_00854	PG JCVI SC001	hypothetical protein	PG W83	PG1494	271, 437	42	125.9	1.40E-27
hypothetical protein	Pgjcvi_00855	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0995	1, 331	92.4	602.4	0
hypothetical protein	Pgjcvi_00855	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0083	1, 331	89.1	590.9	0
hypothetical protein	Pgjcvi_00855	PG JCVI SC001	hypothetical protein	PG W83	PG1494	2, 288	45.9	258.8	0
Transcriptional regulator	Pgjcvi_00856	PG JCVI SC001	transcriptional regulator, TetR family	PG TDC60	PGTDC60_0996	1, 202	99.5	403.3	0
3-oxoacyl-[acyl-carrier-protein] synthase III	Pgjcvi_00857	PG JCVI SC001	3-oxoacyl-(acyl-carrier-protein) synthase III	PG TDC60	PGTDC60_0997	1, 385	100	773.1	0
Arylsulfatase regulator (Fe-S oxidoreductase)	Pgjcvi_00859	PG JCVI SC001	radical SAM domain protein	PG TDC60	PGTDC60_0998	1, 432	100	901	0
hypothetical protein	Pgjcvi_00860	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0999	1, 761	100	1533.1	0
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_00861	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1000	1, 727	100	1436.8	0
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_00861	PG JCVI SC001	ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0949	8, 569	26.6	179.9	3.60E-43
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_00861	PG JCVI SC001	ABC transporter, ATP-binding protein, putative	PG W83	PG1176	17, 558	26.4	179.5	4.70E-43
hypothetical protein	Pgjcvi_00862	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1001	1, 164	100	321.2	0
hypothetical protein	Pgjcvi_00863	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1002	1, 84	100	164.5	1.80E-39
RteC protein.	Pgjcvi_00864	PG JCVI SC001	RteC protein	PG TDC60	PGTDC60_1003	1, 119	99.2	241.1	0
RteC protein.	Pgjcvi_00864	PG JCVI SC001	probable tetracycline resistance element mobilization regulatory protein RteC	PG ATCC 33277	PGN_0080	12, 108	72.2	161.4	2.20E-38
B-box zinc finger.	Pgjcvi_00865	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1004	1, 67	100	141.4	2.90E-32
B-box zinc finger.	Pgjcvi_00865	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0078	1, 70	82.9	130.6	5.10E-29
Type IV secretory pathway, VirD4 components	Pgjcvi_00866	PG JCVI SC001	TraG family protein	PG TDC60	PGTDC60_1006	207, 509	96.8	619.4	0
Type IV secretory pathway, VirD4 components	Pgjcvi_00866	PG JCVI SC001	putative mobilization protein TraG family	PG ATCC 33277	PGN_0076	206, 508	96.5	619	0
Type IV secretory pathway, VirD4 components	Pgjcvi_00866	PG JCVI SC001	TraG family protein	PG W83	PG1490	206, 507	83.5	539.3	0
hypothetical protein	Pgjcvi_00867	PG JCVI SC001	putative mobilization protein TraG family	PG ATCC 33277	PGN_0076	2, 167	95.8	328.2	0
hypothetical protein	Pgjcvi_00867	PG JCVI SC001	TraG family protein	PG TDC60	PGTDC60_1006	1, 168	95.2	326.6	0
hypothetical protein	Pgjcvi_00867	PG JCVI SC001	TraG family protein	PG W83	PG1490	2, 167	59	207.6	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_00868	PG JCVI SC001	mobilization protein	PG TDC60	PGTDC60_1007	19, 372	99.2	715.3	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_00868	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0075	19, 370	79.5	573.9	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_00868	PG JCVI SC001	hypothetical protein	PG W83	PG1489	21, 346	41.8	261.5	0
hypothetical protein	Pgjcvi_00869	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1008	6, 137	94.7	244.2	0
hypothetical protein	Pgjcvi_00869	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0074	4, 137	79.9	204.1	0
hypothetical protein	Pgjcvi_00869	PG JCVI SC001	hypothetical protein	PG W83	PG0829	16, 157	69.7	189.5	0
ATPases involved in chromosome partitioning	Pgjcvi_00871	PG JCVI SC001	putative conserved protein found in conjugate transposon TraA	PG ATCC 33277	PGN_0073	1, 260	97.7	506.1	0
ATPases involved in chromosome partitioning	Pgjcvi_00871	PG JCVI SC001	putative conjugate transposon protein TraA	PG TDC60	PGTDC60_1010	1, 260	95.8	498	0
ATPases involved in chromosome partitioning	Pgjcvi_00871	PG JCVI SC001	conjugative transposon protein TraA	PG W83	PG1486	7, 266	35.4	177.2	8.40E-43
Protein of unknown function (DUF3408).	Pgjcvi_00872	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1011	31, 142	95.5	211.8	0
Protein of unknown function (DUF3408).	Pgjcvi_00872	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0072	31, 143	91.2	200.7	0
Protein of unknown function (DUF3408).	Pgjcvi_00872	PG JCVI SC001	hypothetical protein	PG W83	PG1442	37, 142	56.4	108.6	1.60E-22
Protein of unknown function (DUF3408).	Pgjcvi_00873	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0071	1, 117	93.2	215.7	0
Protein of unknown function (DUF3408).	Pgjcvi_00873	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1012	1, 117	91.5	210.3	0
hypothetical protein	Pgjcvi_00874	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0070	1, 196	95.9	362.5	0
hypothetical protein	Pgjcvi_00874	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1013	1, 197	88.8	335.5	0
CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_00875	PG JCVI SC001	probable conserved protein found in conjugate transposon TraA	PG ATCC 33277	PGN_0069	1, 246	92.7	468.4	0
CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_00875	PG JCVI SC001	conjugative transposon protein TraA	PG TDC60	PGTDC60_1014	1, 246	89.8	449.1	0
CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_00875	PG JCVI SC001	conjugative transposon protein TraA	PG W83	PG1486	10, 238	26.5	79.7	1.70E-13
hypothetical protein	Pgjcvi_00876	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0068	1, 190	84.9	313.2	0
hypothetical protein	Pgjcvi_00876	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1015	1, 190	81.8	299.3	0
hypothetical protein	Pgjcvi_00877	PG JCVI SC001	conjugative transposon protein TraE	PG TDC60	PGTDC60_1016	1, 99	97	187.6	0
hypothetical protein	Pgjcvi_00877	PG JCVI SC001	probable conserved transmembrane protein found in conjugate transposon TraE	PG ATCC 33277	PGN_0067	1, 99	96	189.9	0
hypothetical protein	Pgjcvi_00877	PG JCVI SC001	conjugative transposon protein TraE	PG W83	PG1483	3, 100	81.6	161	2.40E-38
hypothetical protein	Pgjcvi_00878	PG JCVI SC001	probable conserved transmembrane protein found in conjugate transposon TraF	PG ATCC 33277	PGN_0066	1, 125	95.2	244.6	0
hypothetical protein	Pgjcvi_00878	PG JCVI SC001	conjugative transposon protein TraF	PG TDC60	PGTDC60_1017	1, 125	84	216.9	0
hypothetical protein	Pgjcvi_00878	PG JCVI SC001	conjugative transposon protein TraF	PG W83	PG1482	2, 99	67.3	147.9	2.60E-34
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_00879	PG JCVI SC001	conserved protein found in conjugate transposon TraG	PG ATCC 33277	PGN_0065	1, 828	99.3	1644.8	0
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_00879	PG JCVI SC001	conjugative transposon protein TraG	PG TDC60	PGTDC60_1018	1, 828	95.4	1595.9	0
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_00879	PG JCVI SC001	conjugative transposon protein TraG	PG W83	PG1481	1, 829	69.8	1203.7	0
hypothetical protein	Pgjcvi_00880	PG JCVI SC001	putative conserved protein found in conjugate transposon TraI	PG ATCC 33277	PGN_0064	9, 209	100	402.9	0
hypothetical protein	Pgjcvi_00880	PG JCVI SC001	conjugative transposon protein TraI	PG TDC60	PGTDC60_1019	3, 203	97.5	394	0
hypothetical protein	Pgjcvi_00880	PG JCVI SC001	conjugative transposon protein TraI	PG W83	PG1480	9, 209	60.2	246.5	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_00881	PG JCVI SC001	conjugative transposon protein TraJ	PG TDC60	PGTDC60_1020	1, 363	99.4	723	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_00881	PG JCVI SC001	conserved transmembrane protein found in conjugate transposon TraJ	PG ATCC 33277	PGN_0063	1, 358	93	672.9	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_00881	PG JCVI SC001	conjugative transposon protein TraJ	PG W83	PG1479	2, 346	56.4	386.7	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_00882	PG JCVI SC001	conjugative transposon protein TraK	PG TDC60	PGTDC60_1021	1, 207	100	412.5	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_00882	PG JCVI SC001	putative conserved protein found in conjugate transposon TraK	PG ATCC 33277	PGN_0062	1, 207	97.1	401.7	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_00882	PG JCVI SC001	conjugative transposon protein TraK	PG W83	PG1478	1, 207	66.7	301.2	0
hypothetical protein	Pgjcvi_00883	PG JCVI SC001	putative conjugative transposon protein TraL	PG TDC60	PGTDC60_1022	9, 110	100	208.8	0
hypothetical protein	Pgjcvi_00883	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0061	9, 110	73.5	153.3	5.10E-36
Bacteroides conjugative transposon TraM protein	Pgjcvi_00884	PG JCVI SC001	conjugative transposon protein TraM	PG TDC60	PGTDC60_1023	3, 455	99.1	867.8	0
Bacteroides conjugative transposon TraM protein	Pgjcvi_00884	PG JCVI SC001	conserved protein found in conjugate transposon TraM	PG ATCC 33277	PGN_0060	1, 455	84.4	746.1	0
Bacteroides conjugative transposon TraM protein	Pgjcvi_00884	PG JCVI SC001	conjugative transposon protein TraM	PG W83	PG1476	31, 452	36.4	272.3	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_00885	PG JCVI SC001	conserved protein found in conjugate transposon TraN	PG ATCC 33277	PGN_0059	1, 306	99.7	606.3	0

Bacteroides conjugative transposon TraN protein	Pgjcvi_00885	PG JCVI SC001	conjugative transposon protein TraN	PG TDC60	PGTDC60_1024	1, 306	97.1	592.8	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_00885	PG JCVI SC001	conjugative transposon protein TraN	PG W83	PG1475	163, 340	53.6	211.8	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_00885	PG JCVI SC001	conjugative transposon protein TraN	PG W83	PG1475	1, 340	44.8	263.5	0
Conjugative transposon protein TraO.	Pgjcvi_00886	PG JCVI SC001	probable conserved protein found in conjugate transposon	PG ATCC 33277	PGN_0058	1, 194	91.8	364.4	0
Conjugative transposon protein TraO.	Pgjcvi_00886	PG JCVI SC001	conjugative transposon protein TraO	PG TDC60	PGTDC60_1025	1, 194	91.2	365.2	0
Conjugative transposon protein TraO.	Pgjcvi_00886	PG JCVI SC001	conjugative transposon protein TraO	PG W83	PG1474	3, 192	33.7	109	2.10E-22
DNA primase (bacterial type)	Pgjcvi_00887	PG JCVI SC001	probable conserved protein found in conjugate transposon TraP	PG ATCC 33277	PGN_0057	1, 278	88.1	510.8	0
DNA primase (bacterial type)	Pgjcvi_00887	PG JCVI SC001	mobilizable transposon, excision protein	PG TDC60	PGTDC60_1026	1, 280	85	487.6	0
DNA primase (bacterial type)	Pgjcvi_00887	PG JCVI SC001	mobilizable transposon, excision protein, putative	PG W83	PG0841	1, 283	38.9	171	6.50E-41
hypothetical protein	Pgjcvi_00888	PG JCVI SC001	conjugative transposon protein TraQ	PG TDC60	PGTDC60_1027	1, 139	91.4	264.2	0
hypothetical protein	Pgjcvi_00888	PG JCVI SC001	probable conserved protein found in conjugate transposon	PG ATCC 33277	PGN_0056	1, 139	89.2	260	0
hypothetical protein	Pgjcvi_00888	PG JCVI SC001	conjugative transposon protein TraQ	PG W83	PG1473	1, 138	49.3	154.8	2.50E-36
Phage-related lysozyme (muraminidase)	Pgjcvi_00889	PG JCVI SC001	putative lysozyme	PG TDC60	PGTDC60_1028	1, 97	100	194.9	0
Phage-related lysozyme (muraminidase)	Pgjcvi_00889	PG JCVI SC001	lysozyme-related protein	PG W83	PG1441	1, 55	89.1	109.4	1.40E-22
Phage-related lysozyme (muraminidase)	Pgjcvi_00889	PG JCVI SC001	probable lysozyme	PG ATCC 33277	PGN_1286	1, 171	85.4	297	0
hypothetical protein	Pgjcvi_00890	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1029	1, 189	100	372.1	0
hypothetical protein	Pgjcvi_00891	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1031	3, 78	100	155.2	1.00E-36
hypothetical protein	Pgjcvi_00891	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0052	1, 76	82.9	129.4	5.90E-29
hypothetical protein	Pgjcvi_00891	PG JCVI SC001	hypothetical protein	PG W83	PG1470	11, 62	46.2	50.1	4.50E-05
hypothetical protein	Pgjcvi_00892	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1032	261, 424	100	333.6	0
hypothetical protein	Pgjcvi_00892	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0050	261, 424	88.4	293.9	0
hypothetical protein	Pgjcvi_00893	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1032	1, 240	99.6	505	0
hypothetical protein	Pgjcvi_00893	PG JCVI SC001	conserved hypothetical protein related to phage	PG ATCC 33277	PGN_1291	1, 240	93.3	481.5	0
Antirestriction protein (ArdA).	Pgjcvi_00894	PG JCVI SC001	putative anti-restriction protein	PG TDC60	PGTDC60_1033	129, 176	100	106.7	2.90E-22
Antirestriction protein (ArdA).	Pgjcvi_00894	PG JCVI SC001	probable anti-restriction protein	PG ATCC 33277	PGN_0049	129, 175	89.4	94.4	1.50E-18
Antirestriction protein (ArdA).	Pgjcvi_00895	PG JCVI SC001	putative anti-restriction protein	PG TDC60	PGTDC60_1033	1, 147	100	310.1	0
Antirestriction protein (ArdA).	Pgjcvi_00895	PG JCVI SC001	probable anti-restriction protein	PG ATCC 33277	PGN_0049	1, 147	93.9	289.3	0
hypothetical protein	Pgjcvi_00896	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1034	1, 137	100	277.3	0
hypothetical protein	Pgjcvi_00896	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0048	1, 138	92.8	256.9	0
hypothetical protein	Pgjcvi_00897	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1035	1, 196	100	424.5	0
hypothetical protein	Pgjcvi_00898	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1036	1, 93	100	193.7	0
hypothetical protein	Pgjcvi_00898	PG JCVI SC001	hypothetical protein	PG W83	PG1463	1, 90	64.4	123.2	5.10E-27
hypothetical protein	Pgjcvi_00898	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0848	1, 90	63.3	121.3	2.00E-26
hypothetical protein	Pgjcvi_00899	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1037	1, 72	100	145.6	7.50E-34
hypothetical protein	Pgjcvi_00899	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0047	1, 72	94.4	139	7.00E-32
hypothetical protein	Pgjcvi_00900	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1038	1, 69	98.6	138.7	8.80E-32
hypothetical protein	Pgjcvi_00900	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0046	20, 88	91.3	129	7.00E-29
cobyrinic acid a,c-diamide synthase	Pgjcvi_00904	PG JCVI SC001	cobyrinic acid a,c-diamide synthase	PG W83	PG1163	1, 439	98.9	891.7	0
cobyrinic acid a,c-diamide synthase	Pgjcvi_00904	PG JCVI SC001	cobyrinic acid a,c-diamide synthase	PG TDC60	PGTDC60_1052	1, 439	98.9	892.1	0
cobyrinic acid a,c-diamide synthase	Pgjcvi_00904	PG JCVI SC001	cobyrinic acid a,c-diamide synthase	PG ATCC 33277	PGN_1262	3, 439	96.3	862.8	0
ATP:cob(I)alamin adenosyltransferase	Pgjcvi_00905	PG JCVI SC001	putative cobalamin adenosyltransferase	PG TDC60	PGTDC60_1053	1, 188	98.9	380.2	0
ATP:cob(I)alamin adenosyltransferase	Pgjcvi_00905	PG JCVI SC001	probable cobalamin adenosyltransferase	PG ATCC 33277	PGN_1261	1, 188	97.9	375.9	0
ATP:cob(I)alamin adenosyltransferase	Pgjcvi_00905	PG JCVI SC001	ATP:cob(I)alamin adenosyltransferase, putative	PG W83	PG1162	1, 188	96.8	372.5	0
cobyric acid synthase CobQ	Pgjcvi_00906	PG JCVI SC001	cobyric acid synthase	PG ATCC 33277	PGN_1260	1, 498	99.8	1000.3	0
cobyric acid synthase CobQ	Pgjcvi_00906	PG JCVI SC001	cobyric acid synthase	PG TDC60	PGTDC60_1054	1, 498	98.8	993.4	0
L-threonine-O-3-phosphate decarboxylase	Pgjcvi_00907	PG JCVI SC001	L-threonine-O-3-phosphate decarboxylase	PG TDC60	PGTDC60_1055	1, 335	98.2	665.2	0
L-threonine-O-3-phosphate decarboxylase	Pgjcvi_00907	PG JCVI SC001	probable histidinol-phosphate aminotransferase	PG ATCC 33277	PGN_1259	1, 335	97.3	660.2	0
L-threonine-O-3-phosphate decarboxylase	Pgjcvi_00907	PG JCVI SC001	L-threonine-O-3-phosphate decarboxylase, putative	PG W83	PG1160	1, 335	97.3	658.3	0
cobalamin biosynthesis protein CobD	Pgjcvi_00908	PG JCVI SC001	cobalamin biosynthesis protein CbiB	PG TDC60	PGTDC60_1056	1, 296	100	579.3	0
cobalamin biosynthesis protein CobD	Pgjcvi_00908	PG JCVI SC001	cobalamin biosynthesis protein	PG ATCC 33277	PGN_1258	1, 326	99.1	636.3	0
cobalamin biosynthesis protein CobD	Pgjcvi_00908	PG JCVI SC001	cobalamin biosynthesis protein CbiB	PG W83	PG1159	1, 336	98.8	654.8	0
16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	Pgjcvi_00909	PG JCVI SC001	S4 domain protein	PG W83	PG1156	1, 150	100	303.1	0
16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	Pgjcvi_00909	PG JCVI SC001	S4 domain-containing protein	PG TDC60	PGTDC60_1066	1, 150	100	303.1	0
16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	Pgjcvi_00909	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1256	1, 150	99.3	300.8	0
ADP-heptose:LPS heptosyltransferase	Pgjcvi_00910	PG JCVI SC001	putative heptosyltransferase	PG ATCC 33277	PGN_1255	1, 351	100	709.5	0
ADP-heptose:LPS heptosyltransferase	Pgjcvi_00910	PG JCVI SC001	ADP-heptose--LPS heptosyltransferase, putative	PG W83	PG1155	1, 296	100	603.2	0
ADP-heptose:LPS heptosyltransferase	Pgjcvi_00910	PG JCVI SC001	ADP-heptose--LPS heptosyltransferase	PG TDC60	PGTDC60_1065	1, 335	99.7	678.3	0
hypothetical protein	Pgjcvi_00911	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1254	1, 201	99.5	409.8	0
hypothetical protein	Pgjcvi_00911	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1064	1, 201	98.5	406.8	0
hypothetical protein	Pgjcvi_00912	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1063	1, 138	99.3	290	0
hypothetical protein	Pgjcvi_00912	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1253	1, 138	98.6	288.9	0
Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family	Pgjcvi_00913	PG JCVI SC001	alcohol dehydrogenase, iron-containing	PG W83	PG1151	1, 382	100	766.9	0
Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family	Pgjcvi_00913	PG JCVI SC001	iron-containing alcohol dehydrogenase	PG ATCC 33277	PGN_1252	1, 382	99.7	763.8	0
Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family	Pgjcvi_00913	PG JCVI SC001	alcohol dehydrogenase, iron-containing	PG TDC60	PGTDC60_1062	1, 382	99.7	766.5	0
Glycosyltransferase	Pgjcvi_00914	PG JCVI SC001	probable glycosyltransferase	PG ATCC 33277	PGN_1251	14, 375	99.2	713	0
Glycosyltransferase	Pgjcvi_00914	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG W83	PG1149	14, 375	99.2	713	0
Glycosyltransferase	Pgjcvi_00914	PG JCVI SC001	putative glycosyltransferase	PG TDC60	PGTDC60_1060	1, 362	99.2	711.4	0
hypothetical protein	Pgjcvi_00915	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1059	1, 72	98.6	156.8	3.30E-37
hypothetical protein	Pgjcvi_00915	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1250	1, 72	94.4	149.1	6.80E-35
Long-chain acyl-CoA synthetases (AMP-forming)	Pgjcvi_00917	PG JCVI SC001	long-chain-fatty-acid-CoA ligase	PG ATCC 33277	PGN_1245	2, 608	99.7	1206.8	0
Long-chain acyl-CoA synthetases (AMP-forming)	Pgjcvi_00917	PG JCVI SC001	long-chain-fatty-acid--CoA ligase, putative	PG W83	PG1145	1, 607	99.2	1200.7	0
Long-chain acyl-CoA synthetases (AMP-forming)	Pgjcvi_00917	PG JCVI SC001	long-chain-fatty-acid-CoA ligase	PG TDC60	PGTDC60_1067	2, 608	98.7	1198.3	0

Protein chain release factor B	Pgjcvi_00918	PG JCVI SC001	putative peptide chain release factor RF-2	PG ATCC 33277	PGN_1244	1, 319	99.4	636.3	0
Protein chain release factor B	Pgjcvi_00918	PG JCVI SC001	putative peptide chain release factor RF-2	PG TDC60	PGTDC60_1068	1, 319	99.4	636.3	0
Protein chain release factor B	Pgjcvi_00918	PG JCVI SC001	peptide chain release factor 1	PG W83	PG0074	84, 349	39.4	183.7	1.10E-44
nucleotide sugar dehydrogenase	Pgjcvi_00919	PG JCVI SC001	UDP-glucose 6-dehydrogenase	PG ATCC 33277	PGN_1243	1, 522	99.4	1026.9	0
nucleotide sugar dehydrogenase	Pgjcvi_00919	PG JCVI SC001	UDP-glucose 6-dehydrogenase	PG TDC60	PGTDC60_1069	1, 444	99.3	868.6	0
nucleotide sugar dehydrogenase	Pgjcvi_00919	PG JCVI SC001	sugar dehydrogenase, UDP-glucose/GDP-mannose dehydrogenase family	PG W83	PG1143	1, 522	99	1022.7	0
hypothetical protein	Pgjcvi_00920	PG JCVI SC001	exopolysaccharide synthesis-related protein	PG W83	PG1142	1, 302	100	600.1	0
hypothetical protein	Pgjcvi_00920	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1242	1, 347	99.1	684.5	0
hypothetical protein	Pgjcvi_00920	PG JCVI SC001	exopolysaccharide synthesis-like protein	PG TDC60	PGTDC60_1070	1, 347	97.7	679.1	0
hypothetical protein	Pgjcvi_00921	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1241	1, 103	96.1	204.1	0
hypothetical protein	Pgjcvi_00921	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1071	1, 103	95.1	201.1	0
Glycosyltransferase	Pgjcvi_00922	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1240	1, 383	99.7	767.7	0
Glycosyltransferase	Pgjcvi_00922	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG W83	PG1141	15, 397	99.2	763.5	0
Glycosyltransferase	Pgjcvi_00922	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG TDC60	PGTDC60_1072	1, 383	98.7	758.4	0
Predicted glycosyltransferases	Pgjcvi_00923	PG JCVI SC001	probable lipopolysaccharide biosynthesis glycosyltransferase	PG ATCC 33277	PGN_1239	1, 286	99	585.1	0
Predicted glycosyltransferases	Pgjcvi_00923	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG1140	1, 286	99	584.3	0
Predicted glycosyltransferases	Pgjcvi_00923	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_1073	1, 286	97.2	574.7	0
AhpC/TSA family.	Pgjcvi_00924	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1238	4, 378	99.7	746.5	0
AhpC/TSA family.	Pgjcvi_00924	PG JCVI SC001	hypothetical protein	PG W83	PG1139	4, 378	99.5	745.3	0
AhpC/TSA family.	Pgjcvi_00924	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1074	1, 367	98.6	724.5	0
Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	Pgjcvi_00925	PG JCVI SC001	regulator PorR	PG ATCC 33277	PGN_1236	1, 384	99	761.5	0
Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	Pgjcvi_00925	PG JCVI SC001	pigmentation and extracellular proteinase regulator	PG W83	PG1138	1, 384	99	761.5	0
Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	Pgjcvi_00925	PG JCVI SC001	pigmentation and extracellular proteinase regulator PorR	PG TDC60	PGTDC60_1075	1, 374	97.6	735.7	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_00926	PG JCVI SC001	membrane protein PorS	PG TDC60	PGTDC60_1076	1, 419	100	812.8	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_00926	PG JCVI SC001	membrane protein PorS	PG ATCC 33277	PGN_1235	1, 435	99.8	841.6	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_00926	PG JCVI SC001	porS protein	PG W83	PG1137	1, 435	99.8	841.6	0
Asparagine synthase (glutamine-hydrolyzing)	Pgjcvi_00927	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1077	1, 542	99.3	1099.7	0
Asparagine synthase (glutamine-hydrolyzing)	Pgjcvi_00927	PG JCVI SC001	hypothetical protein	PG W83	PG1136	1, 542	98.5	1085.9	0
Asparagine synthase (glutamine-hydrolyzing)	Pgjcvi_00927	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1234	1, 533	98.3	1068.1	0
Sugar transferases involved in lipopolysaccharide synthesis	Pgjcvi_00928	PG JCVI SC001	sugar transferase	PG TDC60	PGTDC60_1078	1, 204	98.5	401.4	0
Sugar transferases involved in lipopolysaccharide synthesis	Pgjcvi_00928	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1233	1, 204	98	400.6	0
Sugar transferases involved in lipopolysaccharide synthesis	Pgjcvi_00928	PG JCVI SC001	bacterial sugar transferase	PG W83	PG1135	1, 204	98	401.7	0
thioredoxin-disulfide reductase	Pgjcvi_00930	PG JCVI SC001	thioredoxin reductase	PG ATCC 33277	PGN_1232	1, 313	100	625.5	0
thioredoxin-disulfide reductase	Pgjcvi_00930	PG JCVI SC001	thioredoxin reductase	PG W83	PG1134	1, 313	100	625.5	0
thioredoxin-disulfide reductase	Pgjcvi_00930	PG JCVI SC001	thioredoxin reductase	PG TDC60	PGTDC60_1079	1, 313	99.4	623.6	0
hypothetical protein	Pgjcvi_00932	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1230	1, 150	100	295.8	0
hypothetical protein	Pgjcvi_00932	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1081	1, 150	100	295.8	0
hypothetical protein	Pgjcvi_00932	PG JCVI SC001	hypothetical protein	PG W83	PG1133	1, 150	99.3	294.7	0
valyl-tRNA synthetase	Pgjcvi_00933	PG JCVI SC001	valyl-tRNA synthetase	PG ATCC 33277	PGN_1229	1, 876	99.8	1787.7	0
valyl-tRNA synthetase	Pgjcvi_00933	PG JCVI SC001	valyl-tRNA synthetase	PG W83	PG1132	1, 876	99.4	1785.4	0
valyl-tRNA synthetase	Pgjcvi_00933	PG JCVI SC001	valyl-tRNA synthetase	PG TDC60	PGTDC60_1082	1, 876	99.3	1783.8	0
Tetratricopeptide repeat.	Pgjcvi_00934	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_1227	379, 724	99.7	690.6	0
Tetratricopeptide repeat.	Pgjcvi_00934	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_1085	379, 724	75.7	495.4	0
Tetratricopeptide repeat.	Pgjcvi_00934	PG JCVI SC001	TPR domain protein	PG W83	PG1130	319, 665	72.9	482.3	0
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_1227	1, 345	99.7	676	0
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain protein	PG W83	PG1130	33, 383	86.6	598.6	0
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_1085	1, 345	85.8	573.5	0
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_1085	387, 529	42.7	104.8	7.40E-21
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain protein	PG W83	PG1130	292, 470	33	90.9	1.10E-16
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_1227	230, 575	32.7	121.7	5.90E-26
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_1085	418, 621	31.9	106.3	2.60E-21
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_1227	69, 437	28.5	120.2	1.70E-25
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain protein	PG W83	PG1130	381, 607	27.5	78.2	7.50E-13
Tetratricopeptide repeat.	Pgjcvi_00935	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_1227	368, 675	25.4	79.7	2.60E-13
ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent	Pgjcvi_00936	PG JCVI SC001	ribonucleotide reductase	PG TDC60	PGTDC60_1086	1, 850	99.9	1728.8	0
ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent	Pgjcvi_00936	PG JCVI SC001	ribonucleotide reductase	PG ATCC 33277	PGN_1226	1, 850	99.8	1726.5	0
ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent	Pgjcvi_00936	PG JCVI SC001	ribonucleotide reductase	PG W83	PG1129	1, 850	99.8	1727.6	0
exodeoxyribonuclease VII, large subunit	Pgjcvi_00937	PG JCVI SC001	exodeoxyribonuclease VII large subunit	PG TDC60	PGTDC60_1087	1, 460	99.6	895.2	0
exodeoxyribonuclease VII, large subunit	Pgjcvi_00937	PG JCVI SC001	probable exodeoxyribonuclease VII large subunit	PG ATCC 33277	PGN_1225	1, 460	99.3	894.4	0
exodeoxyribonuclease VII, large subunit	Pgjcvi_00937	PG JCVI SC001	exodeoxyribonuclease VII large subunit	PG W83	PG1128	1, 459	99.1	890.6	0
Transcriptional regulators	Pgjcvi_00938	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_1224	1, 155	100	311.2	0
Transcriptional regulators	Pgjcvi_00938	PG JCVI SC001	transcriptional regulator, AsnC Family	PG W83	PG1127	1, 155	100	311.2	0
Transcriptional regulators	Pgjcvi_00938	PG JCVI SC001	AsnC family transcriptional regulator	PG TDC60	PGTDC60_1088	1, 155	99.4	309.3	0
uracil-xanthine permease	Pgjcvi_00939	PG JCVI SC001	uracil permease	PG ATCC 33277	PGN_1223	1, 395	100	757.3	0
uracil-xanthine permease	Pgjcvi_00939	PG JCVI SC001	uracil permease	PG W83	PG1126	1, 395	100	757.3	0
uracil-xanthine permease	Pgjcvi_00939	PG JCVI SC001	uracil permease	PG TDC60	PGTDC60_1089	1, 395	99.7	754.2	0
hypothetical protein	Pgjcvi_00940	PG JCVI SC001	hypothetical protein	PG W83	PG1125	3, 218	98.1	421	0
hypothetical protein	Pgjcvi_00940	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1090	1, 216	97.7	419.9	0
hypothetical protein	Pgjcvi_00940	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1222	3, 218	97.2	417.9	0

ATP:cob(I)alamin adenosyltransferase	Pgjcvi_00941	PG JCVI SC001	ATP:cob(I)alamin adenosyltransferase, putative	PG W83	PG1124	1, 183	100	372.5	0
ATP:cob(I)alamin adenosyltransferase	Pgjcvi_00941	PG JCVI SC001	putative ATP:corrinoid adenosyltransferase	PG TDC60	PGTDC60_1091	1, 187	100	379.4	0
ATP:cob(I)alamin adenosyltransferase	Pgjcvi_00941	PG JCVI SC001	probable ATP:corrinoid adenosyltransferase	PG ATCC 33277	PGN_1221	1, 187	99.5	376.7	0
adenylosuccinate lyase	Pgjcvi_00942	PG JCVI SC001	adenylosuccinate lyase	PG ATCC 33277	PGN_1220	1, 447	99.6	884.4	0
adenylosuccinate lyase	Pgjcvi_00942	PG JCVI SC001	adenylosuccinate lyase	PG W83	PG1123	1, 447	99.6	883.6	0
adenylosuccinate lyase	Pgjcvi_00942	PG JCVI SC001	adenylosuccinate lyase	PG TDC60	PGTDC60_1092	1, 447	99.3	880.6	0
pseudouridine synthase	Pgjcvi_00943	PG JCVI SC001	ribosomal large subunit pseudouridine synthase B	PG ATCC 33277	PGN_1219	1, 439	98.6	873.2	0
pseudouridine synthase	Pgjcvi_00943	PG JCVI SC001	ribosomal large subunit pseudouridine synthase B	PG TDC60	PGTDC60_1093	1, 439	98.4	870.2	0
asparaginyl-tRNA synthetase	Pgjcvi_00944	PG JCVI SC001	asparaginyl-tRNA synthetase	PG W83	PG1121	1, 469	99.8	957.2	0
asparaginyl-tRNA synthetase	Pgjcvi_00944	PG JCVI SC001	asparaginyl-tRNA synthetase	PG ATCC 33277	PGN_1218	1, 469	99.6	955.7	0
asparaginyl-tRNA synthetase	Pgjcvi_00944	PG JCVI SC001	asparaginyl-tRNA synthetase	PG TDC60	PGTDC60_1094	1, 469	99.6	953.7	0
6Fe-6S prismane cluster-containing protein	Pgjcvi_00945	PG JCVI SC001	hydroxylamine reductase	PG W83	PG0893	5, 69	92.3	126.7	3.60E-28
6Fe-6S prismane cluster-containing protein	Pgjcvi_00945	PG JCVI SC001	hydroxylamine reductase	PG TDC60	PGTDC60_0821	5, 69	92.3	126.7	3.60E-28
6Fe-6S prismane cluster-containing protein	Pgjcvi_00945	PG JCVI SC001	hydroxylamine reductase	PG ATCC 33277	PGN_1047	5, 69	90.8	124.8	1.40E-27
SEFIR domain.	Pgjcvi_00946	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1246	20, 287	22.7	49.3	0.00045
Flavodoxins	Pgjcvi_00947	PG JCVI SC001	probable flavodoxin	PG ATCC 33277	PGN_1209	1, 186	99.5	367.5	0
Flavodoxins	Pgjcvi_00947	PG JCVI SC001	flavodoxin, putative	PG W83	PG1119	1, 186	99.5	365.9	0
Flavodoxins	Pgjcvi_00947	PG JCVI SC001	flavodoxin	PG TDC60	PGTDC60_1095	1, 186	99.5	365.9	0
ATP-dependent chaperone ClpB	Pgjcvi_00948	PG JCVI SC001	clpB protein	PG W83	PG1118	1, 863	100	1666.4	0
ATP-dependent chaperone ClpB	Pgjcvi_00948	PG JCVI SC001	ClpB protein	PG ATCC 33277	PGN_1208	1, 863	99.9	1664.8	0
ATP-dependent chaperone ClpB	Pgjcvi_00948	PG JCVI SC001	clpB protein	PG TDC60	PGTDC60_1096	14, 876	99.9	1664.8	0
putative efflux protein, MATE family	Pgjcvi_00949	PG JCVI SC001	putative transport multidrug efflux protein	PG ATCC 33277	PGN_1207	1, 448	99.6	872.8	0
putative efflux protein, MATE family	Pgjcvi_00949	PG JCVI SC001	putative transport multidrug efflux protein	PG TDC60	PGTDC60_1098	1, 448	99.6	875.2	0
putative efflux protein, MATE family	Pgjcvi_00949	PG JCVI SC001	MATE efflux family protein	PG W83	PG1117	1, 483	99	939.1	0
5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	Pgjcvi_00950	PG JCVI SC001	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	PG W83	PG1116	1, 296	100	592.8	0
5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	Pgjcvi_00950	PG JCVI SC001	putative methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	PG ATCC 33277	PGN_1206	1, 296	99.7	590.5	0
5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	Pgjcvi_00950	PG JCVI SC001	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase	PG TDC60	PGTDC60_1099	1, 296	99.7	592.4	0
signal recognition particle protein	Pgjcvi_00951	PG JCVI SC001	signal recognition particle protein	PG W83	PG1115	1, 445	100	862.1	0
signal recognition particle protein	Pgjcvi_00951	PG JCVI SC001	signal recognition particle protein	PG TDC60	PGTDC60_1100	1, 445	100	862.1	0
signal recognition particle protein	Pgjcvi_00951	PG JCVI SC001	signal recognition particle protein	PG ATCC 33277	PGN_1205	1, 445	99.8	861.7	0
L-aspartate-alpha-decarboxylase	Pgjcvi_00952	PG JCVI SC001	probable aspartate-1-decarboxylase	PG ATCC 33277	PGN_1204	1, 118	100	235.3	0
L-aspartate-alpha-decarboxylase	Pgjcvi_00952	PG JCVI SC001	aspartate 1-decarboxylase precursor	PG W83	PG1114	1, 118	100	235.3	0
L-aspartate-alpha-decarboxylase	Pgjcvi_00952	PG JCVI SC001	aspartate alpha-decarboxylase	PG TDC60	PGTDC60_1101	1, 118	100	235.3	0
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	Pgjcvi_00953	PG JCVI SC001	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	PG TDC60	PGTDC60_1102	1, 434	99.1	854.4	0
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	Pgjcvi_00953	PG JCVI SC001	UDP-N-acetylmuramoyl-tripeptide?D-alanyl-D- alanine ligase	PG ATCC 33277	PGN_1203	1, 434	98.4	847	0
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	Pgjcvi_00953	PG JCVI SC001	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	PG W83	PG1106	1, 420	98.1	818.9	0
RNA polymerase sigma-54 factor	Pgjcvi_00954	PG JCVI SC001	RNA polymerase sigma-54 factor	PG TDC60	PGTDC60_1103	1, 485	99.8	945.7	0
RNA polymerase sigma-54 factor	Pgjcvi_00954	PG JCVI SC001	RNA polymerase sigma-54 factor	PG W83	PG1105	1, 485	99.6	945.7	0
RNA polymerase sigma-54 factor	Pgjcvi_00954	PG JCVI SC001	RNA polymerase sigma-54 factor	PG ATCC 33277	PGN_1202	1, 485	99.2	943	0
Predicted O-methyltransferase	Pgjcvi_00955	PG JCVI SC001	hypothetical protein	PG W83	PG1104	1, 255	99.6	507.7	0
Predicted O-methyltransferase	Pgjcvi_00955	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1104	1, 255	98.8	504.6	0
Predicted O-methyltransferase	Pgjcvi_00955	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1201	1, 236	98.3	463.8	0
ATPase related to the helicase subunit of the Holliday junction resolvase	Pgjcvi_00956	PG JCVI SC001	ATPase AAA family	PG ATCC 33277	PGN_1200	1, 434	100	858.2	0
ATPase related to the helicase subunit of the Holliday junction resolvase	Pgjcvi_00956	PG JCVI SC001	ATPase, AAA family	PG W83	PG1103	1, 434	100	858.2	0
ATPase related to the helicase subunit of the Holliday junction resolvase	Pgjcvi_00956	PG JCVI SC001	recombination factor protein RarA	PG TDC60	PGTDC60_1105	1, 439	99.8	866.3	0
hypothetical protein	Pgjcvi_00957	PG JCVI SC001	DNA-binding protein histone-like family	PG TDC60	PGTDC60_1106	1, 152	100	303.1	0
hypothetical protein	Pgjcvi_00957	PG JCVI SC001	DNA-binding protein histone-like family	PG ATCC 33277	PGN_1199	1, 152	98.7	298.5	0
hypothetical protein	Pgjcvi_00957	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG1497	1, 152	69.7	212.2	0
Na+/proline symporter	Pgjcvi_00958	PG JCVI SC001	putative sodium-solute transporter	PG ATCC 33277	PGN_1198	1, 486	99.4	963	0
Na+/proline symporter	Pgjcvi_00958	PG JCVI SC001	sodium:solute symporter family protein	PG W83	PG1101	1, 486	98.8	958.7	0
Na+/proline symporter	Pgjcvi_00958	PG JCVI SC001	sodium:solute symporter family protein	PG TDC60	PGTDC60_1107	1, 486	98.8	958.7	0
Predicted N-acetylglucosamine kinase	Pgjcvi_00959	PG JCVI SC001	hypothetical protein	PG W83	PG1100	1, 283	99.6	568.5	0
Predicted N-acetylglucosamine kinase	Pgjcvi_00959	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1108	1, 283	98.6	560.5	0
Predicted N-acetylglucosamine kinase	Pgjcvi_00959	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1197	1, 283	96.5	553.1	0
N-acetylmuramic acid 6-phosphate etherase	Pgjcvi_00960	PG JCVI SC001	hypothetical protein	PG W83	PG1099	1, 274	99.6	535.4	0
N-acetylmuramic acid 6-phosphate etherase	Pgjcvi_00960	PG JCVI SC001	N-acetylmuramic acid-6-phosphate etherase	PG TDC60	PGTDC60_1109	1, 274	99.3	532.7	0
N-acetylmuramic acid 6-phosphate etherase	Pgjcvi_00960	PG JCVI SC001	putative sugar phosphate isomerase	PG ATCC 33277	PGN_1196	1, 274	98.9	530.4	0
hypothetical protein	Pgjcvi_00963	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1110	1, 407	99	800.8	0
hypothetical protein	Pgjcvi_00963	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1195	1, 407	98.3	789.6	0
hypothetical protein	Pgjcvi_00963	PG JCVI SC001	hypothetical protein	PG W83	PG1098	1, 407	97.8	786.6	0
alanine racemase	Pgjcvi_00964	PG JCVI SC001	alanine racemase	PG ATCC 33277	PGN_1194	1, 823	99.3	1622.8	0
alanine racemase	Pgjcvi_00964	PG JCVI SC001	Mur ligase domain protein/alanine racemase	PG W83	PG1097	1, 823	99.3	1620.9	0
alanine racemase	Pgjcvi_00964	PG JCVI SC001	putative bifunctional UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine ligase/alanine racemase	PG TDC60	PGTDC60_1111	1, 719	99.2	1417.5	0
GSCFA family.	Pgjcvi_00965	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1193	41, 368	99.4	661.8	0
GSCFA family.	Pgjcvi_00965	PG JCVI SC001	hypothetical protein	PG W83	PG1096	34, 358	98.5	651.4	0
GSCFA family.	Pgjcvi_00965	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1112	1, 328	98.2	654.4	0

23S rRNA (uracil-5-)-methyltransferase RumA	Pgjcvi_00966	PG JCVI SC001	RNA methyltransferase, TrmA family	PG W83	PG1095	1, 465	99.8	937.9	0
23S rRNA (uracil-5-)-methyltransferase RumA	Pgjcvi_00966	PG JCVI SC001	RNA methyltransferase	PG ATCC 33277	PGN_1190	1, 478	99.4	959.9	0
23S rRNA (uracil-5-)-methyltransferase RumA	Pgjcvi_00966	PG JCVI SC001	RNA methyltransferase	PG TDC60	PGTDC60_1114	1, 478	99.4	959.5	0
phosphoglucosamine mutase	Pgjcvi_00967	PG JCVI SC001	phosphomannomutase	PG W83	PG1094	1, 462	99.4	912.1	0
phosphoglucosamine mutase	Pgjcvi_00967	PG JCVI SC001	phosphoglucomutase/phosphomannomutase	PG ATCC 33277	PGN_1189	1, 462	99.1	911.4	0
phosphoglucosamine mutase	Pgjcvi_00967	PG JCVI SC001	phosphomannomutase	PG TDC60	PGTDC60_1115	1, 462	98.5	901.7	0
hypothetical protein	Pgjcvi_00968	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1188	6, 203	99.5	402.5	0
hypothetical protein	Pgjcvi_00968	PG JCVI SC001	hypothetical protein	PG W83	PG1093	1, 192	98.4	389.8	0
hypothetical protein	Pgjcvi_00968	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1116	1, 198	98	399.4	0
Exopolyphosphatase-related proteins	Pgjcvi_00969	PG JCVI SC001	DHH subfamily 1 protein	PG W83	PG1091	1, 331	99.7	656	0
Exopolyphosphatase-related proteins	Pgjcvi_00969	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1187	1, 347	98.8	682.9	0
Exopolyphosphatase-related proteins	Pgjcvi_00969	PG JCVI SC001	DHH subfamily 1 protein	PG TDC60	PGTDC60_1117	1, 347	98.6	682.6	0
Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	Pgjcvi_00970	PG JCVI SC001	putative DNA-binding response regulator RprY	PG ATCC 33277	PGN_1186	1, 245	100	490.3	0
Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	Pgjcvi_00970	PG JCVI SC001	DNA-binding response regulator RprY	PG W83	PG1089	1, 245	100	490.3	0
Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	Pgjcvi_00970	PG JCVI SC001	DNA-binding response regulator RprY	PG TDC60	PGTDC60_1119	1, 245	100	490.3	0
Acetyltransferases	Pgjcvi_00971	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1185	1, 187	100	383.6	0
Acetyltransferases	Pgjcvi_00971	PG JCVI SC001	acetyltransferase, GNAT family	PG W83	PG1088	8, 194	100	383.6	0
Acetyltransferases	Pgjcvi_00971	PG JCVI SC001	acetyltransferase	PG TDC60	PGTDC60_1120	1, 187	98.4	373.6	0
radical SAM protein, TIGR01212 family	Pgjcvi_00972	PG JCVI SC001	radical SAM protein, TIGR01212 family	PG W83	PG1087	1, 311	100	639	0
radical SAM protein, TIGR01212 family	Pgjcvi_00972	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1184	1, 310	99.7	634.8	0
radical SAM protein, TIGR01212 family	Pgjcvi_00972	PG JCVI SC001	radical SAM family protein	PG TDC60	PGTDC60_1121	1, 311	99.7	638.6	0
hypothetical protein	Pgjcvi_00973	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1182	21, 82	98.4	121.7	1.00E-26
hypothetical protein	Pgjcvi_00973	PG JCVI SC001	hypothetical protein	PG W83	PG1085	21, 82	98.4	121.7	1.00E-26
hypothetical protein	Pgjcvi_00973	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1123	21, 82	98.4	121.7	1.00E-26
Thiol-disulfide isomerase and thioredoxins	Pgjcvi_00974	PG JCVI SC001	putative thiol:disulfide oxidoreductase	PG TDC60	PGTDC60_1124	23, 389	100	729.2	0
Thiol-disulfide isomerase and thioredoxins	Pgjcvi_00974	PG JCVI SC001	probable thiol:disulfide oxidoreductase	PG ATCC 33277	PGN_1181	1, 367	99.7	727.6	0
Thiol-disulfide isomerase and thioredoxins	Pgjcvi_00974	PG JCVI SC001	thioredoxin family protein	PG W83	PG1084	1, 358	99.2	709.9	0
Protein of unknown function (DUF3108).	Pgjcvi_00975	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1125	1, 282	99.6	567	0
Protein of unknown function (DUF3108).	Pgjcvi_00975	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1180	1, 282	98.9	563.5	0
Protein of unknown function (DUF3108).	Pgjcvi_00975	PG JCVI SC001	hypothetical protein	PG W83	PG1083	32, 313	97.9	556.2	0
phosphate acetyltransferase	Pgjcvi_00976	PG JCVI SC001	phosphotransacetylase	PG ATCC 33277	PGN_1179	1, 336	100	642.9	0
phosphate acetyltransferase	Pgjcvi_00976	PG JCVI SC001	phosphotransacetylase	PG TDC60	PGTDC60_1126	1, 336	100	642.9	0
phosphate acetyltransferase	Pgjcvi_00976	PG JCVI SC001	phosphotransacetylase	PG W83	PG1082	1, 336	99.7	639.8	0
acetate kinase	Pgjcvi_00977	PG JCVI SC001	acetate kinase	PG W83	PG1081	1, 398	99.7	786.9	0
acetate kinase	Pgjcvi_00977	PG JCVI SC001	acetate kinase	PG TDC60	PGTDC60_1127	1, 397	99.7	785	0
acetate kinase	Pgjcvi_00977	PG JCVI SC001	acetate kinase	PG ATCC 33277	PGN_1178	1, 398	99.2	784.6	0
3-hydroxyacyl-CoA dehydrogenase	Pgjcvi_00978	PG JCVI SC001	3-hydroxybutyryl-CoA dehydrogenase family protein	PG TDC60	PGTDC60_1128	1, 281	100	542.7	0
3-hydroxyacyl-CoA dehydrogenase	Pgjcvi_00978	PG JCVI SC001	putative 3-hydroxybutyryl-CoA dehydrogenase	PG ATCC 33277	PGN_1176	1, 281	99.6	540	0
3-hydroxyacyl-CoA dehydrogenase	Pgjcvi_00978	PG JCVI SC001	3-hydroxyacyl-CoA dehydrogenase family protein	PG W83	PG1080	1, 281	98.9	539.3	0
Enoyl-CoA hydratase/carnithine racemase	Pgjcvi_00979	PG JCVI SC001	enoyl-CoA hydratase/isomerase family protein	PG W83	PG1079	1, 256	99.2	487.3	0
Enoyl-CoA hydratase/carnithine racemase	Pgjcvi_00979	PG JCVI SC001	putative enoyl-CoA hydratase	PG ATCC 33277	PGN_1175	1, 256	98.4	484.6	0
Enoyl-CoA hydratase/carnithine racemase	Pgjcvi_00979	PG JCVI SC001	enoyl-CoA hydratase/isomerase family protein	PG TDC60	PGTDC60_1129	1, 256	98	482.6	0
Electron transfer flavoprotein, alpha subunit	Pgjcvi_00980	PG JCVI SC001	electron transfer flavoprotein alpha subunit	PG ATCC 33277	PGN_1174	1, 335	100	650.2	0
Electron transfer flavoprotein, alpha subunit	Pgjcvi_00980	PG JCVI SC001	electron transfer flavoprotein, alpha subunit	PG W83	PG1078	1, 335	99.7	648.3	0
Electron transfer flavoprotein, alpha subunit	Pgjcvi_00980	PG JCVI SC001	electron transfer flavoprotein subunit alpha	PG TDC60	PGTDC60_1130	1, 335	98.5	639	0
Electron transfer flavoprotein, beta subunit	Pgjcvi_00981	PG JCVI SC001	putative electron transfer flavoprotein beta subunit	PG ATCC 33277	PGN_1173	1, 261	99.6	515	0
Electron transfer flavoprotein, beta subunit	Pgjcvi_00981	PG JCVI SC001	electron transfer flavoprotein, beta subunit	PG W83	PG1077	1, 261	99.6	515	0
Electron transfer flavoprotein, beta subunit	Pgjcvi_00981	PG JCVI SC001	electron transfer flavoprotein subunit beta	PG TDC60	PGTDC60_1131	1, 261	99.6	515	0
Acyl-CoA dehydrogenases	Pgjcvi_00982	PG JCVI SC001	acyl-CoA dehydrogenase, short-chain specific	PG W83	PG1076	1, 379	100	754.6	0
Acyl-CoA dehydrogenases	Pgjcvi_00982	PG JCVI SC001	acyl-CoA dehydrogenase, short-chain specific	PG TDC60	PGTDC60_1132	1, 379	100	754.6	0
Acyl-CoA dehydrogenases	Pgjcvi_00982	PG JCVI SC001	acyl-CoA dehydrogenase short-chain specific	PG ATCC 33277	PGN_1172	1, 379	99.7	753.1	0
3-oxoacid CoA-transferase, B subunit	Pgjcvi_00983	PG JCVI SC001	coenzyme A transferase subunit beta	PG TDC60	PGTDC60_1133	1, 220	100	435.6	0
3-oxoacid CoA-transferase, B subunit	Pgjcvi_00983	PG JCVI SC001	coenzyme A transferase beta subunit	PG ATCC 33277	PGN_1171	1, 220	99.5	431.8	0
3-oxoacid CoA-transferase, B subunit	Pgjcvi_00983	PG JCVI SC001	coenzyme A transferase, beta subunit	PG W83	PG1075	1, 220	99.1	433.3	0
Predicted cobalamin binding protein	Pgjcvi_00984	PG JCVI SC001	D-lysine 5,6-aminomutase, beta subunit	PG W83	PG1074	1, 263	100	530.4	0
Predicted cobalamin binding protein	Pgjcvi_00984	PG JCVI SC001	D-lysine 5,6-aminomutase subunit beta	PG TDC60	PGTDC60_1134	1, 263	100	530.4	0
Predicted cobalamin binding protein	Pgjcvi_00984	PG JCVI SC001	D-lysine 5,6-aminomutase beta subunit	PG ATCC 33277	PGN_1170	1, 263	99.6	528.1	0
D-Lysine 5,6-aminomutase alpha subunit.	Pgjcvi_00985	PG JCVI SC001	D-lysine 5,6-aminomutase, alpha subunit	PG W83	PG1073	1, 523	100	1033.9	0
D-Lysine 5,6-aminomutase alpha subunit.	Pgjcvi_00985	PG JCVI SC001	D-lysine 5,6-aminomutase alpha subunit	PG ATCC 33277	PGN_1169	1, 523	99.8	1032.7	0
D-Lysine 5,6-aminomutase alpha subunit.	Pgjcvi_00985	PG JCVI SC001	D-lysine 5,6-aminomutase subunit alpha	PG TDC60	PGTDC60_1135	1, 523	99.8	1031.9	0
Mismatch repair ATPase (MutS family)	Pgjcvi_00986	PG JCVI SC001	MutS family protein	PG W83	PG1072	1, 463	100	901.7	0
Mismatch repair ATPase (MutS family)	Pgjcvi_00986	PG JCVI SC001	probable DNA mismatch repair protein MutS	PG ATCC 33277	PGN_1168	1, 463	99.4	895.6	0
Mismatch repair ATPase (MutS family)	Pgjcvi_00986	PG JCVI SC001	MutS family protein	PG TDC60	PGTDC60_1136	3, 465	98.7	888.6	0
hypothetical protein	Pgjcvi_00987	PG JCVI SC001	hypothetical protein	PG W83	PG1071	1, 322	99.7	619.8	0
hypothetical protein	Pgjcvi_00987	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1167	28, 359	98.2	630.6	0
hypothetical protein	Pgjcvi_00987	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1137	1, 322	97.8	610.9	0
lysine-2,3-aminomutase	Pgjcvi_00988	PG JCVI SC001	L-lysine 2,3-aminomutase	PG ATCC 33277	PGN_1166	1, 416	100	860.1	0
lysine-2,3-aminomutase	Pgjcvi_00988	PG JCVI SC001	L-lysine 2,3-aminomutase	PG W83	PG1070	1, 416	100	860.1	0
lysine-2,3-aminomutase	Pgjcvi_00988	PG JCVI SC001	L-lysine 2,3-aminomutase	PG TDC60	PGTDC60_1138	1, 416	100	860.1	0

NADPH:quinone reductase and related Zn-dependent oxidoreductases	Pgjcvi_00989	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1165	1, 347	100	684.9	0
NADPH:quinone reductase and related Zn-dependent oxidoreductases	Pgjcvi_00989	PG JCVI SC001	alcohol dehydrogenase, zinc-containing, putative	PG W83	PG1069	1, 347	100	684.9	0
NADPH:quinone reductase and related Zn-dependent oxidoreductases	Pgjcvi_00989	PG JCVI SC001	alcohol dehydrogenase, zinc-containing	PG TDC60	PGTDC60_1139	1, 347	100	684.9	0
Uncharacterized conserved protein	Pgjcvi_00990	PG JCVI SC001	conserved hypothetical protein with prokaryotic DUF849 domain	PG ATCC 33277	PGN_1164	1, 270	99.6	539.7	0
Uncharacterized conserved protein	Pgjcvi_00990	PG JCVI SC001	hypothetical protein	PG W83	PG1068	1, 273	99.3	544.3	0
Uncharacterized conserved protein	Pgjcvi_00990	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1140	1, 273	99.3	542	0
Acyl-CoA hydrolase	Pgjcvi_00991	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1163	1, 124	100	252.7	0
Acyl-CoA hydrolase	Pgjcvi_00991	PG JCVI SC001	hypothetical protein	PG W83	PG1067	1, 129	100	261.9	0
Acyl-CoA hydrolase	Pgjcvi_00991	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1141	1, 119	100	243.8	0
3-oxoacid CoA-transferase, A subunit	Pgjcvi_00992	PG JCVI SC001	putative CoA transferase subunit A	PG ATCC 33277	PGN_1162	1, 214	100	424.9	0
3-oxoacid CoA-transferase, A subunit	Pgjcvi_00992	PG JCVI SC001	butyrate-acetoacetate CoA-transferase, subunit A	PG W83	PG1066	1, 214	100	424.9	0
3-oxoacid CoA-transferase, A subunit	Pgjcvi_00992	PG JCVI SC001	butyrate-acetoacetate CoA-transferase, subunit A	PG TDC60	PGTDC60_1142	1, 214	99.5	422.5	0
dihydroorotate dehydrogenase (subfamily 1) family protein	Pgjcvi_00993	PG JCVI SC001	dihydroorotate dehydrogenase	PG W83	PG1065	19, 307	99.7	569.7	0
dihydroorotate dehydrogenase (subfamily 1) family protein	Pgjcvi_00993	PG JCVI SC001	dihydroorotate dehydrogenase 1B	PG TDC60	PGTDC60_1143	1, 289	99.7	569.3	0
dihydroorotate dehydrogenase (subfamily 1) family protein	Pgjcvi_00993	PG JCVI SC001	putative dihydroorotate dehydrogenase	PG ATCC 33277	PGN_0905	1, 216	99.5	429.5	0
2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	Pgjcvi_00994	PG JCVI SC001	probable dihydroorotate dehydrogenase electron transfer subunit	PG ATCC 33277	PGN_0906	1, 265	100	541.6	0
2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	Pgjcvi_00994	PG JCVI SC001	dihydroorotate dehydrogenase	PG TDC60	PGTDC60_1144	1, 265	98.9	535.8	0
2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	Pgjcvi_00994	PG JCVI SC001	dihydroorotate dehydrogenase, putative	PG W83	PG1064	1, 265	98.5	532.3	0
Plasmid maintenance system antidote protein	Pgjcvi_00995	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0907	1, 146	100	292.4	0
Plasmid maintenance system antidote protein	Pgjcvi_00995	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_1145	1, 146	100	292.4	0
Plasmid maintenance system antidote protein	Pgjcvi_00995	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG1063	1, 146	99.3	290.4	0
Transposase	Pgjcvi_00996	PG JCVI SC001	ISPg6, transposase	PG W83	PG1061	16, 213	96.5	380.6	0
Transposase	Pgjcvi_00996	PG JCVI SC001	partial transposase in ISPg6	PG ATCC 33277	PGN_0954	1, 166	95.8	316.6	0
Transposase	Pgjcvi_00996	PG JCVI SC001	transposase in ISPg6	PG TDC60	PGTDC60_1147	16, 213	94.9	378.6	0
Transposase domain (DUF772).	Pgjcvi_00997	PG JCVI SC001	transposase in ISPg7	PG TDC60	PGTDC60_0800	11, 128	84.7	212.6	0
Transposase domain (DUF772).	Pgjcvi_00997	PG JCVI SC001	ISPg7, transposase	PG W83	PG0461	28, 145	83.1	209.5	0
C-terminal peptidase (prc)	Pgjcvi_00998	PG JCVI SC001	carboxyl-terminal protease	PG W83	PG1060	1, 569	99.6	1108.2	0
C-terminal peptidase (prc)	Pgjcvi_00998	PG JCVI SC001	carboxyl-terminal protease	PG TDC60	PGTDC60_1149	1, 569	99.5	1106.7	0
C-terminal peptidase (prc)	Pgjcvi_00998	PG JCVI SC001	carboxyl-terminal processing protease	PG ATCC 33277	PGN_0952	1, 569	99.3	1105.9	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_00999	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_1916	1, 568	99.8	1099.7	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_00999	PG JCVI SC001	ABC transporter, ATP-binding protein, putative	PG W83	PG1175	1, 568	99.6	1099	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_00999	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1151	1, 568	99.6	1099	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_01000	PG JCVI SC001	ABC transporter, ATP-binding protein, putative	PG W83	PG1176	1, 573	99.7	1123.2	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_01000	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1152	1, 584	99.7	1141.7	0
ABC-type multidrug transport system, ATPase and permease components	Pgjcvi_01000	PG JCVI SC001	ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0949	1, 584	99.3	1137.9	0
hypothetical protein	Pgjcvi_01001	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1153	1, 425	99.5	869.4	0
hypothetical protein	Pgjcvi_01001	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1918	1, 425	99.1	865.1	0
hypothetical protein	Pgjcvi_01001	PG JCVI SC001	hypothetical protein	PG W83	PG1178	1, 425	99.1	863.6	0
Protein of unknown function (DUF1329).	Pgjcvi_01002	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1919	1, 263	100	535.8	0
Protein of unknown function (DUF1329).	Pgjcvi_01002	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1154	1, 263	100	535.8	0
Protein of unknown function (DUF1329).	Pgjcvi_01002	PG JCVI SC001	hypothetical protein	PG W83	PG1179	1, 263	99.6	535.4	0
Predicted membrane protein involved in D-alanine export	Pgjcvi_01003	PG JCVI SC001	alginate O-acetyltransferase	PG TDC60	PGTDC60_1161	1, 442	100	903.3	0
Predicted membrane protein involved in D-alanine export	Pgjcvi_01003	PG JCVI SC001	alginate O-acetyltransferase	PG ATCC 33277	PGN_0943	1, 448	99.3	911.8	0
Predicted membrane protein involved in D-alanine export	Pgjcvi_01003	PG JCVI SC001	alginate O-acetyltransferase, putative	PG W83	PG1184	1, 448	99.1	909.8	0
Lysophospholipase L1 and related esterases	Pgjcvi_01004	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1162	1, 268	99.3	547	0
Lysophospholipase L1 and related esterases	Pgjcvi_01004	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0942	1, 268	98.5	540.4	0
Lysophospholipase L1 and related esterases	Pgjcvi_01004	PG JCVI SC001	hypothetical protein	PG W83	PG1185	11, 286	97.8	553.1	0
hypothetical protein	Pgjcvi_01005	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1163	1, 463	100	923.7	0
hypothetical protein	Pgjcvi_01005	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0941	1, 463	99.6	918.7	0
hypothetical protein	Pgjcvi_01005	PG JCVI SC001	hypothetical protein	PG W83	PG1186	20, 482	99.4	920.6	0
Domain of Unknown Function (DUF349).	Pgjcvi_01006	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0935	1, 626	99.7	1227.6	0
Domain of Unknown Function (DUF349).	Pgjcvi_01006	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1165	1, 626	99.5	1226.1	0
Domain of Unknown Function (DUF349).	Pgjcvi_01006	PG JCVI SC001	hypothetical protein	PG W83	PG1189	1, 626	99.4	1223	0
Lactate dehydrogenase and related dehydrogenases	Pgjcvi_01007	PG JCVI SC001	glycerate dehydrogenase	PG TDC60	PGTDC60_1166	1, 317	99.4	627.1	0
Lactate dehydrogenase and related dehydrogenases	Pgjcvi_01007	PG JCVI SC001	putative glycerate dehydrogenase	PG ATCC 33277	PGN_0936	1, 317	97.8	611.7	0
Lactate dehydrogenase and related dehydrogenases	Pgjcvi_01007	PG JCVI SC001	glycerate dehydrogenase	PG W83	PG1190	1, 317	95.3	604.4	0
hypothetical protein	Pgjcvi_01008	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1182	1, 515	99.8	1042.7	0
hypothetical protein	Pgjcvi_01008	PG JCVI SC001	hypothetical protein	PG W83	PG1209	2, 516	99.4	1036.6	0
hypothetical protein	Pgjcvi_01008	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0915	1, 515	99.2	1035.8	0
Xaa-Pro aminopeptidase	Pgjcvi_01009	PG JCVI SC001	peptidase, M24 family	PG W83	PG1210	1, 595	99.5	1194.1	0
Xaa-Pro aminopeptidase	Pgjcvi_01009	PG JCVI SC001	peptidase M24 family	PG TDC60	PGTDC60_1183	1, 595	99.2	1189.9	0
Xaa-Pro aminopeptidase	Pgjcvi_01009	PG JCVI SC001	peptidase M24 family	PG ATCC 33277	PGN_0914	1, 595	98.8	1184.9	0
Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	Pgjcvi_01010	PG JCVI SC001	hexapeptide transferase family protein	PG W83	PG1211	14, 192	100	359.4	0
Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	Pgjcvi_01010	PG JCVI SC001	putative acetyltransferase	PG ATCC 33277	PGN_0913	1, 179	99.4	359	0
Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	Pgjcvi_01010	PG JCVI SC001	hexapeptide transferase family protein	PG TDC60	PGTDC60_1184	1, 179	99.4	359	0
hypothetical protein	Pgjcvi_01011	PG JCVI SC001	TPR domain protein	PG W83	PG1212	1, 337	99.7	653.3	0
hypothetical protein	Pgjcvi_01011	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0912	1, 333	98.5	641.3	0
hypothetical protein	Pgjcvi_01011	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_1185	1, 314	98.1	599.4	0
Predicted double-stranded RNA/RNA-DNA hybrid binding protein	Pgjcvi_01012	PG JCVI SC001	ribonuclease H	PG W83	PG1213	1, 216	100	458.8	0
Predicted double-stranded RNA/RNA-DNA hybrid binding protein	Pgjcvi_01012	PG JCVI SC001	ribonuclease H	PG TDC60	PGTDC60_1186	1, 216	99.5	457.6	0
Predicted double-stranded RNA/RNA-DNA hybrid binding protein	Pgjcvi_01012	PG JCVI SC001	putative ribonuclease H	PG ATCC 33277	PGN_0911	1, 216	98.6	454.1	0
hypothetical protein	Pgjcvi_01013	PG JCVI SC001	hypothetical protein	PG W83	PG1214	1, 412	99.8	852.8	0

hypothetical protein	Pgjcvi_01013	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1187	1, 412	99.3	849.4	0
hypothetical protein	Pgjcvi_01013	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0910	1, 390	98.5	797.3	0
outer membrane assembly lipoprotein YfiO	Pgjcvi_01014	PG JCVI SC001	lipoprotein protein, putative	PG W83	PG1215	1, 270	100	546.6	0
outer membrane assembly lipoprotein YfiO	Pgjcvi_01014	PG JCVI SC001	lipoprotein	PG TDC60	PGTDC60_1188	1, 270	100	546.6	0
outer membrane assembly lipoprotein YfiO	Pgjcvi_01014	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1354	41, 310	99.6	545	0
RNA polymerase Rpb6.	Pgjcvi_01015	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1356	1, 110	100	221.1	0
RNA polymerase Rpb6.	Pgjcvi_01015	PG JCVI SC001	hypothetical protein	PG W83	PG1217	1, 110	100	221.1	0
RNA polymerase Rpb6.	Pgjcvi_01015	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1190	1, 110	100	221.1	0
hypothetical protein	Pgjcvi_01016	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1357	1, 136	100	271.6	0
hypothetical protein	Pgjcvi_01016	PG JCVI SC001	hypothetical protein	PG W83	PG1218	1, 152	100	304.3	0
hypothetical protein	Pgjcvi_01016	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1191	1, 152	100	304.3	0
Protein of unknown function (DUF3467).	Pgjcvi_01018	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1358	1, 103	100	211.1	0
Protein of unknown function (DUF3467).	Pgjcvi_01018	PG JCVI SC001	hypothetical protein	PG W83	PG1219	1, 103	100	211.1	0
Protein of unknown function (DUF3467).	Pgjcvi_01018	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1192	1, 103	100	211.1	0
Phosphoglycerate dehydrogenase and related dehydrogenases	Pgjcvi_01019	PG JCVI SC001	erythronate-4-phosphate dehydrogenase	PG W83	PG1220	1, 377	99.7	765	0
Phosphoglycerate dehydrogenase and related dehydrogenases	Pgjcvi_01019	PG JCVI SC001	putative erythronate-4-phosphate dehydrogenase	PG ATCC 33277	PGN_1359	1, 377	98.9	760.4	0
Phosphoglycerate dehydrogenase and related dehydrogenases	Pgjcvi_01019	PG JCVI SC001	erythronate-4-phosphate dehydrogenase	PG TDC60	PGTDC60_1193	1, 377	98.7	760	0
Short-chain dehydrogenases of various substrate specificities	Pgjcvi_01020	PG JCVI SC001	probable oxidoreductase	PG ATCC 33277	PGN_1360	1, 241	100	477.6	0
Short-chain dehydrogenases of various substrate specificities	Pgjcvi_01020	PG JCVI SC001	oxidoreductase, short chain dehydrogenase/reductase family	PG W83	PG1221	1, 241	100	477.6	0
Short-chain dehydrogenases of various substrate specificities	Pgjcvi_01020	PG JCVI SC001	short chain dehydrogenase/reductase family oxidoreductase	PG TDC60	PGTDC60_1194	1, 241	100	477.6	0
Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein	Pgjcvi_01023	PG JCVI SC001	probable exported transglycosylase protein	PG ATCC 33277	PGN_1362	50, 521	99.6	944.1	0
Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein	Pgjcvi_01023	PG JCVI SC001	putative exported transglycosylase protein	PG TDC60	PGTDC60_1197	1, 472	98.9	936.8	0
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01024	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG1225	1, 623	100	1249.2	0
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01024	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1198	1, 623	99.4	1238.4	0
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01024	PG JCVI SC001	ABC transporter ATP-binding protein	PG ATCC 33277	PGN_1363	1, 623	99	1236.5	0
Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	Pgjcvi_01025	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	PG W83	PG1226	14, 234	99.5	440.7	0
Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	Pgjcvi_01025	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	PG TDC60	PGTDC60_1199	1, 221	99.1	438.3	0
Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	Pgjcvi_01025	PG JCVI SC001	probable peptidyl-prolyl cis-trans isomerase cyclophilin-type	PG ATCC 33277	PGN_1364	14, 234	98.2	435.6	0
hypothetical protein	Pgjcvi_01027	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1366	1, 702	99	1404	0
hypothetical protein	Pgjcvi_01027	PG JCVI SC001	hypothetical protein	PG W83	PG1230	1, 702	99	1404	0
hypothetical protein	Pgjcvi_01027	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1201	1, 702	98.1	1393.3	0
Glutamate dehydrogenase/leucine dehydrogenase	Pgjcvi_01028	PG JCVI SC001	NAD-specific glutamate dehydrogenase	PG ATCC 33277	PGN_1367	7, 445	100	908.7	0
Glutamate dehydrogenase/leucine dehydrogenase	Pgjcvi_01028	PG JCVI SC001	glutamate dehydrogenase	PG W83	PG1232	7, 445	100	908.7	0
Glutamate dehydrogenase/leucine dehydrogenase	Pgjcvi_01028	PG JCVI SC001	glutamate dehydrogenase	PG TDC60	PGTDC60_1202	1, 437	99.8	904.4	0
hypothetical protein	Pgjcvi_01029	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1368	4, 36	100	71.6	6.30E-12
hypothetical protein	Pgjcvi_01029	PG JCVI SC001	hypothetical protein	PG W83	PG1233	4, 36	100	71.6	6.30E-12
hypothetical protein	Pgjcvi_01029	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1203	4, 36	97	69.3	3.10E-11
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_01030	PG JCVI SC001	NAD-dependent nucleotide-diphosphate-sugar epimerase	PG ATCC 33277	PGN_1370	1, 318	100	644	0
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_01030	PG JCVI SC001	epimerase/reductase, putative	PG W83	PG1235	1, 318	100	644	0
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_01030	PG JCVI SC001	NAD-dependent nucleotide-diphosphate-sugar epimerase	PG TDC60	PGTDC60_1205	1, 318	99.4	639.4	0
Hemerythrin HHE cation binding domain.	Pgjcvi_01032	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1207	1, 236	99.6	473	0
Hemerythrin HHE cation binding domain.	Pgjcvi_01032	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1372	1, 236	99.2	469.5	0
Hemerythrin HHE cation binding domain.	Pgjcvi_01032	PG JCVI SC001	hypothetical protein	PG W83	PG1236	1, 236	98.7	466.8	0
Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	Pgjcvi_01033	PG JCVI SC001	transcriptional regulator, LuxR family	PG W83	PG1237	1, 199	100	394.8	0
Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	Pgjcvi_01033	PG JCVI SC001	probable transcriptional regulator	PG ATCC 33277	PGN_1373	1, 199	99.5	393.7	0
Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	Pgjcvi_01033	PG JCVI SC001	LuxR family transcriptional regulator	PG TDC60	PGTDC60_1208	1, 199	99.5	393.7	0
Pseudouridylate synthases, 23S RNA-specific	Pgjcvi_01034	PG JCVI SC001	putative ribosomal large subunit pseudouridine synthase D	PG ATCC 33277	PGN_1374	1, 227	99.1	456.1	0
Pseudouridylate synthases, 23S RNA-specific	Pgjcvi_01034	PG JCVI SC001	putative ribosomal large subunit pseudouridine synthase D	PG TDC60	PGTDC60_1209	1, 227	98.2	452.6	0
3-oxoacyl-(acyl-carrier-protein) reductase	Pgjcvi_01035	PG JCVI SC001	putative beta-ketoacyl-acyl carrier protein reductase	PG ATCC 33277	PGN_1375	1, 248	100	480.3	0
3-oxoacyl-(acyl-carrier-protein) reductase	Pgjcvi_01035	PG JCVI SC001	3-oxoacyl-(acyl-carrier-protein) reductase	PG W83	PG1239	1, 248	100	480.3	0
3-oxoacyl-(acyl-carrier-protein) reductase	Pgjcvi_01035	PG JCVI SC001	3-oxoacyl-(acyl-carrier-protein) reductase	PG TDC60	PGTDC60_1210	1, 248	100	480.3	0
Transcriptional regulator	Pgjcvi_01036	PG JCVI SC001	transcriptional regulator, tetR family	PG W83	PG1240	1, 202	100	401.7	0
Transcriptional regulator	Pgjcvi_01036	PG JCVI SC001	putative transcriptional regulator	PG TDC60	PGTDC60_1211	1, 211	99.5	413.7	0
Transcriptional regulator	Pgjcvi_01036	PG JCVI SC001	putative transcriptional regulator	PG ATCC 33277	PGN_1376	1, 211	99.1	412.9	0
GTP-binding protein LepA	Pgjcvi_01038	PG JCVI SC001	GTP-binding protein LepA	PG W83	PG1241	1, 595	100	1172.1	0
GTP-binding protein LepA	Pgjcvi_01038	PG JCVI SC001	GTP-binding protein LepA	PG TDC60	PGTDC60_1212	1, 595	99.8	1169.5	0
GTP-binding protein LepA	Pgjcvi_01038	PG JCVI SC001	GTP-binding protein LepA	PG ATCC 33277	PGN_1377	1, 595	99.5	1166.4	0
replicative DNA helicase	Pgjcvi_01039	PG JCVI SC001	replicative DNA helicase	PG W83	PG1242	1, 528	100	1029.2	0
replicative DNA helicase	Pgjcvi_01039	PG JCVI SC001	replicative DNA helicase	PG TDC60	PGTDC60_1213	1, 528	100	1029.2	0
replicative DNA helicase	Pgjcvi_01039	PG JCVI SC001	replicative DNA helicase	PG ATCC 33277	PGN_1378	1, 509	99.4	989.2	0
hypothetical protein	Pgjcvi_01040	PG JCVI SC001	transposase in ISPg6	PG TDC60	PGTDC60_1147	1, 34	85.3	62.4	7.90E-09
hypothetical protein	Pgjcvi_01040	PG JCVI SC001	partial transposase in ISPg6	PG ATCC 33277	PGN_0111	16, 66	82.4	80.5	2.80E-14
hypothetical protein	Pgjcvi_01040	PG JCVI SC001	ISPg6, transposase	PG W83	PG1061	1, 34	82.4	58.9	8.70E-08
hypothetical protein	Pgjcvi_01040	PG JCVI SC001	transposase in ISPg6	PG TDC60	PGTDC60_1147	312, 362	82.4	80.5	2.80E-14
hypothetical protein	Pgjcvi_01040	PG JCVI SC001	ISPg6, transposase	PG W83	PG1061	312, 362	80.4	79	8.10E-14
hypothetical protein	Pgjcvi_01041	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1217	1, 28	100	59.3	3.80E-08
hypothetical protein	Pgjcvi_01041	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1380	1, 28	96.4	56.2	3.20E-07

alanine--tRNA ligase	Pgjcvi_01042	PG JCVI SC001	alanyl-tRNA synthetase	PG W83	PG1246	1, 876	99.8	1738.4	0
alanine--tRNA ligase	Pgjcvi_01042	PG JCVI SC001	alanyl-tRNA synthetase	PG ATCC 33277	PGN_1381	1, 876	98.9	1723.8	0
alanine--tRNA ligase	Pgjcvi_01042	PG JCVI SC001	alanyl-tRNA synthetase	PG TDC60	PGTDC60_1218	1, 876	98.6	1719.5	0
3-dehydroquinate synthase	Pgjcvi_01043	PG JCVI SC001	3-dehydroquinate synthase	PG W83	PG1247	1, 353	99.4	720.7	0
3-dehydroquinate synthase	Pgjcvi_01043	PG JCVI SC001	3-dehydroquinate synthase	PG TDC60	PGTDC60_1219	1, 353	97.7	706.4	0
3-dehydroquinate synthase	Pgjcvi_01043	PG JCVI SC001	putative 3-dehydroquinate synthase	PG ATCC 33277	PGN_1382	1, 334	96.4	664.1	0
Predicted DNA alkylation repair enzyme	Pgjcvi_01045	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1383	1, 243	98.8	489.6	0
Predicted DNA alkylation repair enzyme	Pgjcvi_01045	PG JCVI SC001	hypothetical protein	PG W83	PG1248	1, 243	98.8	489.6	0
Predicted DNA alkylation repair enzyme	Pgjcvi_01045	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1220	1, 243	98.8	486.5	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01046	PG JCVI SC001	1-acyl-sn-glycerol-3-phosphate acetyltransferase, putative	PG W83	PG1249	1, 204	99	414.8	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01046	PG JCVI SC001	probable 1-acyl-sn-glycerol-3-phosphate acetyltransferase	PG ATCC 33277	PGN_1384	1, 261	98.9	526.6	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01046	PG JCVI SC001	putative 1-acyl-sn-glycerol-3-phosphate acetyltransferase	PG TDC60	PGTDC60_1221	1, 253	98.4	511.1	0
hypothetical protein	Pgjcvi_01047	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1385	1, 88	100	171	2.00E-41
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_01048	PG JCVI SC001	hypothetical protein	PG W83	PG1252	1, 411	99.8	803.5	0
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_01048	PG JCVI SC001	putative ABC transporter permease protein	PG TDC60	PGTDC60_1224	1, 411	99.5	803.1	0
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_01048	PG JCVI SC001	putative ABC transporter permease protein	PG ATCC 33277	PGN_1387	1, 411	99	798.5	0
DNA ligase, NAD-dependent	Pgjcvi_01049	PG JCVI SC001	DNA ligase	PG ATCC 33277	PGN_1388	1, 669	99.6	1313.1	0
DNA ligase, NAD-dependent	Pgjcvi_01049	PG JCVI SC001	NAD-dependent DNA ligase	PG TDC60	PGTDC60_1225	1, 669	99.4	1309.7	0
DNA ligase, NAD-dependent	Pgjcvi_01049	PG JCVI SC001	DNA ligase, NAD-dependent	PG W83	PG1253	1, 669	98.8	1301.2	0
Acetyltransferases, including N-acetylases of ribosomal proteins	Pgjcvi_01050	PG JCVI SC001	probable acetyltransferase	PG ATCC 33277	PGN_1389	1, 175	99.4	355.1	0
Acetyltransferases, including N-acetylases of ribosomal proteins	Pgjcvi_01050	PG JCVI SC001	acetyltransferase, GNAT family	PG W83	PG1254	1, 175	98.9	354.4	0
Acetyltransferases, including N-acetylases of ribosomal proteins	Pgjcvi_01050	PG JCVI SC001	acetyltransferase	PG TDC60	PGTDC60_1226	1, 175	98.3	350.5	0
recombination protein RecR	Pgjcvi_01051	PG JCVI SC001	recombination protein RecR	PG W83	PG1255	1, 207	100	410.6	0
recombination protein RecR	Pgjcvi_01051	PG JCVI SC001	putative recombination protein RecR	PG ATCC 33277	PGN_1390	1, 207	98.1	399.8	0
recombination protein RecR	Pgjcvi_01051	PG JCVI SC001	recombination protein RecR	PG TDC60	PGTDC60_1227	1, 207	97.6	399.1	0
ribonuclease, Rne/Rng family	Pgjcvi_01052	PG JCVI SC001	putative ribonuclease E	PG ATCC 33277	PGN_1391	16, 519	100	979.9	0
ribonuclease, Rne/Rng family	Pgjcvi_01052	PG JCVI SC001	ribonuclease, Rne/Rng family	PG W83	PG1256	1, 504	100	979.9	0
ribonuclease, Rne/Rng family	Pgjcvi_01052	PG JCVI SC001	putative ribonuclease E	PG TDC60	PGTDC60_1228	1, 504	99.6	976.5	0
Bacterial nucleoid DNA-binding protein	Pgjcvi_01054	PG JCVI SC001	putative DNA-binding protein HU	PG ATCC 33277	PGN_1393	1, 92	100	179.5	6.00E-44
Bacterial nucleoid DNA-binding protein	Pgjcvi_01054	PG JCVI SC001	DNA-binding protein HU	PG W83	PG1258	1, 92	100	179.5	6.00E-44
Bacterial nucleoid DNA-binding protein	Pgjcvi_01054	PG JCVI SC001	DNA-binding protein HU	PG TDC60	PGTDC60_1229	1, 92	100	179.5	6.00E-44
anaerobic ribonucleoside-triphosphate reductase activating protein	Pgjcvi_01055	PG JCVI SC001	anaerobic ribonucleoside-triphosphate reductase activating protein	PG W83	PG1259	1, 163	99.4	344.7	0
anaerobic ribonucleoside-triphosphate reductase activating protein	Pgjcvi_01055	PG JCVI SC001	anaerobic ribonucleoside-triphosphate reductase activating protein	PG TDC60	PGTDC60_1230	1, 163	99.4	344.7	0
anaerobic ribonucleoside-triphosphate reductase activating protein	Pgjcvi_01055	PG JCVI SC001	putative anaerobic ribonucleoside-triphosphate reductase activating protein	PG ATCC 33277	PGN_1395	5, 167	98.8	340.5	0
anaerobic ribonucleoside-triphosphate reductase	Pgjcvi_01056	PG JCVI SC001	anaerobic ribonucleoside-triphosphate reductase	PG ATCC 33277	PGN_1396	1, 798	99.6	1605.9	0
anaerobic ribonucleoside-triphosphate reductase	Pgjcvi_01056	PG JCVI SC001	anaerobic ribonucleoside triphosphate reductase	PG W83	PG1260	1, 798	99.6	1606.3	0
anaerobic ribonucleoside-triphosphate reductase	Pgjcvi_01056	PG JCVI SC001	anaerobic ribonucleoside triphosphate reductase	PG TDC60	PGTDC60_1231	1, 798	99.6	1607.4	0
Transposase	Pgjcvi_01059	PG JCVI SC001	transposase in ISPg2	PG TDC60	PGTDC60_1232	1, 342	99.7	677.6	0
Transposase	Pgjcvi_01059	PG JCVI SC001	transposase in ISPg2	PG ATCC 33277	PGN_1160	43, 356	46.1	281.2	0
Transposase	Pgjcvi_01059	PG JCVI SC001	ISPg2, transposase	PG W83	PG1350	37, 376	45.8	303.1	0
hypothetical protein	Pgjcvi_01060	PG JCVI SC001	calcium-transporting ATPase	PG W83	PG0938	13, 41	96.6	60.1	3.30E-08
hypothetical protein	Pgjcvi_01060	PG JCVI SC001	putative DNA methylase	PG TDC60	PGTDC60_2151	13, 42	93.3	61.6	1.10E-08
hypothetical protein	Pgjcvi_01060	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0028	13, 41	93.1	60.1	3.30E-08
Membrane proteins related to metalloendopeptidases	Pgjcvi_01061	PG JCVI SC001	peptidase, M23/M37 family	PG W83	PG2192	1, 337	100	677.6	0
Membrane proteins related to metalloendopeptidases	Pgjcvi_01061	PG JCVI SC001	probable peptidase	PG ATCC 33277	PGN_0099	1, 337	98.8	670.6	0
Membrane proteins related to metalloendopeptidases	Pgjcvi_01061	PG JCVI SC001	M24/M37 family peptidase	PG TDC60	PGTDC60_0047	1, 316	98.7	631.3	0
Predicted ATPase involved in cell division	Pgjcvi_01062	PG JCVI SC001	cell-division ATP-binding protein	PG W83	PG2190	1, 246	99.6	469.5	0
Predicted ATPase involved in cell division	Pgjcvi_01062	PG JCVI SC001	putative cell-division ATP-binding protein	PG ATCC 33277	PGN_0097	1, 246	99.2	467.2	0
Predicted ATPase involved in cell division	Pgjcvi_01062	PG JCVI SC001	cell-division ATP-binding protein	PG TDC60	PGTDC60_0049	1, 246	99.2	467.2	0
aspartate kinase	Pgjcvi_01063	PG JCVI SC001	aspartate kinase	PG W83	PG2189	1, 292	99.7	575.1	0
aspartate kinase	Pgjcvi_01063	PG JCVI SC001	aspartate kinase	PG ATCC 33277	PGN_0096	1, 292	99.3	573.2	0
aspartate kinase	Pgjcvi_01063	PG JCVI SC001	aspartate kinase	PG TDC60	PGTDC60_0050	1, 292	99.3	572.8	0
hypothetical protein	Pgjcvi_01064	PG JCVI SC001	aspartate kinase	PG ATCC 33277	PGN_0096	324, 446	100	241.9	0
hypothetical protein	Pgjcvi_01064	PG JCVI SC001	aspartate kinase	PG W83	PG2189	324, 446	100	241.9	0
hypothetical protein	Pgjcvi_01064	PG JCVI SC001	aspartate kinase	PG TDC60	PGTDC60_0050	324, 446	100	241.9	0
diaminopimelate decarboxylase	Pgjcvi_01065	PG JCVI SC001	diaminopimelate decarboxylase	PG W83	PG2188	1, 382	99.5	755	0
diaminopimelate decarboxylase	Pgjcvi_01065	PG JCVI SC001	diaminopimelate decarboxylase	PG TDC60	PGTDC60_0051	1, 382	99.2	754.2	0
diaminopimelate decarboxylase	Pgjcvi_01065	PG JCVI SC001	diaminopimelate decarboxylase	PG ATCC 33277	PGN_0100	1, 382	98.4	748	0
1,4-dihydroxy-2-naphthoate octaprenyltransferase	Pgjcvi_01066	PG JCVI SC001	1,4-dihydroxy-2-naphthoate octaprenyltransferase	PG W83	PG2187	1, 295	99.7	582.4	0
1,4-dihydroxy-2-naphthoate octaprenyltransferase	Pgjcvi_01066	PG JCVI SC001	1,4-dihydroxy-2-naphthoate octaprenyltransferase	PG TDC60	PGTDC60_0052	1, 295	98.6	577.8	0
1,4-dihydroxy-2-naphthoate octaprenyltransferase	Pgjcvi_01066	PG JCVI SC001	probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase	PG ATCC 33277	PGN_1273	1, 295	98.3	575.5	0
Predicted transcriptional regulator	Pgjcvi_01067	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG2186	1, 111	100	231.9	0
Predicted transcriptional regulator	Pgjcvi_01067	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_0053	1, 126	100	260.4	0
Predicted transcriptional regulator	Pgjcvi_01067	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1274	1, 126	99.2	258.8	0
TonB family C-terminal domain	Pgjcvi_01068	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1275	1, 438	97.5	845.9	0
TonB family C-terminal domain	Pgjcvi_01068	PG JCVI SC001	transporter	PG TDC60	PGTDC60_0054	1, 438	96.8	840.5	0
TonB family C-terminal domain	Pgjcvi_01068	PG JCVI SC001	transporter, putative	PG W83	PG2185	1, 438	93.2	813.9	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, A subunit	Pgjcvi_01070	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase subunit A	PG W83	PG2182	1, 451	98.9	896.3	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, A subunit	Pgjcvi_01070	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase, subunit A	PG TDC60	PGTDC60_1240	1, 451	98.7	893.6	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, A subunit	Pgjcvi_01070	PG JCVI SC001	Na translocating NADH-quinone reductase subunit A	PG ATCC 33277	PGN_0114	1, 451	97.8	885.9	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, B subunit	Pgjcvi_01071	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase subunit B	PG W83	PG2181	1, 399	99.5	784.6	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, B subunit	Pgjcvi_01071	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase, subunit B	PG TDC60	PGTDC60_1241	1, 399	99.5	784.6	0

NADH:ubiquinone oxidoreductase, Na(+)-translocating, B subunit	Pgjcvi_01071	PG JCVI SC001	Na translocating NADH-quinone reductase subunit B	PG ATCC 33277	PGN_0115	1, 399	99.2	784.3	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, C subunit	Pgjcvi_01072	PG JCVI SC001	probable Na translocating NADH-quinone reductase subunit C	PG ATCC 33277	PGN_0116	1, 244	99.6	481.1	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, C subunit	Pgjcvi_01072	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase subunit C	PG W83	PG2180	1, 244	99.6	481.1	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, C subunit	Pgjcvi_01072	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase, subunit C	PG TDC60	PGTDC60_1242	1, 244	99.2	479.6	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, D subunit	Pgjcvi_01073	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase, subunit D	PG TDC60	PGTDC60_1243	1, 209	100	403.7	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, D subunit	Pgjcvi_01073	PG JCVI SC001	putative Na translocating NADH-quinone reductase subunit D	PG ATCC 33277	PGN_0117	1, 209	99.5	400.6	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, D subunit	Pgjcvi_01073	PG JCVI SC001	NADH-ubiquinone oxidoreductase	PG W83	PG2179	1, 209	99.5	403.3	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, E subunit	Pgjcvi_01074	PG JCVI SC001	putative Na translocating NADH-quinone reductase subunit E	PG ATCC 33277	PGN_0118	1, 169	99.4	328.2	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, E subunit	Pgjcvi_01074	PG JCVI SC001	NADH:ubiquinone oxidoreductase, Na translocating, E subunit	PG W83	PG2178	1, 169	99.4	328.2	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, E subunit	Pgjcvi_01074	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase, subunit E	PG TDC60	PGTDC60_1244	1, 169	99.4	328.2	0
Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrE	Pgjcvi_01075	PG JCVI SC001	putative Na translocating NADH-quinone reductase subunit E	PG ATCC 33277	PGN_0118	134, 204	100	142.1	8.20E-33
Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrE	Pgjcvi_01075	PG JCVI SC001	NADH:ubiquinone oxidoreductase, Na translocating, E subunit	PG W83	PG2178	134, 204	100	142.1	8.20E-33
Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrE	Pgjcvi_01075	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase, subunit E	PG TDC60	PGTDC60_1244	134, 204	100	142.1	8.20E-33
NADH:ubiquinone oxidoreductase, Na(+)-translocating, F subunit	Pgjcvi_01076	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase subunit F	PG W83	PG2177	1, 310	100	628.6	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, F subunit	Pgjcvi_01076	PG JCVI SC001	Na(+)-translocating NADH-quinone reductase, subunit F	PG TDC60	PGTDC60_1245	1, 310	100	628.6	0
NADH:ubiquinone oxidoreductase, Na(+)-translocating, F subunit	Pgjcvi_01076	PG JCVI SC001	Na translocating NADH-quinone reductase subunit F	PG ATCC 33277	PGN_0119	1, 310	99.7	628.2	0
Peroxiredoxin	Pgjcvi_01079	PG JCVI SC001	hypothetical protein	PG W83	PG2175	1, 160	99.4	322	0
Peroxiredoxin	Pgjcvi_01079	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1246	1, 160	99.4	321.2	0
Peroxiredoxin	Pgjcvi_01079	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0120	1, 160	98.8	320.1	0
hypothetical protein	Pgjcvi_01080	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1247	1, 581	99.1	1177.2	0
hypothetical protein	Pgjcvi_01080	PG JCVI SC001	hypothetical protein	PG W83	PG2174	1, 581	99	1171.4	0
hypothetical protein	Pgjcvi_01080	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0121	1, 581	98.8	1172.1	0
Outer membrane protein Omp28.	Pgjcvi_01081	PG JCVI SC001	outer membrane lipoprotein Omp28	PG TDC60	PGTDC60_1248	1, 290	96.2	570.1	0
Outer membrane protein Omp28.	Pgjcvi_01081	PG JCVI SC001	28 kDa outer membrane protein Omp28	PG ATCC 33277	PGN_0122	1, 291	95.5	558.9	0
Outer membrane protein Omp28.	Pgjcvi_01081	PG JCVI SC001	outer membrane lipoprotein Omp28	PG W83	PG2173	1, 290	94.8	562	0
hypothetical protein	Pgjcvi_01082	PG JCVI SC001	hypothetical protein	PG W83	PG2172	9, 248	93.3	438.3	0
hypothetical protein	Pgjcvi_01082	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0123	8, 246	92.9	435.3	0
hypothetical protein	Pgjcvi_01082	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1249	1, 240	92.9	434.9	0
Lactate dehydrogenase and related dehydrogenases	Pgjcvi_01083	PG JCVI SC001	D-isomer specific 2-hydroxyacid dehydrogenase family protein	PG W83	PG2171	1, 319	99.4	626.7	0
Lactate dehydrogenase and related dehydrogenases	Pgjcvi_01083	PG JCVI SC001	D-isomer specific 2-hydroxyacid dehydrogenase family protein	PG TDC60	PGTDC60_1251	1, 319	99.4	626.3	0
Lactate dehydrogenase and related dehydrogenases	Pgjcvi_01083	PG JCVI SC001	D-isomer specific 2-hydroxyacid dehydrogenase family protein	PG ATCC 33277	PGN_0125	1, 319	99.1	625.2	0
Fucose permease	Pgjcvi_01084	PG JCVI SC001	sugar transporter	PG W83	PG2170	1, 429	100	845.5	0
Fucose permease	Pgjcvi_01084	PG JCVI SC001	sugar transporter	PG TDC60	PGTDC60_1253	1, 236	99.6	469.9	0
Fucose permease	Pgjcvi_01084	PG JCVI SC001	putative transmembrane glucose/galactose transporter	PG ATCC 33277	PGN_0126	1, 428	99.5	839.3	0
hypothetical protein	Pgjcvi_01085	PG JCVI SC001	histone-like family DNA-binding protein	PG TDC60	PGTDC60_1254	1, 66	95.5	124.4	2.10E-27
hypothetical protein	Pgjcvi_01085	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG2152	77, 142	90.9	114.8	1.70E-24
protoporphyrinogen oxidase	Pgjcvi_01087	PG JCVI SC001	protoporphyrinogen oxidase	PG W83	PG2159	1, 465	99.4	930.6	0
protoporphyrinogen oxidase	Pgjcvi_01087	PG JCVI SC001	protoporphyrinogen oxidase	PG TDC60	PGTDC60_1265	1, 465	99.4	931	0
protoporphyrinogen oxidase	Pgjcvi_01087	PG JCVI SC001	protoporphyrinogen oxidase	PG ATCC 33277	PGN_0204	1, 465	98.3	919.5	0
SufE protein probably involved in Fe-S center assembly	Pgjcvi_01088	PG JCVI SC001	probable SufE Fe/S-cluster-related protein	PG ATCC 33277	PGN_0203	1, 141	100	280.4	0
SufE protein probably involved in Fe-S center assembly	Pgjcvi_01088	PG JCVI SC001	hypothetical protein	PG W83	PG2158	1, 141	100	280.4	0
SufE protein probably involved in Fe-S center assembly	Pgjcvi_01088	PG JCVI SC001	putative SufE Fe/S-cluster-like protein	PG TDC60	PGTDC60_1266	1, 141	100	280.4	0
Predicted aminopeptidases	Pgjcvi_01089	PG JCVI SC001	probable leucine aminopeptidase precursor	PG ATCC 33277	PGN_0202	1, 333	98.8	681.4	0
Predicted aminopeptidases	Pgjcvi_01089	PG JCVI SC001	glutamine cyclotransferase-related protein	PG W83	PG2157	1, 333	98.5	679.5	0
Predicted aminopeptidases	Pgjcvi_01089	PG JCVI SC001	putative leucine aminopeptidase precursor	PG TDC60	PGTDC60_1267	1, 333	98.2	677.6	0
RNA methyltransferase, RsmE family	Pgjcvi_01090	PG JCVI SC001	conserved hypothetical protein with DUF558 domain	PG ATCC 33277	PGN_0201	1, 248	98	484.2	0
RNA methyltransferase, RsmE family	Pgjcvi_01090	PG JCVI SC001	16S ribosomal RNA methyltransferase RsmE	PG TDC60	PGTDC60_1268	1, 248	96.8	478	0
RNA methyltransferase, RsmE family	Pgjcvi_01090	PG JCVI SC001	conserved hypothetical protein TIGR00046	PG W83	PG2156	1, 248	96.4	475.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01091	PG JCVI SC001	lipoprotein, putative	PG W83	PG2155	1, 296	99	584.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01091	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1269	4, 299	98.6	584.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01091	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0200	1, 296	97.6	580.5	0
hypothetical protein	Pgjcvi_01092	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0199	1, 61	98.4	117.1	3.00E-25
hypothetical protein	Pgjcvi_01092	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1270	1, 61	98.4	117.1	3.00E-25
hypothetical protein	Pgjcvi_01092	PG JCVI SC001	hypothetical protein	PG W83	PG2154	1, 61	96.7	115.5	8.70E-25
Predicted glycosyl hydrolase	Pgjcvi_01097	PG JCVI SC001	LysM domain-containing protein	PG TDC60	PGTDC60_1273	1, 501	99.8	994.6	0
Predicted glycosyl hydrolase	Pgjcvi_01097	PG JCVI SC001	LysM domain protein	PG W83	PG2150	1, 501	99.6	991.5	0
Predicted glycosyl hydrolase	Pgjcvi_01097	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0198	1, 501	99.2	988	0
hypothetical protein	Pgjcvi_01098	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0197	1, 223	99.6	445.7	0
hypothetical protein	Pgjcvi_01098	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1274	1, 223	99.6	445.7	0
hypothetical protein	Pgjcvi_01098	PG JCVI SC001	hypothetical protein	PG W83	PG2149	18, 240	98.7	441.8	0
xanthine permease	Pgjcvi_01099	PG JCVI SC001	xanthine/uracil permease	PG ATCC 33277	PGN_0196	1, 445	99.6	844.3	0
xanthine permease	Pgjcvi_01099	PG JCVI SC001	xanthine/uracil permease family protein	PG TDC60	PGTDC60_1275	1, 445	99.3	842.4	0
xanthine permease	Pgjcvi_01099	PG JCVI SC001	xanthine/uracil permease family protein	PG W83	PG2148	1, 445	99.1	841.3	0
xanthine phosphoribosyltransferase	Pgjcvi_01100	PG JCVI SC001	putative xanthine phosphoribosyltransferase	PG ATCC 33277	PGN_0195	1, 193	100	383.3	0
xanthine phosphoribosyltransferase	Pgjcvi_01100	PG JCVI SC001	xanthine phosphoribosyltransferase	PG W83	PG2147	1, 193	100	383.3	0
xanthine phosphoribosyltransferase	Pgjcvi_01100	PG JCVI SC001	xanthine phosphoribosyltransferase	PG TDC60	PGTDC60_1276	1, 193	100	383.3	0
Uncharacterized conserved protein	Pgjcvi_01101	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0194	1, 228	99.6	473	0
Uncharacterized conserved protein	Pgjcvi_01101	PG JCVI SC001	hypothetical protein	PG W83	PG2146	24, 251	98.7	467.6	0
Uncharacterized conserved protein	Pgjcvi_01101	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1277	1, 228	98.7	469.2	0
Predicted xylanase/chitin deacetylase	Pgjcvi_01102	PG JCVI SC001	putative polysaccharide deacetylase	PG ATCC 33277	PGN_0193	1, 215	100	451.8	0
Predicted xylanase/chitin deacetylase	Pgjcvi_01102	PG JCVI SC001	polysaccharide deacetylase	PG W83	PG2145	1, 201	100	424.9	0
Predicted xylanase/chitin deacetylase	Pgjcvi_01102	PG JCVI SC001	polysaccharide deacetylase	PG TDC60	PGTDC60_1278	1, 215	100	451.8	0

4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	Pgjcvi_01103	PG JCVI SC001	hypothetical protein	PG W83	PG2144	1, 1099	99.4	2197.5	0
4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	Pgjcvi_01103	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1279	1, 1099	99.3	2192.9	0
4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	Pgjcvi_01103	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0192	1, 1099	99.1	2189.5	0
ribosome-associated GTPase EngA	Pgjcvi_01104	PG JCVI SC001	GTP-binding protein EngA	PG ATCC 33277	PGN_0191	1, 437	99.5	866.7	0
ribosome-associated GTPase EngA	Pgjcvi_01104	PG JCVI SC001	GTP-binding protein EngA	PG W83	PG2143	1, 437	99.5	866.7	0
ribosome-associated GTPase EngA	Pgjcvi_01104	PG JCVI SC001	GTP-binding protein EngA	PG TDC60	PGTDC60_1280	1, 437	99.5	866.7	0
GTP-binding protein Era	Pgjcvi_01105	PG JCVI SC001	putative GTP-binding protein	PG ATCC 33277	PGN_0190	1, 299	99.7	582	0
GTP-binding protein Era	Pgjcvi_01105	PG JCVI SC001	GTP-binding protein Era	PG TDC60	PGTDC60_1281	1, 299	99.3	580.1	0
GTP-binding protein Era	Pgjcvi_01105	PG JCVI SC001	GTP-binding protein Era	PG W83	PG2142	1, 299	99	578.9	0
3-oxoacyl-(acyl-carrier-protein) synthase III	Pgjcvi_01106	PG JCVI SC001	beta-ketoacyl-acyl-carrier-protein synthase III	PG ATCC 33277	PGN_0189	1, 335	100	689.1	0
3-oxoacyl-(acyl-carrier-protein) synthase III	Pgjcvi_01106	PG JCVI SC001	3-oxoacyl-(acyl carrier protein) synthase	PG W83	PG2141	1, 335	99.7	687.6	0
3-oxoacyl-(acyl-carrier-protein) synthase III	Pgjcvi_01106	PG JCVI SC001	3-oxoacyl-(acyl-carrier-protein) synthase III	PG TDC60	PGTDC60_1282	1, 335	99.7	687.6	0
ribosomal protein L32	Pgjcvi_01107	PG JCVI SC001	50S ribosomal protein L32	PG ATCC 33277	PGN_0188	1, 61	100	136.3	3.90E-31
ribosomal protein L32	Pgjcvi_01107	PG JCVI SC001	ribosomal protein L32	PG W83	PG2140	1, 61	100	136.3	3.90E-31
ribosomal protein L32	Pgjcvi_01107	PG JCVI SC001	50S ribosomal protein L32	PG TDC60	PGTDC60_1283	1, 38	100	90.5	2.40E-17
Predicted metal-binding, possibly nucleic acid-binding protein	Pgjcvi_01108	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0187	1, 183	99.5	364.8	0
Predicted metal-binding, possibly nucleic acid-binding protein	Pgjcvi_01108	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1284	1, 183	99.5	365.5	0
Predicted metal-binding, possibly nucleic acid-binding protein	Pgjcvi_01108	PG JCVI SC001	hypothetical protein	PG W83	PG2139	1, 159	98.7	315.5	0
hypothetical protein	Pgjcvi_01109	PG JCVI SC001	minor component FimE	PG ATCC 33277	PGN_0185	1, 550	99.1	1086.6	0
hypothetical protein	Pgjcvi_01109	PG JCVI SC001	minor component FimE	PG TDC60	PGTDC60_1286	1, 550	98.4	1078.5	0
hypothetical protein	Pgjcvi_01109	PG JCVI SC001	hypothetical protein	PG W83	PG2136	3, 553	42.6	398.7	0
hypothetical protein	Pgjcvi_01110	PG JCVI SC001	minor component FimD	PG TDC60	PGTDC60_1287	1, 634	98.4	1258.8	0
hypothetical protein	Pgjcvi_01110	PG JCVI SC001	minor component FimD	PG ATCC 33277	PGN_0184	1, 670	95.1	1279.6	0
hypothetical protein	Pgjcvi_01110	PG JCVI SC001	lipoprotein, putative	PG W83	PG2135	12, 670	42.6	506.9	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_01111	PG JCVI SC001	minor component FimC	PG ATCC 33277	PGN_0183	1, 462	96.3	886.3	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_01111	PG JCVI SC001	minor component FimC	PG TDC60	PGTDC60_1288	1, 434	93.5	801.6	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_01111	PG JCVI SC001	lipoprotein, putative	PG W83	PG2134	1, 457	80.4	710.3	0
Protein of unknown function (DUF1812).	Pgjcvi_01112	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0181	1, 118	99.2	240	0
Protein of unknown function (DUF1812).	Pgjcvi_01112	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1289	1, 303	99	610.1	0
Protein of unknown function (DUF1812).	Pgjcvi_01112	PG JCVI SC001	lipoprotein, putative	PG W83	PG2133	1, 303	98.7	609	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_01113	PG JCVI SC001	FimA type II fimbrilin	PG TDC60	PGTDC60_1290	1, 389	92.8	720.7	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_01113	PG JCVI SC001	FimA type I fimbrilin	PG ATCC 33277	PGN_0180	1, 383	78.3	592.8	0
Porphyromonas gingivalis major fimbrial subunit protein (FimA).	Pgjcvi_01113	PG JCVI SC001	fimbrilin	PG W83	PG2132	1, 388	52.1	358.6	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01114	PG JCVI SC001	60 kDa protein	PG ATCC 33277	PGN_0179	1, 490	99.2	968	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01114	PG JCVI SC001	60 kDa protein	PG TDC60	PGTDC60_1291	1, 490	99.2	968.4	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01114	PG JCVI SC001	60 kDa protein	PG W83	PG2131	1, 490	99	965.7	0
Protein of unknown function (DUF3575).	Pgjcvi_01115	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0178	1, 193	99	407.9	0
Protein of unknown function (DUF3575).	Pgjcvi_01115	PG JCVI SC001	hypothetical protein	PG W83	PG2130	1, 193	99	404.8	0
Protein of unknown function (DUF3575).	Pgjcvi_01115	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1292	1, 193	99	407.9	0
Protein of unknown function (DUF1661).	Pgjcvi_01116	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1448	21, 55	68.6	46.6	0.00094
Protein of unknown function (DUF1661).	Pgjcvi_01116	PG JCVI SC001	hypothetical protein	PG W83	PG0524	21, 55	68.6	47.8	0.00042
hypothetical protein	Pgjcvi_01117	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0176	1, 147	100	295.4	0
hypothetical protein	Pgjcvi_01117	PG JCVI SC001	hypothetical protein	PG W83	PG2127	1, 147	100	295.4	0
hypothetical protein	Pgjcvi_01117	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1294	1, 147	99.3	293.9	0
pyridoxal phosphate enzyme, YggS family	Pgjcvi_01118	PG JCVI SC001	conserved hypothetical protein TIGR00044	PG W83	PG2126	1, 224	100	433.7	0
pyridoxal phosphate enzyme, YggS family	Pgjcvi_01118	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0175	1, 224	99.6	431	0
pyridoxal phosphate enzyme, YggS family	Pgjcvi_01118	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1295	1, 224	99.1	429.1	0
AraC-type DNA-binding domain-containing proteins	Pgjcvi_01119	PG JCVI SC001	transcriptional regulator, AraC family	PG W83	PG2125	8, 292	98.2	553.5	0
AraC-type DNA-binding domain-containing proteins	Pgjcvi_01119	PG JCVI SC001	probable transcriptional regulator AraC family	PG ATCC 33277	PGN_0174	11, 312	98	583.6	0
AraC-type DNA-binding domain-containing proteins	Pgjcvi_01119	PG JCVI SC001	AraC family transcriptional regulator	PG TDC60	PGTDC60_1296	14, 315	96.4	571.6	0
glyceraldehyde-3-phosphate dehydrogenase, type I	Pgjcvi_01120	PG JCVI SC001	glyceraldehyde 3-phosphate dehydrogenase type I	PG ATCC 33277	PGN_0173	1, 336	100	667.5	0
glyceraldehyde-3-phosphate dehydrogenase, type I	Pgjcvi_01120	PG JCVI SC001	glyceraldehyde 3-phosphate dehydrogenase, type I	PG W83	PG2124	1, 336	100	667.5	0
glyceraldehyde-3-phosphate dehydrogenase, type I	Pgjcvi_01120	PG JCVI SC001	glyceraldehyde 3-phosphate dehydrogenase, type I	PG TDC60	PGTDC60_1297	1, 336	100	667.5	0
hypothetical protein	Pgjcvi_01121	PG JCVI SC001	partial transposase in ISPg2	PG ATCC 33277	PGN_0171	9, 97	98.9	177.2	3.30E-43
hypothetical protein	Pgjcvi_01121	PG JCVI SC001	ISPg2, transposase	PG W83	PG1350	11, 40	76.7	47.4	0.00039
L-asparaginases, type I	Pgjcvi_01122	PG JCVI SC001	L-asparaginase	PG ATCC 33277	PGN_0170	1, 337	100	673.7	0
L-asparaginases, type I	Pgjcvi_01122	PG JCVI SC001	L-asparaginase	PG W83	PG2121	1, 359	99.7	713.8	0
L-asparaginases, type I	Pgjcvi_01122	PG JCVI SC001	L-asparaginase	PG TDC60	PGTDC60_1300	1, 337	99.4	666.8	0
Metal-dependent hydrolases of the beta-lactamase superfamily I	Pgjcvi_01123	PG JCVI SC001	probable metallo-beta-lactamase superfamily protein	PG ATCC 33277	PGN_0169	1, 269	99.6	557	0
Metal-dependent hydrolases of the beta-lactamase superfamily I	Pgjcvi_01123	PG JCVI SC001	metallo-beta-lactamase superfamily protein	PG W83	PG2120	1, 269	99.6	557	0
Metal-dependent hydrolases of the beta-lactamase superfamily I	Pgjcvi_01123	PG JCVI SC001	metallo-beta-lactamase superfamily protein	PG TDC60	PGTDC60_1301	1, 269	99.3	555.4	0
tmRNA	Pgjcvi_01125	PG JCVI SC001	Gfo/Idh/MocA family oxidoreductase	PG TDC60	PGTDC60_1302	1, 323	100	666.8	0
tmRNA	Pgjcvi_01125	PG JCVI SC001	putative oxidoreductase	PG ATCC 33277	PGN_0168	1, 323	99.4	660.2	0
tmRNA	Pgjcvi_01125	PG JCVI SC001	oxidoreductase, Gfo/Idh/MocA family	PG W83	PG2119	1, 323	99.1	659.8	0
ribosomal protein S16	Pgjcvi_01126	PG JCVI SC001	30S ribosomal protein S16	PG TDC60	PGTDC60_1303	1, 192	100	371.7	0
ribosomal protein S16	Pgjcvi_01126	PG JCVI SC001	30S ribosomal protein S16	PG W83	PG2117	1, 192	99.5	370.5	0
ribosomal protein S16	Pgjcvi_01126	PG JCVI SC001	30S ribosomal protein S16	PG ATCC 33277	PGN_0167	1, 192	99	369	0
hypothetical protein	Pgjcvi_01127	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0165	1, 51	90.2	100.1	6.90E-20
hypothetical protein	Pgjcvi_01127	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0752	11, 102	46.7	78.2	2.80E-13

hypothetical protein	Pgjcvi_01127	PG JCVI SC001	hypothetical protein	PG W83	PG1547	11, 102	44.6	74.7	3.10E-12
hypothetical protein	Pgjcvi_01128	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1306	1, 215	94	421.4	0
hypothetical protein	Pgjcvi_01129	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1307	1, 90	98.9	191.8	0
hypothetical protein	Pgjcvi_01129	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0163	1, 102	98	215.3	0
hypothetical protein	Pgjcvi_01130	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0162	1, 256	98.4	517.3	0
hypothetical protein	Pgjcvi_01130	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1308	1, 240	97.5	481.1	0
hypothetical protein	Pgjcvi_01130	PG JCVI SC001	hypothetical protein	PG W83	PG2112	112, 367	97.3	513.1	0
hypothetical protein	Pgjcvi_01131	PG JCVI SC001	hypothetical protein	PG W83	PG2112	35, 107	95.9	142.9	5.10E-33
thiamine biosynthesis protein ThiS	Pgjcvi_01133	PG JCVI SC001	thiS protein	PG W83	PG2111	1, 66	93.9	125.9	5.60E-28
thiamine biosynthesis protein ThiS	Pgjcvi_01133	PG JCVI SC001	thiS protein	PG TDC60	PGTDC60_1309	1, 66	93.9	125.9	5.60E-28
thiamine biosynthesis protein ThiS	Pgjcvi_01133	PG JCVI SC001	putative thiamine biosynthesis protein ThiS	PG ATCC 33277	PGN_0161	19, 84	92.4	122.1	8.10E-27
thiamine biosynthesis protein ThiC	Pgjcvi_01134	PG JCVI SC001	thiamine biosynthesis protein ThiC	PG TDC60	PGTDC60_1310	1, 587	99.1	1198.3	0
thiamine biosynthesis protein ThiC	Pgjcvi_01134	PG JCVI SC001	thiamine biosynthesis protein ThiC	PG W83	PG2110	1, 587	98.8	1195.6	0
thiamine biosynthesis protein ThiC	Pgjcvi_01134	PG JCVI SC001	thiamine biosynthesis protein	PG ATCC 33277	PGN_0160	1, 587	98.5	1192.9	0
thiamine-phosphate pyrophosphorylase	Pgjcvi_01135	PG JCVI SC001	probable thiamin-phosphate pyrophosphorylase	PG ATCC 33277	PGN_0159	1, 647	97.7	1270	0
thiamine-phosphate pyrophosphorylase	Pgjcvi_01135	PG JCVI SC001	thiamine-phosphate pyrophosphorylase	PG W83	PG2109	1, 647	96.9	1263.1	0
thiamine-phosphate pyrophosphorylase	Pgjcvi_01135	PG JCVI SC001	thiamine-phosphate pyrophosphorylase	PG TDC60	PGTDC60_1311	1, 647	95.5	1250.3	0
Uncharacterized enzyme of thiazole biosynthesis	Pgjcvi_01136	PG JCVI SC001	putative thiazole biosynthesis protein ThiG	PG ATCC 33277	PGN_0158	3, 259	99.2	485.7	0
Uncharacterized enzyme of thiazole biosynthesis	Pgjcvi_01136	PG JCVI SC001	thiazole synthase	PG W83	PG2108	4, 259	98.8	480.3	0
Uncharacterized enzyme of thiazole biosynthesis	Pgjcvi_01136	PG JCVI SC001	thiazole synthase	PG TDC60	PGTDC60_1312	3, 259	97.7	476.5	0
thiazole biosynthesis protein ThiH	Pgjcvi_01137	PG JCVI SC001	thiamine biosynthesis protein ThiH	PG W83	PG2107	1, 370	98.9	741.9	0
thiazole biosynthesis protein ThiH	Pgjcvi_01137	PG JCVI SC001	thiamine biosynthesis protein ThiH	PG TDC60	PGTDC60_1313	1, 370	98.4	735.3	0
thiazole biosynthesis protein ThiH	Pgjcvi_01137	PG JCVI SC001	putative thiamine biosynthesis protein ThiH	PG ATCC 33277	PGN_0157	1, 370	98.1	734.2	0
hypothetical protein	Pgjcvi_01138	PG JCVI SC001	hypothetical protein	PG W83	PG2106	3, 227	99.6	438	0
hypothetical protein	Pgjcvi_01138	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0156	3, 227	98.7	434.5	0
hypothetical protein	Pgjcvi_01138	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1314	3, 227	97.8	432.2	0
hypothetical protein	Pgjcvi_01139	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1316	1, 166	100	326.2	0
hypothetical protein	Pgjcvi_01139	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0154	1, 186	99.5	366.3	0
hypothetical protein	Pgjcvi_01139	PG JCVI SC001	lipoprotein, putative	PG W83	PG2105	1, 166	98.8	322	0
Por secretion system C-terminal sorting domain	Pgjcvi_01141	PG JCVI SC001	immunoreactive 61 kDa antigen	PG ATCC 33277	PGN_0152	1, 540	99.6	1107.8	0
Por secretion system C-terminal sorting domain	Pgjcvi_01141	PG JCVI SC001	immunoreactive 61 kDa antigen PG91	PG W83	PG2102	1, 540	99.3	1104.4	0
Por secretion system C-terminal sorting domain	Pgjcvi_01141	PG JCVI SC001	immunoreactive 61 kDa antigen PG91	PG TDC60	PGTDC60_1319	1, 540	98.9	1098.6	0
Protein of unknown function (DUF3108).	Pgjcvi_01142	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1320	1, 297	99.3	585.9	0
Protein of unknown function (DUF3108).	Pgjcvi_01142	PG JCVI SC001	hypothetical protein	PG W83	PG2101	8, 331	98.8	638.3	0
Protein of unknown function (DUF3108).	Pgjcvi_01142	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0151	1, 324	98.1	634	0
Superfamily II DNA and RNA helicases	Pgjcvi_01144	PG JCVI SC001	putative ATP-dependent RNA helicase	PG ATCC 33277	PGN_0150	1, 427	99.8	840.5	0
Superfamily II DNA and RNA helicases	Pgjcvi_01144	PG JCVI SC001	DEAD-box ATP dependent DNA helicase	PG TDC60	PGTDC60_1321	1, 427	99.8	840.5	0
Superfamily II DNA and RNA helicases	Pgjcvi_01144	PG JCVI SC001	ATP-dependent RNA helicase, DEAD/DEAH box family	PG W83	PG2099	1, 427	97.7	820.1	0
ribose-phosphate pyrophosphokinase	Pgjcvi_01145	PG JCVI SC001	ribose-phosphate pyrophosphokinase	PG ATCC 33277	PGN_0149	1, 313	100	621.7	0
ribose-phosphate pyrophosphokinase	Pgjcvi_01145	PG JCVI SC001	ribose-phosphate pyrophosphokinase	PG TDC60	PGTDC60_1322	1, 313	100	621.7	0
ribose-phosphate pyrophosphokinase	Pgjcvi_01145	PG JCVI SC001	ribose-phosphate pyrophosphokinase	PG W83	PG2097	1, 313	99.7	620.5	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01146	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0148	1, 1582	99.4	3094.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01146	PG JCVI SC001	hypothetical protein	PG W83	PG2096	1, 1596	99.4	3118.2	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01146	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1323	1, 1596	99.3	3121.3	0
Outer membrane protein/protective antigen OMA87	Pgjcvi_01147	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1324	1, 775	99.6	1554.7	0
Outer membrane protein/protective antigen OMA87	Pgjcvi_01147	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0147	1, 775	99.4	1551.6	0
Outer membrane protein/protective antigen OMA87	Pgjcvi_01147	PG JCVI SC001	lipoprotein, putative	PG W83	PG2095	1, 775	99.2	1548.1	0
Uncharacterized protein involved in outer membrane biogenesis	Pgjcvi_01148	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0145	10, 1515	98.7	2914.8	0
Uncharacterized protein involved in outer membrane biogenesis	Pgjcvi_01148	PG JCVI SC001	hypothetical protein	PG W83	PG2094	10, 1515	98.7	2914.4	0
Uncharacterized protein involved in outer membrane biogenesis	Pgjcvi_01148	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1326	1, 1485	98.7	2876.3	0
Sigma-70 region 2.	Pgjcvi_01150	PG JCVI SC001	RNA polymerase sigma factor RpoD	PG ATCC 33277	PGN_0638	8, 125	40.7	96.7	2.20E-18
Sigma-70 region 2.	Pgjcvi_01150	PG JCVI SC001	RNA polymerase sigma-70 factor	PG W83	PG0594	8, 125	40.7	96.7	2.20E-18
Sigma-70 region 2.	Pgjcvi_01150	PG JCVI SC001	RNA polymerase sigma-70 factor	PG TDC60	PGTDC60_1719	8, 125	40.7	96.7	2.20E-18
riboflavin synthase, alpha subunit	Pgjcvi_01152	PG JCVI SC001	putative riboflavin synthase alpha subunit	PG ATCC 33277	PGN_0764	1, 200	99	401.4	0
riboflavin synthase, alpha subunit	Pgjcvi_01152	PG JCVI SC001	riboflavin synthase subunit alpha	PG TDC60	PGTDC60_1855	1, 200	99	401.4	0
riboflavin synthase, alpha subunit	Pgjcvi_01152	PG JCVI SC001	riboflavin synthase subunit alpha	PG W83	PG0733	1, 200	98.5	398.3	0
Nitroreductase	Pgjcvi_01153	PG JCVI SC001	nitroreductase family protein	PG W83	PG0734	1, 183	100	369.8	0
Nitroreductase	Pgjcvi_01153	PG JCVI SC001	probable nitroreductase	PG ATCC 33277	PGN_0765	1, 183	99.5	369.4	0
Nitroreductase	Pgjcvi_01153	PG JCVI SC001	nitroreductase family protein	PG TDC60	PGTDC60_1856	1, 183	99.5	369.4	0
cysteine desulfurases, SufSfamily	Pgjcvi_01154	PG JCVI SC001	aminotransferase class V	PG ATCC 33277	PGN_0766	1, 404	99.5	801.2	0
cysteine desulfurases, SufSfamily	Pgjcvi_01154	PG JCVI SC001	aminotransferase, class V	PG W83	PG0735	1, 404	99	797.3	0
cysteine desulfurases, SufSfamily	Pgjcvi_01154	PG JCVI SC001	aminotransferase, class V	PG TDC60	PGTDC60_1857	1, 404	99	797.3	0
Ribonuclease HII	Pgjcvi_01155	PG JCVI SC001	putative ribonuclease HII	PG ATCC 33277	PGN_0767	1, 201	99.5	412.9	0
Ribonuclease HII	Pgjcvi_01155	PG JCVI SC001	ribonuclease HII	PG TDC60	PGTDC60_1858	1, 201	99.5	412.9	0
Ribonuclease HII	Pgjcvi_01155	PG JCVI SC001	ribonuclease HII	PG W83	PG0736	1, 201	99	411.4	0
hypothetical protein	Pgjcvi_01156	PG JCVI SC001	hypothetical protein	PG W83	PG0737	18, 92	100	152.5	6.40E-36
hypothetical protein	Pgjcvi_01156	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1859	1, 61	100	124.4	1.90E-27
hypothetical protein	Pgjcvi_01156	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0768	18, 92	98.7	150.2	3.20E-35
Cytosine/adenosine deaminases	Pgjcvi_01157	PG JCVI SC001	putative cytosine/adenosine deaminase	PG ATCC 33277	PGN_0769	1, 150	100	306.6	0
Cytosine/adenosine deaminases	Pgjcvi_01157	PG JCVI SC001	cytidine/deoxycytidylate deaminase family protein	PG W83	PG0738	1, 150	100	306.6	0
Cytosine/adenosine deaminases	Pgjcvi_01157	PG JCVI SC001	cytidine/deoxycytidylate deaminase family protein	PG TDC60	PGTDC60_1860	1, 150	99.3	303.5	0
ribonuclease Z	Pgjcvi_01158	PG JCVI SC001	ribonuclease Z	PG W83	PG0739	1, 304	99.7	624.4	0

ribonuclease Z	Pgjcvi_01158	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0770	1, 304	99.3	621.3	0
ribonuclease Z	Pgjcvi_01158	PG JCVI SC001	ribonuclease Z	PG TDC60	PGTDC60_1861	4, 307	99.3	624.4	0
Cell wall-associated hydrolases (invasion-associated proteins)	Pgjcvi_01159	PG JCVI SC001	NLP/P60 family protein	PG W83	PG0740	1, 189	99.5	389.4	0
Cell wall-associated hydrolases (invasion-associated proteins)	Pgjcvi_01159	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0771	1, 189	98.4	383.3	0
Cell wall-associated hydrolases (invasion-associated proteins)	Pgjcvi_01159	PG JCVI SC001	NLP/P60 family protein	PG TDC60	PGTDC60_1862	1, 173	98.3	352.4	0
hypothetical protein	Pgjcvi_01160	PG JCVI SC001	hypothetical protein	PG W83	PG2092	1, 419	99.8	844	0
hypothetical protein	Pgjcvi_01160	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1327	1, 352	99.7	709.1	0
hypothetical protein	Pgjcvi_01160	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0144	1, 419	99	837.8	0
dihydroneopterin aldolase	Pgjcvi_01161	PG JCVI SC001	probable dihydroneopterin aldolase	PG ATCC 33277	PGN_0143	1, 103	100	204.5	0
dihydroneopterin aldolase	Pgjcvi_01161	PG JCVI SC001	dihydroneopterin aldolase	PG W83	PG2091	1, 103	100	204.5	0
dihydroneopterin aldolase	Pgjcvi_01161	PG JCVI SC001	dihydroneopterin aldolase	PG TDC60	PGTDC60_1328	14, 116	100	204.5	0
cation diffusion facilitator family transporter	Pgjcvi_01162	PG JCVI SC001	putative cation efflux protein	PG ATCC 33277	PGN_0142	1, 302	100	595.1	0
cation diffusion facilitator family transporter	Pgjcvi_01162	PG JCVI SC001	cation efflux family protein	PG W83	PG2090	1, 302	100	595.1	0
cation diffusion facilitator family transporter	Pgjcvi_01162	PG JCVI SC001	cation efflux family protein	PG TDC60	PGTDC60_1329	1, 302	99.3	592.4	0
hypothetical protein	Pgjcvi_01163	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0141	1, 394	99.7	772.3	0
hypothetical protein	Pgjcvi_01163	PG JCVI SC001	hypothetical protein	PG W83	PG2089	1, 394	99.7	772.3	0
hypothetical protein	Pgjcvi_01163	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1330	1, 394	99.5	770.4	0
methionine-R-sulfoxide reductase/methionine-S-sulfoxide reductase	Pgjcvi_01164	PG JCVI SC001	bifunctional methionine sulfoxide reductase A/B protein	PG W83	PG2088	1, 352	99.7	721.1	0
methionine-R-sulfoxide reductase/methionine-S-sulfoxide reductase	Pgjcvi_01164	PG JCVI SC001	bifunctional methionine sulfoxide reductase A/B protein	PG TDC60	PGTDC60_1331	1, 352	99.7	720.3	0
methionine-R-sulfoxide reductase/methionine-S-sulfoxide reductase	Pgjcvi_01164	PG JCVI SC001	peptide methionine sulfoxide reductase	PG ATCC 33277	PGN_0140	1, 352	99.4	718.8	0
Uncharacterized conserved protein	Pgjcvi_01165	PG JCVI SC001	hypothetical protein	PG W83	PG2087	1, 157	100	307	0
Uncharacterized conserved protein	Pgjcvi_01165	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0139	1, 157	98.1	301.6	0
Uncharacterized conserved protein	Pgjcvi_01165	PG JCVI SC001	rRNA large subunit methyltransferase	PG TDC60	PGTDC60_1332	1, 157	98.1	302.4	0
Protein of unknown function (DUF3127).	Pgjcvi_01166	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0138	1, 139	100	295.8	0
Protein of unknown function (DUF3127).	Pgjcvi_01166	PG JCVI SC001	hypothetical protein	PG W83	PG2086	1, 139	100	295.8	0
Protein of unknown function (DUF3127).	Pgjcvi_01166	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1333	1, 139	100	295.8	0
tryptophanyl-tRNA synthetase	Pgjcvi_01167	PG JCVI SC001	putative tryptophanyl-tRNA synthetase	PG ATCC 33277	PGN_0137	1, 327	100	654.8	0
tryptophanyl-tRNA synthetase	Pgjcvi_01167	PG JCVI SC001	tryptophanyl-tRNA synthetase	PG W83	PG2085	1, 327	100	654.8	0
tryptophanyl-tRNA synthetase	Pgjcvi_01167	PG JCVI SC001	tryptophanyl-tRNA synthetase	PG TDC60	PGTDC60_1334	1, 327	99.7	650.6	0
hypothetical protein	Pgjcvi_01168	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0136	1, 363	98.1	706.1	0
hypothetical protein	Pgjcvi_01168	PG JCVI SC001	hypothetical protein	PG W83	PG2083	3, 365	98.1	707.2	0
hypothetical protein	Pgjcvi_01168	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1335	1, 363	97.5	701.8	0
Dipeptide/tripeptide permease	Pgjcvi_01169	PG JCVI SC001	putative H+/peptide symporter	PG TDC60	PGTDC60_1336	1, 510	100	1011.5	0
Dipeptide/tripeptide permease	Pgjcvi_01169	PG JCVI SC001	putative H+/peptide symporter	PG ATCC 33277	PGN_0135	1, 513	60.7	620.9	0
Dipeptide/tripeptide permease	Pgjcvi_01169	PG JCVI SC001	POT family protein	PG W83	PG2082	1, 513	60.7	620.9	0
biotin synthase	Pgjcvi_01170	PG JCVI SC001	biotin synthetase	PG TDC60	PGTDC60_1337	1, 330	98.8	654.1	0
biotin synthase	Pgjcvi_01170	PG JCVI SC001	biotin synthetase	PG W83	PG2081	1, 330	98.5	652.5	0
biotin synthase	Pgjcvi_01170	PG JCVI SC001	putative biotin synthetase	PG ATCC 33277	PGN_0134	23, 352	96.4	639.4	0
adenosylmethionine-8-amino-7-oxononanoate transaminase	Pgjcvi_01171	PG JCVI SC001	adenosylmethionine--8-amino-7-oxononanoate transaminase	PG TDC60	PGTDC60_1338	1, 433	99.5	871.7	0
adenosylmethionine-8-amino-7-oxononanoate transaminase	Pgjcvi_01171	PG JCVI SC001	adenosylmethionine--8-amino-7-oxononanoate transaminase	PG W83	PG2080	1, 433	98.4	862.8	0
adenosylmethionine-8-amino-7-oxononanoate transaminase	Pgjcvi_01171	PG JCVI SC001	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	PG ATCC 33277	PGN_0133	1, 433	98.2	862.1	0
hypothetical protein	Pgjcvi_01172	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0132	1, 158	100	327.8	0
hypothetical protein	Pgjcvi_01172	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1339	1, 158	99.4	323.6	0
hypothetical protein	Pgjcvi_01172	PG JCVI SC001	hypothetical protein	PG W83	PG2079	1, 158	98.1	321.2	0
Predicted ATPase (AAA+ superfamily)	Pgjcvi_01173	PG JCVI SC001	hypothetical protein	PG W83	PG2078	1, 390	99.5	779.6	0
Predicted ATPase (AAA+ superfamily)	Pgjcvi_01173	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1239	1, 390	99.5	780.8	0
Predicted ATPase (AAA+ superfamily)	Pgjcvi_01173	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0211	1, 390	99.2	779.2	0
hypothetical protein	Pgjcvi_01174	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1238	1, 70	100	145.2	1.70E-33
hypothetical protein	Pgjcvi_01174	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0213	2, 128	96.9	241.5	0
hypothetical protein	Pgjcvi_01174	PG JCVI SC001	hypothetical protein	PG W83	PG2077	2, 128	89.8	225.3	0
Protein of unknown function (DUF3078).	Pgjcvi_01175	PG JCVI SC001	hypothetical protein	PG W83	PG1786	1, 294	99.3	594.7	0
Protein of unknown function (DUF3078).	Pgjcvi_01175	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1349	1, 294	99	592.4	0
Protein of unknown function (DUF3078).	Pgjcvi_01175	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0109	1, 108	96.3	223	0
Predicted xylanase/chitin deacetylase	Pgjcvi_01177	PG JCVI SC001	probable polysaccharide deacetylase	PG ATCC 33277	PGN_1725	1, 264	99.2	547.4	0
Predicted xylanase/chitin deacetylase	Pgjcvi_01177	PG JCVI SC001	hypothetical protein	PG W83	PG1784	1, 264	99.2	547.4	0
Predicted xylanase/chitin deacetylase	Pgjcvi_01177	PG JCVI SC001	putative polysaccharide deacetylase	PG TDC60	PGTDC60_1351	1, 264	98.1	541.2	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01178	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG1783	1, 236	99.6	476.1	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01178	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_1352	1, 236	99.2	471.5	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01178	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1724	1, 231	99.1	465.3	0
Protein of unknown function (DUF2029).	Pgjcvi_01179	PG JCVI SC001	hypothetical protein	PG W83	PG1782	1, 395	99.2	790.4	0
Protein of unknown function (DUF2029).	Pgjcvi_01179	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1723	1, 395	99	788.9	0
Protein of unknown function (DUF2029).	Pgjcvi_01179	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1353	1, 395	98.7	783.1	0
uridine kinase	Pgjcvi_01180	PG JCVI SC001	putative uridine kinase	PG ATCC 33277	PGN_1722	1, 207	100	407.9	0
uridine kinase	Pgjcvi_01180	PG JCVI SC001	uridine kinase	PG W83	PG1781	1, 209	99.5	411	0
uridine kinase	Pgjcvi_01180	PG JCVI SC001	uridine kinase	PG TDC60	PGTDC60_1354	1, 209	99.5	411	0
7-keto-8-aminopelargonate synthetase and related enzymes	Pgjcvi_01181	PG JCVI SC001	8-amino-7-oxononanoate synthase	PG ATCC 33277	PGN_1721	1, 395	99.7	787.7	0
7-keto-8-aminopelargonate synthetase and related enzymes	Pgjcvi_01181	PG JCVI SC001	8-amino-7-oxononanoate synthase	PG W83	PG1780	1, 395	99.7	787.3	0
7-keto-8-aminopelargonate synthetase and related enzymes	Pgjcvi_01181	PG JCVI SC001	8-amino-7-oxononanoate synthase	PG TDC60	PGTDC60_1355	1, 395	99.5	786.6	0
Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	Pgjcvi_01182	PG JCVI SC001	conserved hypothetical protein with appr-1-p processing enzyme domain	PG ATCC 33277	PGN_1719	1, 164	98.8	334.7	0
Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	Pgjcvi_01182	PG JCVI SC001	hypothetical protein	PG W83	PG1779	1, 164	98.8	334.7	0
Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	Pgjcvi_01182	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1357	1, 164	98.8	334.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01183	PG JCVI SC001	hypothetical protein	PG W83	PG1778	1, 262	99.2	546.6	0

Uncharacterized protein conserved in bacteria	Pgjcvi_01183	PG JCVI SC001	probable UDP-2,3-diacylglucosamine hydrolase	PG ATCC 33277	PGN_1718	1, 262	98.9	546.6	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01183	PG JCVI SC001	putative UDP-2,3-diacylglucosamine hydrolase	PG TDC60	PGTDC60_1358	1, 276	98.6	572.8	0
Predicted metal-sulfur cluster biosynthetic enzyme	Pgjcvi_01184	PG JCVI SC001	hypothetical protein	PG W83	PG1777	1, 105	100	213.4	0
Predicted metal-sulfur cluster biosynthetic enzyme	Pgjcvi_01184	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1359	1, 105	100	213.4	0
Predicted metal-sulfur cluster biosynthetic enzyme	Pgjcvi_01184	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1717	1, 105	99	211.8	0
chaperone protein DnaJ	Pgjcvi_01185	PG JCVI SC001	chaperone protein DnaJ	PG ATCC 33277	PGN_1716	1, 383	99.7	773.1	0
chaperone protein DnaJ	Pgjcvi_01185	PG JCVI SC001	chaperone protein DnaJ	PG TDC60	PGTDC60_1360	1, 383	99.2	771.5	0
chaperone protein DnaJ	Pgjcvi_01185	PG JCVI SC001	dnaJ protein	PG W83	PG1776	1, 383	98.7	766.5	0
Molecular chaperone GrpE (heat shock protein)	Pgjcvi_01186	PG JCVI SC001	putative chaperone protein GrpE	PG ATCC 33277	PGN_1715	1, 194	99.5	384.4	0
Molecular chaperone GrpE (heat shock protein)	Pgjcvi_01186	PG JCVI SC001	grpE protein	PG W83	PG1775	1, 194	99.5	386	0
Molecular chaperone GrpE (heat shock protein)	Pgjcvi_01186	PG JCVI SC001	grpE protein	PG TDC60	PGTDC60_1361	1, 194	99.5	385.6	0
transcription-repair coupling factor (mfd)	Pgjcvi_01187	PG JCVI SC001	transcription-repair coupling factor	PG TDC60	PGTDC60_1362	1, 1122	98.8	2170.6	0
transcription-repair coupling factor (mfd)	Pgjcvi_01187	PG JCVI SC001	transcription-repair coupling factor	PG ATCC 33277	PGN_1714	1, 1122	98.5	2162.1	0
transcription-repair coupling factor (mfd)	Pgjcvi_01187	PG JCVI SC001	transcription-repair coupling factor	PG W83	PG1774	1, 1122	98.4	2162.5	0
Membrane-associated phospholipid phosphatase	Pgjcvi_01188	PG JCVI SC001	PAP2 superfamily protein	PG W83	PG1773	1, 445	99.3	895.2	0
Membrane-associated phospholipid phosphatase	Pgjcvi_01188	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1713	1, 445	98.9	891.7	0
Membrane-associated phospholipid phosphatase	Pgjcvi_01188	PG JCVI SC001	PAP2 superfamily protein	PG TDC60	PGTDC60_1363	1, 417	98.8	837.4	0
endonuclease III	Pgjcvi_01189	PG JCVI SC001	endonuclease III	PG W83	PG1772	1, 224	100	454.5	0
endonuclease III	Pgjcvi_01189	PG JCVI SC001	endonuclease III	PG TDC60	PGTDC60_1364	1, 224	100	454.5	0
endonuclease III	Pgjcvi_01189	PG JCVI SC001	putative endonuclease III	PG ATCC 33277	PGN_1712	1, 224	99.6	451.1	0
phenylalanyl-tRNA synthetase, alpha subunit	Pgjcvi_01190	PG JCVI SC001	phenylalanyl-tRNA synthetase alpha subunit	PG ATCC 33277	PGN_1711	58, 340	100	585.1	0
phenylalanyl-tRNA synthetase, alpha subunit	Pgjcvi_01190	PG JCVI SC001	phenylalanyl-tRNA synthetase alpha subunit	PG W83	PG1771	58, 340	100	585.1	0
phenylalanyl-tRNA synthetase, alpha subunit	Pgjcvi_01190	PG JCVI SC001	phenylalanyl-tRNA synthetase subunit alpha	PG TDC60	PGTDC60_1365	58, 340	99.6	583.6	0
hypothetical protein	Pgjcvi_01191	PG JCVI SC001	phenylalanyl-tRNA synthetase alpha subunit	PG ATCC 33277	PGN_1711	1, 42	100	83.2	3.60E-15
hypothetical protein	Pgjcvi_01191	PG JCVI SC001	phenylalanyl-tRNA synthetase alpha subunit	PG W83	PG1771	1, 42	100	83.2	3.60E-15
hypothetical protein	Pgjcvi_01191	PG JCVI SC001	phenylalanyl-tRNA synthetase subunit alpha	PG TDC60	PGTDC60_1365	1, 42	100	83.2	3.60E-15
hypothetical protein	Pgjcvi_01192	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1366	1, 188	97.3	379	0
Mg chelatase-related protein	Pgjcvi_01193	PG JCVI SC001	magnesium chelatase subunit ChlI	PG ATCC 33277	PGN_1708	1, 513	99.8	1011.1	0
Mg chelatase-related protein	Pgjcvi_01193	PG JCVI SC001	magnesium chelatase subunit ChlI	PG TDC60	PGTDC60_1368	1, 513	99.8	1011.1	0
Mg chelatase-related protein	Pgjcvi_01193	PG JCVI SC001	magnesium chelatase, subunit D/I family	PG W83	PG1768	1, 513	99.6	1008.8	0
Peroxiredoxin	Pgjcvi_01194	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1707	7, 346	99.7	672.5	0
Peroxiredoxin	Pgjcvi_01194	PG JCVI SC001	lipoprotein, putative	PG W83	PG1767	7, 346	98.5	661.8	0
Peroxiredoxin	Pgjcvi_01194	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1369	1, 339	98.2	657.9	0
Folate-dependent phosphoribosylglycinamide formyltransferase PurN	Pgjcvi_01195	PG JCVI SC001	probable phosphoribosylglycinamide formyltransferase	PG ATCC 33277	PGN_1706	1, 193	100	391.3	0
Folate-dependent phosphoribosylglycinamide formyltransferase PurN	Pgjcvi_01195	PG JCVI SC001	phosphoribosylglycinamide formyltransferase	PG TDC60	PGTDC60_1370	1, 193	99.5	388.7	0
Folate-dependent phosphoribosylglycinamide formyltransferase PurN	Pgjcvi_01195	PG JCVI SC001	phosphoribosylglycinamide formyltransferase	PG W83	PG1766	1, 193	97.9	387.9	0
acyl carrier protein	Pgjcvi_01196	PG JCVI SC001	putative acyl carrier protein	PG ATCC 33277	PGN_1705	1, 78	100	152.1	8.70E-36
acyl carrier protein	Pgjcvi_01196	PG JCVI SC001	acyl carrier protein	PG W83	PG1765	1, 78	100	152.1	8.70E-36
acyl carrier protein	Pgjcvi_01196	PG JCVI SC001	acyl carrier protein	PG TDC60	PGTDC60_1371	1, 78	100	152.1	8.70E-36
beta-ketoacyl-acyl-carrier-protein synthase II	Pgjcvi_01197	PG JCVI SC001	beta-ketoacyl-acyl-carrier-protein synthase II	PG ATCC 33277	PGN_1704	1, 418	100	832.8	0
beta-ketoacyl-acyl-carrier-protein synthase II	Pgjcvi_01197	PG JCVI SC001	3-oxoacyl-(acyl-carrier-protein) synthase II	PG W83	PG1764	1, 418	100	832.8	0
beta-ketoacyl-acyl-carrier-protein synthase II	Pgjcvi_01197	PG JCVI SC001	3-oxoacyl-(acyl-carrier-protein) synthase II	PG TDC60	PGTDC60_1372	1, 418	100	832.8	0
ribonuclease III, bacterial	Pgjcvi_01198	PG JCVI SC001	putative ribonuclease III	PG ATCC 33277	PGN_1703	1, 261	100	522.3	0
ribonuclease III, bacterial	Pgjcvi_01198	PG JCVI SC001	ribonuclease III	PG W83	PG1763	1, 237	99.6	474.2	0
ribonuclease III, bacterial	Pgjcvi_01198	PG JCVI SC001	ribonuclease III	PG TDC60	PGTDC60_1373	1, 237	99.6	474.2	0
protein-export membrane protein, SecD/SecF family	Pgjcvi_01199	PG JCVI SC001	protein-export membrane protein SecD/SecF	PG ATCC 33277	PGN_1702	1, 981	99.8	1870.5	0
protein-export membrane protein, SecD/SecF family	Pgjcvi_01199	PG JCVI SC001	protein-export membrane protein SecD/protein-export membrane protein SecF	PG W83	PG1762	1, 944	99.8	1800	0
protein-export membrane protein, SecD/SecF family	Pgjcvi_01199	PG JCVI SC001	bifunctional preprotein translocase subunit SecD/SecF	PG TDC60	PGTDC60_1374	1, 981	99.8	1869.4	0
Acetyltransferases	Pgjcvi_01200	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1701	1, 179	98.9	365.5	0
Acetyltransferases	Pgjcvi_01200	PG JCVI SC001	acetyltransferase	PG TDC60	PGTDC60_1375	1, 184	98.9	372.5	0
Acetyltransferases	Pgjcvi_01200	PG JCVI SC001	acetyltransferase, GNAT family	PG W83	PG1761	1, 184	98.4	370.9	0
ABC-type Mn/Zn transport systems, ATPase component	Pgjcvi_01201	PG JCVI SC001	probable metal uptake system ABC transporter ATP-binding protein	PG ATCC 33277	PGN_1700	1, 204	99	394.4	0
ABC-type Mn/Zn transport systems, ATPase component	Pgjcvi_01201	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG1760	1, 209	99	403.3	0
ABC-type Mn/Zn transport systems, ATPase component	Pgjcvi_01201	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1376	1, 209	99	403.3	0
ABC-type metal ion transport system, periplasmic component/surface adhesin	Pgjcvi_01202	PG JCVI SC001	probable zinc ABC transporter zinc-binding protein	PG ATCC 33277	PGN_1699	1, 315	99.7	630.9	0
ABC-type metal ion transport system, periplasmic component/surface adhesin	Pgjcvi_01202	PG JCVI SC001	adhesion protein, putative	PG W83	PG1759	1, 315	99	627.1	0
ABC-type metal ion transport system, periplasmic component/surface adhesin	Pgjcvi_01202	PG JCVI SC001	adhesion protein	PG TDC60	PGTDC60_1377	1, 315	99	627.1	0
ribosomal protein S15, bacterial/organelle	Pgjcvi_01203	PG JCVI SC001	putative 30S ribosomal protein S15	PG ATCC 33277	PGN_1698	1, 89	100	175.6	8.40E-43
ribosomal protein S15, bacterial/organelle	Pgjcvi_01203	PG JCVI SC001	ribosomal protein S15	PG W83	PG1758	1, 89	100	175.6	8.40E-43
ribosomal protein S15, bacterial/organelle	Pgjcvi_01203	PG JCVI SC001	30S ribosomal protein S15	PG TDC60	PGTDC60_1378	1, 89	100	175.6	8.40E-43
hypothetical protein	Pgjcvi_01204	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0030	31, 265	99.1	474.6	0
hypothetical protein	Pgjcvi_01204	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1697	109, 343	97.9	470.3	0
hypothetical protein	Pgjcvi_01204	PG JCVI SC001	hypothetical protein	PG W83	PG1757	109, 343	96.2	465.3	0
Fructose-1,6-bisphosphate aldolase	Pgjcvi_01206	PG JCVI SC001	fructose-1,6-bisphosphate aldolase	PG TDC60	PGTDC60_1381	1, 293	100	580.5	0
Fructose-1,6-bisphosphate aldolase	Pgjcvi_01206	PG JCVI SC001	putative fructose-bisphosphate aldolase class I	PG ATCC 33277	PGN_1695	1, 293	99.7	578.9	0
Fructose-1,6-bisphosphate aldolase	Pgjcvi_01206	PG JCVI SC001	fructose-bisphosphate aldolase	PG W83	PG1755	1, 293	99.7	578.9	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01207	PG JCVI SC001	hypothetical protein	PG W83	PG1754	7, 841	100	1711	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01207	PG JCVI SC001	putative alanyl dipeptidyl peptidase	PG TDC60	PGTDC60_1382	7, 841	99.9	1708	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01207	PG JCVI SC001	putative alanyl dipeptidyl peptidase	PG ATCC 33277	PGN_1694	7, 841	99.8	1708	0
selenium donor protein	Pgjcvi_01208	PG JCVI SC001	selenide, water dikinase	PG W83	PG1753	1, 348	100	694.5	0
selenium donor protein	Pgjcvi_01208	PG JCVI SC001	selenide, water dikinase	PG TDC60	PGTDC60_1383	1, 348	99.7	693	0
selenium donor protein	Pgjcvi_01208	PG JCVI SC001	selenide water dikinase	PG ATCC 33277	PGN_1693	1, 348	99.4	689.9	0

Protein of unknown function (DUF3343).	Pgjcvi_01209	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1692	1, 74	98.6	146.4	4.50E-34
Protein of unknown function (DUF3343).	Pgjcvi_01209	PG JCVI SC001	hypothetical protein	PG W83	PG1752	1, 74	98.6	146.4	4.50E-34
Protein of unknown function (DUF3343).	Pgjcvi_01209	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1384	1, 74	97.3	144.8	1.30E-33
cysteine desulfurase family protein	Pgjcvi_01210	PG JCVI SC001	aminotransferase, class V	PG TDC60	PGTDC60_1385	1, 376	98.9	748.8	0
cysteine desulfurase family protein	Pgjcvi_01210	PG JCVI SC001	putative cysteine desulfurase	PG ATCC 33277	PGN_1691	1, 376	98.4	741.1	0
cysteine desulfurase family protein	Pgjcvi_01210	PG JCVI SC001	aminotransferase, class V	PG W83	PG1751	1, 376	98.4	741.5	0
Alpha-L-fucosidase	Pgjcvi_01211	PG JCVI SC001	putative exported fucosidase	PG ATCC 33277	PGN_1690	1, 606	98.7	1224.5	0
Alpha-L-fucosidase	Pgjcvi_01211	PG JCVI SC001	alpha-1,3/4-fucosidase, putative	PG W83	PG1750	1, 606	98.7	1223	0
Alpha-L-fucosidase	Pgjcvi_01211	PG JCVI SC001	alpha-1,3/4-fucosidase	PG TDC60	PGTDC60_1386	1, 606	98.2	1215.3	0
Transketolase	Pgjcvi_01212	PG JCVI SC001	transketolase	PG ATCC 33277	PGN_1689	1, 675	99.9	1348.6	0
Transketolase	Pgjcvi_01212	PG JCVI SC001	transketolase	PG TDC60	PGTDC60_1387	1, 675	99.9	1348.6	0
Transketolase	Pgjcvi_01212	PG JCVI SC001	transketolase	PG W83	PG1748	1, 675	99.7	1345.9	0
ribose 5-phosphate isomerase B	Pgjcvi_01213	PG JCVI SC001	putative ribose 5-phosphate isomerase B	PG ATCC 33277	PGN_1688	1, 145	100	299.7	0
ribose 5-phosphate isomerase B	Pgjcvi_01213	PG JCVI SC001	ribose 5-phosphate isomerase B, putative	PG W83	PG1747	1, 145	100	299.7	0
ribose 5-phosphate isomerase B	Pgjcvi_01213	PG JCVI SC001	putative ribose 5-phosphate isomerase B	PG TDC60	PGTDC60_1388	1, 145	100	299.7	0
hypothetical protein	Pgjcvi_01214	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1687	1, 145	100	283.5	0
hypothetical protein	Pgjcvi_01214	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1389	1, 145	99.3	281.2	0
hypothetical protein	Pgjcvi_01214	PG JCVI SC001	hypothetical protein	PG W83	PG0278	1, 116	99.1	230.7	0
Malic enzyme	Pgjcvi_01215	PG JCVI SC001	malic enzyme	PG TDC60	PGTDC60_1391	1, 760	99.9	1498.4	0
Malic enzyme	Pgjcvi_01215	PG JCVI SC001	NADP-dependent malic enzyme	PG W83	PG0279	1, 759	99.6	1489.6	0
Malic enzyme	Pgjcvi_01215	PG JCVI SC001	NADP-dependent malate dehydrogenase	PG ATCC 33277	PGN_1685	1, 760	99.5	1493.8	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01216	PG JCVI SC001	ABC transporter, permease protein, putative	PG W83	PG0280	1, 442	99.1	880.2	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01216	PG JCVI SC001	putative ABC transporter permease protein	PG TDC60	PGTDC60_1393	1, 442	98.6	866.7	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01216	PG JCVI SC001	probable ABC transporter permease protein	PG ATCC 33277	PGN_1683	1, 442	98.2	871.3	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01217	PG JCVI SC001	probable ABC transporter permease protein	PG ATCC 33277	PGN_1682	1, 458	99.6	907.5	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01217	PG JCVI SC001	ABC transporter, permease protein, putative	PG W83	PG0281	1, 458	99.3	905.6	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01217	PG JCVI SC001	putative ABC transporter permease protein	PG TDC60	PGTDC60_1394	1, 458	99.3	907.1	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_01218	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_1681	1, 223	100	438.7	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_01218	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG0282	1, 223	100	438.7	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_01218	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1395	1, 223	100	438.7	0
Multidrug resistance efflux pump	Pgjcvi_01219	PG JCVI SC001	putative ABC transporter permease protein	PG ATCC 33277	PGN_1680	30, 445	99.3	790	0
Multidrug resistance efflux pump	Pgjcvi_01219	PG JCVI SC001	efflux transporter, MFP component, RND family	PG W83	PG0283	1, 416	98.8	786.6	0
Multidrug resistance efflux pump	Pgjcvi_01219	PG JCVI SC001	RND family efflux transporter MFP subunit	PG TDC60	PGTDC60_1396	1, 416	98.8	786.9	0
Outer membrane protein	Pgjcvi_01220	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1679	1, 501	99.4	975.3	0
Outer membrane protein	Pgjcvi_01220	PG JCVI SC001	hypothetical protein	PG W83	PG0285	1, 501	99.4	976.9	0
Outer membrane protein	Pgjcvi_01220	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1397	1, 501	99.2	973	0
Protein of unknown function (DUF2795).	Pgjcvi_01221	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1678	13, 85	100	157.1	2.50E-37
Protein of unknown function (DUF2795).	Pgjcvi_01221	PG JCVI SC001	hypothetical protein	PG W83	PG0286	13, 85	100	157.1	2.50E-37
Protein of unknown function (DUF2795).	Pgjcvi_01221	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1398	1, 73	100	157.1	2.50E-37
Bacteroidetes-specific putative membrane protein	Pgjcvi_01222	PG JCVI SC001	hypothetical protein	PG W83	PG0287	1, 313	98.7	625.2	0
Bacteroidetes-specific putative membrane protein	Pgjcvi_01222	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1399	1, 313	98.4	624.8	0
Bacteroidetes-specific putative membrane protein	Pgjcvi_01222	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1677	1, 313	98.1	623.6	0
Uncharacterized conserved protein	Pgjcvi_01223	PG JCVI SC001	lipoprotein, putative	PG W83	PG0288	1, 491	100	1015.4	0
Uncharacterized conserved protein	Pgjcvi_01223	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1676	1, 491	99.8	1013.1	0
Uncharacterized conserved protein	Pgjcvi_01223	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1400	1, 491	99.8	1013.4	0
gliding motility-associated protein GldL	Pgjcvi_01224	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1401	1, 309	100	605.9	0
gliding motility-associated protein GldL	Pgjcvi_01224	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1675	1, 309	99.7	604	0
gliding motility-associated protein GldL	Pgjcvi_01224	PG JCVI SC001	hypothetical protein	PG W83	PG0289	38, 346	99.7	604	0
gliding motility-associated protein GldM	Pgjcvi_01225	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1674	1, 516	100	1000.3	0
gliding motility-associated protein GldM	Pgjcvi_01225	PG JCVI SC001	hypothetical protein	PG W83	PG0290	1, 516	99.6	998	0
gliding motility-associated protein GldM	Pgjcvi_01225	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1402	1, 516	99.4	997.7	0
gliding motility associated protien GldN	Pgjcvi_01226	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1403	1, 359	99.7	719.9	0
gliding motility associated protien GldN	Pgjcvi_01226	PG JCVI SC001	hypothetical protein	PG W83	PG0291	3, 361	99.2	714.5	0
gliding motility associated protien GldN	Pgjcvi_01226	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1673	1, 359	98.9	713.8	0
Chromate transport protein ChrA	Pgjcvi_01227	PG JCVI SC001	probable chromate transport protein	PG ATCC 33277	PGN_1672	1, 193	99.5	381.7	0
Chromate transport protein ChrA	Pgjcvi_01227	PG JCVI SC001	putative chromate transport protein	PG TDC60	PGTDC60_1404	1, 196	98	383.6	0
Chromate transport protein ChrA	Pgjcvi_01228	PG JCVI SC001	probable chromate transport protein	PG ATCC 33277	PGN_1671	1, 197	98.5	380.6	0
Chromate transport protein ChrA	Pgjcvi_01228	PG JCVI SC001	putative chromate transport protein	PG TDC60	PGTDC60_1405	1, 197	97	378.6	0
Putative secretion activating protein	Pgjcvi_01229	PG JCVI SC001	conserved hypothetical protein with predicted lysozyme domain	PG ATCC 33277	PGN_1670	1, 192	99.5	392.5	0
Putative secretion activating protein	Pgjcvi_01229	PG JCVI SC001	secretion activator protein, putative	PG W83	PG0293	1, 192	99.5	392.5	0
Putative secretion activating protein	Pgjcvi_01229	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1406	1, 192	99.5	392.5	0
Uncharacterized conserved protein	Pgjcvi_01230	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1730	1, 307	99	621.3	0
Uncharacterized conserved protein	Pgjcvi_01230	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1415	1, 309	98.4	620.5	0
Uncharacterized conserved protein	Pgjcvi_01230	PG JCVI SC001	hypothetical protein	PG W83	PG1841	1, 307	98	614.8	0
hypothetical protein	Pgjcvi_01231	PG JCVI SC001	probable acetyltransferase	PG ATCC 33277	PGN_1729	1, 330	98.8	674.5	0
hypothetical protein	Pgjcvi_01231	PG JCVI SC001	acetyltransferase, GNAT family	PG W83	PG1842	1, 330	98.2	669.8	0
hypothetical protein	Pgjcvi_01231	PG JCVI SC001	acetyltransferase	PG TDC60	PGTDC60_1414	1, 339	97.9	682.6	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	1, 946	99.2	1900.2	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG ATCC 33277	PGN_1728	1, 946	96.9	1862	0

Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1380, 1630	90.4	470.7	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG ATCC 33277	PGN_1728	1304, 1392	61.1	107.1	3.90E-21
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	1306, 1394	58.9	102.4	9.70E-20
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1270, 1375	54.2	105.5	1.10E-20
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	525, 925	46.9	338.6	0
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	1575, 1651	37.2	50.4	0.00044
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG ATCC 33277	PGN_1728	1344, 1647	31	114.8	1.90E-23
Domain of unknown function (DUF2436)./Peptidase family C25, C terminal ig-like domain./Peptidase family C25./Propeptide_C25.	Pgjcvi_01233	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	10, 542	25.5	171.8	1.30E-40
Predicted glycosyltransferases	Pgjcvi_01234	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_1408	1, 296	98.6	582	0
Predicted glycosyltransferases	Pgjcvi_01234	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG0294	1, 296	98.3	579.7	0
Predicted glycosyltransferases	Pgjcvi_01234	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1668	1, 296	98	577.4	0
DNA protecting protein DprA	Pgjcvi_01235	PG JCVI SC001	DNA processing protein DprA, putative	PG W83	PG0295	1, 374	99.5	725.7	0
DNA protecting protein DprA	Pgjcvi_01235	PG JCVI SC001	DNA processing protein DprA	PG TDC60	PGTDC60_1409	1, 374	99.5	726.9	0
DNA protecting protein DprA	Pgjcvi_01235	PG JCVI SC001	putative DNA processing Smf-like protein	PG ATCC 33277	PGN_1667	1, 374	98.9	723.4	0
phosphoribosylformylglycinamidine synthase, single chain form	Pgjcvi_01236	PG JCVI SC001	phosphoribosylformylglycinamidine synthase	PG ATCC 33277	PGN_1666	1, 1234	99.5	2483.4	0
phosphoribosylformylglycinamidine synthase, single chain form	Pgjcvi_01236	PG JCVI SC001	phosphoribosylformylglycinamidine synthase	PG W83	PG0296	1, 1234	99.5	2483	0
phosphoribosylformylglycinamidine synthase, single chain form	Pgjcvi_01236	PG JCVI SC001	phosphoribosylformylglycinamidine synthase	PG TDC60	PGTDC60_1410	1, 1234	99.4	2480.3	0
hypothetical protein	Pgjcvi_01237	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1411	1, 56	96.4	109.4	4.60E-23
hypothetical protein	Pgjcvi_01237	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1664	1, 56	89.3	100.9	1.60E-20
hypothetical protein	Pgjcvi_01237	PG JCVI SC001	hypothetical protein	PG W83	PG0297	1, 56	89.3	100.5	2.20E-20
hypothetical protein	Pgjcvi_01238	PG JCVI SC001	partial transposase in ISPg3	PG ATCC 33277	PGN_1662	18, 112	100	202.2	0
hypothetical protein	Pgjcvi_01238	PG JCVI SC001	ISPg3, transposase	PG W83	PG1262	48, 122	70.7	107.8	2.30E-22
hypothetical protein	Pgjcvi_01239	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1661	1, 430	98.1	835.5	0
hypothetical protein	Pgjcvi_01239	PG JCVI SC001	TPR domain protein	PG W83	PG0300	1, 430	97.9	836.6	0
hypothetical protein	Pgjcvi_01239	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_1421	1, 430	97.2	831.6	0
Positive regulator of sigma E activity	Pgjcvi_01241	PG JCVI SC001	hypothetical protein	PG W83	PG0302	1, 140	98.6	272.3	0
Positive regulator of sigma E activity	Pgjcvi_01241	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1660	1, 127	98.4	247.3	0
Positive regulator of sigma E activity	Pgjcvi_01241	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1422	1, 140	97.9	270	0
Predicted NADH:ubiquinone oxidoreductase, subunit RnfB	Pgjcvi_01242	PG JCVI SC001	putative electron transport complex RnfABCDGE type B subunit	PG ATCC 33277	PGN_1659	1, 290	99.7	595.1	0
Predicted NADH:ubiquinone oxidoreductase, subunit RnfB	Pgjcvi_01242	PG JCVI SC001	ferredoxin	PG W83	PG0303	1, 290	99.3	593.2	0
Predicted NADH:ubiquinone oxidoreductase, subunit RnfB	Pgjcvi_01242	PG JCVI SC001	ferredoxin	PG TDC60	PGTDC60_1423	1, 290	99.3	593.2	0
electron transport complex, RnfABCDGE type, C subunit	Pgjcvi_01243	PG JCVI SC001	electron transport complex RnfABCDGE type C subunit	PG ATCC 33277	PGN_1658	1, 443	100	877.5	0
electron transport complex, RnfABCDGE type, C subunit	Pgjcvi_01243	PG JCVI SC001	electron transport complex, RnfABCDGE type, C subunit	PG W83	PG0304	1, 443	99.8	875.9	0
electron transport complex, RnfABCDGE type, C subunit	Pgjcvi_01243	PG JCVI SC001	electron transport complex RnfABCDGE type, C subunit	PG TDC60	PGTDC60_1424	1, 443	99.1	869.4	0
electron transport complex, RnfABCDGE type, D subunit	Pgjcvi_01244	PG JCVI SC001	electron transport complex RnfABCDGE type D subunit	PG ATCC 33277	PGN_1657	1, 327	100	647.1	0
electron transport complex, RnfABCDGE type, D subunit	Pgjcvi_01244	PG JCVI SC001	electron transport complex, RnfABCDGE type, D subunit	PG W83	PG0305	1, 327	100	647.1	0
electron transport complex, RnfABCDGE type, D subunit	Pgjcvi_01244	PG JCVI SC001	electron transport complex RnfABCDGE type, D subunit	PG TDC60	PGTDC60_1425	1, 327	100	647.1	0
electron transport complex, RnfABCDGE type, G subunit	Pgjcvi_01245	PG JCVI SC001	putative electron transport complex RnfABCDGE type G subunit	PG ATCC 33277	PGN_1656	1, 225	100	443.7	0
electron transport complex, RnfABCDGE type, G subunit	Pgjcvi_01245	PG JCVI SC001	electron transport complex, RnfABCDGE type, G subunit	PG TDC60	PGTDC60_1426	1, 225	96.4	429.5	0
electron transport complex, RnfABCDGE type, G subunit	Pgjcvi_01245	PG JCVI SC001	electron transport complex, RnfABCDGE type, G subunit	PG W83	PG0306	1, 215	96.3	410.6	0
electron transport complex, RnfABCDGE type, E subunit	Pgjcvi_01246	PG JCVI SC001	putative electron transport complex RnfABCDGE type E subunit	PG ATCC 33277	PGN_1655	1, 196	100	374.8	0
electron transport complex, RnfABCDGE type, E subunit	Pgjcvi_01246	PG JCVI SC001	NADH-ubiquinone oxidoreductase	PG W83	PG0307	1, 196	100	374.8	0
electron transport complex, RnfABCDGE type, E subunit	Pgjcvi_01246	PG JCVI SC001	electron transport complex RsxE subunit	PG TDC60	PGTDC60_1427	1, 196	100	374.8	0
electron transport complex, RnfABCDGE type, A subunit	Pgjcvi_01247	PG JCVI SC001	putative electron transport complex RnfABCDGE type A subunit	PG ATCC 33277	PGN_1654	1, 190	100	360.9	0
electron transport complex, RnfABCDGE type, A subunit	Pgjcvi_01247	PG JCVI SC001	electron transport complex, RnfABCDGE type, A subunit	PG W83	PG0308	1, 190	100	360.9	0
electron transport complex, RnfABCDGE type, A subunit	Pgjcvi_01247	PG JCVI SC001	electron transport complex, RnfABCDGE type, A subunit	PG TDC60	PGTDC60_1428	1, 190	100	360.9	0
Membrane-associated lipoprotein involved in thiamine biosynthesis	Pgjcvi_01248	PG JCVI SC001	thiamine biosynthesis lipoprotein ApbE	PG W83	PG0309	1, 337	99.4	674.9	0
Membrane-associated lipoprotein involved in thiamine biosynthesis	Pgjcvi_01248	PG JCVI SC001	putative thiamine biosynthesis lipoprotein ApbE	PG ATCC 33277	PGN_1653	1, 337	98.8	671.8	0
Membrane-associated lipoprotein involved in thiamine biosynthesis	Pgjcvi_01248	PG JCVI SC001	thiamine biosynthesis lipoprotein ApbE	PG TDC60	PGTDC60_1429	1, 337	98.8	672.9	0
Nitroreductase	Pgjcvi_01249	PG JCVI SC001	probable nitroreductase	PG ATCC 33277	PGN_1652	1, 179	100	372.1	0
Nitroreductase	Pgjcvi_01249	PG JCVI SC001	nitroreductase family protein	PG W83	PG0310	1, 179	99.4	370.9	0
Nitroreductase	Pgjcvi_01249	PG JCVI SC001	nitroreductase family protein	PG TDC60	PGTDC60_1430	1, 179	99.4	369	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01250	PG JCVI SC001	putative glycosyltransferase	PG ATCC 33277	PGN_1651	1, 317	100	640.2	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01250	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG0311	1, 317	99.7	638.6	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01250	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_1431	1, 317	99.4	636.3	0
hypothetical protein	Pgjcvi_01251	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1650	1, 179	99.4	363.2	0
hypothetical protein	Pgjcvi_01251	PG JCVI SC001	hypothetical protein	PG W83	PG0312	1, 179	99.4	365.9	0
hypothetical protein	Pgjcvi_01251	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1432	1, 179	97.2	359	0
ribosomal protein L21	Pgjcvi_01252	PG JCVI SC001	ribosomal protein L21	PG W83	PG0314	16, 120	100	208.8	0
ribosomal protein L21	Pgjcvi_01252	PG JCVI SC001	50S ribosomal protein L21	PG TDC60	PGTDC60_1434	1, 105	100	208.8	0
ribosomal protein L21	Pgjcvi_01252	PG JCVI SC001	putative 50S ribosomal protein L21	PG ATCC 33277	PGN_1648	1, 105	99	206.8	0
ribosomal protein L27	Pgjcvi_01253	PG JCVI SC001	putative 50S ribosomal protein L27	PG ATCC 33277	PGN_1647	1, 85	100	172.2	8.80E-42
ribosomal protein L27	Pgjcvi_01253	PG JCVI SC001	50S ribosomal protein L27	PG W83	PG0315	1, 85	100	172.2	8.80E-42
ribosomal protein L27	Pgjcvi_01253	PG JCVI SC001	50S ribosomal protein L27	PG TDC60	PGTDC60_1435	1, 85	100	172.2	8.80E-42

seryl-tRNA synthetase	Pgjcvi_01254	PG JCVI SC001	seryl-tRNA synthetase	PG W83	PG0316	1, 423	99.1	835.5	0
seryl-tRNA synthetase	Pgjcvi_01254	PG JCVI SC001	seryl-tRNA synthetase	PG TDC60	PGTDC60_1436	1, 423	99.1	837.4	0
seryl-tRNA synthetase	Pgjcvi_01254	PG JCVI SC001	seryl-tRNA synthetase	PG ATCC 33277	PGN_1646	1, 423	98.8	833.9	0
DNA alkylation repair enzyme./Peptidase family M49.	Pgjcvi_01255	PG JCVI SC001	putative dipeptidyl-peptidase III	PG ATCC 33277	PGN_1645	21, 906	98.2	1750.7	0
DNA alkylation repair enzyme./Peptidase family M49.	Pgjcvi_01255	PG JCVI SC001	putative dipeptidyl-peptidase III	PG TDC60	PGTDC60_1437	1, 886	98.1	1748	0
DNA alkylation repair enzyme./Peptidase family M49.	Pgjcvi_01255	PG JCVI SC001	peptidase, M49 family	PG W83	PG0317	1, 886	97.4	1739.2	0
hypothetical protein	Pgjcvi_01256	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0307	16, 69	57.4	52.4	9.80E-06
Protein of unknown function (DUF1573).	Pgjcvi_01257	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1643	1, 127	100	253.1	0
Protein of unknown function (DUF1573).	Pgjcvi_01257	PG JCVI SC001	hypothetical protein	PG W83	PG0319	16, 142	100	253.1	0
Protein of unknown function (DUF1573).	Pgjcvi_01257	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1438	1, 127	100	253.1	0
Protein of unknown function (DUF1573).	Pgjcvi_01258	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1642	1, 362	98.6	691	0
Protein of unknown function (DUF1573).	Pgjcvi_01258	PG JCVI SC001	hypothetical protein	PG W83	PG0320	1, 362	98.6	693	0
Protein of unknown function (DUF1573).	Pgjcvi_01258	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1439	1, 362	98.3	693	0
LAO/AO transport system ATPase	Pgjcvi_01259	PG JCVI SC001	arginine/ornithine transport system ATPase	PG TDC60	PGTDC60_1440	1, 368	100	734.2	0
LAO/AO transport system ATPase	Pgjcvi_01259	PG JCVI SC001	arginine/ornithine transport system ATPase	PG ATCC 33277	PGN_1641	1, 368	99.7	731.5	0
LAO/AO transport system ATPase	Pgjcvi_01259	PG JCVI SC001	arginine/ornithine transport system ATPase	PG W83	PG0321	1, 343	99.7	678.3	0
Na+/H+-dicarboxylate symporters	Pgjcvi_01260	PG JCVI SC001	serine/threonine transporter	PG ATCC 33277	PGN_1640	1, 392	99.7	753.8	0
Na+/H+-dicarboxylate symporters	Pgjcvi_01260	PG JCVI SC001	serine/threonine transporter	PG TDC60	PGTDC60_1441	1, 392	99.7	753.8	0
Na+/H+-dicarboxylate symporters	Pgjcvi_01260	PG JCVI SC001	serine/threonine transporter	PG W83	PG0322	1, 392	99.5	752.7	0
Uncharacterized conserved protein, contains double-stranded beta-helix domain	Pgjcvi_01261	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1639	1, 109	99.1	211.5	0
Uncharacterized conserved protein, contains double-stranded beta-helix domain	Pgjcvi_01261	PG JCVI SC001	hypothetical protein	PG W83	PG0323	1, 109	99.1	211.5	0
Uncharacterized conserved protein, contains double-stranded beta-helix domain	Pgjcvi_01261	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1442	1, 109	98.2	211.1	0
histidine ammonia-lyase	Pgjcvi_01262	PG JCVI SC001	histidine ammonia-lyase	PG TDC60	PGTDC60_1443	1, 497	99.8	980.7	0
histidine ammonia-lyase	Pgjcvi_01262	PG JCVI SC001	histidine ammonia-lyase	PG W83	PG0324	1, 497	99.6	979.2	0
histidine ammonia-lyase	Pgjcvi_01262	PG JCVI SC001	histidine ammonia-lyase	PG ATCC 33277	PGN_1638	1, 497	99.4	977.6	0
Methenyl tetrahydrofolate cyclohydrolase	Pgjcvi_01263	PG JCVI SC001	putative methenyltetrahydrofolate cyclohydrolase	PG ATCC 33277	PGN_1637	1, 209	100	396.4	0
Methenyl tetrahydrofolate cyclohydrolase	Pgjcvi_01263	PG JCVI SC001	hypothetical protein	PG W83	PG0325	1, 209	100	396.4	0
Methenyl tetrahydrofolate cyclohydrolase	Pgjcvi_01263	PG JCVI SC001	putative methenyltetrahydrofolate cyclohydrolase	PG TDC60	PGTDC60_1444	1, 209	99.5	394.8	0
hypothetical protein	Pgjcvi_01264	PG JCVI SC001	hypothetical protein	PG W83	PG0326	37, 411	99.7	780.8	0
hypothetical protein	Pgjcvi_01264	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1636	8, 382	99.5	780	0
hypothetical protein	Pgjcvi_01264	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1445	8, 382	99.5	780.4	0
hypothetical protein	Pgjcvi_01265	PG JCVI SC001	conserved hypothetical protein with nucleoside recognition domain	PG ATCC 33277	PGN_1635	1, 384	99.7	756.1	0
hypothetical protein	Pgjcvi_01265	PG JCVI SC001	hypothetical protein	PG W83	PG0327	1, 384	99.7	756.1	0
hypothetical protein	Pgjcvi_01265	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1446	1, 384	99.7	756.1	0
imidazolonepropionase	Pgjcvi_01266	PG JCVI SC001	imidazolonepropionase	PG W83	PG0328	8, 423	99.8	827.4	0
imidazolonepropionase	Pgjcvi_01266	PG JCVI SC001	imidazolonepropionase	PG TDC60	PGTDC60_1447	8, 423	99.8	827.4	0
imidazolonepropionase	Pgjcvi_01266	PG JCVI SC001	imidazolonepropionase	PG ATCC 33277	PGN_1634	8, 423	99.3	823.9	0
glutamate formiminotransferase	Pgjcvi_01267	PG JCVI SC001	formiminotransferase-cyclodeaminase	PG ATCC 33277	PGN_1633	1, 300	100	596.7	0
glutamate formiminotransferase	Pgjcvi_01267	PG JCVI SC001	formiminotransferase-cyclodeaminase-related protein	PG W83	PG0329	1, 300	99.7	595.1	0
glutamate formiminotransferase	Pgjcvi_01267	PG JCVI SC001	formiminotransferase-cyclodeaminase	PG TDC60	PGTDC60_1448	1, 294	99.7	585.5	0
DNA-binding protein, histone-like, putative	Pgjcvi_01268	PG JCVI SC001	piutative DNA-binding protein histone-like family	PG ATCC 33277	PGN_1631	1, 170	99.4	338.2	0
DNA-binding protein, histone-like, putative	Pgjcvi_01268	PG JCVI SC001	piutative DNA-binding protein histone-likefamily	PG TDC60	PGTDC60_1450	1, 170	99.4	338.2	0
DNA-binding protein, histone-like, putative	Pgjcvi_01268	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG0330	1, 171	98.8	337	0
transcription termination factor Rho	Pgjcvi_01269	PG JCVI SC001	transcription termination factor Rho	PG W83	PG0332	1, 658	99.2	1280.8	0
transcription termination factor Rho	Pgjcvi_01269	PG JCVI SC001	transcription termination factor Rho	PG TDC60	PGTDC60_1451	1, 658	99.2	1280	0
transcription termination factor Rho	Pgjcvi_01269	PG JCVI SC001	transcription termination factor Rho	PG ATCC 33277	PGN_1630	1, 658	99.1	1280	0
Predicted permeases	Pgjcvi_01270	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1452	1, 302	100	579.7	0
Predicted permeases	Pgjcvi_01270	PG JCVI SC001	hypothetical protein	PG W83	PG0333	1, 302	99.7	579.3	0
Predicted permeases	Pgjcvi_01270	PG JCVI SC001	conserved hypothetical protein with integral membrane domain DUF6	PG ATCC 33277	PGN_1629	56, 357	99.3	578.9	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01271	PG JCVI SC001	putative glycosyltransferases	PG ATCC 33277	PGN_1628	1, 319	99.7	633.6	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01271	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG0334	1, 319	97.5	626.3	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01271	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_1453	1, 319	97.2	625.2	0
4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	Pgjcvi_01272	PG JCVI SC001	probable 4-amino-4-deoxy-L-arabinose transferase	PG ATCC 33277	PGN_1627	1, 504	99.6	1018.1	0
tRNA dimethylallyltransferase	Pgjcvi_01273	PG JCVI SC001	tRNA delta(2)-isopentenylpyrophosphate transferase	PG W83	PG0335	1, 300	98.3	598.6	0
tRNA dimethylallyltransferase	Pgjcvi_01273	PG JCVI SC001	putative tRNA isopentenyltransferase	PG ATCC 33277	PGN_1626	1, 300	98	597.4	0
tRNA dimethylallyltransferase	Pgjcvi_01273	PG JCVI SC001	tRNA delta(2)-isopentenylpyrophosphate transferase	PG TDC60	PGTDC60_1454	1, 300	97.7	596.3	0
hypothetical protein	Pgjcvi_01274	PG JCVI SC001	hypothetical protein	PG W83	PG0336	1, 189	100	381.3	0
hypothetical protein	Pgjcvi_01274	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1455	1, 189	100	381.3	0
hypothetical protein	Pgjcvi_01274	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1625	1, 189	99.5	379.4	0
hypothetical protein	Pgjcvi_01275	PG JCVI SC001	hypothetical protein	PG W83	PG0338	1, 1175	97.6	2325.1	0
hypothetical protein	Pgjcvi_01275	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1623	807, 1119	89	558.9	0
hypothetical protein	Pgjcvi_01275	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1457	807, 1119	87.7	545.4	0
hypothetical protein	Pgjcvi_01275	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1623	1, 995	84.3	1698.7	0
hypothetical protein	Pgjcvi_01275	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1457	1, 995	83.4	1679.5	0
hypothetical protein	Pgjcvi_01276	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1458	2, 181	99.4	356.7	0
hypothetical protein	Pgjcvi_01276	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1622	2, 181	98.9	357.5	0
hypothetical protein	Pgjcvi_01276	PG JCVI SC001	hypothetical protein	PG W83	PG0339	2, 181	98.3	354	0
hypothetical protein	Pgjcvi_01277	PG JCVI SC001	hypothetical protein	PG W83	PG1222	1, 63	42.9	48.5	0.00014
methionine gamma-lyase	Pgjcvi_01278	PG JCVI SC001	methionine gamma-lyase	PG TDC60	PGTDC60_1459	7, 399	99.7	791.2	0
methionine gamma-lyase	Pgjcvi_01278	PG JCVI SC001	methionine gamma-lyase	PG ATCC 33277	PGN_1618	7, 399	99.5	790	0
methionine gamma-lyase	Pgjcvi_01278	PG JCVI SC001	methionine gamma-lyase	PG W83	PG0343	1, 393	99.5	790	0

Predicted phosphohydrolases	Pgjcvi_01279	PG JCVI SC001	probable metallophosphoesterase	PG ATCC 33277	PGN_1617	1, 489	99.8	1023.1	0
Predicted phosphohydrolases	Pgjcvi_01279	PG JCVI SC001	purple acid phosphatase	PG W83	PG0344	1, 489	99.6	1018.8	0
Predicted phosphohydrolases	Pgjcvi_01279	PG JCVI SC001	purple acid phosphatase	PG TDC60	PGTDC60_1460	1, 450	99.3	940.3	0
hypothetical protein	Pgjcvi_01280	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1616	1, 197	100	397.1	0
hypothetical protein	Pgjcvi_01280	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1461	1, 197	100	397.1	0
hypothetical protein	Pgjcvi_01280	PG JCVI SC001	hypothetical protein	PG W83	PG0345	1, 197	99.5	396.7	0
ribosome biogenesis GTP-binding protein YsxC/EngB	Pgjcvi_01281	PG JCVI SC001	ribosome biogenesis GTP-binding protein YsxC	PG TDC60	PGTDC60_1462	1, 201	100	404.4	0
ribosome biogenesis GTP-binding protein YsxC/EngB	Pgjcvi_01281	PG JCVI SC001	putative GTP-binding protein	PG ATCC 33277	PGN_1615	1, 201	99.5	402.1	0
ribosome biogenesis GTP-binding protein YsxC/EngB	Pgjcvi_01281	PG JCVI SC001	GTP-binding protein	PG W83	PG0346	1, 201	99.5	402.1	0
UDP-glucose-4-epimerase	Pgjcvi_01282	PG JCVI SC001	UDP-glucose 4-epimerase	PG W83	PG0347	1, 342	99.4	678.7	0
UDP-glucose-4-epimerase	Pgjcvi_01282	PG JCVI SC001	UDP-glucose 4-epimerase	PG ATCC 33277	PGN_1614	1, 342	98.8	676	0
UDP-glucose-4-epimerase	Pgjcvi_01282	PG JCVI SC001	UDP-glucose 4-epimerase	PG TDC60	PGTDC60_1463	1, 342	98.8	674.5	0
ATP-dependent DNA helicase RecG	Pgjcvi_01283	PG JCVI SC001	ATP-dependent DNA helicase RecG	PG ATCC 33277	PGN_1613	1, 698	99.9	1369.8	0
ATP-dependent DNA helicase RecG	Pgjcvi_01283	PG JCVI SC001	ATP-dependent DNA helicase RecG	PG W83	PG0348	1, 698	99.4	1365.1	0
ATP-dependent DNA helicase RecG	Pgjcvi_01283	PG JCVI SC001	ATP-dependent DNA helicase RecG	PG TDC60	PGTDC60_1464	1, 698	99.3	1362.4	0
Predicted phosphatase/phosphohexomutase	Pgjcvi_01284	PG JCVI SC001	putative beta-phosphoglucomutase	PG TDC60	PGTDC60_1465	7, 256	99.6	501.5	0
Predicted phosphatase/phosphohexomutase	Pgjcvi_01284	PG JCVI SC001	probable beta-phosphoglucomutase	PG ATCC 33277	PGN_1612	1, 250	99.2	499.6	0
Predicted phosphatase/phosphohexomutase	Pgjcvi_01284	PG JCVI SC001	hydrolase, haloacid dehalogenase-like family	PG W83	PG0349	1, 250	98.8	498.4	0
hypothetical protein	Pgjcvi_01285	PG JCVI SC001	internalin-like protein	PG TDC60	PGTDC60_1466	1, 485	95.7	911	0
hypothetical protein	Pgjcvi_01285	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1611	1, 485	95.3	907.9	0
hypothetical protein	Pgjcvi_01285	PG JCVI SC001	internalin-related protein	PG W83	PG0350	1, 484	95.3	902.5	0
BNR/Asp-box repeat.	Pgjcvi_01286	PG JCVI SC001	sialidase, putative	PG W83	PG0352	1, 526	97.1	1025	0
BNR/Asp-box repeat.	Pgjcvi_01286	PG JCVI SC001	putative sialidase	PG TDC60	PGTDC60_1468	1, 502	97	983	0
BNR/Asp-box repeat.	Pgjcvi_01286	PG JCVI SC001	probable sialidase	PG ATCC 33277	PGN_1608	1, 526	96.2	1017.7	0
Site-specific recombinase XerD	Pgjcvi_01288	PG JCVI SC001	integrase	PG TDC60	PGTDC60_2028	353, 403	80.4	82	7.80E-15
Site-specific recombinase XerD	Pgjcvi_01288	PG JCVI SC001	integrase	PG W83	PG1113	352, 402	53.7	63.2	3.70E-09
Site-specific recombinase XerD	Pgjcvi_01288	PG JCVI SC001	tyrosine type site-specific recombinase	PG ATCC 33277	PGN_0917	368, 401	50	42.7	0.0052
Domain of unknown function (DUF1896).	Pgjcvi_01289	PG JCVI SC001	hypothetical protein	PG W83	PG0816	1, 157	98.7	313.2	0
Domain of unknown function (DUF1896).	Pgjcvi_01289	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1950	1, 150	71.3	223.4	0
Domain of unknown function (DUF1896).	Pgjcvi_01289	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0844	4, 146	45.5	129.4	1.20E-28
hypothetical protein	Pgjcvi_01290	PG JCVI SC001	hypothetical protein	PG W83	PG0814	1, 115	99.1	221.9	0
hypothetical protein	Pgjcvi_01292	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0048	1, 137	60	169.9	7.20E-41
hypothetical protein	Pgjcvi_01292	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1034	1, 136	58.7	169.1	1.20E-40
hypothetical protein	Pgjcvi_01293	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0050	1, 424	78.3	696.8	0
hypothetical protein	Pgjcvi_01293	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1032	1, 424	77.4	691	0
hypothetical protein	Pgjcvi_01294	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0051	1, 84	78.6	148.7	1.00E-34
Phage-related lysozyme (muraminidase)	Pgjcvi_01295	PG JCVI SC001	lysozyme-related protein	PG W83	PG1441	1, 55	80	102.8	1.30E-20
Phage-related lysozyme (muraminidase)	Pgjcvi_01295	PG JCVI SC001	putative lysozyme	PG TDC60	PGTDC60_1028	1, 97	77.3	161.8	2.30E-38
Phage-related lysozyme (muraminidase)	Pgjcvi_01295	PG JCVI SC001	probable lysozyme	PG ATCC 33277	PGN_1286	9, 171	70.6	244.6	0
hypothetical protein	Pgjcvi_01296	PG JCVI SC001	probable conserved protein found in conjugate transposon	PG ATCC 33277	PGN_0056	1, 144	72.2	223.8	0
hypothetical protein	Pgjcvi_01296	PG JCVI SC001	conjugative transposon protein TraQ	PG TDC60	PGTDC60_1027	1, 148	71.6	221.9	0
hypothetical protein	Pgjcvi_01296	PG JCVI SC001	conjugative transposon protein TraQ	PG W83	PG1473	1, 154	50	165.2	2.00E-39
Conjugative transposon protein TraO.	Pgjcvi_01297	PG JCVI SC001	conjugative transposon protein TraO	PG W83	PG1474	3, 191	68.2	265.4	0
Conjugative transposon protein TraO.	Pgjcvi_01297	PG JCVI SC001	conjugative transposon protein TraO	PG TDC60	PGTDC60_2000	3, 191	67.2	263.1	0
Conjugative transposon protein TraO.	Pgjcvi_01297	PG JCVI SC001	putative conserved protein found in conjugate transposon TraO	PG ATCC 33277	PGN_0593	2, 191	32.8	97.8	4.80E-19
Bacteroides conjugative transposon TraN protein	Pgjcvi_01298	PG JCVI SC001	conjugative transposon protein TraN	PG TDC60	PGTDC60_1999	1, 300	68	392.5	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_01298	PG JCVI SC001	conjugative transposon protein TraN	PG W83	PG1475	127, 341	66.4	285.4	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_01298	PG JCVI SC001	conjugative transposon protein TraN	PG TDC60	PGTDC60_1999	86, 300	66.4	285	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_01298	PG JCVI SC001	conjugative transposon protein TraN	PG W83	PG1475	1, 341	65	426.8	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_01298	PG JCVI SC001	conserved protein found in conjugate transposon TraN	PG ATCC 33277	PGN_0594	2, 311	53.8	341.3	0
Bacteroides conjugative transposon TraM protein	Pgjcvi_01299	PG JCVI SC001	conjugative transposon protein TraM	PG W83	PG1476	35, 453	55.8	449.1	0
Bacteroides conjugative transposon TraM protein	Pgjcvi_01299	PG JCVI SC001	conjugative transposon protein TraM	PG TDC60	PGTDC60_1998	35, 453	55.1	445.3	0
Bacteroides conjugative transposon TraM protein	Pgjcvi_01299	PG JCVI SC001	putative conserved protein found in conjugate transposon TraM	PG ATCC 33277	PGN_0595	35, 450	32.6	229.9	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_01301	PG JCVI SC001	conjugative transposon protein TraK	PG W83	PG1478	1, 207	71.5	317.4	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_01301	PG JCVI SC001	conjugative transposon protein TraK	PG TDC60	PGTDC60_1996	1, 207	71	317	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_01301	PG JCVI SC001	putative conserved protein found in conjugate transposon TraK	PG ATCC 33277	PGN_0597	1, 207	63.8	289.3	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_01302	PG JCVI SC001	conjugative transposon protein TraJ	PG W83	PG1479	1, 344	75	531.2	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_01302	PG JCVI SC001	conjugative transposon protein TraJ	PG TDC60	PGTDC60_1995	5, 315	73.3	473.4	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_01302	PG JCVI SC001	conserved transmembrane protein found in conjugate transposon TraJ	PG ATCC 33277	PGN_0063	4, 350	57.7	402.9	0
hypothetical protein	Pgjcvi_01303	PG JCVI SC001	conjugative transposon protein TraI	PG W83	PG1480	4, 209	68.6	283.5	0
hypothetical protein	Pgjcvi_01303	PG JCVI SC001	conjugative transposon protein TraI	PG TDC60	PGTDC60_1994	4, 209	68.1	280.8	0
hypothetical protein	Pgjcvi_01303	PG JCVI SC001	putative conserved protein found in conjugate transposon TraI	PG ATCC 33277	PGN_0064	1, 209	61.7	256.5	0
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_01304	PG JCVI SC001	conjugative transposon protein TraG	PG W83	PG1481	1, 836	77.3	1337	0
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_01304	PG JCVI SC001	conjugative transposon protein TraG	PG TDC60	PGTDC60_1993	1, 836	77.3	1335.5	0
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_01304	PG JCVI SC001	conserved protein found in conjugate transposon TraG	PG ATCC 33277	PGN_0065	1, 830	71.4	1211.1	0
hypothetical protein	Pgjcvi_01305	PG JCVI SC001	conjugative transposon protein TraF	PG W83	PG1482	2, 92	76.9	154.8	1.90E-36
hypothetical protein	Pgjcvi_01305	PG JCVI SC001	conjugative transposon protein TraF	PG TDC60	PGTDC60_1992	2, 92	76.9	153.7	4.30E-36
hypothetical protein	Pgjcvi_01305	PG JCVI SC001	probable conserved transmembrane protein found in conjugate transposon TraF	PG ATCC 33277	PGN_0066	1, 116	53.4	135.6	1.20E-30
hypothetical protein	Pgjcvi_01306	PG JCVI SC001	conjugative transposon protein TraE	PG TDC60	PGTDC60_1991	1, 100	82	166.4	5.70E-40
hypothetical protein	Pgjcvi_01306	PG JCVI SC001	conjugative transposon protein TraE	PG W83	PG1483	1, 100	81	165.2	1.30E-39
hypothetical protein	Pgjcvi_01306	PG JCVI SC001	probable conserved transmembrane protein found in conjugate transposon TraE	PG ATCC 33277	PGN_0067	3, 99	78.4	156.4	5.90E-37
hypothetical protein	Pgjcvi_01308	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1955	1, 149	38.3	99.8	1.10E-19

CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_01309	PG JCVI SC001	conjugative transposon protein TraA	PG W83	PG1486	3, 263	45.4	236.1	0
CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_01309	PG JCVI SC001	conjugative transposon protein TraA	PG TDC60	PGTDC60_1988	3, 263	45	236.1	0
CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_01309	PG JCVI SC001	putative conserved protein found in conjugate transposon TraA	PG ATCC 33277	PGN_0073	2, 248	31	141.4	5.20E-32
hypothetical protein	Pgjcvi_01310	PG JCVI SC001	hypothetical protein	PG W83	PG1488	15, 129	50	119.8	8.40E-26
hypothetical protein	Pgjcvi_01310	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1986	15, 129	50	115.5	1.60E-24
Relaxase/Mobilisation nuclease domain.	Pgjcvi_01311	PG JCVI SC001	hypothetical protein	PG W83	PG1489	1, 412	49.6	392.5	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_01311	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1985	1, 412	48.4	389	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_01311	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0075	1, 410	40.1	299.3	0
Type IV secretory pathway, VirD4 components	Pgjcvi_01312	PG JCVI SC001	TraG family protein	PG TDC60	PGTDC60_1984	1, 655	85.5	1141.7	0
Type IV secretory pathway, VirD4 components	Pgjcvi_01312	PG JCVI SC001	TraG family protein	PG W83	PG1490	1, 667	84.3	1143.6	0
Type IV secretory pathway, VirD4 components	Pgjcvi_01312	PG JCVI SC001	putative mobilization protein TraG family	PG ATCC 33277	PGN_0076	1, 665	75.9	1065.8	0
Transposase	Pgjcvi_01313	PG JCVI SC001	ISPg2, transposase	PG W83	PG0277	1, 376	100	748.8	0
Transposase	Pgjcvi_01313	PG JCVI SC001	transposase in ISPg2	PG ATCC 33277	PGN_1394	1, 376	98.7	734.6	0
Transposase	Pgjcvi_01313	PG JCVI SC001	transposase in ISPg2	PG TDC60	PGTDC60_1232	5, 342	45.7	299.7	0
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_01316	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1000	1, 726	47.2	671.8	0
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_01316	PG JCVI SC001	ABC transporter, ATP-binding protein, putative	PG W83	PG1176	27, 561	26.7	185.3	8.40E-45
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_01316	PG JCVI SC001	ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0949	38, 572	26.2	186.4	4.20E-45
hypothetical protein	Pgjcvi_01321	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1970	221, 335	47.8	119.8	7.80E-26
hypothetical protein	Pgjcvi_01324	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1969	1, 469	60.6	563.1	0
hypothetical protein	Pgjcvi_01324	PG JCVI SC001	hypothetical protein	PG W83	PG1494	1, 437	59.5	521.5	0
hypothetical protein	Pgjcvi_01324	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0083	10, 464	46.6	399.4	0
Topoisomerase IA	Pgjcvi_01325	PG JCVI SC001	DNA topoisomerase III	PG TDC60	PGTDC60_1968	3, 694	58.8	800.4	0
Topoisomerase IA	Pgjcvi_01325	PG JCVI SC001	DNA topoisomerase III	PG W83	PG1495	3, 694	58.4	797	0
Topoisomerase IA	Pgjcvi_01325	PG JCVI SC001	DNA topoisomerase I	PG ATCC 33277	PGN_0582	4, 690	51.8	681	0
Helicase conserved C-terminal domain./Protein of unknown function (DUF2958).	Pgjcvi_01326	PG JCVI SC001	hypothetical protein	PG W83	PG0847	2, 506	93.5	937.2	0
Helicase conserved C-terminal domain./Protein of unknown function (DUF2958).	Pgjcvi_01326	PG JCVI SC001	DNA methylase	PG TDC60	PGTDC60_0992	343, 1780	59	1662.9	0
Helicase conserved C-terminal domain./Protein of unknown function (DUF2958).	Pgjcvi_01326	PG JCVI SC001	putative DNA methylase	PG ATCC 33277	PGN_0086	272, 1827	55.9	1662.9	0
Helicase conserved C-terminal domain./Protein of unknown function (DUF2958).	Pgjcvi_01326	PG JCVI SC001	DNA methylase	PG TDC60	PGTDC60_0992	3, 442	40.4	307	0
Helicase conserved C-terminal domain./Protein of unknown function (DUF2958).	Pgjcvi_01326	PG JCVI SC001	putative DNA methylase	PG ATCC 33277	PGN_0086	4, 466	39.3	305.8	0
Uncharacterized conserved protein	Pgjcvi_01327	PG JCVI SC001	hypothetical protein	PG W83	PG0848	1, 332	98.8	639.8	0
hypothetical protein	Pgjcvi_01328	PG JCVI SC001	hypothetical protein	PG W83	PG0849	22, 256	97.9	454.9	0
Predicted site-specific integrase-resolvase	Pgjcvi_01330	PG JCVI SC001	DNA binding protein, excisionase family, putative	PG W83	PG0850	1, 101	98	207.2	0
hypothetical protein	Pgjcvi_01331	PG JCVI SC001	hypothetical protein	PG W83	PG0851	1, 388	99.5	766.9	0
hypothetical protein	Pgjcvi_01331	PG JCVI SC001	TOPRIM domain-containing protein	PG TDC60	PGTDC60_0766	5, 678	57.5	795	0
hypothetical protein	Pgjcvi_01331	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0584	16, 436	51.6	450.7	0
hypothetical protein	Pgjcvi_01334	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1471	1, 263	98.5	543.9	0
hypothetical protein	Pgjcvi_01334	PG JCVI SC001	hypothetical protein	PG W83	PG0355	30, 327	98.3	608.2	0
hypothetical protein	Pgjcvi_01334	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1606	29, 327	97.3	604	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01335	PG JCVI SC001	hypothetical protein	PG W83	PG0356	16, 260	100	474.6	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01335	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1605	1, 245	99.6	473	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01335	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1472	1, 245	99.2	470.7	0
aspartate carbamoyltransferase	Pgjcvi_01336	PG JCVI SC001	aspartate carbamoyltransferase catalytic subunit	PG W83	PG0357	1, 304	100	607.4	0
aspartate carbamoyltransferase	Pgjcvi_01336	PG JCVI SC001	aspartate carbamoyltransferase, catalytic subunit	PG TDC60	PGTDC60_1473	1, 304	100	607.4	0
aspartate carbamoyltransferase	Pgjcvi_01336	PG JCVI SC001	aspartate carbamoyltransferase catalytic subunit	PG ATCC 33277	PGN_1604	1, 304	99.7	606.3	0
aspartate carbamoyltransferase, regulatory subunit	Pgjcvi_01337	PG JCVI SC001	aspartate carbamoyltransferase regulatory subunit	PG ATCC 33277	PGN_1603	6, 151	100	293.9	0
aspartate carbamoyltransferase, regulatory subunit	Pgjcvi_01337	PG JCVI SC001	aspartate carbamoyltransferase regulatory subunit	PG W83	PG0358	6, 151	100	293.9	0
aspartate carbamoyltransferase, regulatory subunit	Pgjcvi_01337	PG JCVI SC001	aspartate carbamoyltransferase, regulatory subunit	PG TDC60	PGTDC60_1474	6, 151	100	293.9	0
Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	Pgjcvi_01338	PG JCVI SC001	flavin reductase domain protein	PG W83	PG0359	1, 195	100	406.4	0
Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	Pgjcvi_01338	PG JCVI SC001	putative flavoredoxin	PG ATCC 33277	PGN_1602	1, 195	99.5	404.8	0
Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	Pgjcvi_01338	PG JCVI SC001	flavin reductase domain-containing protein	PG TDC60	PGTDC60_1475	1, 195	99.5	404.4	0
Uncharacterized conserved protein	Pgjcvi_01339	PG JCVI SC001	conserved hypothetical protein with lemA family domain	PG ATCC 33277	PGN_1601	3, 198	100	382.5	0
Uncharacterized conserved protein	Pgjcvi_01339	PG JCVI SC001	lemA protein	PG W83	PG0360	1, 196	100	382.5	0
Uncharacterized conserved protein	Pgjcvi_01339	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1476	3, 198	99	378.3	0
Beta-propeller domains of methanol dehydrogenase type	Pgjcvi_01340	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1477	1, 382	99.2	781.6	0
Beta-propeller domains of methanol dehydrogenase type	Pgjcvi_01340	PG JCVI SC001	hypothetical protein	PG W83	PG0361	1, 435	99.1	885.2	0
Beta-propeller domains of methanol dehydrogenase type	Pgjcvi_01340	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1600	1, 422	98.6	859.4	0
hypothetical protein	Pgjcvi_01341	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1478	35, 720	99.9	1410.2	0
hypothetical protein	Pgjcvi_01341	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1599	11, 696	99.6	1405.6	0
hypothetical protein	Pgjcvi_01341	PG JCVI SC001	hypothetical protein	PG W83	PG0362	37, 722	99.4	1407.9	0
Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein	Pgjcvi_01342	PG JCVI SC001	probable glutamine ABC transporter	PG ATCC 33277	PGN_1598	3, 275	98.9	535	0
Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein	Pgjcvi_01342	PG JCVI SC001	putative glutamine ABC transporter	PG TDC60	PGTDC60_1479	3, 275	98.9	533.9	0
Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein	Pgjcvi_01342	PG JCVI SC001	hypothetical protein	PG W83	PG0363	3, 275	98.2	529.6	0
Predicted SAM-dependent methyltransferases	Pgjcvi_01343	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1597	1, 401	99.3	796.6	0

Predicted SAM-dependent methyltransferases	Pgjcvi_01343	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1480	1, 401	99	795	0
Predicted SAM-dependent methyltransferases	Pgjcvi_01343	PG JCVI SC001	hypothetical protein	PG W83	PG0364	1, 401	98.5	791.6	0
Ribonuclease D	Pgjcvi_01344	PG JCVI SC001	probable 3'-5' exonuclease	PG ATCC 33277	PGN_1596	1, 200	99	388.7	0
Ribonuclease D	Pgjcvi_01344	PG JCVI SC001	3'-5' exonuclease domain-containing protein	PG TDC60	PGTDC60_1481	1, 200	99	388.7	0
Ribonuclease D	Pgjcvi_01344	PG JCVI SC001	3'-5' exonuclease domain protein	PG W83	PG0365	1, 188	98.9	367.5	0
hypothetical protein	Pgjcvi_01345	PG JCVI SC001	hypothetical protein	PG W83	PG0366	1, 186	99.5	371.7	0
hypothetical protein	Pgjcvi_01345	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1595	1, 186	98.9	370.2	0
hypothetical protein	Pgjcvi_01345	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1482	1, 186	98.4	366.7	0
Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	Pgjcvi_01347	PG JCVI SC001	DNA topoisomerase IV B subunit	PG ATCC 33277	PGN_1594	1, 644	100	1282.7	0
Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	Pgjcvi_01347	PG JCVI SC001	DNA topoisomerase IV subunit B	PG W83	PG0368	1, 644	99.8	1281.5	0
Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	Pgjcvi_01347	PG JCVI SC001	DNA topoisomerase IV, subunit B	PG TDC60	PGTDC60_1483	1, 644	99.7	1278.1	0
pantetheine-phosphate adenylyltransferase, bacterial	Pgjcvi_01348	PG JCVI SC001	putative phosphopantetheine adenylyltransferase	PG ATCC 33277	PGN_1593	1, 153	99.3	296.2	0
pantetheine-phosphate adenylyltransferase, bacterial	Pgjcvi_01348	PG JCVI SC001	phosphopantetheine adenylyltransferase	PG W83	PG0369	1, 153	99.3	296.2	0
pantetheine-phosphate adenylyltransferase, bacterial	Pgjcvi_01348	PG JCVI SC001	phosphopantetheine adenylyltransferase	PG TDC60	PGTDC60_1484	1, 153	99.3	296.2	0
hypothetical protein	Pgjcvi_01349	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1591	1, 222	99.1	450.3	0
hypothetical protein	Pgjcvi_01349	PG JCVI SC001	hypothetical protein	PG W83	PG0373	1, 222	98.2	446.4	0
hypothetical protein	Pgjcvi_01349	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1487	1, 222	97.3	441.8	0
ribosomal protein L13, bacterial type	Pgjcvi_01350	PG JCVI SC001	putative 50S ribosomal protein L13	PG ATCC 33277	PGN_1590	1, 151	99.3	312	0
ribosomal protein L13, bacterial type	Pgjcvi_01350	PG JCVI SC001	50S ribosomal protein L13	PG TDC60	PGTDC60_1490	1, 151	99.3	312	0
ribosomal protein L13, bacterial type	Pgjcvi_01350	PG JCVI SC001	50S ribosomal protein L13	PG W83	PG0375	1, 151	98.7	310.5	0
Ribosomal protein S9	Pgjcvi_01351	PG JCVI SC001	putative 30S ribosomal protein S9	PG ATCC 33277	PGN_1589	1, 128	100	250.8	0
Ribosomal protein S9	Pgjcvi_01351	PG JCVI SC001	30S ribosomal protein S9	PG W83	PG0376	1, 128	100	250.8	0
Ribosomal protein S9	Pgjcvi_01351	PG JCVI SC001	30S ribosomal protein S9	PG TDC60	PGTDC60_1491	1, 128	100	250.8	0
ribosomal protein S2, bacterial type	Pgjcvi_01352	PG JCVI SC001	putative 30S ribosomal protein S2	PG ATCC 33277	PGN_1588	1, 281	100	549.3	0
ribosomal protein S2, bacterial type	Pgjcvi_01352	PG JCVI SC001	30S ribosomal protein S2	PG W83	PG0377	1, 281	100	549.3	0
ribosomal protein S2, bacterial type	Pgjcvi_01352	PG JCVI SC001	30S ribosomal protein S2	PG TDC60	PGTDC60_1492	1, 281	100	549.3	0
translation elongation factor Ts	Pgjcvi_01353	PG JCVI SC001	putative translation elongation factor Ts	PG ATCC 33277	PGN_1587	1, 274	99.6	529.6	0
translation elongation factor Ts	Pgjcvi_01353	PG JCVI SC001	elongation factor Ts	PG W83	PG0378	1, 274	99.6	529.6	0
translation elongation factor Ts	Pgjcvi_01353	PG JCVI SC001	elongation factor Ts	PG TDC60	PGTDC60_1493	1, 274	99.6	529.6	0
excinuclease ABC, B subunit	Pgjcvi_01354	PG JCVI SC001	excinuclease ABC subunit B	PG W83	PG0380	1, 678	99.9	1328.9	0
excinuclease ABC, B subunit	Pgjcvi_01354	PG JCVI SC001	excinuclease ABC, B subunit	PG TDC60	PGTDC60_1495	1, 678	99.9	1329.3	0
excinuclease ABC, B subunit	Pgjcvi_01354	PG JCVI SC001	excinuclease ABC B subunit	PG ATCC 33277	PGN_1585	1, 678	99.7	1328.2	0
NhaP-type Na+/H+ and K+/H+ antiporters with a unique C-terminal domain	Pgjcvi_01355	PG JCVI SC001	putative sodium/hydrogen antiporter	PG ATCC 33277	PGN_1584	1, 506	99.4	973	0
NhaP-type Na+/H+ and K+/H+ antiporters with a unique C-terminal domain	Pgjcvi_01355	PG JCVI SC001	cell volume regulation protein CvrA	PG W83	PG0381	1, 506	99.4	973.4	0
NhaP-type Na+/H+ and K+/H+ antiporters with a unique C-terminal domain	Pgjcvi_01355	PG JCVI SC001	potassium/proton antiporter	PG TDC60	PGTDC60_1496	1, 506	99	969.1	0
RIP metalloprotease RseP	Pgjcvi_01356	PG JCVI SC001	membrane-associated zinc metalloprotease	PG TDC60	PGTDC60_1498	1, 439	99.5	863.2	0
RIP metalloprotease RseP	Pgjcvi_01356	PG JCVI SC001	membrane-associated zinc metalloprotease, putative	PG W83	PG0383	1, 439	99.1	860.1	0
RIP metalloprotease RseP	Pgjcvi_01356	PG JCVI SC001	membrane-associated zinc metalloprotease	PG ATCC 33277	PGN_1582	1, 439	98.6	855.1	0
Mismatch repair ATPase (MutS family)	Pgjcvi_01357	PG JCVI SC001	MutS2 family protein	PG TDC60	PGTDC60_1499	1, 840	98.9	1633.2	0
Mismatch repair ATPase (MutS family)	Pgjcvi_01357	PG JCVI SC001	MutS2 family protein	PG W83	PG0384	1, 840	98.8	1628.2	0
Mismatch repair ATPase (MutS family)	Pgjcvi_01357	PG JCVI SC001	DNA mismatch repair protein MutS	PG ATCC 33277	PGN_1581	1, 840	98.7	1624.8	0
ribosomal protein S21	Pgjcvi_01358	PG JCVI SC001	ribosomal protein S21	PG W83	PG0385	1, 63	100	122.5	5.90E-27
ribosomal protein S21	Pgjcvi_01358	PG JCVI SC001	30S ribosomal protein S21	PG TDC60	PGTDC60_1500	1, 63	100	122.5	5.90E-27
ribosomal protein S21	Pgjcvi_01358	PG JCVI SC001	putative 30S ribosomal protein S21	PG ATCC 33277	PGN_1580	1, 63	98.4	121.3	1.30E-26
ribosomal subunit interface protein	Pgjcvi_01359	PG JCVI SC001	site-specific recombinase, phage integrase family/ribosomal subunit interface protein	PG W83	PG0386	1, 400	99.2	782.3	0
ribosomal subunit interface protein	Pgjcvi_01359	PG JCVI SC001	phage integrase family site specific recombinase	PG TDC60	PGTDC60_1501	1, 400	99	780	0
ribosomal subunit interface protein	Pgjcvi_01359	PG JCVI SC001	putative site-specific recombinase	PG ATCC 33277	PGN_1579	1, 401	98.8	776.9	0
translation elongation factor TU	Pgjcvi_01362	PG JCVI SC001	elongation factor Tu	PG W83	PG0387	1, 395	100	797	0
translation elongation factor TU	Pgjcvi_01362	PG JCVI SC001	elongation factor Tu	PG TDC60	PGTDC60_1502	1, 395	100	797	0
translation elongation factor TU	Pgjcvi_01362	PG JCVI SC001	translation elongation factor Tu	PG ATCC 33277	PGN_1578	1, 395	99.7	795	0
preprotein translocase, SecE subunit, bacterial	Pgjcvi_01364	PG JCVI SC001	putative preprotein translocase SecE subunit	PG ATCC 33277	PGN_1577	1, 67	100	131	1.80E-29
preprotein translocase, SecE subunit, bacterial	Pgjcvi_01364	PG JCVI SC001	putative preprotein translocase SecE subunit	PG TDC60	PGTDC60_1503	1, 67	100	131	1.80E-29
transcription termination/antitermination factor NusG	Pgjcvi_01365	PG JCVI SC001	putative transcription antitermination protein	PG ATCC 33277	PGN_1576	1, 179	100	352.1	0
transcription termination/antitermination factor NusG	Pgjcvi_01365	PG JCVI SC001	transcription antitermination protein NusG	PG W83	PG0389	1, 179	100	352.1	0
transcription termination/antitermination factor NusG	Pgjcvi_01365	PG JCVI SC001	transcription antitermination protein NusG	PG TDC60	PGTDC60_1504	1, 179	100	352.1	0
50S ribosomal protein L11	Pgjcvi_01366	PG JCVI SC001	50S ribosomal protein L11	PG ATCC 33277	PGN_1575	1, 145	100	287.7	0
50S ribosomal protein L11	Pgjcvi_01366	PG JCVI SC001	50S ribosomal protein L11	PG W83	PG0390	1, 145	100	287.7	0
50S ribosomal protein L11	Pgjcvi_01366	PG JCVI SC001	50S ribosomal protein L11	PG TDC60	PGTDC60_1505	1, 145	99.3	286.2	0
ribosomal protein L1, bacterial/chloroplast	Pgjcvi_01367	PG JCVI SC001	50S ribosomal protein L1	PG ATCC 33277	PGN_1574	1, 232	100	453.8	0
ribosomal protein L1, bacterial/chloroplast	Pgjcvi_01367	PG JCVI SC001	50S ribosomal protein L1	PG W83	PG0391	1, 232	100	453.8	0
ribosomal protein L1, bacterial/chloroplast	Pgjcvi_01367	PG JCVI SC001	50S ribosomal protein L1	PG TDC60	PGTDC60_1506	1, 232	100	453.8	0
Ribosomal protein L10	Pgjcvi_01368	PG JCVI SC001	putative 50S ribosomal protein L10	PG ATCC 33277	PGN_1573	1, 174	100	340.9	0
Ribosomal protein L10	Pgjcvi_01368	PG JCVI SC001	50S ribosomal protein L10	PG TDC60	PGTDC60_1507	1, 174	100	340.9	0
Ribosomal protein L10	Pgjcvi_01368	PG JCVI SC001	ribosomal protein L10	PG W83	PG0392	1, 174	99.4	339.3	0
ribosomal protein L7/L12	Pgjcvi_01369	PG JCVI SC001	putative 50S ribosomal protein L7/L12	PG ATCC 33277	PGN_1572	1, 125	99.2	229.6	0
ribosomal protein L7/L12	Pgjcvi_01369	PG JCVI SC001	ribosomal protein L7/L12	PG W83	PG0393	1, 125	99.2	229.6	0
ribosomal protein L7/L12	Pgjcvi_01369	PG JCVI SC001	50S ribosomal protein L7/L12	PG TDC60	PGTDC60_1508	1, 125	99.2	229.6	0
DNA-directed RNA polymerase, beta subunit	Pgjcvi_01370	PG JCVI SC001	DNA-directed RNA polymerase beta subunit	PG ATCC 33277	PGN_1571	1, 1269	99.8	2516.1	0
DNA-directed RNA polymerase, beta subunit	Pgjcvi_01370	PG JCVI SC001	DNA-directed RNA polymerase beta subunit	PG W83	PG0394	1, 1269	99.8	2516.9	0
DNA-directed RNA polymerase, beta subunit	Pgjcvi_01370	PG JCVI SC001	DNA-directed RNA polymerase subunit beta	PG TDC60	PGTDC60_1509	1, 1269	99.8	2518	0
DNA-directed RNA polymerase, beta'' subunit, predominant form	Pgjcvi_01371	PG JCVI SC001	DNA-directed RNA polymerase, beta' subunit	PG TDC60	PGTDC60_1510	1, 1433	100	2815.4	0
DNA-directed RNA polymerase, beta'' subunit, predominant form	Pgjcvi_01371	PG JCVI SC001	DNA-directed RNA polymerase beta' subunit	PG ATCC 33277	PGN_1570	1, 1433	99.9	2813.1	0

DNA-directed RNA polymerase, beta'' subunit, predominant form	Pgjcvi_01371	PG JCVI SC001	DNA-directed RNA polymerase beta' subunit	PG W83	PG0395	1, 1433	99.9	2813.9	0
cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Pgjcvi_01372	PG JCVI SC001	probable transcriptional regulator Crp/Fnr family	PG ATCC 33277	PGN_1569	1, 232	100	458.8	0
cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Pgjcvi_01372	PG JCVI SC001	Crp/FNR family transcriptional regulator	PG TDC60	PGTDC60_1511	1, 232	100	458.8	0
cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Pgjcvi_01372	PG JCVI SC001	transcriptional regulator, Crp/Fnr family	PG W83	PG0396	1, 232	99.6	457.2	0
Protein of unknown function (DUF721).	Pgjcvi_01373	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1568	1, 96	100	186	0
Protein of unknown function (DUF721).	Pgjcvi_01373	PG JCVI SC001	hypothetical protein	PG W83	PG0397	1, 96	99	183.3	4.20E-45
Protein of unknown function (DUF721).	Pgjcvi_01373	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1512	1, 96	99	183.3	4.20E-45
recF protein	Pgjcvi_01374	PG JCVI SC001	DNA replication and repair protein RecF	PG TDC60	PGTDC60_1513	1, 364	100	727.6	0
recF protein	Pgjcvi_01374	PG JCVI SC001	putative DNA replication and repair protein RecF	PG ATCC 33277	PGN_1567	1, 364	99.5	723.8	0
recF protein	Pgjcvi_01374	PG JCVI SC001	recF protein	PG W83	PG0398	1, 364	99.2	720.7	0
gliding motility-associated lipoprotein GldH	Pgjcvi_01375	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1566	1, 176	100	357.1	0
gliding motility-associated lipoprotein GldH	Pgjcvi_01375	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1514	1, 176	98.9	354.4	0
gliding motility-associated lipoprotein GldH	Pgjcvi_01375	PG JCVI SC001	lipoprotein, putative	PG W83	PG0399	1, 176	98.3	353.2	0
Uncharacterized homolog of PSP1	Pgjcvi_01376	PG JCVI SC001	conserved hypothetical protein with PSP1 C-terminal conserved region	PG ATCC 33277	PGN_1565	1, 469	99.6	952.6	0
Uncharacterized homolog of PSP1	Pgjcvi_01376	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1515	1, 470	99.6	954.9	0
Uncharacterized homolog of PSP1	Pgjcvi_01376	PG JCVI SC001	hypothetical protein	PG W83	PG0400	1, 427	99.3	859.4	0
conserved hypothetical protein YmdA/YtgF	Pgjcvi_01377	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1564	1, 513	100	978	0
conserved hypothetical protein YmdA/YtgF	Pgjcvi_01377	PG JCVI SC001	hypothetical protein	PG W83	PG0401	1, 513	100	978	0
conserved hypothetical protein YmdA/YtgF	Pgjcvi_01377	PG JCVI SC001	phosphodiesterase	PG TDC60	PGTDC60_1516	1, 513	100	978	0
Cell division protein ZapA.	Pgjcvi_01378	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1562	1, 102	100	204.9	0
Cell division protein ZapA.	Pgjcvi_01378	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1517	1, 102	100	204.9	0
Cell division protein ZapA.	Pgjcvi_01378	PG JCVI SC001	hypothetical protein	PG W83	PG0403	1, 102	99	203.4	0
hypothetical protein	Pgjcvi_01379	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1561	1, 98	100	184.1	2.80E-45
hypothetical protein	Pgjcvi_01379	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1518	1, 98	100	184.1	2.80E-45
hypothetical protein	Pgjcvi_01379	PG JCVI SC001	hypothetical protein	PG W83	PG0404	1, 112	99.1	212.2	0
hypothetical protein	Pgjcvi_01380	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1521	1, 94	98.9	178.3	1.50E-43
hypothetical protein	Pgjcvi_01381	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1557	1, 273	99.6	537	0
hypothetical protein	Pgjcvi_01381	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1522	1, 273	98.5	531.9	0
hypothetical protein	Pgjcvi_01381	PG JCVI SC001	hypothetical protein	PG W83	PG0409	1, 273	97.1	525.8	0
Por secretion system C-terminal sorting domain	Pgjcvi_01382	PG JCVI SC001	hemagglutinin, putative	PG W83	PG0411	5, 925	99.1	1897.5	0
Por secretion system C-terminal sorting domain	Pgjcvi_01382	PG JCVI SC001	putative hemagglutinin	PG ATCC 33277	PGN_1556	5, 925	98.6	1891.3	0
Por secretion system C-terminal sorting domain	Pgjcvi_01382	PG JCVI SC001	hemagglutinin	PG TDC60	PGTDC60_1523	5, 925	98.6	1882.5	0
DNA mismatch repair protein MutL	Pgjcvi_01383	PG JCVI SC001	DNA mismatch repair protein MutL	PG W83	PG0412	1, 618	99	1196.4	0
DNA mismatch repair protein MutL	Pgjcvi_01383	PG JCVI SC001	DNA mismatch repair protein MutL	PG ATCC 33277	PGN_1555	1, 618	98.9	1194.9	0
DNA mismatch repair protein MutL	Pgjcvi_01383	PG JCVI SC001	DNA mismatch repair protein MutL	PG TDC60	PGTDC60_1524	1, 618	98.7	1193.7	0
hypothetical protein	Pgjcvi_01384	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1554	1, 114	100	230.3	0
hypothetical protein	Pgjcvi_01384	PG JCVI SC001	hypothetical protein	PG W83	PG0413	1, 114	100	230.3	0
hypothetical protein	Pgjcvi_01384	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1525	1, 114	100	230.3	0
hypothetical protein	Pgjcvi_01385	PG JCVI SC001	hypothetical protein	PG W83	PG0414	1, 626	99.7	1246.1	0
hypothetical protein	Pgjcvi_01385	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1553	1, 626	99.2	1241.5	0
hypothetical protein	Pgjcvi_01385	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1526	1, 626	98.6	1232.6	0
Parvulin-like peptidyl-prolyl isomerase	Pgjcvi_01386	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, PPIC-type	PG W83	PG0415	6, 460	100	898.7	0
Parvulin-like peptidyl-prolyl isomerase	Pgjcvi_01386	PG JCVI SC001	putative peptidyl-prolyl cis-trans isomerase	PG ATCC 33277	PGN_1552	6, 460	99.8	897.1	0
Parvulin-like peptidyl-prolyl isomerase	Pgjcvi_01386	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, PPIC-type	PG TDC60	PGTDC60_1527	1, 455	99.8	895.6	0
ATP-dependent DNA helicase RecQ	Pgjcvi_01387	PG JCVI SC001	ATP-dependent DNA helicase RecQ	PG W83	PG0416	1, 725	100	1436.4	0
ATP-dependent DNA helicase RecQ	Pgjcvi_01387	PG JCVI SC001	ATP-dependent DNA helicase RecQ	PG ATCC 33277	PGN_1551	1, 725	99.6	1431.8	0
ATP-dependent DNA helicase RecQ	Pgjcvi_01387	PG JCVI SC001	ATP-dependent DNA helicase RecQ	PG TDC60	PGTDC60_1528	1, 725	99.6	1432.5	0
endopeptidase Clp ATP-binding regulatory subunit (clpX)	Pgjcvi_01388	PG JCVI SC001	ATP-dependent Clp protease ATP-binding subunit ClpX	PG ATCC 33277	PGN_1550	15, 411	99.7	776.9	0
endopeptidase Clp ATP-binding regulatory subunit (clpX)	Pgjcvi_01388	PG JCVI SC001	ATP-dependent protease ATP-binding subunit	PG W83	PG0417	15, 411	99.7	776.9	0
endopeptidase Clp ATP-binding regulatory subunit (clpX)	Pgjcvi_01388	PG JCVI SC001	ATP-dependent protease ATP-binding subunit ClpX	PG TDC60	PGTDC60_1529	15, 411	99.5	775	0
Protease subunit of ATP-dependent Clp proteases	Pgjcvi_01389	PG JCVI SC001	ATP-dependent Clp protease, proteolytic subunit	PG TDC60	PGTDC60_1530	1, 228	99.6	448	0
Protease subunit of ATP-dependent Clp proteases	Pgjcvi_01389	PG JCVI SC001	ATP-dependent Clp protease, proteolytic subunit	PG W83	PG0418	1, 222	99.5	437.2	0
Protease subunit of ATP-dependent Clp proteases	Pgjcvi_01389	PG JCVI SC001	putative ATP-dependent Clp protease proteolytic subunit	PG ATCC 33277	PGN_1549	1, 222	99.1	435.6	0
Protein of unknown function (DUF2807).	Pgjcvi_01390	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1548	1, 286	99.7	547.4	0
Protein of unknown function (DUF2807).	Pgjcvi_01390	PG JCVI SC001	hypothetical protein	PG W83	PG0419	16, 301	99.7	548.5	0
Protein of unknown function (DUF2807).	Pgjcvi_01390	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1531	1, 286	99.7	548.1	0
Protein of unknown function (DUF2807).	Pgjcvi_01391	PG JCVI SC001	hypothetical protein	PG W83	PG0421	1, 285	100	549.7	0
Protein of unknown function (DUF2807).	Pgjcvi_01391	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1547	1, 285	98.6	543.5	0
Protein of unknown function (DUF2807).	Pgjcvi_01391	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1532	1, 265	98.1	504.6	0
hypothetical protein	Pgjcvi_01392	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1534	1, 39	97.4	87.4	2.10E-16
hypothetical protein	Pgjcvi_01392	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1545	1, 61	95.1	127.1	2.30E-28
hypothetical protein	Pgjcvi_01393	PG JCVI SC001	hypothetical protein	PG W83	PG0423	1, 80	100	168.7	1.30E-40
hypothetical protein	Pgjcvi_01393	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1535	1, 114	100	235.3	0
hypothetical protein	Pgjcvi_01393	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1544	1, 114	99.1	232.6	0
Orthopoxvirus protein of unknown function (DUF830).	Pgjcvi_01394	PG JCVI SC001	hypothetical protein	PG W83	PG0424	3, 221	100	438.7	0
Orthopoxvirus protein of unknown function (DUF830).	Pgjcvi_01394	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1543	1, 219	99.5	436.4	0
Orthopoxvirus protein of unknown function (DUF830).	Pgjcvi_01394	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1536	1, 219	99.5	435.6	0
Predicted esterase	Pgjcvi_01395	PG JCVI SC001	putative esterase	PG ATCC 33277	PGN_1542	1, 279	99.3	570.5	0
Predicted esterase	Pgjcvi_01395	PG JCVI SC001	esterase, putative	PG W83	PG0425	1, 256	98.4	526.6	0

Predicted esterase	Pgjcvi_01395	PG JCVI SC001	esterase	PG TDC60	PGTDC60_1537	1, 279	96.4	553.9	0
hypothetical protein	Pgjcvi_01396	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1541	1, 41	97.6	84.3	2.20E-15
hypothetical protein	Pgjcvi_01396	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1538	1, 41	97.6	84.3	2.20E-15
Cation/multidrug efflux pump	Pgjcvi_01397	PG JCVI SC001	putative ABC transport membrane protein	PG TDC60	PGTDC60_1539	1, 1055	99.1	2029.2	0
Cation/multidrug efflux pump	Pgjcvi_01397	PG JCVI SC001	putative ABC transport membrane protein	PG ATCC 33277	PGN_1540	1, 1043	99	2004.6	0
Cation/multidrug efflux pump	Pgjcvi_01397	PG JCVI SC001	heavy metal efflux pump, CzcA family	PG W83	PG0064	15, 524	22.8	137.9	2.30E-30
Outer membrane protein	Pgjcvi_01398	PG JCVI SC001	putative ABC transport system exported protein	PG ATCC 33277	PGN_1539	1, 496	99	965.3	0
Outer membrane protein	Pgjcvi_01398	PG JCVI SC001	putative ABC transport system exported protein	PG TDC60	PGTDC60_1540	1, 457	98.7	889	0
Cation/multidrug efflux pump	Pgjcvi_01399	PG JCVI SC001	putative cation efflux system	PG ATCC 33277	PGN_1538	1, 1023	98.8	1939.9	0
Cation/multidrug efflux pump	Pgjcvi_01399	PG JCVI SC001	putative cation efflux system	PG TDC60	PGTDC60_1541	1, 1010	98.7	1911	0
Cation/multidrug efflux pump	Pgjcvi_01399	PG JCVI SC001	AcrB/AcrD/AcrF family protein	PG W83	PG0540	834, 1022	32	120.2	4.80E-25
Cation/multidrug efflux pump	Pgjcvi_01399	PG JCVI SC001	AcrB/AcrD/AcrF family protein	PG W83	PG0540	8, 664	26.8	226.5	0
Cation/multidrug efflux pump	Pgjcvi_01399	PG JCVI SC001	AcrB/AcrD/AcrF family protein	PG W83	PG0540	92, 481	20.8	66.2	8.20E-09
RND family efflux transporter, MFP subunit	Pgjcvi_01400	PG JCVI SC001	putative cation efflux system protein	PG TDC60	PGTDC60_1542	1, 366	98.4	710.7	0
RND family efflux transporter, MFP subunit	Pgjcvi_01400	PG JCVI SC001	probable cation efflux system protein	PG ATCC 33277	PGN_1537	1, 366	97.5	703.7	0
hypothetical protein	Pgjcvi_01401	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1536	1, 346	98	679.9	0
hypothetical protein	Pgjcvi_01401	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1543	1, 318	97.8	626.3	0
hypothetical protein	Pgjcvi_01402	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1544	1, 350	99.7	702.6	0
hypothetical protein	Pgjcvi_01402	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1535	1, 350	98	689.5	0
hypothetical protein	Pgjcvi_01403	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1545	1, 355	97.2	694.9	0
hypothetical protein	Pgjcvi_01403	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1534	1, 355	96.9	691	0
Carbonic anhydrase	Pgjcvi_01404	PG JCVI SC001	putative carbonic anhydrase	PG ATCC 33277	PGN_1533	1, 242	99.2	471.1	0
Carbonic anhydrase	Pgjcvi_01404	PG JCVI SC001	putative carbonic anhydrase	PG TDC60	PGTDC60_1546	1, 242	99.2	466.8	0
Protein of unknown function (DUF1661).	Pgjcvi_01405	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1532	6, 70	95.4	125.9	5.60E-28
Protein of unknown function (DUF1661).	Pgjcvi_01405	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1547	1, 65	93.8	123.6	2.80E-27
Protein of unknown function (DUF1661).	Pgjcvi_01405	PG JCVI SC001	hypothetical protein	PG W83	PG1722	37, 93	77.2	88.2	1.30E-16
hypothetical protein	Pgjcvi_01406	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1531	1, 47	97.9	90.9	1.80E-17
2-oxoacid:acceptor oxidoreductase, alpha subunit	Pgjcvi_01407	PG JCVI SC001	putative 2-oxoglutarate ferredoxin oxidoreductase subunit	PG TDC60	PGTDC60_1549	1, 619	100	1241.5	0
2-oxoacid:acceptor oxidoreductase, alpha subunit	Pgjcvi_01407	PG JCVI SC001	putative 2-oxoglutarate ferredoxin oxidoreductase subunit	PG ATCC 33277	PGN_1530	1, 619	99.8	1237.6	0
2-oxoacid:acceptor oxidoreductase, alpha subunit	Pgjcvi_01407	PG JCVI SC001	pyruvate synthase	PG W83	PG0429	1, 619	99.7	1236.9	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	Pgjcvi_01408	PG JCVI SC001	putative oxidoreductase	PG ATCC 33277	PGN_1529	1, 335	100	684.9	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	Pgjcvi_01408	PG JCVI SC001	ferrodoxin oxidoreductase beta subunit	PG W83	PG0430	1, 335	99.4	681.8	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	Pgjcvi_01408	PG JCVI SC001	2-oxoglutarate ferredoxin oxidoreductase subunit beta	PG TDC60	PGTDC60_1550	1, 345	99.4	701.4	0
tRNA and rRNA cytosine-C5-methylases	Pgjcvi_01409	PG JCVI SC001	NOL1/NOP2/sun family protein	PG W83	PG0432	1, 468	98.3	946	0
tRNA and rRNA cytosine-C5-methylases	Pgjcvi_01409	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1528	1, 468	98.1	944.9	0
tRNA and rRNA cytosine-C5-methylases	Pgjcvi_01409	PG JCVI SC001	NOL1/NOP2/sun family protein	PG TDC60	PGTDC60_1552	1, 468	98.1	944.5	0
Predicted methyltransferases	Pgjcvi_01410	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1527	1, 236	99.6	475.7	0
Predicted methyltransferases	Pgjcvi_01410	PG JCVI SC001	tetrapyrrole methylase family protein	PG TDC60	PGTDC60_1553	1, 237	99.6	477.6	0
Predicted methyltransferases	Pgjcvi_01410	PG JCVI SC001	tetrapyrrole methylase family protein	PG W83	PG0433	1, 237	99.2	475.7	0
hypothetical protein	Pgjcvi_01411	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1554	1, 335	100	683.7	0
hypothetical protein	Pgjcvi_01411	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1526	1, 371	99.5	751.5	0
hypothetical protein	Pgjcvi_01411	PG JCVI SC001	hypothetical protein	PG W83	PG0434	1, 359	98.3	719.2	0
Capsular polysaccharide biosynthesis protein	Pgjcvi_01412	PG JCVI SC001	capsular polysaccharide biosythesis protein, putative	PG W83	PG0435	1, 247	99.2	484.2	0
Capsular polysaccharide biosynthesis protein	Pgjcvi_01412	PG JCVI SC001	putative capsular polysaccharide biosynthesis protein	PG TDC60	PGTDC60_1556	1, 247	98.8	482.6	0
Capsular polysaccharide biosynthesis protein	Pgjcvi_01412	PG JCVI SC001	probable capsular polysaccharide biosynthesis protein	PG ATCC 33277	PGN_1525	1, 247	98.4	481.1	0
capsular exopolysaccharide family	Pgjcvi_01413	PG JCVI SC001	capsular polysaccharide transport protein, putative	PG W83	PG0436	1, 822	99.6	1585.9	0
capsular exopolysaccharide family	Pgjcvi_01413	PG JCVI SC001	capsular polysaccharide transport protein	PG TDC60	PGTDC60_1557	1, 821	87.5	1409.8	0
capsular exopolysaccharide family	Pgjcvi_01413	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1524	1, 821	87.3	1406.7	0
Periplasmic protein involved in polysaccharide export	Pgjcvi_01414	PG JCVI SC001	polysaccharide export protein, BexD/CtrA/VexA family	PG W83	PG0437	1, 307	99.7	599	0
Periplasmic protein involved in polysaccharide export	Pgjcvi_01414	PG JCVI SC001	putative polysaccharide export outer membrane protein	PG ATCC 33277	PGN_1523	1, 267	94.8	498.8	0
Periplasmic protein involved in polysaccharide export	Pgjcvi_01414	PG JCVI SC001	BexD/CtrA/VexA family polysaccharide export protein	PG TDC60	PGTDC60_1558	1, 267	94.4	497.3	0
Protein of unknown function (Porph_ging).	Pgjcvi_01415	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1559	26, 315	98.3	576.2	0
Protein of unknown function (Porph_ging).	Pgjcvi_01415	PG JCVI SC001	hypothetical protein	PG W83	PG0438	26, 316	97.9	579.3	0
Protein of unknown function (Porph_ging).	Pgjcvi_01415	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1522	24, 313	95.5	561.6	0
Protein of unknown function (Porph_ging).	Pgjcvi_01416	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1521	9, 299	99.7	606.7	0
Protein of unknown function (Porph_ging).	Pgjcvi_01416	PG JCVI SC001	hypothetical protein	PG W83	PG0439	9, 299	98.6	599.7	0
Protein of unknown function (Porph_ging).	Pgjcvi_01416	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1560	1, 278	97.8	571.6	0
hypothetical protein	Pgjcvi_01417	PG JCVI SC001	hypothetical protein	PG W83	PG0441	2, 877	97.5	1704.5	0
hypothetical protein	Pgjcvi_01417	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1520	1, 876	97	1696	0
hypothetical protein	Pgjcvi_01417	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1561	2, 877	96.9	1700.3	0
hypothetical protein	Pgjcvi_01418	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1562	1, 86	90.7	157.1	4.20E-37
hypothetical protein	Pgjcvi_01418	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0717	18, 73	55.4	55.5	1.70E-06
hypothetical protein	Pgjcvi_01418	PG JCVI SC001	hypothetical protein	PG W83	PG0681	18, 73	53.6	53.5	6.50E-06
hypothetical protein	Pgjcvi_01419	PG JCVI SC001	hemagglutinin-related protein	PG ATCC 33277	PGN_1519	10, 348	99.7	674.9	0
hypothetical protein	Pgjcvi_01419	PG JCVI SC001	hemagglutinin-related protein	PG W83	PG0443	10, 348	99.7	674.9	0
hypothetical protein	Pgjcvi_01419	PG JCVI SC001	hemagglutinin-like protein	PG TDC60	PGTDC60_1563	1, 339	99.1	669.5	0
putative oligopeptide transporter, OPT family	Pgjcvi_01420	PG JCVI SC001	putative oligopeptide transporter	PG ATCC 33277	PGN_1518	1, 659	99.1	1277.3	0
putative oligopeptide transporter, OPT family	Pgjcvi_01420	PG JCVI SC001	putative oligopeptide transporter	PG TDC60	PGTDC60_1564	1, 659	99.1	1276.2	0
putative oligopeptide transporter, OPT family	Pgjcvi_01420	PG JCVI SC001	oligopeptide transporter, OPT family	PG W83	PG0444	1, 659	98.9	1271.5	0

peptidase T	Pgjcvi_01421	PG JCVI SC001	peptidase T	PG ATCC 33277	PGN_1517	1, 405	98	810.1	0
peptidase T	Pgjcvi_01421	PG JCVI SC001	peptidase T	PG TDC60	PGTDC60_1565	1, 405	98	810.4	0
peptidase T	Pgjcvi_01421	PG JCVI SC001	peptidase T	PG W83	PG0445	1, 405	97.5	809.7	0
Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	Pgjcvi_01422	PG JCVI SC001	thiF protein	PG W83	PG0446	1, 235	97.9	454.5	0
Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	Pgjcvi_01422	PG JCVI SC001	probable molybdopterin biosynthesis MoeB protein	PG ATCC 33277	PGN_1516	1, 249	96.8	474.9	0
Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	Pgjcvi_01422	PG JCVI SC001	thiF protein	PG TDC60	PGTDC60_1566	1, 235	96.2	446.8	0
pantothenate kinase, type III	Pgjcvi_01423	PG JCVI SC001	hypothetical protein	PG W83	PG0447	29, 272	99.6	477.6	0
pantothenate kinase, type III	Pgjcvi_01423	PG JCVI SC001	pantothenate kinase	PG TDC60	PGTDC60_1567	1, 244	99.2	476.1	0
pantothenate kinase, type III	Pgjcvi_01423	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1515	1, 244	98.8	475.7	0
hypothetical protein	Pgjcvi_01424	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1568	1, 434	99.8	881.7	0
hypothetical protein	Pgjcvi_01424	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1514	1, 434	99.5	879.8	0
hypothetical protein	Pgjcvi_01424	PG JCVI SC001	hypothetical protein	PG W83	PG0448	1, 434	99.1	870.9	0
hypothetical protein	Pgjcvi_01425	PG JCVI SC001	TPR domain protein	PG W83	PG0449	11, 460	100	914.8	0
hypothetical protein	Pgjcvi_01425	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_1569	1, 450	100	914.8	0
hypothetical protein	Pgjcvi_01425	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1513	1, 450	99.6	911.8	0
Protein of unknown function (DUF1239).	Pgjcvi_01426	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1512	1, 234	99.1	481.1	0
Protein of unknown function (DUF1239).	Pgjcvi_01426	PG JCVI SC001	hypothetical protein	PG W83	PG0450	3, 236	98.7	479.6	0
Protein of unknown function (DUF1239).	Pgjcvi_01426	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1570	1, 195	97.4	399.8	0
Hemolysins and related proteins containing CBS domains	Pgjcvi_01427	PG JCVI SC001	probable hemolysin	PG ATCC 33277	PGN_1511	1, 417	99.8	811.2	0
Hemolysins and related proteins containing CBS domains	Pgjcvi_01427	PG JCVI SC001	CBS domain protein	PG W83	PG0451	1, 417	99.8	811.2	0
Hemolysins and related proteins containing CBS domains	Pgjcvi_01427	PG JCVI SC001	CBS domain-containing protein	PG TDC60	PGTDC60_1571	1, 417	99.8	811.2	0
PPIC-type PPIASE domain.	Pgjcvi_01428	PG JCVI SC001	putative peptidyl-prolyl cis-trans isomerase	PG ATCC 33277	PGN_1510	1, 715	99.6	1378.6	0
PPIC-type PPIASE domain.	Pgjcvi_01428	PG JCVI SC001	hypothetical protein	PG W83	PG0452	1, 715	99.4	1375.1	0
PPIC-type PPIASE domain.	Pgjcvi_01428	PG JCVI SC001	putative peptidyl-prolyl cis-trans isomerase	PG TDC60	PGTDC60_1572	1, 715	99.4	1376.7	0
Predicted membrane protein	Pgjcvi_01429	PG JCVI SC001	hypothetical protein	PG W83	PG0453	1, 424	99.8	823.5	0
Predicted membrane protein	Pgjcvi_01429	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1573	1, 410	99.3	790	0
Predicted membrane protein	Pgjcvi_01429	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1509	1, 424	98.6	815.8	0
Nitrate/nitrite transporter	Pgjcvi_01432	PG JCVI SC001	transporter	PG TDC60	PGTDC60_1579	1, 467	99.6	905.2	0
Nitrate/nitrite transporter	Pgjcvi_01432	PG JCVI SC001	transporter, putative	PG W83	PG0462	1, 467	99.4	903.7	0
Nitrate/nitrite transporter	Pgjcvi_01432	PG JCVI SC001	putative transporter	PG ATCC 33277	PGN_1506	1, 467	99.1	903.3	0
folylpolyglutamate synthase/dihydrofolate synthase	Pgjcvi_01433	PG JCVI SC001	putative folylpolyglutamate synthase	PG ATCC 33277	PGN_1505	1, 428	97.9	833.6	0
folylpolyglutamate synthase/dihydrofolate synthase	Pgjcvi_01433	PG JCVI SC001	folylpolyglutamate synthase	PG TDC60	PGTDC60_1580	1, 429	97.9	834.7	0
folylpolyglutamate synthase/dihydrofolate synthase	Pgjcvi_01433	PG JCVI SC001	folylpolyglutamate synthase	PG W83	PG0463	1, 429	97.7	833.2	0
adenylosuccinate synthase	Pgjcvi_01434	PG JCVI SC001	adenylosuccinate synthetase	PG ATCC 33277	PGN_1504	1, 423	99.3	849.7	0
adenylosuccinate synthase	Pgjcvi_01434	PG JCVI SC001	adenylosuccinate synthetase	PG W83	PG0464	1, 423	99.1	847.4	0
adenylosuccinate synthase	Pgjcvi_01434	PG JCVI SC001	adenylosuccinate synthetase	PG TDC60	PGTDC60_1581	1, 423	99.1	845.9	0
Fe2+/Zn2+ uptake regulation proteins	Pgjcvi_01435	PG JCVI SC001	ferric uptake transcriptional regulator	PG W83	PG0465	1, 166	100	336.3	0
Fe2+/Zn2+ uptake regulation proteins	Pgjcvi_01435	PG JCVI SC001	probable ferric uptake transcriptional regulator	PG ATCC 33277	PGN_1503	1, 166	99.4	335.5	0
Fe2+/Zn2+ uptake regulation proteins	Pgjcvi_01435	PG JCVI SC001	ferric uptake transcriptional regulator	PG TDC60	PGTDC60_1582	1, 166	99.4	335.5	0
Protein of unknown function (DUF3298).	Pgjcvi_01436	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1502	1, 290	100	574.3	0
Protein of unknown function (DUF3298).	Pgjcvi_01436	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1583	1, 290	99.3	569.7	0
Protein of unknown function (DUF3298).	Pgjcvi_01436	PG JCVI SC001	hypothetical protein	PG W83	PG0466	1, 251	99.2	498.4	0
Phosphomannose isomerase	Pgjcvi_01437	PG JCVI SC001	putative mannose-6-phosphate isomerase	PG ATCC 33277	PGN_1501	1, 336	99.7	688.3	0
Phosphomannose isomerase	Pgjcvi_01437	PG JCVI SC001	mannose-6-phosphate isomerase, class I	PG W83	PG0468	1, 336	99.4	686.4	0
Phosphomannose isomerase	Pgjcvi_01437	PG JCVI SC001	mannose-6-phosphate isomerase, class I	PG TDC60	PGTDC60_1584	1, 336	99.1	684.9	0
hypothetical protein	Pgjcvi_01438	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1585	1, 83	100	169.1	7.30E-41
hypothetical protein	Pgjcvi_01438	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1500	1, 83	98.8	166.8	3.60E-40
hypothetical protein	Pgjcvi_01438	PG JCVI SC001	hypothetical protein	PG W83	PG0469	1, 83	98.8	167.5	2.10E-40
hypothetical protein	Pgjcvi_01439	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1498	1, 352	99.7	691	0
hypothetical protein	Pgjcvi_01439	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1588	1, 352	99.7	691	0
hypothetical protein	Pgjcvi_01439	PG JCVI SC001	hypothetical protein	PG W83	PG0471	3, 354	98.9	682.9	0
Uncharacterized Fe-S protein	Pgjcvi_01440	PG JCVI SC001	putative iron-sulfur cluster binding protein	PG ATCC 33277	PGN_1497	52, 323	100	570.5	0
Uncharacterized Fe-S protein	Pgjcvi_01440	PG JCVI SC001	iron-sulfur cluster binding protein, putative	PG W83	PG0472	60, 331	100	570.5	0
Uncharacterized Fe-S protein	Pgjcvi_01440	PG JCVI SC001	iron-sulfur cluster binding protein	PG TDC60	PGTDC60_1589	60, 331	100	570.5	0
hypothetical protein	Pgjcvi_01441	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1496	46, 121	100	154.8	1.40E-36
hypothetical protein	Pgjcvi_01441	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1590	46, 121	98.7	153.3	4.00E-36
Threonine aldolase	Pgjcvi_01442	PG JCVI SC001	low-specificity L-threonine aldolase	PG W83	PG0474	1, 345	99.7	694.9	0
Threonine aldolase	Pgjcvi_01442	PG JCVI SC001	low-specificity L-threonine aldolase	PG TDC60	PGTDC60_1591	1, 345	98	682.6	0
Threonine aldolase	Pgjcvi_01442	PG JCVI SC001	putative low-specificity L-threonine aldolase	PG ATCC 33277	PGN_1495	1, 344	96.8	670.6	0
putative oxygen-independent coproporphyrinogen III oxidase	Pgjcvi_01443	PG JCVI SC001	oxygen-independent coproporphyrinogen III oxidase, putative	PG W83	PG0475	1, 376	99.5	753.4	0
putative oxygen-independent coproporphyrinogen III oxidase	Pgjcvi_01443	PG JCVI SC001	oxygen-independent coproporphyrinogen III oxidase	PG TDC60	PGTDC60_1592	1, 376	98.9	748.8	0
putative oxygen-independent coproporphyrinogen III oxidase	Pgjcvi_01443	PG JCVI SC001	putative oxygen-independent coproporphyrinogen III oxidase	PG ATCC 33277	PGN_1494	1, 376	98.7	747.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01444	PG JCVI SC001	yngK protein	PG TDC60	PGTDC60_1593	1, 515	99.2	1052.4	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01444	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1493	1, 515	98.8	1047.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01444	PG JCVI SC001	yngK protein	PG W83	PG0476	1, 515	98.6	1046.2	0
pantoate--beta-alanine ligase	Pgjcvi_01445	PG JCVI SC001	pantoate--beta-alanine ligase	PG W83	PG0477	1, 281	99.3	563.9	0
pantoate--beta-alanine ligase	Pgjcvi_01445	PG JCVI SC001	pantoate--beta-alanine ligase	PG TDC60	PGTDC60_1594	1, 281	99.3	564.3	0
pantoate--beta-alanine ligase	Pgjcvi_01445	PG JCVI SC001	putative pantoate-beta-alanine ligase	PG ATCC 33277	PGN_1492	1, 281	98.6	560.5	0
hypothetical protein	Pgjcvi_01446	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1491	9, 252	98.4	506.1	0

hypothetical protein	Pgjcvi_01446	PG JCVI SC001	hypothetical protein	PG W83	PG0479	16, 259	98.4	510.8	0
hypothetical protein	Pgjcvi_01446	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1595	9, 252	98	509.6	0
Precorrin-2 methylase	Pgjcvi_01447	PG JCVI SC001	precorrin-2 C20-methyltransferase	PG TDC60	PGTDC60_1596	1, 237	99.6	470.3	0
Precorrin-2 methylase	Pgjcvi_01447	PG JCVI SC001	probable precorrin-2 C20-methyltransferase	PG ATCC 33277	PGN_1490	1, 237	99.2	468	0
Precorrin-2 methylase	Pgjcvi_01447	PG JCVI SC001	precorrin-2 C20-methyltransferase, putative	PG W83	PG0480	1, 237	99.2	467.6	0
2-amino-3-ketobutyrate coenzyme A ligase	Pgjcvi_01448	PG JCVI SC001	2-amino-3-ketobutyrate coenzyme A ligase	PG W83	PG0481	1, 396	100	792.7	0
2-amino-3-ketobutyrate coenzyme A ligase	Pgjcvi_01448	PG JCVI SC001	2-amino-3-ketobutyrate coenzyme A ligase	PG TDC60	PGTDC60_1597	1, 396	99.5	788.5	0
2-amino-3-ketobutyrate coenzyme A ligase	Pgjcvi_01448	PG JCVI SC001	2-amino-3-ketobutyrate CoA ligase	PG ATCC 33277	PGN_1489	1, 396	99	787.3	0
hypothetical protein	Pgjcvi_01449	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1488	1, 143	100	285.8	0
hypothetical protein	Pgjcvi_01449	PG JCVI SC001	hypothetical protein	PG W83	PG0482	1, 143	100	285.8	0
hypothetical protein	Pgjcvi_01449	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1598	1, 143	99.3	283.1	0
dephospho-CoA kinase	Pgjcvi_01450	PG JCVI SC001	probable dephospho-CoA kinase	PG ATCC 33277	PGN_1487	1, 202	99.5	396.7	0
dephospho-CoA kinase	Pgjcvi_01450	PG JCVI SC001	kinase, putative	PG W83	PG0483	1, 202	98.5	391.3	0
dephospho-CoA kinase	Pgjcvi_01450	PG JCVI SC001	putative dephospho-CoA kinase	PG TDC60	PGTDC60_1599	1, 202	97	389	0
YbbR-like protein.	Pgjcvi_01451	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1600	1, 335	100	656.8	0
YbbR-like protein.	Pgjcvi_01451	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1486	1, 335	99.7	655.2	0
YbbR-like protein.	Pgjcvi_01451	PG JCVI SC001	hypothetical protein	PG W83	PG0484	1, 335	99.7	656.4	0
preprotein translocase, YajC subunit	Pgjcvi_01452	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1485	1, 112	100	218.4	0
preprotein translocase, YajC subunit	Pgjcvi_01452	PG JCVI SC001	preprotein translocase, YajC subunit	PG W83	PG0485	1, 112	100	218.4	0
preprotein translocase, YajC subunit	Pgjcvi_01452	PG JCVI SC001	preprotein translocase subunit YajC	PG TDC60	PGTDC60_1601	1, 112	100	218.4	0
O-6-methylguanine DNA methyltransferase	Pgjcvi_01453	PG JCVI SC001	methylated-DNA--protein-cysteine S-methyltransferase	PG W83	PG0486	1, 175	100	362.1	0
O-6-methylguanine DNA methyltransferase	Pgjcvi_01453	PG JCVI SC001	putative methylated-DNA-protein-cysteine methyltransferase	PG ATCC 33277	PGN_1484	1, 170	98.2	344	0
O-6-methylguanine DNA methyltransferase	Pgjcvi_01453	PG JCVI SC001	methylated-DNA--protein-cysteine S-methyltransferase	PG TDC60	PGTDC60_1602	1, 175	97.7	353.2	0
Holliday junction DNA helicase, RuvB subunit	Pgjcvi_01455	PG JCVI SC001	Holliday junction DNA helicase RuvB	PG W83	PG0488	1, 343	99.4	673.3	0
Holliday junction DNA helicase, RuvB subunit	Pgjcvi_01455	PG JCVI SC001	holliday junction DNA helicase RuvB	PG ATCC 33277	PGN_1482	15, 364	99.1	686.4	0
Holliday junction DNA helicase, RuvB subunit	Pgjcvi_01455	PG JCVI SC001	Holliday junction DNA helicase RuvB	PG TDC60	PGTDC60_1603	15, 364	99.1	685.3	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_01456	PG JCVI SC001	putative polysaccharide biosynthesis protein	PG TDC60	PGTDC60_1604	1, 493	99	991.9	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_01456	PG JCVI SC001	putative polysaccharide biosynthesis protein	PG ATCC 33277	PGN_1481	2, 494	98.8	988.8	0
Membrane protein involved in the export of O-antigen and teichoic acid	Pgjcvi_01456	PG JCVI SC001	polysaccharide biosynthesis-related protein	PG W83	PG0489	1, 493	98.6	989.6	0
Predicted membrane protein	Pgjcvi_01457	PG JCVI SC001	hypothetical protein	PG W83	PG0490	1, 446	99.6	853.2	0
Predicted membrane protein	Pgjcvi_01457	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1605	1, 472	99.6	906.7	0
Predicted membrane protein	Pgjcvi_01457	PG JCVI SC001	conserved hypothetical protein with DUF389 domain	PG ATCC 33277	PGN_1480	1, 446	99.3	850.9	0
Peptidase S46.	Pgjcvi_01458	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1479	1, 712	99.7	1435.2	0
Peptidase S46.	Pgjcvi_01458	PG JCVI SC001	hypothetical protein	PG W83	PG0491	1, 712	99.7	1435.2	0
Peptidase S46.	Pgjcvi_01458	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1606	1, 712	99.7	1435.2	0
hypothetical protein	Pgjcvi_01459	PG JCVI SC001	hypothetical protein	PG W83	PG0492	51, 86	100	74.3	1.10E-12
Por secretion system C-terminal sorting domain	Pgjcvi_01460	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1476	1, 464	99.4	932.9	0
Por secretion system C-terminal sorting domain	Pgjcvi_01460	PG JCVI SC001	hypothetical protein	PG W83	PG0495	6, 469	98.9	932.6	0
Por secretion system C-terminal sorting domain	Pgjcvi_01460	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1611	1, 441	98.9	883.2	0
5''-methylthioadenosine/S-adenosylhomocysteine nucleosidase	Pgjcvi_01461	PG JCVI SC001	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	PG W83	PG0497	1, 228	99.6	454.5	0
5''-methylthioadenosine/S-adenosylhomocysteine nucleosidase	Pgjcvi_01461	PG JCVI SC001	probable 5'-methylthioadenosine/S- adenosylhomocysteine nucleosidase	PG ATCC 33277	PGN_1475	1, 228	98.7	447.2	0
5''-methylthioadenosine/S-adenosylhomocysteine nucleosidase	Pgjcvi_01461	PG JCVI SC001	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	PG TDC60	PGTDC60_1613	1, 228	98.2	447.2	0
LuxS protein involved in autoinducer AI2 synthesis	Pgjcvi_01462	PG JCVI SC001	S-ribosylhomocysteinase	PG W83	PG0498	1, 159	100	335.5	0
LuxS protein involved in autoinducer AI2 synthesis	Pgjcvi_01462	PG JCVI SC001	putative autoinducer-2 production protein LuxS	PG ATCC 33277	PGN_1474	1, 159	99.4	333.6	0
LuxS protein involved in autoinducer AI2 synthesis	Pgjcvi_01462	PG JCVI SC001	S-ribosylhomocysteinase	PG TDC60	PGTDC60_1614	1, 161	99.4	337.4	0
hypothetical protein	Pgjcvi_01463	PG JCVI SC001	hypothetical protein	PG W83	PG1493	1, 891	99.7	1766.5	0
hypothetical protein	Pgjcvi_01463	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0836	1, 891	99	1751.5	0
Predicted site-specific integrase-resolvase	Pgjcvi_01464	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1671	1, 83	83.1	143.3	5.10E-33
Predicted site-specific integrase-resolvase	Pgjcvi_01464	PG JCVI SC001	hypothetical protein	PG W83	PG0546	10, 69	71.7	84.7	2.10E-15
Predicted site-specific integrase-resolvase	Pgjcvi_01464	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0092	4, 99	37.5	77.4	3.40E-13
hypothetical protein	Pgjcvi_01465	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0089	41, 83	48.8	45.8	0.001
hypothetical protein	Pgjcvi_01465	PG JCVI SC001	excisionase family DNA binding protein	PG TDC60	PGTDC60_1953	1, 88	44.3	79.7	6.30E-14
Predicted P-loop ATPase and inactivated derivatives	Pgjcvi_01466	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0922	1, 394	60.8	473	0
hypothetical protein	Pgjcvi_01468	PG JCVI SC001	probable conserved protein found in conjugate transposon TraP	PG ATCC 33277	PGN_0057	2, 274	39.9	171.4	5.70E-41
hypothetical protein	Pgjcvi_01468	PG JCVI SC001	mobilizable transposon, excision protein, putative	PG W83	PG0841	3, 297	39.7	184.9	5.60E-45
hypothetical protein	Pgjcvi_01468	PG JCVI SC001	CHC2 zinc finger containing protein	PG TDC60	PGTDC60_1942	2, 315	36.9	172.6	2.50E-41
Plasmid recombination enzyme.	Pgjcvi_01470	PG JCVI SC001	mobilization protein	PG W83	PG1109	1, 445	39.6	311.6	0
tRNA-guanine transglycosylase, queuosine-34-forming	Pgjcvi_01472	PG JCVI SC001	queuine tRNA-ribosyltransferase	PG W83	PG0500	1, 376	99.7	770.8	0
tRNA-guanine transglycosylase, queuosine-34-forming	Pgjcvi_01472	PG JCVI SC001	queuine tRNA-ribosyltransferase	PG TDC60	PGTDC60_1617	1, 376	99.7	773.5	0
tRNA-guanine transglycosylase, queuosine-34-forming	Pgjcvi_01472	PG JCVI SC001	queuine tRNA-ribosyltransferase	PG ATCC 33277	PGN_1472	1, 376	98.9	764.6	0
Predicted permeases	Pgjcvi_01473	PG JCVI SC001	hypothetical protein	PG W83	PG0501	1, 360	99.7	700.7	0
Predicted permeases	Pgjcvi_01473	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1618	1, 360	99.7	700.7	0
Predicted permeases	Pgjcvi_01473	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1471	4, 363	99.4	698.4	0
SsrA-binding protein	Pgjcvi_01474	PG JCVI SC001	SsrA-binding protein	PG W83	PG0502	1, 153	100	305.8	0
SsrA-binding protein	Pgjcvi_01474	PG JCVI SC001	putative SsrA-binding protein	PG ATCC 33277	PGN_1470	1, 153	99.3	304.3	0
SsrA-binding protein	Pgjcvi_01474	PG JCVI SC001	SsrA-binding protein	PG TDC60	PGTDC60_1619	1, 153	99.3	304.3	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01475	PG JCVI SC001	dipeptidyl aminopeptidase IV	PG W83	PG0503	1, 723	99.6	1462.6	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01475	PG JCVI SC001	dipeptidyl peptidase	PG ATCC 33277	PGN_1469	1, 723	99	1458.7	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01475	PG JCVI SC001	dipeptidyl aminopeptidase IV	PG TDC60	PGTDC60_1620	1, 709	98.9	1427.9	0
lipoate synthase	Pgjcvi_01476	PG JCVI SC001	putative Lipoic acid synthase	PG ATCC 33277	PGN_1468	1, 282	100	571.6	0
lipoate synthase	Pgjcvi_01476	PG JCVI SC001	lipoyl synthase	PG TDC60	PGTDC60_1621	1, 282	100	571.6	0
lipoate synthase	Pgjcvi_01476	PG JCVI SC001	lipoyl synthase	PG W83	PG0504	1, 282	99.6	569.7	0

Peptidase family C25./Propeptide_C25.	Pgjcvi_01477	PG JCVI SC001	arginine-specific cysteine proteinase	PG W83	PG0506	1, 272	100	529.6	0
Peptidase family C25./Propeptide_C25.	Pgjcvi_01477	PG JCVI SC001	arginine-specific cysteine proteinase RgpB	PG TDC60	PGTDC60_1623	1, 272	99.6	526.9	0
Peptidase family C25./Propeptide_C25.	Pgjcvi_01477	PG JCVI SC001	arginine-specific cysteine proteinase RgpB	PG ATCC 33277	PGN_1466	1, 272	98.5	519.6	0
Por secretion system C-terminal sorting domain	Pgjcvi_01478	PG JCVI SC001	arginine-specific cysteine proteinase RgpB	PG ATCC 33277	PGN_1466	544, 736	99.5	374.4	0
Por secretion system C-terminal sorting domain	Pgjcvi_01478	PG JCVI SC001	arginine-specific cysteine proteinase RgpB	PG TDC60	PGTDC60_1623	544, 736	99.5	374.4	0
Por secretion system C-terminal sorting domain	Pgjcvi_01478	PG JCVI SC001	arginine-specific cysteine proteinase	PG W83	PG0506	544, 736	99	372.9	0
HAD-superfamily subfamily IB hydrolase, TIGR01490	Pgjcvi_01479	PG JCVI SC001	HAD-superfamily subfamily IB hydrolase, TIGR01490	PG W83	PG0508	1, 200	99.5	416.4	0
HAD-superfamily subfamily IB hydrolase, TIGR01490	Pgjcvi_01479	PG JCVI SC001	probable HAD-superfamily subfamily IB hydrolase	PG ATCC 33277	PGN_1464	1, 200	99	415.6	0
HAD-superfamily subfamily IB hydrolase, TIGR01490	Pgjcvi_01479	PG JCVI SC001	putative HAD-superfamily subfamily IB hydrolase	PG TDC60	PGTDC60_1627	1, 200	98.5	412.5	0
4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	Pgjcvi_01480	PG JCVI SC001	hypothetical protein	PG W83	PG0509	1, 286	99.3	558.9	0
4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	Pgjcvi_01480	PG JCVI SC001	phosphoribose diphosphate:decaprenyl-phosphate phosphoribosyltransferase	PG TDC60	PGTDC60_1628	1, 286	99.3	560.1	0
4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	Pgjcvi_01480	PG JCVI SC001	probable UbiA prenyltransferase	PG ATCC 33277	PGN_1463	1, 286	98.3	554.7	0
metalloprotein, YbeY/UPF0054 family	Pgjcvi_01481	PG JCVI SC001	hypothetical protein	PG W83	PG0510	1, 151	99.3	301.6	0
metalloprotein, YbeY/UPF0054 family	Pgjcvi_01481	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1629	1, 151	99.3	301.2	0
metalloprotein, YbeY/UPF0054 family	Pgjcvi_01481	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1462	1, 151	98	298.5	0
Uncharacterized membrane protein, required for spore maturation in B.subtilis.	Pgjcvi_01482	PG JCVI SC001	putative spore maturation protein A/B	PG ATCC 33277	PGN_1461	1, 410	99	774.6	0
Uncharacterized membrane protein, required for spore maturation in B.subtilis.	Pgjcvi_01482	PG JCVI SC001	spore maturation protein A/spore maturation protein B	PG W83	PG0511	1, 410	98.8	773.5	0
Uncharacterized membrane protein, required for spore maturation in B.subtilis.	Pgjcvi_01482	PG JCVI SC001	spore maturation protein A/spore maturation protein B	PG TDC60	PGTDC60_1630	1, 410	98.5	771.5	0
guanylate kinase	Pgjcvi_01483	PG JCVI SC001	guanylate kinase	PG W83	PG0512	1, 188	100	367.9	0
guanylate kinase	Pgjcvi_01483	PG JCVI SC001	putative guanylate kinase	PG ATCC 33277	PGN_1460	1, 188	99.5	367.1	0
guanylate kinase	Pgjcvi_01483	PG JCVI SC001	guanylate kinase	PG TDC60	PGTDC60_1631	1, 188	99.5	367.1	0
TIGR00255 family protein	Pgjcvi_01484	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1632	1, 296	99	570.5	0
TIGR00255 family protein	Pgjcvi_01484	PG JCVI SC001	conserved hypothetical protein TIGR00255	PG W83	PG0513	1, 296	98.7	569.3	0
TIGR00255 family protein	Pgjcvi_01484	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1459	1, 292	98.3	558.5	0
preprotein translocase, SecA subunit	Pgjcvi_01485	PG JCVI SC001	preprotein translocase SecA subunit	PG ATCC 33277	PGN_1458	1, 1113	99.8	2187.9	0
preprotein translocase, SecA subunit	Pgjcvi_01485	PG JCVI SC001	translocase	PG W83	PG0514	1, 1107	99.7	2173.3	0
preprotein translocase, SecA subunit	Pgjcvi_01485	PG JCVI SC001	preprotein translocase subunit SecA	PG TDC60	PGTDC60_1633	1, 1113	99.6	2184.1	0
Uncharacterized proteins of the AP superfamily	Pgjcvi_01486	PG JCVI SC001	hypothetical protein	PG W83	PG0515	1, 531	99.2	1047	0
Uncharacterized proteins of the AP superfamily	Pgjcvi_01486	PG JCVI SC001	probable alkaline phosphatase	PG ATCC 33277	PGN_1457	1, 525	98.9	1033.1	0
Uncharacterized proteins of the AP superfamily	Pgjcvi_01486	PG JCVI SC001	putative alkaline phosphatase	PG TDC60	PGTDC60_1634	1, 531	98.9	1044.3	0
hypothetical protein	Pgjcvi_01487	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1635	1, 415	99.3	836.6	0
hypothetical protein	Pgjcvi_01487	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1456	1, 415	99	832.8	0
hypothetical protein	Pgjcvi_01487	PG JCVI SC001	hypothetical protein	PG W83	PG0516	1, 415	98.8	831.6	0
hypothetical protein	Pgjcvi_01488	PG JCVI SC001	hypothetical protein	PG W83	PG0517	1, 960	99.5	1910.2	0
hypothetical protein	Pgjcvi_01488	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1455	1, 1007	99.2	2003.8	0
hypothetical protein	Pgjcvi_01488	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1636	1, 1007	98.5	1989.9	0
CAAX amino terminal protease family.	Pgjcvi_01489	PG JCVI SC001	probable abortive infection protein	PG ATCC 33277	PGN_1454	1, 241	97.9	474.9	0
CAAX amino terminal protease family.	Pgjcvi_01489	PG JCVI SC001	abortive infection protein family	PG W83	PG0518	1, 241	97.9	474.9	0
CAAX amino terminal protease family.	Pgjcvi_01489	PG JCVI SC001	putative abortive infection protein	PG TDC60	PGTDC60_1637	1, 104	96.2	207.2	0
chaperonin GroL	Pgjcvi_01491	PG JCVI SC001	chaperonin GroEL	PG W83	PG0520	1, 545	99.8	1045.8	0
chaperonin GroL	Pgjcvi_01491	PG JCVI SC001	chaperonin GroEL	PG TDC60	PGTDC60_1639	1, 545	99.8	1045.8	0
chaperonin GroL	Pgjcvi_01491	PG JCVI SC001	chaperonin GroEL	PG ATCC 33277	PGN_1452	1, 545	99.6	1044.3	0
Co-chaperonin GroES (HSP10)	Pgjcvi_01492	PG JCVI SC001	chaperonin GroES	PG ATCC 33277	PGN_1451	1, 89	100	173.7	3.20E-42
Co-chaperonin GroES (HSP10)	Pgjcvi_01492	PG JCVI SC001	co-chaperonin GroES	PG W83	PG0521	1, 89	100	173.7	3.20E-42
Co-chaperonin GroES (HSP10)	Pgjcvi_01492	PG JCVI SC001	co-chaperonin GroES	PG TDC60	PGTDC60_1640	1, 89	100	173.7	3.20E-42
tRNA dimethylallyltransferase	Pgjcvi_01493	PG JCVI SC001	putative tRNA isopentenyltransferase	PG ATCC 33277	PGN_1450	1, 302	99.3	609.8	0
tRNA dimethylallyltransferase	Pgjcvi_01493	PG JCVI SC001	tRNA delta(2)-isopentenylpyrophosphate transferase	PG TDC60	PGTDC60_1641	1, 302	99	608.2	0
tRNA dimethylallyltransferase	Pgjcvi_01493	PG JCVI SC001	tRNA delta(2)-isopentenylpyrophosphate transferase	PG W83	PG0522	1, 302	98.7	606.7	0
IMP dehydrogenase/GMP reductase	Pgjcvi_01494	PG JCVI SC001	inosine-5'-monophosphate dehydrogenase	PG ATCC 33277	PGN_1449	1, 498	100	999.2	0
IMP dehydrogenase/GMP reductase	Pgjcvi_01494	PG JCVI SC001	inositol-5-monophosphate dehydrogenase	PG W83	PG0523	1, 498	100	999.2	0
IMP dehydrogenase/GMP reductase	Pgjcvi_01494	PG JCVI SC001	inosine 5-monophosphate dehydrogenase	PG TDC60	PGTDC60_1642	1, 498	99.6	995.3	0
CTP synthase	Pgjcvi_01495	PG JCVI SC001	CTP synthetase	PG TDC60	PGTDC60_1644	1, 539	100	1082.4	0
CTP synthase	Pgjcvi_01495	PG JCVI SC001	CTP synthase	PG ATCC 33277	PGN_1447	1, 539	99.8	1082	0
CTP synthase	Pgjcvi_01495	PG JCVI SC001	CTP synthetase	PG W83	PG0525	1, 539	99.8	1080.9	0
membrane protein insertase, YidC/Oxa1 family, N-terminal domain	Pgjcvi_01496	PG JCVI SC001	putative inner membrane protein translocase component YidC	PG TDC60	PGTDC60_1645	1, 627	99.7	1244.2	0
membrane protein insertase, YidC/Oxa1 family, N-terminal domain	Pgjcvi_01496	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1446	1, 627	99.5	1244.6	0
membrane protein insertase, YidC/Oxa1 family, N-terminal domain	Pgjcvi_01496	PG JCVI SC001	putative inner membrane protein translocase component YidC	PG W83	PG0526	1, 627	99.4	1240.7	0
Glutamine phosphoribosylpyrophosphate amidotransferase	Pgjcvi_01497	PG JCVI SC001	amidophosphoribosyltransferase	PG TDC60	PGTDC60_1646	1, 627	99.8	1262.3	0
Glutamine phosphoribosylpyrophosphate amidotransferase	Pgjcvi_01497	PG JCVI SC001	amidophosphoribosyltransferase, putative	PG W83	PG0528	1, 627	99.7	1259.2	0
Glutamine phosphoribosylpyrophosphate amidotransferase	Pgjcvi_01497	PG JCVI SC001	putative amidophosphoribosyltransferase	PG ATCC 33277	PGN_1445	1, 627	99.5	1259.6	0
carbamoyl-phosphate synthase, small subunit	Pgjcvi_01498	PG JCVI SC001	carbamoyl-phosphate synthase small subunit	PG W83	PG0529	1, 357	99.4	736.5	0
carbamoyl-phosphate synthase, small subunit	Pgjcvi_01498	PG JCVI SC001	carbamoyl phosphate synthase, small subunit	PG TDC60	PGTDC60_1647	1, 357	99.4	736.5	0
carbamoyl-phosphate synthase, small subunit	Pgjcvi_01498	PG JCVI SC001	carbamoyl-phosphate synthase small subunit	PG ATCC 33277	PGN_1444	1, 357	99.2	733	0
carbamoyl-phosphate synthase, large subunit	Pgjcvi_01499	PG JCVI SC001	carbamoyl-phosphate synthase large subunit	PG ATCC 33277	PGN_1443	1, 1075	100	2110.9	0
carbamoyl-phosphate synthase, large subunit	Pgjcvi_01499	PG JCVI SC001	carbamoyl-phosphate synthase, large subunit	PG W83	PG0530	1, 1075	99.8	2109	0
carbamoyl-phosphate synthase, large subunit	Pgjcvi_01499	PG JCVI SC001	carbamoyl phosphate synthase, large subunit	PG TDC60	PGTDC60_1648	1, 1075	99.8	2107.8	0
NAD+ synthetase	Pgjcvi_01500	PG JCVI SC001	glutamine-dependent NAD synthetase	PG ATCC 33277	PGN_1441	1, 647	99.5	1297.3	0
NAD+ synthetase	Pgjcvi_01500	PG JCVI SC001	NAD(+) synthetase	PG W83	PG0531	1, 647	99.5	1297.3	0
NAD+ synthetase	Pgjcvi_01500	PG JCVI SC001	NAD synthetase	PG TDC60	PGTDC60_1649	1, 642	99.4	1283.9	0
Uncharacterized vancomycin resistance protein	Pgjcvi_01501	PG JCVI SC001	putative vancomycin B-type resistance protein VanW	PG ATCC 33277	PGN_1440	1, 282	98.6	578.9	0
Uncharacterized vancomycin resistance protein	Pgjcvi_01501	PG JCVI SC001	putative vancomycin B-type resistance protein VanW	PG TDC60	PGTDC60_1650	1, 229	98.3	471.9	0
Uncharacterized vancomycin resistance protein	Pgjcvi_01501	PG JCVI SC001	hypothetical protein	PG W83	PG0532	18, 299	97.9	577.8	0

Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_01506	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1652	1, 827	99.4	1642.5	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_01506	PG JCVI SC001	hypothetical protein	PG W83	PG0534	1, 827	99.2	1640.6	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_01506	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1437	1, 827	98.7	1629.4	0
Outer membrane protein	Pgjcvi_01507	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1653	1, 206	100	394.8	0
Outer membrane protein	Pgjcvi_01507	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1436	1, 206	99.5	393.3	0
Outer membrane protein	Pgjcvi_01507	PG JCVI SC001	hypothetical protein	PG W83	PG0535	1, 206	99	391.3	0
hypothetical protein	Pgjcvi_01508	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1435	1, 71	100	148.3	1.10E-34
hypothetical protein	Pgjcvi_01508	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1654	1, 71	98.6	146.7	3.30E-34
Xaa-His dipeptidase	Pgjcvi_01509	PG JCVI SC001	aminoacyl-histidine dipeptidase	PG W83	PG0537	1, 486	99.8	988.8	0
Xaa-His dipeptidase	Pgjcvi_01509	PG JCVI SC001	aminoacyl-histidine dipeptidase	PG TDC60	PGTDC60_1655	1, 486	99.8	988.8	0
Xaa-His dipeptidase	Pgjcvi_01509	PG JCVI SC001	aminoacyl-histidine dipeptidase	PG ATCC 33277	PGN_1434	1, 486	99.6	986.5	0
Outer membrane protein	Pgjcvi_01510	PG JCVI SC001	outer membrane efflux protein	PG W83	PG0538	1, 462	99.6	899	0
Outer membrane protein	Pgjcvi_01510	PG JCVI SC001	outer membrane efflux protein	PG TDC60	PGTDC60_1656	1, 437	99.5	845.5	0
Outer membrane protein	Pgjcvi_01510	PG JCVI SC001	probable outer membrane efflux protein	PG ATCC 33277	PGN_1432	1, 462	98.9	892.9	0
RND family efflux transporter, MFP subunit	Pgjcvi_01511	PG JCVI SC001	efflux transporter, MFP component, RND family	PG W83	PG0539	1, 350	99.7	669.8	0
RND family efflux transporter, MFP subunit	Pgjcvi_01511	PG JCVI SC001	putative cation efflux system protein	PG ATCC 33277	PGN_1431	1, 353	99.4	674.1	0
RND family efflux transporter, MFP subunit	Pgjcvi_01511	PG JCVI SC001	RND family efflux transporter MFP subunit	PG TDC60	PGTDC60_1657	1, 311	99	594.7	0
Cation/multidrug efflux pump	Pgjcvi_01512	PG JCVI SC001	AcrB/AcrD/AcrF family protein	PG W83	PG0540	1, 1049	99.4	2000.3	0
Cation/multidrug efflux pump	Pgjcvi_01512	PG JCVI SC001	AcrB/AcrD/AcrF family protein	PG TDC60	PGTDC60_1658	1, 1049	99.3	2001.1	0
Cation/multidrug efflux pump	Pgjcvi_01512	PG JCVI SC001	putative transmembrane Acr-type transport protein	PG ATCC 33277	PGN_1430	1, 1049	99.1	1993.8	0
hypothetical protein	Pgjcvi_01513	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1429	1, 99	99	207.2	0
hypothetical protein	Pgjcvi_01513	PG JCVI SC001	hypothetical protein	PG W83	PG0541	1, 99	99	207.2	0
hypothetical protein	Pgjcvi_01513	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1659	1, 99	98	205.3	0
Predicted transcriptional regulators	Pgjcvi_01514	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG0543	1, 67	100	132.9	4.70E-30
Predicted transcriptional regulators	Pgjcvi_01514	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_1176	5, 63	57.6	74.3	2.00E-12
Predicted transcriptional regulators	Pgjcvi_01514	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0927	1, 63	57.1	78.2	1.40E-13
Type I restriction-modification system methyltransferase subunit	Pgjcvi_01515	PG JCVI SC001	type I restriction-modification system, M subunit, putative	PG W83	PG0544	1, 648	100	1309.7	0
Type I restriction-modification system methyltransferase subunit	Pgjcvi_01515	PG JCVI SC001	putative type I restriction-modification system, M subunit	PG TDC60	PGTDC60_1939	10, 135	37.1	70.9	2.30E-10
Restriction endonuclease S subunits	Pgjcvi_01516	PG JCVI SC001	hypothetical protein	PG W83	PG0545	1, 701	77	1026.2	0
hypothetical protein	Pgjcvi_01517	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1671	1, 35	97.1	69.7	9.70E-11
Predicted ATPase (AAA+ superfamily)	Pgjcvi_01519	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1419	1, 393	100	797.7	0
Predicted ATPase (AAA+ superfamily)	Pgjcvi_01519	PG JCVI SC001	hypothetical protein	PG W83	PG0547	6, 398	100	797.7	0
Predicted ATPase (AAA+ superfamily)	Pgjcvi_01519	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1672	1, 370	100	751.5	0
pyruvate:ferredoxin (flavodoxin) oxidoreductase, homodimeric	Pgjcvi_01520	PG JCVI SC001	pyruvate ferredoxin/flavodoxin oxidoreductase family protein	PG TDC60	PGTDC60_1673	1, 1193	100	2430.2	0
pyruvate:ferredoxin (flavodoxin) oxidoreductase, homodimeric	Pgjcvi_01520	PG JCVI SC001	pyruvate-flavodoxin oxidoreductase	PG ATCC 33277	PGN_1418	1, 1193	99.9	2427.1	0
pyruvate:ferredoxin (flavodoxin) oxidoreductase, homodimeric	Pgjcvi_01520	PG JCVI SC001	pyruvate ferredoxin/flavodoxin oxidoreductase family protein	PG W83	PG0548	1, 1193	99.9	2427.1	0
Site-specific recombinase XerD	Pgjcvi_01521	PG JCVI SC001	integrase	PG W83	PG1454	1, 409	50.2	403.7	0
Site-specific recombinase XerD	Pgjcvi_01521	PG JCVI SC001	putative bacteriophage integrase	PG ATCC 33277	PGN_0094	2, 388	32.7	213.4	0
Site-specific recombinase XerD	Pgjcvi_01521	PG JCVI SC001	integrase	PG TDC60	PGTDC60_1949	2, 391	26.1	173.7	1.50E-41
Site-specific recombinase XerD	Pgjcvi_01522	PG JCVI SC001	integrase	PG TDC60	PGTDC60_1667	5, 218	83.3	369.8	0
Site-specific recombinase XerD	Pgjcvi_01522	PG JCVI SC001	integrase	PG W83	PG1453	1, 394	42.7	308.5	0
Site-specific recombinase XerD	Pgjcvi_01522	PG JCVI SC001	putative bacteriophage integrase	PG ATCC 33277	PGN_0094	1, 396	31.7	190.7	0
hypothetical protein	Pgjcvi_01523	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0838	1, 70	92.9	127.5	3.80E-28
hypothetical protein	Pgjcvi_01523	PG JCVI SC001	hypothetical protein	PG W83	PG1491	1, 70	92.9	127.5	3.80E-28
Protein of unknown function (Porph_ging).	Pgjcvi_01524	PG JCVI SC001	hypothetical protein	PG W83	PG1492	1, 238	100	473	0
Protein of unknown function (Porph_ging).	Pgjcvi_01524	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0837	1, 238	99.2	469.2	0
Protein of unknown function (Porph_ging).	Pgjcvi_01524	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0177	145, 253	35.1	51.2	6.40E-05
Por secretion system C-terminal sorting domain	Pgjcvi_01525	PG JCVI SC001	extracellular protease, putative	PG W83	PG0553	1, 940	99.4	1893.2	0
Por secretion system C-terminal sorting domain	Pgjcvi_01525	PG JCVI SC001	probable lysyl endopeptidase precursor	PG ATCC 33277	PGN_1416	1, 940	99.1	1887.8	0
Por secretion system C-terminal sorting domain	Pgjcvi_01525	PG JCVI SC001	putative lysyl endopeptidase precursor	PG TDC60	PGTDC60_1678	1, 940	98.9	1884	0
DNA-binding protein, histone-like, putative	Pgjcvi_01526	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG0555	1, 172	100	345.9	0
DNA-binding protein, histone-like, putative	Pgjcvi_01526	PG JCVI SC001	DNA-binding protein histone-like family	PG ATCC 33277	PGN_1415	1, 172	99.4	344	0
DNA-binding protein, histone-like, putative	Pgjcvi_01526	PG JCVI SC001	histone-like family DNA-binding protein	PG TDC60	PGTDC60_1680	1, 172	99.4	345.5	0
hypothetical protein	Pgjcvi_01528	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1413	2, 181	97.2	370.5	0
hypothetical protein	Pgjcvi_01528	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1683	1, 224	95.5	443.4	0
hypothetical protein	Pgjcvi_01528	PG JCVI SC001	hypothetical protein	PG W83	PG0557	7, 230	94.2	444.5	0
purine nucleoside phosphorylase I, inosine and guanosine-specific	Pgjcvi_01529	PG JCVI SC001	putative purine nucleoside phosphorylase I	PG ATCC 33277	PGN_1412	1, 273	99.6	547.4	0
purine nucleoside phosphorylase I, inosine and guanosine-specific	Pgjcvi_01529	PG JCVI SC001	purine nucleoside phosphorylase	PG W83	PG0558	1, 273	99.6	547.4	0
purine nucleoside phosphorylase I, inosine and guanosine-specific	Pgjcvi_01529	PG JCVI SC001	purine nucleoside phosphorylase	PG TDC60	PGTDC60_1684	1, 273	99.6	547.4	0
Cytosine deaminase and related metal-dependent hydrolases	Pgjcvi_01530	PG JCVI SC001	chlorohydrolase family protein	PG W83	PG0559	1, 381	99.7	774.2	0
Cytosine deaminase and related metal-dependent hydrolases	Pgjcvi_01530	PG JCVI SC001	putative N-ethylammeline chlorohydrolase	PG ATCC 33277	PGN_1411	1, 424	98.8	848.2	0
Cytosine deaminase and related metal-dependent hydrolases	Pgjcvi_01530	PG JCVI SC001	putative N-ethylammeline chlorohydrolase	PG TDC60	PGTDC60_1685	1, 424	98.6	847	0
Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	Pgjcvi_01531	PG JCVI SC001	M20/M25/M40 family peptidase	PG TDC60	PGTDC60_1686	1, 451	99.8	915.2	0
Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	Pgjcvi_01531	PG JCVI SC001	putative peptidase	PG ATCC 33277	PGN_1409	1, 451	99.6	914.1	0
Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	Pgjcvi_01531	PG JCVI SC001	peptidase, M20/M25/M40 family	PG W83	PG0561	1, 451	99.3	911.8	0
Predicted permease	Pgjcvi_01532	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1687	1, 558	99.8	1094.3	0
Predicted permease	Pgjcvi_01532	PG JCVI SC001	potassium uptake protein TrkA, putative	PG W83	PG0562	1, 558	99.6	1093.2	0
Predicted permease	Pgjcvi_01532	PG JCVI SC001	conserved hypothetical protein with predicted permease membrane region	PG ATCC 33277	PGN_1408	1, 558	99.5	1089.7	0
hypothetical protein	Pgjcvi_01534	PG JCVI SC001	hypothetical protein	PG W83	PG0569	1, 508	99.8	1033.5	0

hypothetical protein	Pgjcvi_01534	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1694	1, 518	99.4	1050.4	0
hypothetical protein	Pgjcvi_01534	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0617	1, 518	98.8	1045	0
aspartate-semialdehyde dehydrogenase (peptidoglycan organisms)	Pgjcvi_01535	PG JCVI SC001	aspartate-semialdehyde dehydrogenase	PG W83	PG0571	1, 337	99.7	669.5	0
aspartate-semialdehyde dehydrogenase (peptidoglycan organisms)	Pgjcvi_01535	PG JCVI SC001	aspartate-semialdehyde dehydrogenase	PG ATCC 33277	PGN_0618	1, 337	99.4	669.1	0
aspartate-semialdehyde dehydrogenase (peptidoglycan organisms)	Pgjcvi_01535	PG JCVI SC001	aspartate-semialdehyde dehydrogenase	PG TDC60	PGTDC60_1695	1, 337	99.1	664.5	0
S-adenosyl-methyltransferase MraW	Pgjcvi_01536	PG JCVI SC001	S-adenosyl-methyltransferase MraW	PG W83	PG0573	1, 311	99.7	620.9	0
S-adenosyl-methyltransferase MraW	Pgjcvi_01536	PG JCVI SC001	S-adenosyl-methyltransferase MraW	PG TDC60	PGTDC60_1697	1, 311	99.4	618.2	0
S-adenosyl-methyltransferase MraW	Pgjcvi_01536	PG JCVI SC001	putative S-adenosyl-methyltransferase MraW	PG ATCC 33277	PGN_0620	1, 311	99	617.8	0
hypothetical protein	Pgjcvi_01537	PG JCVI SC001	hypothetical protein	PG W83	PG0574	1, 157	100	318.5	0
hypothetical protein	Pgjcvi_01537	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0621	1, 157	99.4	317	0
hypothetical protein	Pgjcvi_01537	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1698	1, 157	98.1	313.5	0
Cell division protein FtsI/penicillin-binding protein 2	Pgjcvi_01538	PG JCVI SC001	penicillin-binding protein 2, putative	PG W83	PG0575	1, 733	99.7	1456	0
Cell division protein FtsI/penicillin-binding protein 2	Pgjcvi_01538	PG JCVI SC001	penicillin-binding protein 2	PG TDC60	PGTDC60_1699	1, 733	99.7	1457.2	0
Cell division protein FtsI/penicillin-binding protein 2	Pgjcvi_01538	PG JCVI SC001	penicillin-binding protein	PG ATCC 33277	PGN_0622	1, 733	99.2	1451.4	0
UDP-N-acetylmuramyl-tripeptide synthetase	Pgjcvi_01539	PG JCVI SC001	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	PG W83	PG0576	1, 487	99.8	968.8	0
UDP-N-acetylmuramyl-tripeptide synthetase	Pgjcvi_01539	PG JCVI SC001	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6- diaminopimelate ligase	PG ATCC 33277	PGN_0623	1, 487	99.6	968.4	0
UDP-N-acetylmuramyl-tripeptide synthetase	Pgjcvi_01539	PG JCVI SC001	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	PG TDC60	PGTDC60_1700	1, 487	99.2	965.3	0
phospho-N-acetylmuramoyl-pentapeptide-transferase	Pgjcvi_01540	PG JCVI SC001	phospho-N-acetylmuramoyl-pentapeptide- transferase	PG W83	PG0577	1, 419	100	817.8	0
phospho-N-acetylmuramoyl-pentapeptide-transferase	Pgjcvi_01540	PG JCVI SC001	phospho-N-acetylmuramoyl-pentapeptide- transferase	PG TDC60	PGTDC60_1701	1, 419	100	817.8	0
phospho-N-acetylmuramoyl-pentapeptide-transferase	Pgjcvi_01540	PG JCVI SC001	phospho-N-acetylmuramoyl-pentapeptide- transferase	PG ATCC 33277	PGN_0624	1, 419	99.3	814.7	0
UDP-N-acetylmuramoylalanine--D-glutamate ligase	Pgjcvi_01541	PG JCVI SC001	UDP-N-acetylmuramoylalanine--D-glutamate ligase	PG W83	PG0578	1, 450	99.8	902.9	0
UDP-N-acetylmuramoylalanine--D-glutamate ligase	Pgjcvi_01541	PG JCVI SC001	UDP-N-acetylmuramoylalanine--D-glutamate ligase	PG ATCC 33277	PGN_0625	1, 450	99.6	902.5	0
UDP-N-acetylmuramoylalanine--D-glutamate ligase	Pgjcvi_01541	PG JCVI SC001	UDP-N-acetylmuramoylalanine--D-glutamate ligase	PG TDC60	PGTDC60_1702	1, 450	99.6	901.4	0
Bacterial cell division membrane protein	Pgjcvi_01542	PG JCVI SC001	cell division protein FtsW	PG TDC60	PGTDC60_1703	1, 418	100	808.9	0
Bacterial cell division membrane protein	Pgjcvi_01542	PG JCVI SC001	cell division protein FtsW, putative	PG W83	PG0579	1, 418	99.5	804.7	0
Bacterial cell division membrane protein	Pgjcvi_01542	PG JCVI SC001	putative rod shape-determining protein RodA	PG ATCC 33277	PGN_0626	1, 418	99.3	803.9	0
undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	Pgjcvi_01543	PG JCVI SC001	N-acetylglucosaminyl transferase	PG W83	PG0580	1, 379	100	749.2	0
undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	Pgjcvi_01543	PG JCVI SC001	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	PG TDC60	PGTDC60_1704	1, 379	99.7	747.7	0
undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	Pgjcvi_01543	PG JCVI SC001	N-acetylglucosaminyl transferase	PG ATCC 33277	PGN_0627	1, 379	98.7	740	0
UDP-N-acetylmuramate--alanine ligase	Pgjcvi_01544	PG JCVI SC001	UDP-N-acetylmuramate--L-alanine ligase	PG TDC60	PGTDC60_1705	1, 456	99.3	907.1	0
UDP-N-acetylmuramate--alanine ligase	Pgjcvi_01544	PG JCVI SC001	UDP-N-acetylmuramate--L-alanine ligase	PG W83	PG0581	1, 456	99.1	903.7	0
UDP-N-acetylmuramate--alanine ligase	Pgjcvi_01544	PG JCVI SC001	UDP-N-acetylmuramate-alanine ligase	PG ATCC 33277	PGN_0628	1, 456	98.5	899.4	0
hypothetical protein	Pgjcvi_01545	PG JCVI SC001	putative cell division protein FtsQ	PG ATCC 33277	PGN_0629	1, 258	99.2	509.2	0
hypothetical protein	Pgjcvi_01545	PG JCVI SC001	cell division protein FtsQ, putative	PG W83	PG0582	1, 258	98.1	502.7	0
hypothetical protein	Pgjcvi_01545	PG JCVI SC001	cell division protein FtsQ	PG TDC60	PGTDC60_1706	1, 258	97.7	500.7	0
Actin-like ATPase involved in cell division	Pgjcvi_01546	PG JCVI SC001	cell division protein FtsA	PG TDC60	PGTDC60_1707	1, 476	100	943	0
Actin-like ATPase involved in cell division	Pgjcvi_01546	PG JCVI SC001	probable cell division protein FtsA	PG ATCC 33277	PGN_0630	1, 476	99.6	939.1	0
Actin-like ATPase involved in cell division	Pgjcvi_01546	PG JCVI SC001	cell division protein FtsA	PG W83	PG0583	4, 479	99.2	934.9	0
cell division protein FtsZ	Pgjcvi_01547	PG JCVI SC001	cell division protein FtsZ	PG TDC60	PGTDC60_1708	1, 457	100	892.5	0
cell division protein FtsZ	Pgjcvi_01547	PG JCVI SC001	putative cell division protein FtsZ	PG ATCC 33277	PGN_0631	1, 457	99.8	891.7	0
cell division protein FtsZ	Pgjcvi_01547	PG JCVI SC001	cell division protein FtsZ	PG W83	PG0584	1, 457	99.8	889.4	0
Uncharacterized conserved protein	Pgjcvi_01548	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0632	1, 149	100	280	0
Uncharacterized conserved protein	Pgjcvi_01548	PG JCVI SC001	YqeY family protein	PG W83	PG0585	1, 149	100	280	0
Uncharacterized conserved protein	Pgjcvi_01548	PG JCVI SC001	YqeY family protein	PG TDC60	PGTDC60_1709	1, 149	100	280	0
Predicted membrane protein	Pgjcvi_01549	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0633	1, 210	100	424.5	0
Predicted membrane protein	Pgjcvi_01549	PG JCVI SC001	yadS protein	PG W83	PG0587	1, 210	100	424.5	0
Predicted membrane protein	Pgjcvi_01549	PG JCVI SC001	yadS protein	PG TDC60	PGTDC60_1713	1, 210	100	424.5	0
3-methyl-2-oxobutanoate hydroxymethyltransferase	Pgjcvi_01550	PG JCVI SC001	3-methyl-2-oxobutanoate hydroxymethyltransferase	PG ATCC 33277	PGN_0634	1, 273	100	534.3	0
3-methyl-2-oxobutanoate hydroxymethyltransferase	Pgjcvi_01550	PG JCVI SC001	3-methyl-2-oxobutanoate hydroxymethyltransferase	PG W83	PG0588	1, 273	100	534.3	0
3-methyl-2-oxobutanoate hydroxymethyltransferase	Pgjcvi_01550	PG JCVI SC001	3-methyl-2-oxobutanoate hydroxymethyltransferase	PG TDC60	PGTDC60_1714	1, 273	100	534.3	0
GMP synthase (glutamine-hydrolyzing), C-terminal domain or B subunit/GMP synthase (glutamine-hydrolyzing), N-terminal domain or A subunit	Pgjcvi_01551	PG JCVI SC001	bifunctional GMP synthase/glutamine amidotransferase protein	PG W83	PG0589	1, 506	100	1017.7	0
GMP synthase (glutamine-hydrolyzing), C-terminal domain or B subunit/GMP synthase (glutamine-hydrolyzing), N-terminal domain or A subunit	Pgjcvi_01551	PG JCVI SC001	glutamine-hydrolyzing GMP synthase	PG ATCC 33277	PGN_0635	1, 506	99.8	1016.1	0
GMP synthase (glutamine-hydrolyzing), C-terminal domain or B subunit/GMP synthase (glutamine-hydrolyzing), N-terminal domain or A subunit	Pgjcvi_01551	PG JCVI SC001	GMP synthase	PG TDC60	PGTDC60_1715	1, 506	99.8	1016.1	0
ribosomal protein L31	Pgjcvi_01552	PG JCVI SC001	50S ribosomal protein L31	PG ATCC 33277	PGN_0636	1, 85	100	174.9	1.40E-42
ribosomal protein L31	Pgjcvi_01552	PG JCVI SC001	50S ribosomal protein L31	PG W83	PG0592	1, 85	100	174.9	1.40E-42
ribosomal protein L31	Pgjcvi_01552	PG JCVI SC001	50S ribosomal protein L31 type B	PG TDC60	PGTDC60_1717	1, 85	100	174.9	1.40E-42
periplasmic serine protease, Do/DeqQ family	Pgjcvi_01553	PG JCVI SC001	putative heat shock-related protease htrA protein	PG ATCC 33277	PGN_0637	1, 498	100	960.7	0
periplasmic serine protease, Do/DeqQ family	Pgjcvi_01553	PG JCVI SC001	htrA protein	PG W83	PG0593	1, 498	99.6	957.6	0
periplasmic serine protease, Do/DeqQ family	Pgjcvi_01553	PG JCVI SC001	heat shock-related protease htrA	PG TDC60	PGTDC60_1718	1, 498	99.4	956.4	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_01554	PG JCVI SC001	RNA polymerase sigma-70 factor	PG W83	PG0594	1, 287	100	549.7	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_01554	PG JCVI SC001	RNA polymerase sigma-70 factor	PG TDC60	PGTDC60_1719	1, 287	100	549.7	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_01554	PG JCVI SC001	RNA polymerase sigma factor RpoD	PG ATCC 33277	PGN_0638	1, 287	99.7	548.1	0
ribosomal protein S6	Pgjcvi_01555	PG JCVI SC001	30S ribosomal protein S6	PG ATCC 33277	PGN_0639	1, 117	100	231.5	0
ribosomal protein S6	Pgjcvi_01555	PG JCVI SC001	30S ribosomal protein S6	PG W83	PG0595	1, 117	100	231.5	0
ribosomal protein S6	Pgjcvi_01555	PG JCVI SC001	30S ribosomal protein S6	PG TDC60	PGTDC60_1720	1, 117	100	231.5	0
ribosomal protein S18	Pgjcvi_01556	PG JCVI SC001	30S ribosomal protein S18	PG ATCC 33277	PGN_0640	1, 90	100	183	5.60E-45
ribosomal protein S18	Pgjcvi_01556	PG JCVI SC001	ribosomal protein S18	PG W83	PG0596	1, 90	100	183	5.60E-45
ribosomal protein S18	Pgjcvi_01556	PG JCVI SC001	30S ribosomal protein S18	PG TDC60	PGTDC60_1721	1, 90	100	183	5.60E-45
ribosomal protein L9	Pgjcvi_01557	PG JCVI SC001	ribosomal protein L9	PG W83	PG0597	1, 179	99.4	337	0

ribosomal protein L9	Pgjcvi_01557	PG JCVI SC001	50S ribosomal protein L9	PG ATCC 33277	PGN_0641	1, 179	98.9	334	0
ribosomal protein L9	Pgjcvi_01557	PG JCVI SC001	50S ribosomal protein L9	PG TDC60	PGTDC60_1722	1, 179	98.9	335.1	0
Predicted permeases	Pgjcvi_01558	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0642	1, 651	99.8	1290.8	0
Predicted permeases	Pgjcvi_01558	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1723	1, 651	99.7	1287.7	0
Predicted permeases	Pgjcvi_01558	PG JCVI SC001	hypothetical protein	PG W83	PG0598	1, 651	99.4	1283.5	0
GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase	Pgjcvi_01559	PG JCVI SC001	3,4-dihydroxy-2-butanone 4-phosphate synthase	PG ATCC 33277	PGN_0643	1, 405	100	816.6	0
GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase	Pgjcvi_01559	PG JCVI SC001	3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	PG W83	PG0599	1, 405	100	816.6	0
GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase	Pgjcvi_01559	PG JCVI SC001	3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	PG TDC60	PGTDC60_1724	1, 406	100	818.5	0
hypothetical protein	Pgjcvi_01560	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1728	1, 346	99.7	705.3	0
hypothetical protein	Pgjcvi_01560	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0645	1, 346	99.4	703.7	0
hypothetical protein	Pgjcvi_01560	PG JCVI SC001	hypothetical protein	PG W83	PG0602	1, 346	99.4	704.1	0
cytidylate kinase	Pgjcvi_01561	PG JCVI SC001	probable cytidylate kinase	PG ATCC 33277	PGN_0646	1, 231	100	453	0
cytidylate kinase	Pgjcvi_01561	PG JCVI SC001	cytidylate kinase	PG TDC60	PGTDC60_1729	1, 231	100	453	0
cytidylate kinase	Pgjcvi_01561	PG JCVI SC001	cytidylate kinase	PG W83	PG0603	1, 231	99.6	451.1	0
(E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate reductase (IPP and DMAPP forming)	Pgjcvi_01562	PG JCVI SC001	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	PG W83	PG0604	1, 289	99.7	572.8	0
(E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate reductase (IPP and DMAPP forming)	Pgjcvi_01562	PG JCVI SC001	hydroxymethylbutenyl pyrophosphate reductase	PG ATCC 33277	PGN_0647	1, 289	99	571.2	0
(E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate reductase (IPP and DMAPP forming)	Pgjcvi_01562	PG JCVI SC001	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	PG TDC60	PGTDC60_1730	1, 289	99	570.1	0
Predicted extracellular nuclease	Pgjcvi_01563	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1731	1, 346	99.7	708	0
Predicted extracellular nuclease	Pgjcvi_01563	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0648	5, 350	99.4	705.3	0
Predicted extracellular nuclease	Pgjcvi_01563	PG JCVI SC001	hypothetical protein	PG W83	PG0605	67, 412	99.4	705.3	0
hypothetical protein	Pgjcvi_01564	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1732	1, 164	100	319.3	0
hypothetical protein	Pgjcvi_01564	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0650	1, 120	99.2	241.1	0
hypothetical protein	Pgjcvi_01564	PG JCVI SC001	hypothetical protein	PG W83	PG0607	1, 120	98.3	239.2	0
hypothetical protein	Pgjcvi_01567	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1029	2, 187	36.1	113.2	1.20E-23
hypothetical protein	Pgjcvi_01575	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0654	3, 312	98.7	619	0
hypothetical protein	Pgjcvi_01575	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1739	1, 265	94.7	512.7	0
hypothetical protein	Pgjcvi_01575	PG JCVI SC001	lipoprotein, putative	PG W83	PG0611	7, 316	89.1	557	0
hypothetical protein	Pgjcvi_01576	PG JCVI SC001	hypothetical protein	PG W83	PG0612	1, 67	100	132.9	4.70E-30
hypothetical protein	Pgjcvi_01576	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1740	1, 64	100	128.3	1.20E-28
hypothetical protein	Pgjcvi_01576	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0655	1, 67	92.5	124.8	1.30E-27
hypothetical protein	Pgjcvi_01577	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1741	1, 232	95.7	455.7	0
hypothetical protein	Pgjcvi_01577	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0656	1, 231	95.2	449.9	0
hypothetical protein	Pgjcvi_01577	PG JCVI SC001	hypothetical protein	PG W83	PG0613	1, 229	92.6	434.1	0
hypothetical protein	Pgjcvi_01578	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0657	1, 308	96.8	610.9	0
hypothetical protein	Pgjcvi_01578	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1742	1, 261	94.3	503.8	0
hypothetical protein	Pgjcvi_01578	PG JCVI SC001	hypothetical protein	PG W83	PG0614	13, 326	91.1	576.2	0
GTP-binding protein TypA/BipA	Pgjcvi_01579	PG JCVI SC001	GTP-binding elongation factor family protein TypA/BipA	PG ATCC 33277	PGN_0658	1, 599	100	1188.3	0
GTP-binding protein TypA/BipA	Pgjcvi_01579	PG JCVI SC001	GTP-binding elongation factor family protein TypA/BipA	PG TDC60	PGTDC60_1743	1, 599	100	1188.3	0
GTP-binding protein TypA/BipA	Pgjcvi_01579	PG JCVI SC001	GTP-binding protein TypA	PG W83	PG0615	1, 599	99.8	1186.4	0
hypothetical protein	Pgjcvi_01580	PG JCVI SC001	35 kDa hemin binding protein	PG ATCC 33277	PGN_0659	1, 344	100	685.6	0
hypothetical protein	Pgjcvi_01580	PG JCVI SC001	thioredoxin, putative	PG W83	PG0616	1, 344	99.7	683.3	0
hypothetical protein	Pgjcvi_01580	PG JCVI SC001	35 kDa hemin binding protein	PG TDC60	PGTDC60_1744	1, 344	99.7	682.6	0
hypothetical protein	Pgjcvi_01581	PG JCVI SC001	hypothetical protein	PG W83	PG0617	28, 99	98.6	147.1	2.60E-34
hypothetical protein	Pgjcvi_01581	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1745	28, 99	98.6	147.1	2.60E-34
peroxiredoxin	Pgjcvi_01582	PG JCVI SC001	putative alkyl hydroperoxide reductase C subunit	PG ATCC 33277	PGN_0660	1, 188	100	389	0
peroxiredoxin	Pgjcvi_01582	PG JCVI SC001	alkyl hydroperoxide reductase, C subunit	PG W83	PG0618	1, 188	100	389	0
peroxiredoxin	Pgjcvi_01582	PG JCVI SC001	alkyl hydroperoxide reductase, subunit C	PG TDC60	PGTDC60_1746	1, 188	100	389	0
alkyl hydroperoxide reductase, F subunit	Pgjcvi_01583	PG JCVI SC001	alkyl hydroperoxide reductase, F subunit	PG W83	PG0619	1, 515	99.2	1001.1	0
alkyl hydroperoxide reductase, F subunit	Pgjcvi_01583	PG JCVI SC001	alkyl hydroperoxide reductase F subunit	PG ATCC 33277	PGN_0661	1, 515	98.8	996.1	0
alkyl hydroperoxide reductase, F subunit	Pgjcvi_01583	PG JCVI SC001	alkyl hydroperoxide reductase, F subunit	PG TDC60	PGTDC60_1747	1, 515	98.4	993.4	0
ATP-dependent protease La	Pgjcvi_01585	PG JCVI SC001	ATP-dependent protease La	PG ATCC 33277	PGN_0662	1, 845	99.8	1649.8	0
ATP-dependent protease La	Pgjcvi_01585	PG JCVI SC001	ATP-dependent protease La	PG TDC60	PGTDC60_1748	1, 845	99.6	1647.9	0
ATP-dependent protease La	Pgjcvi_01585	PG JCVI SC001	ATP-dependent protease La	PG W83	PG0620	1, 810	99.5	1573.1	0
Domain of Unknown Function (DUF1599).	Pgjcvi_01586	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0663	1, 182	100	362.5	0
Domain of Unknown Function (DUF1599).	Pgjcvi_01586	PG JCVI SC001	hypothetical protein	PG W83	PG0621	1, 182	100	362.5	0
Domain of Unknown Function (DUF1599).	Pgjcvi_01586	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1749	1, 182	99.5	359.8	0
Predicted membrane protein	Pgjcvi_01587	PG JCVI SC001	hypothetical protein	PG W83	PG0622	1, 430	100	866.7	0
Predicted membrane protein	Pgjcvi_01587	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1750	1, 430	99.8	865.1	0
Predicted membrane protein	Pgjcvi_01587	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0664	1, 430	99.5	863.6	0
triosephosphate isomerase	Pgjcvi_01588	PG JCVI SC001	putative triosephosphate isomerase	PG ATCC 33277	PGN_0665	1, 251	99.2	489.6	0
triosephosphate isomerase	Pgjcvi_01588	PG JCVI SC001	triosephosphate isomerase	PG TDC60	PGTDC60_1751	1, 251	99.2	491.5	0
triosephosphate isomerase	Pgjcvi_01588	PG JCVI SC001	triosephosphate isomerase	PG W83	PG0623	1, 251	98.8	488.4	0
Sporulation related domain.	Pgjcvi_01589	PG JCVI SC001	hypothetical protein	PG W83	PG0624	1, 168	100	331.3	0
Sporulation related domain.	Pgjcvi_01589	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1752	1, 168	100	331.3	0
Sporulation related domain.	Pgjcvi_01589	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0666	1, 168	99.4	330.5	0
GTP cyclohydrolase I	Pgjcvi_01590	PG JCVI SC001	putative GTP cyclohydrolase I	PG ATCC 33277	PGN_0667	1, 193	100	386.7	0
GTP cyclohydrolase I	Pgjcvi_01590	PG JCVI SC001	GTP cyclohydrolase I	PG W83	PG0625	1, 193	100	386.7	0
GTP cyclohydrolase I	Pgjcvi_01590	PG JCVI SC001	GTP cyclohydrolase I	PG TDC60	PGTDC60_1753	1, 193	100	386.7	0
Por secretion system C-terminal sorting domain	Pgjcvi_01591	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1754	16, 48	100	69.7	2.00E-10
Por secretion system C-terminal sorting domain	Pgjcvi_01591	PG JCVI SC001	hypothetical protein	PG W83	PG0626	9, 288	99.6	583.2	0
RNA-binding proteins (RRM domain)	Pgjcvi_01592	PG JCVI SC001	RNA-binding protein	PG ATCC 33277	PGN_0668	3, 97	100	192.2	0
RNA-binding proteins (RRM domain)	Pgjcvi_01592	PG JCVI SC001	RNA-binding protein	PG W83	PG0627	3, 97	100	192.2	0

RNA-binding proteins (RRM domain)	Pgjcvi_01592	PG JCVI SC001	RNA-binding protein	PG TDC60	PGTDC60_1756	3, 97	100	192.2	0
ABC-type (unclassified) transport system, ATPase component	Pgjcvi_01593	PG JCVI SC001	ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0669	7, 251	100	480.7	0
ABC-type (unclassified) transport system, ATPase component	Pgjcvi_01593	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG0628	7, 251	100	480.7	0
ABC-type (unclassified) transport system, ATPase component	Pgjcvi_01593	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1757	7, 251	100	480.7	0
Predicted sugar kinase	Pgjcvi_01594	PG JCVI SC001	probable inorganic polyphosphate/ATP-NAD kinase	PG ATCC 33277	PGN_0670	1, 288	99.3	568.5	0
Predicted sugar kinase	Pgjcvi_01594	PG JCVI SC001	inorganic polyphosphate/ATP-NAD kinase	PG TDC60	PGTDC60_1758	1, 288	99	568.2	0
Predicted sugar kinase	Pgjcvi_01594	PG JCVI SC001	inorganic polyphosphate/ATP-NAD kinase	PG W83	PG0629	1, 288	98.6	565.5	0
pyridoxine 5''-phosphate synthase	Pgjcvi_01595	PG JCVI SC001	putative pyridoxal phosphate biosynthetic protein	PG ATCC 33277	PGN_0671	1, 238	99.6	482.6	0
pyridoxine 5''-phosphate synthase	Pgjcvi_01595	PG JCVI SC001	pyridoxal phosphate biosynthetic protein	PG W83	PG0630	1, 238	98.7	479.6	0
pyridoxine 5''-phosphate synthase	Pgjcvi_01595	PG JCVI SC001	pyridoxine 5'-phosphate synthase	PG TDC60	PGTDC60_1759	1, 238	98.3	477.6	0
Biopolymer transport proteins	Pgjcvi_01596	PG JCVI SC001	probable biopolymer transport protein	PG ATCC 33277	PGN_0672	1, 204	100	394.8	0
Biopolymer transport proteins	Pgjcvi_01596	PG JCVI SC001	MotA/TolQ/ExbB proton channel family protein	PG W83	PG0631	1, 204	100	394.8	0
Biopolymer transport proteins	Pgjcvi_01596	PG JCVI SC001	MotA/TolQ/ExbB proton channel family protein	PG TDC60	PGTDC60_1760	1, 244	99.6	468.4	0
Biopolymer transport protein	Pgjcvi_01597	PG JCVI SC001	probable biopolymer transport protein	PG ATCC 33277	PGN_0673	1, 139	100	267.3	0
Biopolymer transport protein	Pgjcvi_01597	PG JCVI SC001	biopolymer transport protein ExbD, putative	PG W83	PG0632	1, 139	100	267.3	0
Biopolymer transport protein	Pgjcvi_01597	PG JCVI SC001	biopolymer transport protein ExbD	PG TDC60	PGTDC60_1761	1, 139	100	267.3	0
TonB family C-terminal domain	Pgjcvi_01598	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1762	1, 275	99.6	533.5	0
TonB family C-terminal domain	Pgjcvi_01598	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0674	1, 275	99.3	533.1	0
TonB family C-terminal domain	Pgjcvi_01598	PG JCVI SC001	hypothetical protein	PG W83	PG0633	1, 275	98.9	531.6	0
DJ-1 family protein	Pgjcvi_01599	PG JCVI SC001	ThiJ/PfpI family protein	PG W83	PG0634	1, 181	100	363.6	0
DJ-1 family protein	Pgjcvi_01599	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0675	1, 181	99.4	361.7	0
DJ-1 family protein	Pgjcvi_01599	PG JCVI SC001	ThiJ/PfpI family protein	PG TDC60	PGTDC60_1763	1, 181	99.4	361.7	0
Ribosomal protein L11 methylase	Pgjcvi_01600	PG JCVI SC001	ribosomal protein L11 methyltransferase	PG W83	PG0635	22, 311	99	583.2	0
Ribosomal protein L11 methylase	Pgjcvi_01600	PG JCVI SC001	putative ribosomal protein L11 methyltransferase	PG ATCC 33277	PGN_0676	22, 311	98.6	580.9	0
Ribosomal protein L11 methylase	Pgjcvi_01600	PG JCVI SC001	ribosomal protein L11 methyltransferase	PG TDC60	PGTDC60_1764	1, 290	98.6	578.6	0
putative efflux protein, MATE family	Pgjcvi_01601	PG JCVI SC001	putative multi antimicrobial extrusion protein MatE	PG ATCC 33277	PGN_0677	1, 454	98.9	875.2	0
putative efflux protein, MATE family	Pgjcvi_01601	PG JCVI SC001	MATE efflux family protein	PG W83	PG0636	1, 454	98.7	872.8	0
putative efflux protein, MATE family	Pgjcvi_01601	PG JCVI SC001	putative multi antimicrobial extrusion protein MatE	PG TDC60	PGTDC60_1765	1, 454	98.7	875.2	0
thiamine-monophosphate kinase	Pgjcvi_01602	PG JCVI SC001	thiamine monophosphate kinase	PG W83	PG0637	1, 346	99.7	683.3	0
thiamine-monophosphate kinase	Pgjcvi_01602	PG JCVI SC001	thiamine monophosphate kinase	PG TDC60	PGTDC60_1766	1, 346	99.7	683.3	0
thiamine-monophosphate kinase	Pgjcvi_01602	PG JCVI SC001	thiamine monophosphate kinase	PG ATCC 33277	PGN_0678	1, 346	99.4	682.9	0
tetraacyldisaccharide 4''-kinase	Pgjcvi_01603	PG JCVI SC001	tetraacyldisaccharide 4'-kinase	PG TDC60	PGTDC60_1767	1, 357	99.7	716.8	0
tetraacyldisaccharide 4''-kinase	Pgjcvi_01603	PG JCVI SC001	putative tetraacyldisaccharide 4'-kinase	PG ATCC 33277	PGN_0679	1, 357	99.2	715.7	0
tetraacyldisaccharide 4''-kinase	Pgjcvi_01603	PG JCVI SC001	tetraacyldisaccharide 4'-kinase	PG W83	PG0638	1, 357	98.9	715.7	0
signal peptide peptidase SppA, 67K type	Pgjcvi_01604	PG JCVI SC001	signal peptide peptidase SppA, 67K type	PG TDC60	PGTDC60_1768	1, 595	99.7	1151	0
signal peptide peptidase SppA, 67K type	Pgjcvi_01604	PG JCVI SC001	signal peptide peptidase SppA 67K type	PG ATCC 33277	PGN_0680	1, 595	99.3	1147.5	0
signal peptide peptidase SppA, 67K type	Pgjcvi_01604	PG JCVI SC001	signal peptide peptidase SppA, 67K type	PG W83	PG0639	1, 595	99.3	1145.6	0
TonB-dependent heme/hemoglobin receptor family protein/TonB-dependent hemoglobin/transferrin/lactoferrin receptor family protein	Pgjcvi_01606	PG JCVI SC001	TonB-linked receptor Tlr	PG ATCC 33277	PGN_0683	1, 706	99.7	1423.7	0
TonB-dependent heme/hemoglobin receptor family protein/TonB-dependent hemoglobin/transferrin/lactoferrin receptor family protein	Pgjcvi_01606	PG JCVI SC001	TonB-linked receptor Tlr	PG TDC60	PGTDC60_1772	1, 706	99.6	1420.6	0
TonB-dependent heme/hemoglobin receptor family protein/TonB-dependent hemoglobin/transferrin/lactoferrin receptor family protein	Pgjcvi_01606	PG JCVI SC001	TonB-dependent receptor HmuR	PG W83	PG1552	7, 249	27.3	78.6	1.10E-12
Uncharacterized conserved protein	Pgjcvi_01607	PG JCVI SC001	conserved hypothetical protein with adenosylcobinamide amidohydrolase domain	PG ATCC 33277	PGN_0684	1, 387	99.2	759.2	0
Uncharacterized conserved protein	Pgjcvi_01607	PG JCVI SC001	hypothetical protein	PG W83	PG0645	1, 358	98.9	694.9	0
Uncharacterized conserved protein	Pgjcvi_01607	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1773	10, 396	98.7	753.8	0
ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components	Pgjcvi_01608	PG JCVI SC001	putative iron compound ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0685	1, 333	99.4	655.6	0
ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components	Pgjcvi_01608	PG JCVI SC001	iron compound ABC transporter, ATP-binding protein	PG W83	PG0646	1, 333	99.1	653.7	0
ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components	Pgjcvi_01608	PG JCVI SC001	iron compound ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1774	1, 333	99.1	653.7	0
ABC-type Fe3+-siderophore transport system, permease component	Pgjcvi_01609	PG JCVI SC001	iron compound ABC transporter permease	PG TDC60	PGTDC60_1775	1, 344	100	663.7	0
ABC-type Fe3+-siderophore transport system, permease component	Pgjcvi_01609	PG JCVI SC001	putative iron compound ABC transporter permease protein	PG ATCC 33277	PGN_0686	1, 344	99.4	659.4	0
ABC-type Fe3+-siderophore transport system, permease component	Pgjcvi_01609	PG JCVI SC001	iron compound ABC transporter, permease protein	PG W83	PG0647	1, 344	99.4	660.6	0
ABC-type Fe3+-hydroxamate transport system, periplasmic component	Pgjcvi_01610	PG JCVI SC001	iron compound ABC transporter, periplasmic iron compound-binding protein, putative	PG W83	PG0648	1, 391	99.7	804.7	0
ABC-type Fe3+-hydroxamate transport system, periplasmic component	Pgjcvi_01610	PG JCVI SC001	iron compound ABC transporter, periplasmic iron compound-binding protein	PG TDC60	PGTDC60_1776	1, 391	99.7	805.4	0
ABC-type Fe3+-hydroxamate transport system, periplasmic component	Pgjcvi_01610	PG JCVI SC001	putative iron compound ABC transporter periplasmic iron compound-binding protein	PG ATCC 33277	PGN_0687	1, 391	99.2	802.7	0
Protein of unknown function (DUF3109).	Pgjcvi_01612	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1777	1, 194	99.5	403.3	0
Protein of unknown function (DUF3109).	Pgjcvi_01612	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0688	1, 194	99	401	0
Protein of unknown function (DUF3109).	Pgjcvi_01612	PG JCVI SC001	hypothetical protein	PG W83	PG0649	1, 194	98.5	399.1	0
Protein of unknown function (DUF3276).	Pgjcvi_01613	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0689	1, 127	100	252.7	0
Protein of unknown function (DUF3276).	Pgjcvi_01613	PG JCVI SC001	hypothetical protein	PG W83	PG0650	1, 127	99.2	251.1	0
Protein of unknown function (DUF3276).	Pgjcvi_01613	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1778	1, 127	99.2	250.4	0
uncharacterized domain HDIG	Pgjcvi_01614	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0690	1, 182	98.9	366.3	0
uncharacterized domain HDIG	Pgjcvi_01614	PG JCVI SC001	HDIG domain-containing protein	PG TDC60	PGTDC60_1779	1, 183	98.4	366.3	0
uncharacterized domain HDIG	Pgjcvi_01614	PG JCVI SC001	HDIG domain protein	PG W83	PG0651	1, 183	97.8	363.2	0
Stress responsive A/B Barrel Domain.	Pgjcvi_01616	PG JCVI SC001	hypothetical protein	PG W83	PG0652	1, 100	99	198.7	0
Stress responsive A/B Barrel Domain.	Pgjcvi_01616	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0691	1, 100	98	196.4	0
Stress responsive A/B Barrel Domain.	Pgjcvi_01616	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1780	1, 100	98	196.4	0
phosphoserine phosphatase SerB	Pgjcvi_01617	PG JCVI SC001	phosphoserine phosphatase	PG ATCC 33277	PGN_0692	1, 413	100	795.4	0
phosphoserine phosphatase SerB	Pgjcvi_01617	PG JCVI SC001	phosphoserine phosphatase	PG W83	PG0653	1, 413	100	795.4	0
phosphoserine phosphatase SerB	Pgjcvi_01617	PG JCVI SC001	phosphoserine phosphatase	PG TDC60	PGTDC60_1781	1, 413	100	795.4	0
Por secretion system C-terminal sorting domain	Pgjcvi_01618	PG JCVI SC001	hypothetical protein	PG W83	PG0654	1, 390	99	777.7	0
Por secretion system C-terminal sorting domain	Pgjcvi_01618	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1782	1, 390	98.5	774.6	0

Por secretion system C-terminal sorting domain	Pgjcvi_01618	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0693	1, 390	98.2	772.7	0
ribosomal protein L34, bacterial type	Pgjcvi_01619	PG JCVI SC001	50S ribosomal protein L34	PG ATCC 33277	PGN_0694	1, 50	100	101.7	8.60E-21
ribosomal protein L34, bacterial type	Pgjcvi_01619	PG JCVI SC001	50S ribosomal protein L34	PG W83	PG0656	1, 50	100	101.7	8.60E-21
ribosomal protein L34, bacterial type	Pgjcvi_01619	PG JCVI SC001	50S ribosomal protein L34	PG TDC60	PGTDC60_1783	1, 50	100	101.7	8.60E-21
MAF protein	Pgjcvi_01620	PG JCVI SC001	Maf-like protein	PG TDC60	PGTDC60_1784	1, 199	99	396	0
MAF protein	Pgjcvi_01620	PG JCVI SC001	Maf-like protein	PG W83	PG0657	9, 207	98.5	392.5	0
MAF protein	Pgjcvi_01620	PG JCVI SC001	probable septum formation protein Maf	PG ATCC 33277	PGN_0695	1, 199	98	393.7	0
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family	Pgjcvi_01621	PG JCVI SC001	probable hydrolase	PG ATCC 33277	PGN_0696	1, 173	99.4	348.2	0
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family	Pgjcvi_01621	PG JCVI SC001	phosphatase, YrbI family	PG W83	PG0658	1, 173	99.4	345.1	0
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family	Pgjcvi_01621	PG JCVI SC001	YrbI family phosphatase	PG TDC60	PGTDC60_1785	1, 173	99.4	345.1	0
Uncharacterized conserved protein	Pgjcvi_01622	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1786	1, 270	99.3	534.3	0
Uncharacterized conserved protein	Pgjcvi_01622	PG JCVI SC001	hypothetical protein	PG W83	PG0659	1, 270	98.5	530.8	0
Uncharacterized conserved protein	Pgjcvi_01622	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0697	1, 270	98.1	529.3	0
Nitroreductase	Pgjcvi_01623	PG JCVI SC001	probable nitroreductase	PG ATCC 33277	PGN_0698	1, 184	100	372.5	0
Nitroreductase	Pgjcvi_01623	PG JCVI SC001	nitroreductase family protein	PG TDC60	PGTDC60_1787	1, 184	100	372.5	0
Nitroreductase	Pgjcvi_01623	PG JCVI SC001	nitroreductase family protein	PG W83	PG0660	1, 184	99.5	370.2	0
Predicted dehydrogenases and related proteins	Pgjcvi_01624	PG JCVI SC001	Gfo/Idh/MocA family oxidoreductase	PG TDC60	PGTDC60_1790	1, 468	99.8	965.3	0
Predicted dehydrogenases and related proteins	Pgjcvi_01624	PG JCVI SC001	putative oxidoreductase Gfo/Idh/MocA family	PG ATCC 33277	PGN_0700	1, 495	99.6	1015.8	0
Predicted dehydrogenases and related proteins	Pgjcvi_01624	PG JCVI SC001	oxidoreductase, Gfo/Idh/MocA family	PG W83	PG0664	1, 495	99.4	1015.8	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_01625	PG JCVI SC001	beta-galactosidase	PG TDC60	PGTDC60_1791	1, 1123	98.6	2299.6	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_01625	PG JCVI SC001	beta-galactosidase	PG W83	PG0665	1, 1112	98.5	2283.4	0
Beta-galactosidase/beta-glucuronidase	Pgjcvi_01625	PG JCVI SC001	beta-galactosidase	PG ATCC 33277	PGN_0701	1, 1123	98.4	2293.8	0
Putative homoserine kinase type II (protein kinase fold)	Pgjcvi_01626	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0702	1, 362	99.7	740.7	0
Putative homoserine kinase type II (protein kinase fold)	Pgjcvi_01626	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1792	1, 362	98.6	731.5	0
Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_01628	PG JCVI SC001	TonB-dependent receptor	PG W83	PG0668	1, 757	99.7	1520.4	0
Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_01628	PG JCVI SC001	putative tonB-linked outer membrane receptor	PG ATCC 33277	PGN_0704	1, 757	99.5	1516.1	0
Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_01628	PG JCVI SC001	TonB-dependent receptor	PG TDC60	PGTDC60_1793	1, 757	99.5	1514.6	0
Cobalamin biosynthesis protein CbiK, Co2+ chelatase	Pgjcvi_01629	PG JCVI SC001	heme-binding protein FetB	PG ATCC 33277	PGN_0705	1, 293	99.7	578.9	0
Cobalamin biosynthesis protein CbiK, Co2+ chelatase	Pgjcvi_01629	PG JCVI SC001	heme-binding protein FetB	PG W83	PG0669	1, 293	99.3	576.6	0
Cobalamin biosynthesis protein CbiK, Co2+ chelatase	Pgjcvi_01629	PG JCVI SC001	heme-binding protein FetB	PG TDC60	PGTDC60_1794	1, 293	99.3	576.6	0
ABC-type Fe3+-hydroxamate transport system, periplasmic component	Pgjcvi_01630	PG JCVI SC001	putative exported periplasmic protein	PG ATCC 33277	PGN_0706	1, 379	99.5	765	0
ABC-type Fe3+-hydroxamate transport system, periplasmic component	Pgjcvi_01630	PG JCVI SC001	putative exported periplasmic protein	PG TDC60	PGTDC60_1795	1, 379	99.5	766.5	0
ABC-type Fe3+-hydroxamate transport system, periplasmic component	Pgjcvi_01630	PG JCVI SC001	lipoprotein, putative	PG W83	PG0670	1, 379	98.9	763.5	0
ABC-type Fe3+-siderophore transport system, permease component	Pgjcvi_01631	PG JCVI SC001	putative iron compound ABC transporter permease protein	PG ATCC 33277	PGN_0707	1, 356	100	676	0
ABC-type Fe3+-siderophore transport system, permease component	Pgjcvi_01631	PG JCVI SC001	iron compound ABC transporter, permease protein	PG W83	PG0671	1, 356	99.7	674.5	0
ABC-type Fe3+-siderophore transport system, permease component	Pgjcvi_01631	PG JCVI SC001	iron compound ABC transporter permease	PG TDC60	PGTDC60_1796	1, 356	99.4	673.7	0
ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components	Pgjcvi_01632	PG JCVI SC001	putative iron compound ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0708	1, 252	99.6	493.4	0
ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components	Pgjcvi_01632	PG JCVI SC001	iron compound ABC transporter, ATP-binding protein	PG W83	PG0672	1, 252	98.8	488.8	0
ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components	Pgjcvi_01632	PG JCVI SC001	iron compound ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1797	1, 252	97.2	478	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit	Pgjcvi_01633	PG JCVI SC001	putative indolepyruvate ferredoxin oxidoreductase beta subunit	PG ATCC 33277	PGN_0709	1, 197	100	385.6	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit	Pgjcvi_01633	PG JCVI SC001	indolepyruvate ferredoxin oxidoreductase, beta subunit	PG W83	PG0674	1, 197	100	385.6	0
Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit	Pgjcvi_01633	PG JCVI SC001	indolepyruvate oxidoreductase subunit beta	PG TDC60	PGTDC60_1798	1, 197	100	385.6	0
Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits	Pgjcvi_01634	PG JCVI SC001	indolepyruvate ferredoxin oxidoreductase alpha subunit	PG ATCC 33277	PGN_0710	1, 535	99.6	1068.5	0
Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits	Pgjcvi_01634	PG JCVI SC001	indolepyruvate ferredoxin oxidoreductase, alpha subunit	PG W83	PG0675	1, 535	99.4	1066.2	0
Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits	Pgjcvi_01634	PG JCVI SC001	indolepyruvate ferredoxin oxidoreductase subunit alpha	PG TDC60	PGTDC60_1799	1, 535	98.9	1064.3	0
Short-chain alcohol dehydrogenase of unknown specificity	Pgjcvi_01635	PG JCVI SC001	short chain dehydrogenase/reductase family oxidoreductase	PG TDC60	PGTDC60_1800	1, 253	99.2	500	0
Short-chain alcohol dehydrogenase of unknown specificity	Pgjcvi_01635	PG JCVI SC001	putative oxidoreductase short chain dehydrogenase/reductase family	PG ATCC 33277	PGN_0711	1, 253	98.8	498.8	0
Short-chain alcohol dehydrogenase of unknown specificity	Pgjcvi_01635	PG JCVI SC001	oxidoreductase, short chain dehydrogenase/reductase family	PG W83	PG0676	1, 253	98.8	499.2	0
Saccharopine dehydrogenase and related proteins	Pgjcvi_01636	PG JCVI SC001	saccharopine dehydrogenase	PG TDC60	PGTDC60_1802	1, 397	100	827.4	0
Saccharopine dehydrogenase and related proteins	Pgjcvi_01636	PG JCVI SC001	saccharopine dehydrogenase	PG W83	PG0677	1, 397	99.7	824.3	0
Saccharopine dehydrogenase and related proteins	Pgjcvi_01636	PG JCVI SC001	saccharopine dehydrogenase	PG ATCC 33277	PGN_0713	1, 397	99.5	825.1	0
Amidases related to nicotinamidase	Pgjcvi_01637	PG JCVI SC001	pyrazinamidase/nicotinamidase, putative	PG W83	PG0678	1, 170	100	338.6	0
Amidases related to nicotinamidase	Pgjcvi_01637	PG JCVI SC001	probable pyrazinamidase/nicotinamidase	PG ATCC 33277	PGN_0714	1, 170	99.4	337.4	0
Amidases related to nicotinamidase	Pgjcvi_01637	PG JCVI SC001	pyrazinamidase/nicotinamidase	PG TDC60	PGTDC60_1803	1, 170	99.4	337	0
Outer membrane protein	Pgjcvi_01638	PG JCVI SC001	outer membrane efflux protein	PG ATCC 33277	PGN_0715	1, 444	98.9	857.1	0
Outer membrane protein	Pgjcvi_01638	PG JCVI SC001	outer membrane efflux protein	PG W83	PG0679	1, 444	98.6	855.1	0
Outer membrane protein	Pgjcvi_01638	PG JCVI SC001	outer membrane efflux protein	PG TDC60	PGTDC60_1804	1, 444	98.4	855.1	0
RND family efflux transporter, MFP subunit	Pgjcvi_01639	PG JCVI SC001	ABC transporter permease	PG ATCC 33277	PGN_0716	1, 417	99.5	817	0
RND family efflux transporter, MFP subunit	Pgjcvi_01639	PG JCVI SC001	RND family efflux transporter MFP subunit	PG TDC60	PGTDC60_1805	1, 417	99.5	817	0
RND family efflux transporter, MFP subunit	Pgjcvi_01639	PG JCVI SC001	efflux transporter, MFP component, RND family	PG W83	PG0680	1, 417	99	815.1	0
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_01640	PG JCVI SC001	ABC transporter, permease protein, putative	PG W83	PG0683	1, 788	98.9	1543.5	0
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_01640	PG JCVI SC001	probable ABC transporter permease protein	PG ATCC 33277	PGN_0719	1, 789	60.1	955.3	0
ABC-type transport system, involved in lipoprotein release, permease component	Pgjcvi_01640	PG JCVI SC001	ABC transporter permease	PG TDC60	PGTDC60_1808	1, 789	59.7	949.5	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01641	PG JCVI SC001	ABC transporter, permease protein, putative	PG W83	PG0684	1, 791	99.6	1533.1	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01641	PG JCVI SC001	ABC transporter permease	PG TDC60	PGTDC60_1809	1, 791	99.6	1533.1	0
ABC-type antimicrobial peptide transport system, permease component	Pgjcvi_01641	PG JCVI SC001	putative ABC transporter permease protein	PG ATCC 33277	PGN_0720	1, 791	99.5	1532.3	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_01642	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0721	1, 219	100	424.9	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_01642	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG0685	1, 219	100	424.9	0
ABC-type antimicrobial peptide transport system, ATPase component	Pgjcvi_01642	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1810	1, 219	100	424.9	0

Uncharacterized conserved protein	Pgjcvi_01643	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1811	1, 517	99.8	1031.9	0
Uncharacterized conserved protein	Pgjcvi_01643	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0722	1, 517	99.6	1028.5	0
Uncharacterized conserved protein	Pgjcvi_01643	PG JCVI SC001	hypothetical protein	PG W83	PG0686	1, 517	99.4	1026.5	0
hypothetical protein	Pgjcvi_01644	PG JCVI SC001	hypothetical protein	PG W83	PG0700	78, 123	52.2	53.1	3.50E-06
hypothetical protein	Pgjcvi_01644	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0585	62, 106	46.7	42.7	0.0048
NAD-dependent aldehyde dehydrogenases	Pgjcvi_01645	PG JCVI SC001	succinate-semialdehyde dehydrogenase	PG W83	PG0687	1, 451	99.8	892.9	0
NAD-dependent aldehyde dehydrogenases	Pgjcvi_01645	PG JCVI SC001	succinate-semialdehyde dehydrogenase	PG TDC60	PGTDC60_1813	1, 451	99.8	894.4	0
NAD-dependent aldehyde dehydrogenases	Pgjcvi_01645	PG JCVI SC001	succinate-semialdehyde dehydrogenase	PG ATCC 33277	PGN_0723	1, 451	99.6	892.5	0
Alcohol dehydrogenase, class IV	Pgjcvi_01646	PG JCVI SC001	NAD-dependent 4-hydroxybutyrate dehydrogenase	PG ATCC 33277	PGN_0724	1, 371	100	753.4	0
Alcohol dehydrogenase, class IV	Pgjcvi_01646	PG JCVI SC001	NAD-dependent 4-hydroxybutyrate dehydrogenase	PG W83	PG0689	1, 371	100	753.4	0
Alcohol dehydrogenase, class IV	Pgjcvi_01646	PG JCVI SC001	NAD-dependent 4-hydroxybutyrate dehydrogenase	PG TDC60	PGTDC60_1814	1, 371	99.2	747.7	0
Acetyl-CoA hydrolase	Pgjcvi_01647	PG JCVI SC001	4-hydroxybutyrate CoA-transferase	PG TDC60	PGTDC60_1815	1, 431	99.5	856.3	0
Acetyl-CoA hydrolase	Pgjcvi_01647	PG JCVI SC001	4-hydroxybutyrate CoA-transferase	PG ATCC 33277	PGN_0725	1, 431	99.3	856.3	0
Acetyl-CoA hydrolase	Pgjcvi_01647	PG JCVI SC001	4-hydroxybutyrate CoA-transferase	PG W83	PG0690	1, 431	99.3	855.9	0
Thioredoxin-like proteins and domains	Pgjcvi_01648	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0726	1, 94	100	186	0
Thioredoxin-like proteins and domains	Pgjcvi_01648	PG JCVI SC001	NifU-related protein	PG W83	PG0691	1, 94	100	186	0
Thioredoxin-like proteins and domains	Pgjcvi_01648	PG JCVI SC001	NifU-like protein	PG TDC60	PGTDC60_1816	1, 94	98.9	184.5	1.40E-45
Aromatic ring hydroxylase	Pgjcvi_01649	PG JCVI SC001	4-hydroxybutyryl-CoA dehydratase	PG W83	PG0692	1, 486	99.8	973.4	0
Aromatic ring hydroxylase	Pgjcvi_01649	PG JCVI SC001	4-hydroxybutyryl-CoA dehydratase	PG ATCC 33277	PGN_0727	1, 486	99.6	972.2	0
Aromatic ring hydroxylase	Pgjcvi_01649	PG JCVI SC001	4-hydroxybutyryl-CoA dehydratase	PG TDC60	PGTDC60_1817	1, 486	99.6	972.2	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01651	PG JCVI SC001	immunoreactive 42 kDa antigen PG33	PG W83	PG0694	1, 380	99.7	778.1	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01651	PG JCVI SC001	immunoreactive 42 kDa antigen PG33	PG TDC60	PGTDC60_1818	6, 385	98.9	771.9	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01651	PG JCVI SC001	outer membrane protein 40 precursor	PG ATCC 33277	PGN_0728	1, 380	98.7	769.6	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01652	PG JCVI SC001	immunoreactive 43 kDa antigen PG32	PG W83	PG0695	1, 391	99.5	786.2	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01652	PG JCVI SC001	outer membrane protein 41 precursor	PG ATCC 33277	PGN_0729	1, 391	99.2	783.9	0
Outer membrane protein and related peptidoglycan-associated (lipo)proteins	Pgjcvi_01652	PG JCVI SC001	immunoreactive 43 kDa antigen PG32	PG TDC60	PGTDC60_1819	1, 390	98.2	771.2	0
hypothetical protein	Pgjcvi_01653	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1821	1, 317	99.4	630.6	0
hypothetical protein	Pgjcvi_01653	PG JCVI SC001	lipoprotein, putative	PG W83	PG0698	5, 327	99.1	641	0
hypothetical protein	Pgjcvi_01653	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0732	5, 327	98.8	637.5	0
alpha-glucan phosphorylases	Pgjcvi_01654	PG JCVI SC001	maltodextrin phosphorylase	PG W83	PG0699	1, 856	99.8	1765.7	0
alpha-glucan phosphorylases	Pgjcvi_01654	PG JCVI SC001	maltodextrin phosphorylase	PG TDC60	PGTDC60_1822	1, 856	99.5	1763	0
alpha-glucan phosphorylases	Pgjcvi_01654	PG JCVI SC001	alpha-glucan phosphorylase	PG ATCC 33277	PGN_0733	1, 856	99.2	1755.7	0
hypothetical protein	Pgjcvi_01655	PG JCVI SC001	hypothetical protein	PG W83	PG0700	101, 170	100	149.1	7.60E-35
Adenosyl cobinamide kinase/adenosyl cobinamide phosphate guanylyltransferase	Pgjcvi_01656	PG JCVI SC001	cobinamide kinase/cobinamide phosphate guanylyltransferase	PG W83	PG0701	1, 178	100	357.5	0
Adenosyl cobinamide kinase/adenosyl cobinamide phosphate guanylyltransferase	Pgjcvi_01656	PG JCVI SC001	putative bifunctional cobalamin biosynthesis protein	PG ATCC 33277	PGN_0735	1, 178	99.4	356.3	0
Adenosyl cobinamide kinase/adenosyl cobinamide phosphate guanylyltransferase	Pgjcvi_01656	PG JCVI SC001	cobinamide kinase/cobinamide phosphate guanylyltransferase	PG TDC60	PGTDC60_1824	1, 178	99.4	356.3	0
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	Pgjcvi_01657	PG JCVI SC001	putative nicotinate-nucleotide- dimethylbenzimidazole phosphoribosyltransferase	PG ATCC 33277	PGN_0736	1, 345	99.7	693.7	0
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	Pgjcvi_01657	PG JCVI SC001	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase, putative	PG W83	PG0702	1, 345	99.7	693.7	0
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	Pgjcvi_01657	PG JCVI SC001	nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	PG TDC60	PGTDC60_1825	1, 345	99.7	693.7	0
Cobalamin-5-phosphate synthase	Pgjcvi_01658	PG JCVI SC001	cobalamin (5'-phosphate) synthase, putative	PG W83	PG0703	1, 260	100	522.7	0
Cobalamin-5-phosphate synthase	Pgjcvi_01658	PG JCVI SC001	putative cobalamin-5'-phosphate synthase	PG TDC60	PGTDC60_1826	1, 260	100	522.7	0
Cobalamin-5-phosphate synthase	Pgjcvi_01658	PG JCVI SC001	probable cobalamin-5'-phosphate synthase	PG ATCC 33277	PGN_0737	1, 260	99.6	520.8	0
alpha-ribazole phosphatase	Pgjcvi_01659	PG JCVI SC001	putative phosphoglycerate mutase	PG ATCC 33277	PGN_0738	1, 179	98.9	369.4	0
alpha-ribazole phosphatase	Pgjcvi_01659	PG JCVI SC001	putative phosphoglycerate mutase	PG TDC60	PGTDC60_1827	1, 179	98.9	367.1	0
alpha-ribazole phosphatase	Pgjcvi_01659	PG JCVI SC001	phosphoglycerate mutase family protein	PG W83	PG0704	1, 179	98.3	367.9	0
glutamate racemase	Pgjcvi_01660	PG JCVI SC001	glutamate racemase	PG ATCC 33277	PGN_0739	1, 274	99.6	545.4	0
glutamate racemase	Pgjcvi_01660	PG JCVI SC001	glutamate racemase	PG W83	PG0705	1, 274	99.6	547.4	0
glutamate racemase	Pgjcvi_01660	PG JCVI SC001	glutamate racemase	PG TDC60	PGTDC60_1828	1, 274	99.6	546.6	0
Heat shock protein	Pgjcvi_01661	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0740	1, 143	98.6	283.9	0
Heat shock protein	Pgjcvi_01661	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1829	8, 150	98.6	283.9	0
Heat shock protein	Pgjcvi_01661	PG JCVI SC001	hypothetical protein	PG W83	PG0706	8, 150	96.5	276.9	0
Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_01662	PG JCVI SC001	TonB-dependent receptor	PG ATCC 33277	PGN_0741	1, 848	99.4	1708.3	0
Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_01662	PG JCVI SC001	TonB-dependent receptor	PG TDC60	PGTDC60_1830	1, 848	99.4	1708.3	0
Outer membrane receptor for ferrienterochelin and colicins	Pgjcvi_01662	PG JCVI SC001	TonB-dependent receptor, putative	PG W83	PG0707	1, 848	99.3	1708.3	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01664	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, FKBP-type	PG TDC60	PGTDC60_1831	1, 276	100	539.7	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01664	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, FKBP-type	PG W83	PG0708	1, 276	99.6	537.7	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01664	PG JCVI SC001	probable FKBP-type peptidyl-prolyl cis-trans isomerase	PG ATCC 33277	PGN_0742	1, 276	99.3	537.7	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01665	PG JCVI SC001	probable FKBP-type peptidyl-prolyl cis-trans isomerase FkpA	PG ATCC 33277	PGN_0743	1, 257	100	510	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01665	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase FkpA, FKBP-type	PG TDC60	PGTDC60_1832	1, 257	100	510	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01665	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase FkpA, FKBP-type	PG W83	PG0709	1, 253	99.2	500.7	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01666	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, FKBP-type	PG W83	PG0710	1, 195	100	391.3	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01666	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase, FKBP-type	PG TDC60	PGTDC60_1833	1, 195	100	391.3	0
FKBP-type peptidyl-prolyl cis-trans isomerases 1	Pgjcvi_01666	PG JCVI SC001	probable FKBP-type peptidyl-prolyl cis-trans isomerase	PG ATCC 33277	PGN_0744	1, 194	99.5	387.1	0
PAS fold.	Pgjcvi_01667	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0746	1, 115	100	240	0
PAS fold.	Pgjcvi_01667	PG JCVI SC001	hypothetical protein	PG W83	PG0712	1, 115	100	240	0
PAS fold.	Pgjcvi_01667	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1835	1, 115	100	240	0
glutamine amidotransferase of anthranilate synthase or aminodeoxychorismate synthase	Pgjcvi_01668	PG JCVI SC001	probable anthranilate synthase component II	PG ATCC 33277	PGN_0747	1, 198	99	414.1	0
glutamine amidotransferase of anthranilate synthase or aminodeoxychorismate synthase	Pgjcvi_01668	PG JCVI SC001	anthranilate synthase component II	PG W83	PG0713	1, 198	99	414.1	0
glutamine amidotransferase of anthranilate synthase or aminodeoxychorismate synthase	Pgjcvi_01668	PG JCVI SC001	anthranilate synthase component II	PG TDC60	PGTDC60_1836	1, 198	98.5	414.8	0

hypothetical protein	Pgjcvi_01669	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0748	1, 1530	99.8	3009.9	0
Uncharacterized protein involved in copper resistance	Pgjcvi_01671	PG JCVI SC001	copper homeostasis protein CutC	PG TDC60	PGTDC60_1837	1, 248	99.2	490.3	0
Uncharacterized protein involved in copper resistance	Pgjcvi_01671	PG JCVI SC001	putative copper homeostasis protein CutC	PG ATCC 33277	PGN_0750	1, 248	98.4	487.3	0
Uncharacterized protein involved in copper resistance	Pgjcvi_01671	PG JCVI SC001	copper homeostasis protein CutC	PG W83	PG0714	1, 248	98.4	486.9	0
Mg2+ and Co2+ transporters	Pgjcvi_01672	PG JCVI SC001	putative cationic transporter	PG ATCC 33277	PGN_0751	1, 306	100	602.1	0
Mg2+ and Co2+ transporters	Pgjcvi_01672	PG JCVI SC001	transporter	PG W83	PG0715	1, 306	99.7	600.5	0
Mg2+ and Co2+ transporters	Pgjcvi_01672	PG JCVI SC001	transporter	PG TDC60	PGTDC60_1838	1, 306	99.7	600.5	0
Protein of unknown function (DUF2874).	Pgjcvi_01674	PG JCVI SC001	lipoprotein, putative	PG W83	PG0717	1, 335	99.7	684.1	0
Protein of unknown function (DUF2874).	Pgjcvi_01674	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1839	1, 335	99.1	684.5	0
Protein of unknown function (DUF2874).	Pgjcvi_01674	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0752	9, 53	62.2	64.3	1.10E-08
Protein of unknown function (DUF2874).	Pgjcvi_01674	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1839	173, 434	36.7	151	9.00E-35
Protein of unknown function (DUF2874).	Pgjcvi_01675	PG JCVI SC001	hypothetical protein	PG W83	PG0718	1, 145	100	294.7	0
Protein of unknown function (DUF2874).	Pgjcvi_01675	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1840	1, 145	99.3	293.1	0
Signal transduction histidine kinase	Pgjcvi_01676	PG JCVI SC001	sensor histidine kinase	PG W83	PG0719	1, 427	99.8	848.6	0
Signal transduction histidine kinase	Pgjcvi_01676	PG JCVI SC001	sensor histidine kinase	PG TDC60	PGTDC60_1841	1, 427	99.5	847.4	0
Signal transduction histidine kinase	Pgjcvi_01676	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0752	1, 24	91.7	53.5	2.30E-05
Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	Pgjcvi_01677	PG JCVI SC001	probable two component system response regulator	PG ATCC 33277	PGN_0753	1, 225	100	446	0
Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	Pgjcvi_01677	PG JCVI SC001	DNA-binding response regulator	PG TDC60	PGTDC60_1842	1, 229	100	454.1	0
Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	Pgjcvi_01677	PG JCVI SC001	DNA-binding response regulator	PG W83	PG0720	1, 229	99.6	452.6	0
Cell wall-associated hydrolases (invasion-associated proteins)	Pgjcvi_01678	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0754	1, 202	99	397.9	0
Cell wall-associated hydrolases (invasion-associated proteins)	Pgjcvi_01678	PG JCVI SC001	NLP/P60 family protein	PG W83	PG0721	1, 202	99	397.9	0
Cell wall-associated hydrolases (invasion-associated proteins)	Pgjcvi_01678	PG JCVI SC001	NLP/P60 family protein	PG TDC60	PGTDC60_1843	1, 202	99	397.9	0
hypothetical protein	Pgjcvi_01679	PG JCVI SC001	hypothetical protein	PG W83	PG0722	1, 50	96	100.5	1.90E-20
hypothetical protein	Pgjcvi_01679	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1894	1, 50	70	73.2	3.30E-12
hypothetical protein	Pgjcvi_01679	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0235	1, 50	70	73.2	3.30E-12
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01680	PG JCVI SC001	prolyl oligopeptidase	PG ATCC 33277	PGN_0756	9, 684	99.6	1406	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01680	PG JCVI SC001	prolyl oligopeptidase family protein	PG W83	PG0724	1, 648	99.4	1347	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01680	PG JCVI SC001	prolyl oligopeptidase	PG TDC60	PGTDC60_1845	9, 684	99	1396.7	0
haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	Pgjcvi_01681	PG JCVI SC001	hydrolase, haloacid dehalogenase-like family	PG W83	PG0725	1, 208	99.5	418.7	0
haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	Pgjcvi_01681	PG JCVI SC001	HAD superfamily hydrolase	PG TDC60	PGTDC60_1846	1, 208	99	416.8	0
haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	Pgjcvi_01681	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0757	1, 208	98.1	412.9	0
PEGA domain.	Pgjcvi_01682	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0758	1, 129	100	264.6	0
PEGA domain.	Pgjcvi_01682	PG JCVI SC001	lipoprotein, putative	PG W83	PG0726	1, 129	100	264.6	0
PEGA domain.	Pgjcvi_01682	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_1847	11, 139	100	264.6	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01683	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1849	3, 388	100	775.8	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01683	PG JCVI SC001	hypothetical protein	PG W83	PG0728	3, 388	99	766.9	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01683	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0759	1, 386	98.2	765.4	0
D-alanine-D-alanine ligase and related ATP-grasp enzymes	Pgjcvi_01684	PG JCVI SC001	D-alanylalanine synthetase	PG W83	PG0729	1, 330	99.4	648.3	0
D-alanine-D-alanine ligase and related ATP-grasp enzymes	Pgjcvi_01684	PG JCVI SC001	D-alanyl-alanine synthetase A	PG TDC60	PGTDC60_1850	1, 331	99.4	650.2	0
D-alanine-D-alanine ligase and related ATP-grasp enzymes	Pgjcvi_01684	PG JCVI SC001	putative D-alanine--D-alanine ligase	PG ATCC 33277	PGN_0760	1, 330	99.1	643.7	0
pseudouridine synthase, RluA family	Pgjcvi_01685	PG JCVI SC001	ribosomal large subunit pseudouridine synthase	PG ATCC 33277	PGN_0761	1, 365	99.7	747.7	0
pseudouridine synthase, RluA family	Pgjcvi_01685	PG JCVI SC001	ribosomal large subunit pseudouridine synthase	PG TDC60	PGTDC60_1851	1, 373	99.2	758.4	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01686	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1852	1, 200	100	391.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01686	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0762	1, 218	99.5	427.9	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01686	PG JCVI SC001	hypothetical protein	PG W83	PG0731	1, 218	99.5	427.9	0
hypothetical protein	Pgjcvi_01687	PG JCVI SC001	hypothetical protein	PG W83	PG0732	31, 105	98.7	147.1	2.70E-34
hypothetical protein	Pgjcvi_01687	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0763	31, 105	94.7	141.4	1.50E-32
hypothetical protein	Pgjcvi_01687	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1853	11, 37	85.2	48.1	0.00017
rRNA methylases	Pgjcvi_01688	PG JCVI SC001	probable tRNA/rRNA methyltransferase	PG ATCC 33277	PGN_0772	1, 254	98.8	500	0
rRNA methylases	Pgjcvi_01688	PG JCVI SC001	RNA methyltransferase, TrmH family	PG W83	PG0744	1, 254	98	495.7	0
rRNA methylases	Pgjcvi_01688	PG JCVI SC001	RNA methyltransferase	PG TDC60	PGTDC60_1863	1, 254	98	495.7	0
Lactoylglutathione lyase and related lyases	Pgjcvi_01689	PG JCVI SC001	putative lactoylglutathione lyase	PG ATCC 33277	PGN_0773	1, 132	100	286.2	0
Lactoylglutathione lyase and related lyases	Pgjcvi_01689	PG JCVI SC001	lactoylglutathione lyase, putative	PG W83	PG0745	1, 132	98.5	281.6	0
Lactoylglutathione lyase and related lyases	Pgjcvi_01689	PG JCVI SC001	lactoylglutathione lyase	PG TDC60	PGTDC60_1864	1, 132	98.5	281.6	0
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_01690	PG JCVI SC001	sensor histidine kinase	PG W83	PG0746	11, 455	99.3	871.7	0
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_01690	PG JCVI SC001	sensor histidine kinase	PG TDC60	PGTDC60_1865	1, 445	98.7	866.7	0
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_01690	PG JCVI SC001	two-component system sensor histidine kinase	PG ATCC 33277	PGN_0774	1, 445	98	860.1	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_01691	PG JCVI SC001	two-component system response regulator	PG ATCC 33277	PGN_0775	1, 464	99.6	903.3	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_01691	PG JCVI SC001	sigma-54 dependent DNA-binding response regulator	PG TDC60	PGTDC60_1866	1, 464	99.6	899	0
Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	Pgjcvi_01691	PG JCVI SC001	sigma-54 dependent DNA-binding response regulator	PG W83	PG0747	1, 464	99.1	897.1	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01693	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG TDC60	PGTDC60_1867	1, 248	99.6	501.1	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01693	PG JCVI SC001	glycosyl transferase, group 2 family protein	PG W83	PG0750	1, 248	99.2	497.3	0
Glycosyltransferases involved in cell wall biogenesis	Pgjcvi_01693	PG JCVI SC001	probable glycosyl transferase	PG ATCC 33277	PGN_0777	1, 248	98.8	494.2	0

hypothetical protein	Pgjcvi_01694	PG JCVI SC001	membrane-associated protein PorT	PG ATCC 33277	PGN_0778	1, 244	99.6	503.4	0
hypothetical protein	Pgjcvi_01694	PG JCVI SC001	porT protein	PG W83	PG0751	1, 244	99.6	503.4	0
hypothetical protein	Pgjcvi_01694	PG JCVI SC001	membrane-associated protein PorT	PG TDC60	PGTDC60_1868	1, 244	99.6	503.4	0
Uracil phosphoribosyltransferase	Pgjcvi_01695	PG JCVI SC001	probable uracil phosphoribosyltransferase	PG ATCC 33277	PGN_0779	1, 216	100	434.1	0
Uracil phosphoribosyltransferase	Pgjcvi_01695	PG JCVI SC001	uracil phosphoribosyltransferase	PG W83	PG0752	1, 216	100	434.1	0
Uracil phosphoribosyltransferase	Pgjcvi_01695	PG JCVI SC001	uracil phosphoribosyltransferase	PG TDC60	PGTDC60_1869	1, 216	99.5	432.6	0
Collagenase and related proteases	Pgjcvi_01696	PG JCVI SC001	protease	PG W83	PG0753	1, 635	99.5	1253.4	0
Collagenase and related proteases	Pgjcvi_01696	PG JCVI SC001	PrtQ, protease	PG TDC60	PGTDC60_1870	1, 635	98.7	1242.6	0
Collagenase and related proteases	Pgjcvi_01696	PG JCVI SC001	PrtQ, protease	PG ATCC 33277	PGN_0780	1, 635	98.6	1238.8	0
DNA topoisomerase I, bacterial	Pgjcvi_01697	PG JCVI SC001	DNA topoisomerase I	PG W83	PG0754	1, 788	99.5	1553.5	0
DNA topoisomerase I, bacterial	Pgjcvi_01697	PG JCVI SC001	DNA topoisomerase I	PG ATCC 33277	PGN_0781	1, 788	99.2	1550.4	0
DNA topoisomerase I, bacterial	Pgjcvi_01697	PG JCVI SC001	DNA topoisomerase I	PG TDC60	PGTDC60_1872	1, 788	99.1	1549.6	0
pseudouridylate synthase I	Pgjcvi_01698	PG JCVI SC001	putative tRNA pseudouridine synthase A	PG ATCC 33277	PGN_0782	1, 252	99.6	506.5	0
pseudouridylate synthase I	Pgjcvi_01698	PG JCVI SC001	tRNA pseudouridine synthase A	PG TDC60	PGTDC60_1873	1, 252	99.6	506.5	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01699	PG JCVI SC001	hypothetical protein	PG W83	PG0756	1, 450	99.3	871.3	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01699	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0786	1, 450	98.9	867.8	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01699	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1878	1, 450	98.9	867.1	0
hypothetical protein	Pgjcvi_01700	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0787	1, 215	99.1	422.5	0
hypothetical protein	Pgjcvi_01700	PG JCVI SC001	hypothetical protein	PG W83	PG0757	1, 215	99.1	422.5	0
hypothetical protein	Pgjcvi_01700	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1879	1, 215	98.1	419.5	0
Zn-dependent oligopeptidases	Pgjcvi_01701	PG JCVI SC001	peptidyl-dipeptidase Dcp	PG TDC60	PGTDC60_1880	1, 695	99.6	1385.9	0
Zn-dependent oligopeptidases	Pgjcvi_01701	PG JCVI SC001	peptidyl-dipeptidase Dcp	PG W83	PG0758	1, 695	99.4	1384.8	0
Zn-dependent oligopeptidases	Pgjcvi_01701	PG JCVI SC001	peptidyl-dipeptidase	PG ATCC 33277	PGN_0788	1, 708	99.3	1404.8	0
hypothetical protein	Pgjcvi_01702	PG JCVI SC001	TPR domain protein	PG W83	PG0759	6, 717	100	1407.1	0
hypothetical protein	Pgjcvi_01702	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_1881	1, 712	99.9	1404.8	0
hypothetical protein	Pgjcvi_01702	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0789	1, 712	99.4	1398.6	0
trigger factor	Pgjcvi_01703	PG JCVI SC001	trigger factor, putative	PG W83	PG0762	1, 458	99.8	900.6	0
trigger factor	Pgjcvi_01703	PG JCVI SC001	trigger factor	PG TDC60	PGTDC60_1882	1, 458	99.8	901.7	0
trigger factor	Pgjcvi_01703	PG JCVI SC001	putative cell division trigger factor	PG ATCC 33277	PGN_0791	33, 490	99.3	899.8	0
polyribonucleotide nucleotidyltransferase	Pgjcvi_01704	PG JCVI SC001	polyribonucleotide nucleotidyltransferase	PG W83	PG0766	1, 743	100	1480.3	0
polyribonucleotide nucleotidyltransferase	Pgjcvi_01704	PG JCVI SC001	polynucleotide phosphorylase/polyadenylase	PG TDC60	PGTDC60_1883	1, 743	100	1480.3	0
polyribonucleotide nucleotidyltransferase	Pgjcvi_01704	PG JCVI SC001	polyribonucleotide nucleotidyltransferase	PG ATCC 33277	PGN_0792	32, 774	99.9	1478.4	0
4-alpha-glucanotransferase	Pgjcvi_01705	PG JCVI SC001	4-alpha-glucanotransferase	PG TDC60	PGTDC60_1884	1, 897	98.6	1838.9	0
4-alpha-glucanotransferase	Pgjcvi_01705	PG JCVI SC001	4-alpha-glucanotransferase	PG ATCC 33277	PGN_0793	1, 897	98.4	1837.4	0
4-alpha-glucanotransferase	Pgjcvi_01705	PG JCVI SC001	4-alpha-glucanotransferase	PG W83	PG0767	1, 658	98.2	1335.5	0
Protein of unknown function (DUF2891).	Pgjcvi_01706	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0794	1, 368	98.6	744.2	0
Protein of unknown function (DUF2891).	Pgjcvi_01706	PG JCVI SC001	hypothetical protein	PG W83	PG0768	1, 368	97.8	737.6	0
Protein of unknown function (DUF2891).	Pgjcvi_01706	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1885	1, 338	97	684.9	0
hypothetical protein	Pgjcvi_01707	PG JCVI SC001	fibronectin type III domain protein	PG W83	PG0769	1, 540	99.3	1092	0
hypothetical protein	Pgjcvi_01707	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0795	1, 713	99.2	1438.3	0
hypothetical protein	Pgjcvi_01707	PG JCVI SC001	fibronectin type III domain-containing protein	PG TDC60	PGTDC60_1886	1, 713	99	1437.2	0
hypothetical protein	Pgjcvi_01709	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1889	1, 414	98.3	817.8	0
hypothetical protein	Pgjcvi_01709	PG JCVI SC001	hypothetical protein	PG W83	PG0774	1, 414	97.8	812.4	0
hypothetical protein	Pgjcvi_01709	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0798	1, 374	96.5	721.5	0
Acyl-CoA dehydrogenases	Pgjcvi_01712	PG JCVI SC001	putative acyl-CoA dehydrogenase	PG ATCC 33277	PGN_0799	1, 573	99.8	1147.5	0
Acyl-CoA dehydrogenases	Pgjcvi_01712	PG JCVI SC001	acyl-CoA dehydrogenase family protein	PG W83	PG0775	1, 573	99.8	1147.5	0
Acyl-CoA dehydrogenases	Pgjcvi_01712	PG JCVI SC001	acyl-CoA dehydrogenase family protein	PG TDC60	PGTDC60_1890	1, 573	99.8	1147.5	0
Electron transfer flavoprotein, alpha subunit	Pgjcvi_01713	PG JCVI SC001	electron transfer flavoprotein subunit alpha	PG TDC60	PGTDC60_1891	1, 339	100	664.8	0
Electron transfer flavoprotein, alpha subunit	Pgjcvi_01713	PG JCVI SC001	putative electron transfer flavoprotein alpha subunit	PG ATCC 33277	PGN_0800	1, 339	99.7	663.3	0
Electron transfer flavoprotein, alpha subunit	Pgjcvi_01713	PG JCVI SC001	electron transfer flavoprotein, alpha subunit	PG W83	PG0776	1, 339	99.7	664.5	0
Electron transfer flavoprotein, beta subunit	Pgjcvi_01714	PG JCVI SC001	probable electron transfer flavoprotein beta subunit	PG ATCC 33277	PGN_0801	1, 288	99.7	556.6	0
Electron transfer flavoprotein, beta subunit	Pgjcvi_01714	PG JCVI SC001	electron transfer flavoprotein, beta subunit	PG W83	PG0777	1, 288	99.7	556.6	0
Electron transfer flavoprotein, beta subunit	Pgjcvi_01714	PG JCVI SC001	electron transfer flavoprotein subunit beta	PG TDC60	PGTDC60_1892	1, 288	99.7	556.6	0
universal bacterial protein YeaZ	Pgjcvi_01715	PG JCVI SC001	hypothetical protein	PG W83	PG0778	1, 238	97.9	464.5	0
universal bacterial protein YeaZ	Pgjcvi_01715	PG JCVI SC001	putative glycoprotease	PG TDC60	PGTDC60_1893	1, 238	97.5	463.8	0
universal bacterial protein YeaZ	Pgjcvi_01715	PG JCVI SC001	probable glycoprotease	PG ATCC 33277	PGN_0802	1, 238	97.1	458	0
Biopolymer transport protein	Pgjcvi_01716	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0803	1, 157	100	315.1	0
Biopolymer transport protein	Pgjcvi_01716	PG JCVI SC001	hypothetical protein	PG W83	PG0779	1, 157	100	315.1	0
Biopolymer transport protein	Pgjcvi_01716	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1894	1, 157	100	315.1	0
Biopolymer transport protein ExbD/TolR.	Pgjcvi_01717	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0804	1, 204	100	401.4	0
Biopolymer transport protein ExbD/TolR.	Pgjcvi_01717	PG JCVI SC001	hypothetical protein	PG W83	PG0780	1, 204	100	401.4	0
Biopolymer transport protein ExbD/TolR.	Pgjcvi_01717	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1895	1, 204	100	401.4	0
hypothetical protein	Pgjcvi_01718	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0805	1, 156	100	306.2	0
hypothetical protein	Pgjcvi_01718	PG JCVI SC001	hypothetical protein	PG W83	PG0781	1, 156	100	306.2	0
hypothetical protein	Pgjcvi_01718	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1896	1, 156	100	306.2	0
Biopolymer transport proteins	Pgjcvi_01719	PG JCVI SC001	putative MotA/TolQ/ExbB proton channel protein	PG ATCC 33277	PGN_0806	1, 270	100	512.3	0
Biopolymer transport proteins	Pgjcvi_01719	PG JCVI SC001	MotA/TolQ/ExbB proton channel family protein	PG W83	PG0782	1, 270	100	512.3	0
Biopolymer transport proteins	Pgjcvi_01719	PG JCVI SC001	MotA/TolQ/ExbB proton channel family protein	PG TDC60	PGTDC60_1897	1, 270	100	512.3	0
hydrolase, TatD family	Pgjcvi_01721	PG JCVI SC001	hydrolase, putative	PG W83	PG0783	9, 275	100	543.5	0
hydrolase, TatD family	Pgjcvi_01721	PG JCVI SC001	putative DNase-like protein	PG TDC60	PGTDC60_1898	1, 267	99.3	539.3	0
hydrolase, TatD family	Pgjcvi_01721	PG JCVI SC001	putative DNAse related protein	PG ATCC 33277	PGN_0807	9, 275	98.1	535.4	0
Geranylgeranyl pyrophosphate synthase	Pgjcvi_01722	PG JCVI SC001	polyprenyl synthetase	PG W83	PG0784	1, 325	100	647.5	0

Geranylgeranyl pyrophosphate synthase	Pgjcvi_01722	PG JCVI SC001	probable isoprenyl synthetase	PG ATCC 33277	PGN_0808	1, 325	99.7	646	0
Geranylgeranyl pyrophosphate synthase	Pgjcvi_01722	PG JCVI SC001	polyprenyl synthetase	PG TDC60	PGTDC60_1899	1, 325	99.7	646.4	0
TonB family C-terminal domain	Pgjcvi_01723	PG JCVI SC001	tonB protein, putative	PG W83	PG0785	1, 230	100	455.7	0
TonB family C-terminal domain	Pgjcvi_01723	PG JCVI SC001	putative TonB protein	PG ATCC 33277	PGN_0809	1, 230	99.6	455.3	0
TonB family C-terminal domain	Pgjcvi_01723	PG JCVI SC001	putative TonB protein	PG TDC60	PGTDC60_1900	1, 230	96.1	441.4	0
hypothetical protein	Pgjcvi_01724	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0810	1, 55	100	113.6	4.80E-24
hypothetical protein	Pgjcvi_01724	PG JCVI SC001	hypothetical protein	PG W83	PG0787	1, 56	100	115.2	1.60E-24
hypothetical protein	Pgjcvi_01725	PG JCVI SC001	hypothetical protein	PG W83	PG0788	6, 877	99.5	1767.7	0
hypothetical protein	Pgjcvi_01725	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0811	1, 872	99.4	1763.8	0
hypothetical protein	Pgjcvi_01725	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1903	1, 851	99.4	1728.4	0
Uncharacterized conserved protein	Pgjcvi_01726	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0812	1, 238	99.6	475.7	0
Uncharacterized conserved protein	Pgjcvi_01726	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1904	1, 238	99.2	473.4	0
Uncharacterized conserved protein	Pgjcvi_01726	PG JCVI SC001	hypothetical protein	PG W83	PG0789	1, 238	97.9	468.4	0
Obg family GTPase CgtA	Pgjcvi_01727	PG JCVI SC001	GTP-binding protein	PG ATCC 33277	PGN_0813	1, 394	100	797	0
Obg family GTPase CgtA	Pgjcvi_01727	PG JCVI SC001	GTP-binding protein Obg	PG W83	PG0790	1, 394	100	797	0
Obg family GTPase CgtA	Pgjcvi_01727	PG JCVI SC001	GTPase ObgE	PG TDC60	PGTDC60_1905	1, 394	99.7	794.3	0
Adenylate kinase and related kinases	Pgjcvi_01728	PG JCVI SC001	probable adenylate kinase	PG ATCC 33277	PGN_0814	1, 194	100	381.7	0
Adenylate kinase and related kinases	Pgjcvi_01728	PG JCVI SC001	adenylate kinase	PG W83	PG0791	1, 194	99.5	381.3	0
Adenylate kinase and related kinases	Pgjcvi_01728	PG JCVI SC001	adenylate kinase	PG TDC60	PGTDC60_1906	1, 194	99.5	380.2	0
Hypoxanthine-guanine phosphoribosyltransferase	Pgjcvi_01729	PG JCVI SC001	putative hypoxanthine phosphoribosyltransferase	PG ATCC 33277	PGN_0815	1, 178	100	359.8	0
Hypoxanthine-guanine phosphoribosyltransferase	Pgjcvi_01729	PG JCVI SC001	hypoxanthine phosphoribosyltransferase	PG W83	PG0792	1, 178	100	359.8	0
Hypoxanthine-guanine phosphoribosyltransferase	Pgjcvi_01729	PG JCVI SC001	hypoxanthine phosphoribosyltransferase	PG TDC60	PGTDC60_1907	1, 178	100	359.8	0
hypothetical protein	Pgjcvi_01732	PG JCVI SC001	putative DNA-binding protein histone-like family	PG TDC60	PGTDC60_0392	4, 159	54.8	165.2	2.00E-39
hypothetical protein	Pgjcvi_01732	PG JCVI SC001	putative DNA-binding protein histone-like family	PG ATCC 33277	PGN_0229	4, 159	53.2	158.3	2.50E-37
hypothetical protein	Pgjcvi_01732	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG1205	3, 154	51.6	158.3	2.50E-37
Uncharacterized protein conserved in bacteria	Pgjcvi_01735	PG JCVI SC001	fructose-1,6-bisphosphatase	PG ATCC 33277	PGN_0816	1, 665	100	1345.1	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01735	PG JCVI SC001	fructose-1,6-bisphosphatase	PG TDC60	PGTDC60_1909	1, 665	100	1345.1	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01735	PG JCVI SC001	fructose-1,6-bisphosphatase	PG W83	PG0793	1, 655	99.8	1324.3	0
Membrane carboxypeptidase/penicillin-binding protein	Pgjcvi_01736	PG JCVI SC001	penicillin-binding protein 1A	PG ATCC 33277	PGN_0817	1, 784	99.6	1589.3	0
Membrane carboxypeptidase/penicillin-binding protein	Pgjcvi_01736	PG JCVI SC001	penicillin-binding protein 1A, putative	PG W83	PG0794	1, 784	99.6	1590.1	0
Membrane carboxypeptidase/penicillin-binding protein	Pgjcvi_01736	PG JCVI SC001	penicillin-binding protein 1A	PG TDC60	PGTDC60_1910	1, 784	99.5	1587	0
Integral membrane protein, interacts with FtsH	Pgjcvi_01737	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1911	1, 236	100	456.8	0
Integral membrane protein, interacts with FtsH	Pgjcvi_01737	PG JCVI SC001	hypothetical protein	PG W83	PG0795	1, 236	99.2	453	0
Integral membrane protein, interacts with FtsH	Pgjcvi_01737	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0818	1, 236	98.7	449.9	0
leucyl-tRNA synthetase, eubacterial and mitochondrial family	Pgjcvi_01738	PG JCVI SC001	leucyl-tRNA synthetase	PG ATCC 33277	PGN_0819	1, 925	99.4	1895.9	0
leucyl-tRNA synthetase, eubacterial and mitochondrial family	Pgjcvi_01738	PG JCVI SC001	leucyl-tRNA synthetase	PG W83	PG0796	1, 925	99.1	1892.1	0
leucyl-tRNA synthetase, eubacterial and mitochondrial family	Pgjcvi_01738	PG JCVI SC001	leucyl-tRNA synthetase	PG TDC60	PGTDC60_1912	1, 925	99.1	1892.9	0
Uncharacterized FAD-dependent dehydrogenases	Pgjcvi_01740	PG JCVI SC001	NAD-utilizing dehydrogenases	PG ATCC 33277	PGN_0823	1, 519	99.4	1042	0
Uncharacterized FAD-dependent dehydrogenases	Pgjcvi_01740	PG JCVI SC001	hypothetical protein	PG W83	PG0800	1, 519	99.2	1040.8	0
Uncharacterized FAD-dependent dehydrogenases	Pgjcvi_01740	PG JCVI SC001	NAD-utilizing dehydrogenase	PG TDC60	PGTDC60_1917	1, 519	99.2	1040.4	0
uncharacterized domain HDIG	Pgjcvi_01741	PG JCVI SC001	tRNA nucleotidyltransferase	PG ATCC 33277	PGN_0824	1, 483	100	964.9	0
uncharacterized domain HDIG	Pgjcvi_01741	PG JCVI SC001	polyA polymerase family protein	PG W83	PG0801	1, 483	100	964.9	0
uncharacterized domain HDIG	Pgjcvi_01741	PG JCVI SC001	tRNA nucleotidyltransferase	PG TDC60	PGTDC60_1918	1, 483	100	964.9	0
dihydrolipoamide dehydrogenase	Pgjcvi_01743	PG JCVI SC001	alpha keto acid dehydrogenase complex, E3 component, lipoamide dehydrogenase	PG W83	PG0802	1, 449	100	879.8	0
dihydrolipoamide dehydrogenase	Pgjcvi_01743	PG JCVI SC001	alpha keto acid dehydrogenase complex, E3 component, lipoamide dehydrogenase	PG TDC60	PGTDC60_1921	1, 449	100	879.8	0
dihydrolipoamide dehydrogenase	Pgjcvi_01743	PG JCVI SC001	dihydrolipoamide dehydrogenase	PG ATCC 33277	PGN_0826	1, 449	99.3	874	0
glucosamine-6-phosphate isomerase	Pgjcvi_01744	PG JCVI SC001	glucosamine-6-phosphate deaminase	PG W83	PG0803	1, 263	100	535	0
glucosamine-6-phosphate isomerase	Pgjcvi_01744	PG JCVI SC001	glucosamine-6-phosphate deaminase	PG TDC60	PGTDC60_1922	1, 263	100	535	0
glucosamine-6-phosphate isomerase	Pgjcvi_01744	PG JCVI SC001	glucosamine-6-phosphate isomerase	PG ATCC 33277	PGN_0827	1, 263	99.2	530.8	0
Uncharacterized flavoproteins	Pgjcvi_01745	PG JCVI SC001	flavodoxin	PG W83	PG0804	1, 402	99.8	823.9	0
Uncharacterized flavoproteins	Pgjcvi_01745	PG JCVI SC001	flavodoxin	PG TDC60	PGTDC60_1923	1, 403	99.8	825.9	0
Uncharacterized flavoproteins	Pgjcvi_01745	PG JCVI SC001	flavoprotein	PG ATCC 33277	PGN_0828	1, 403	99.3	821.6	0
prolipoprotein diacylglyceryl transferase	Pgjcvi_01746	PG JCVI SC001	putative prolipoprotein diacylglyceryl transferase	PG ATCC 33277	PGN_0829	1, 283	100	587.4	0
prolipoprotein diacylglyceryl transferase	Pgjcvi_01746	PG JCVI SC001	prolipoprotein diacylglyceryl transferase	PG W83	PG0805	1, 283	100	587.4	0
prolipoprotein diacylglyceryl transferase	Pgjcvi_01746	PG JCVI SC001	prolipoprotein diacylglyceryl transferase	PG TDC60	PGTDC60_1924	1, 283	99.3	581.3	0
diaminopimelate dehydrogenase	Pgjcvi_01747	PG JCVI SC001	Gfo/Idh/MocA family oxidoreductase	PG TDC60	PGTDC60_1925	1, 301	99.3	593.2	0
diaminopimelate dehydrogenase	Pgjcvi_01747	PG JCVI SC001	oxidoreductase, Gfo/Idh/MocA family	PG W83	PG0806	1, 301	99	590.1	0
diaminopimelate dehydrogenase	Pgjcvi_01747	PG JCVI SC001	meso-diaminopimelate D-dehydrogenase	PG ATCC 33277	PGN_0830	1, 301	98.3	589.3	0
transcription antitermination factor NusB	Pgjcvi_01748	PG JCVI SC001	probable nitrogen utilization substance protein	PG ATCC 33277	PGN_0831	1, 348	99.7	683.7	0
transcription antitermination factor NusB	Pgjcvi_01748	PG JCVI SC001	NusB family protein	PG TDC60	PGTDC60_1926	1, 348	99.7	683.7	0
transcription antitermination factor NusB	Pgjcvi_01748	PG JCVI SC001	NusB family protein	PG W83	PG0807	17, 364	99.1	679.9	0
hypothetical protein	Pgjcvi_01750	PG JCVI SC001	hypothetical protein	PG W83	PG0809	7, 2316	99.8	4638.2	0
hypothetical protein	Pgjcvi_01750	PG JCVI SC001	gliding motility protein SprA	PG ATCC 33277	PGN_0832	1, 2499	99.6	5007.2	0
hypothetical protein	Pgjcvi_01750	PG JCVI SC001	gliding motility protein SprA	PG TDC60	PGTDC60_1927	1, 2499	99.5	5003	0
Holliday junction DNA helicase, RuvA subunit	Pgjcvi_01751	PG JCVI SC001	Holliday junction DNA helicase motor protein	PG W83	PG0811	1, 202	100	381.3	0
Holliday junction DNA helicase, RuvA subunit	Pgjcvi_01751	PG JCVI SC001	probable Holliday junction DNA helicase RuvA	PG ATCC 33277	PGN_0833	1, 202	99.5	379.8	0
Holliday junction DNA helicase, RuvA subunit	Pgjcvi_01751	PG JCVI SC001	Holliday junction DNA helicase RuvA	PG TDC60	PGTDC60_1928	1, 202	99.5	379.8	0
Uncharacterized conserved protein	Pgjcvi_01752	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0553	1, 108	100	214.5	0
Uncharacterized conserved protein	Pgjcvi_01752	PG JCVI SC001	hypothetical protein	PG W83	PG1556	1, 108	100	214.5	0
Uncharacterized conserved protein	Pgjcvi_01752	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0743	1, 108	100	214.5	0
Biopolymer transport proteins	Pgjcvi_01753	PG JCVI SC001	hypothetical protein	PG W83	PG1555	1, 192	100	378.3	0
Biopolymer transport proteins	Pgjcvi_01753	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0554	1, 189	99.5	370.9	0

Biopolymer transport proteins	Pgjcvi_01753	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0744	1, 192	99.5	373.6	0
hypothetical protein	Pgjcvi_01754	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0555	1, 225	100	444.9	0
hypothetical protein	Pgjcvi_01754	PG JCVI SC001	hypothetical protein	PG W83	PG1554	1, 225	99.6	443.7	0
hypothetical protein	Pgjcvi_01754	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0745	1, 225	99.6	443.4	0
Cobalamin biosynthesis protein CobN and related Mg-chelatases	Pgjcvi_01755	PG JCVI SC001	CobN/magnesium chelatase family protein	PG TDC60	PGTDC60_0746	1, 1469	99.4	2882.4	0
Cobalamin biosynthesis protein CobN and related Mg-chelatases	Pgjcvi_01755	PG JCVI SC001	CobN/magnesium chelatase family protein	PG W83	PG1553	1, 1469	99.1	2875.9	0
Cobalamin biosynthesis protein CobN and related Mg-chelatases	Pgjcvi_01755	PG JCVI SC001	putative cobalamin biosynthesis-related protein	PG ATCC 33277	PGN_0556	1, 1469	98.8	2871.3	0
Outer membrane cobalamin receptor protein	Pgjcvi_01756	PG JCVI SC001	TonB-dependent receptor HmuR	PG ATCC 33277	PGN_0557	1, 646	99.8	1303.9	0
Outer membrane cobalamin receptor protein	Pgjcvi_01756	PG JCVI SC001	TonB-dependent receptor HmuR	PG W83	PG1552	1, 646	99.8	1305.4	0
Outer membrane cobalamin receptor protein	Pgjcvi_01756	PG JCVI SC001	TonB-dependent receptor HmuR	PG TDC60	PGTDC60_0747	1, 646	99.8	1303.9	0
hypothetical protein	Pgjcvi_01757	PG JCVI SC001	hmuY protein	PG W83	PG1551	1, 142	100	296.2	0
hypothetical protein	Pgjcvi_01757	PG JCVI SC001	hmuY protein	PG TDC60	PGTDC60_0748	1, 216	100	447.2	0
hypothetical protein	Pgjcvi_01757	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0558	1, 216	99.5	445.7	0
hypothetical protein	Pgjcvi_01759	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0559	1, 46	100	91.3	1.10E-17
hypothetical protein	Pgjcvi_01759	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0749	1, 46	100	91.3	1.10E-17
hypothetical protein	Pgjcvi_01759	PG JCVI SC001	hypothetical protein	PG W83	PG1549	1, 46	97.8	89	5.30E-17
Por secretion system C-terminal sorting domain	Pgjcvi_01760	PG JCVI SC001	trypsin like proteinase PrtT	PG TDC60	PGTDC60_0751	1, 789	98.7	1588.9	0
Por secretion system C-terminal sorting domain	Pgjcvi_01760	PG JCVI SC001	trypsin like proteinase PrtT	PG ATCC 33277	PGN_0561	1, 840	97	1660.2	0
Por secretion system C-terminal sorting domain	Pgjcvi_01760	PG JCVI SC001	thiol protease/hemagglutinin PrtT precursor, putative	PG W83	PG1427	1, 841	34.9	486.9	0
hypothetical protein	Pgjcvi_01762	PG JCVI SC001	hypothetical protein	PG W83	PG1547	1, 117	99.1	236.5	0
hypothetical protein	Pgjcvi_01762	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0562	1, 117	97.4	232.3	0
hypothetical protein	Pgjcvi_01762	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0752	1, 117	96.6	231.9	0
Superoxide dismutase	Pgjcvi_01763	PG JCVI SC001	superoxide dismutase Fe-Mn	PG ATCC 33277	PGN_0564	1, 191	100	399.8	0
Superoxide dismutase	Pgjcvi_01763	PG JCVI SC001	superoxide dismutase, Fe-Mn	PG W83	PG1545	1, 191	100	399.8	0
Superoxide dismutase	Pgjcvi_01763	PG JCVI SC001	superoxide dismutase Fe-Mn	PG TDC60	PGTDC60_0753	1, 191	100	399.8	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01764	PG JCVI SC001	hypothetical protein	PG W83	PG1544	1, 256	99.6	519.6	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01764	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0754	1, 256	99.6	519.6	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01764	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0565	8, 263	98	508.8	0
Predicted thioesterase	Pgjcvi_01765	PG JCVI SC001	probable thioesterase protein	PG ATCC 33277	PGN_0566	1, 139	100	288.5	0
Predicted thioesterase	Pgjcvi_01765	PG JCVI SC001	putative thioesterase protein	PG TDC60	PGTDC60_0755	1, 139	100	288.5	0
Predicted thioesterase	Pgjcvi_01765	PG JCVI SC001	thioesterase family protein	PG W83	PG1543	1, 139	99.3	283.9	0
Collagenase and related proteases	Pgjcvi_01766	PG JCVI SC001	collagenase	PG TDC60	PGTDC60_0756	4, 417	99	822	0
Collagenase and related proteases	Pgjcvi_01766	PG JCVI SC001	collagenase	PG ATCC 33277	PGN_0567	4, 417	98.8	820.1	0
Collagenase and related proteases	Pgjcvi_01766	PG JCVI SC001	collagenase	PG W83	PG1542	1, 414	98.8	818.9	0
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	Pgjcvi_01767	PG JCVI SC001	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase	PG W83	PG1541	3, 149	100	303.1	0
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	Pgjcvi_01767	PG JCVI SC001	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase	PG TDC60	PGTDC60_0757	1, 147	100	303.1	0
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	Pgjcvi_01767	PG JCVI SC001	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase	PG ATCC 33277	PGN_0568	1, 144	99.3	297	0
S-adenosylmethionine:tRNA ribosyltransferase-isomerase	Pgjcvi_01768	PG JCVI SC001	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	PG W83	PG1540	1, 350	99.7	708	0
S-adenosylmethionine:tRNA ribosyltransferase-isomerase	Pgjcvi_01768	PG JCVI SC001	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	PG TDC60	PGTDC60_0758	1, 350	99.7	706.8	0
S-adenosylmethionine:tRNA ribosyltransferase-isomerase	Pgjcvi_01768	PG JCVI SC001	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	PG ATCC 33277	PGN_0569	1, 350	99.4	706.8	0
tRNA pseudouridine 55 synthase	Pgjcvi_01769	PG JCVI SC001	putative tRNA pseudouridine synthase B	PG TDC60	PGTDC60_0759	1, 258	99.2	515	0
tRNA pseudouridine 55 synthase	Pgjcvi_01769	PG JCVI SC001	putative tRNA pseudouridine synthase B	PG ATCC 33277	PGN_0570	1, 258	98.1	509.2	0
undecaprenyl-diphosphatase UppP	Pgjcvi_01770	PG JCVI SC001	undecaprenol kinase, putative	PG W83	PG1538	1, 280	98.9	533.1	0
undecaprenyl-diphosphatase UppP	Pgjcvi_01770	PG JCVI SC001	putative undecaprenol kinase	PG ATCC 33277	PGN_0571	1, 280	98.6	530.8	0
undecaprenyl-diphosphatase UppP	Pgjcvi_01770	PG JCVI SC001	undecaprenol kinase	PG TDC60	PGTDC60_0760	1, 280	97.9	528.5	0
Protein of unknown function (DUF3098).	Pgjcvi_01771	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0572	1, 75	98.7	147.9	1.60E-34
Protein of unknown function (DUF3098).	Pgjcvi_01771	PG JCVI SC001	hypothetical protein	PG W83	PG1537	25, 99	98.7	147.9	1.60E-34
Protein of unknown function (DUF3098).	Pgjcvi_01771	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0761	1, 75	96	146	6.00E-34
Cell division protein	Pgjcvi_01772	PG JCVI SC001	putative cell division protein FtsX	PG ATCC 33277	PGN_0573	21, 295	100	529.6	0
Cell division protein	Pgjcvi_01772	PG JCVI SC001	cell division protein FtsX	PG TDC60	PGTDC60_0762	1, 275	100	529.6	0
Cell division protein	Pgjcvi_01772	PG JCVI SC001	cell division protein FtsX, putative	PG W83	PG1536	21, 295	99.6	526.6	0
hypothetical protein	Pgjcvi_01773	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0763	1, 43	93	87.4	4.50E-16
hypothetical protein	Pgjcvi_01773	PG JCVI SC001	hypothetical protein	PG W83	PG2064	2, 38	51.4	43.1	0.0098
hypothetical protein	Pgjcvi_01773	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1607	2, 47	50	47.4	0.00052
hypothetical protein	Pgjcvi_01774	PG JCVI SC001	transcriptional regulator, putative	PG W83	PG1535	1, 113	100	225.3	0
hypothetical protein	Pgjcvi_01774	PG JCVI SC001	transcriptional regulator	PG TDC60	PGTDC60_0764	1, 113	98.2	221.5	0
hypothetical protein	Pgjcvi_01774	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0574	1, 113	97.3	217.2	0
hypothetical protein	Pgjcvi_01775	PG JCVI SC001	hypothetical protein	PG W83	PG1534	1, 129	100	258.5	0
hypothetical protein	Pgjcvi_01775	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0765	1, 129	99.2	258.1	0
hypothetical protein	Pgjcvi_01776	PG JCVI SC001	Toprim domain protein	PG W83	PG1533	1, 682	99	1375.5	0
hypothetical protein	Pgjcvi_01776	PG JCVI SC001	TOPRIM domain-containing protein	PG TDC60	PGTDC60_0766	1, 682	98.5	1365.1	0
hypothetical protein	Pgjcvi_01776	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0584	17, 439	54.3	464.9	0
hypothetical protein	Pgjcvi_01777	PG JCVI SC001	hypothetical protein	PG W83	PG1532	1, 64	95.3	132.9	4.50E-30
hypothetical protein	Pgjcvi_01777	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0767	1, 64	93.8	131.3	1.30E-29
hypothetical protein	Pgjcvi_01778	PG JCVI SC001	hypothetical protein	PG W83	PG0849	26, 208	29.5	56.6	1.30E-06
Domain of unknown function (DUF1814).	Pgjcvi_01779	PG JCVI SC001	hypothetical protein	PG W83	PG1510	1, 35	80	58.5	5.60E-07
Domain of unknown function (DUF1814).	Pgjcvi_01779	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0783	1, 35	80	58.5	5.60E-07
SNF2 family N-terminal domain./N-6 DNA Methylase./MutS domain I./Protein of unknown function (DUF2958).	Pgjcvi_01780	PG JCVI SC001	hypothetical protein	PG W83	PG1500	8, 763	98.8	1489.6	0
SNF2 family N-terminal domain./N-6 DNA Methylase./MutS domain I./Protein of unknown function (DUF2958).	Pgjcvi_01780	PG JCVI SC001	DNA methylase	PG TDC60	PGTDC60_1966	1, 1128	98.7	2243	0

SNF2 family N-terminal domain./N-6 DNA Methylase./MutS domain I./Protein of unknown function (DUF2958).	Pgjcvi_01780	PG JCVI SC001	putative DNA methylase	PG ATCC 33277	PGN_0086	381, 1777	59	1611.7	0
SNF2 family N-terminal domain./N-6 DNA Methylase./MutS domain I./Protein of unknown function (DUF2958).	Pgjcvi_01780	PG JCVI SC001	putative DNA methylase	PG ATCC 33277	PGN_0086	4, 443	44.9	361.7	0
Topoisomerase IA	Pgjcvi_01781	PG JCVI SC001	DNA topoisomerase III	PG TDC60	PGTDC60_1968	1, 697	98.6	1378.2	0
Topoisomerase IA	Pgjcvi_01781	PG JCVI SC001	DNA topoisomerase III	PG W83	PG1495	1, 697	98.4	1378.6	0
Topoisomerase IA	Pgjcvi_01781	PG JCVI SC001	DNA topoisomerase I	PG ATCC 33277	PGN_0582	1, 690	50.2	654.8	0
hypothetical protein	Pgjcvi_01782	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0835	1, 54	100	107.5	1.50E-21
hypothetical protein	Pgjcvi_01782	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1969	1, 469	98.3	911.8	0
hypothetical protein	Pgjcvi_01782	PG JCVI SC001	hypothetical protein	PG W83	PG1494	1, 437	97.5	843.2	0
hypothetical protein	Pgjcvi_01783	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1970	1, 336	100	683.3	0
hypothetical protein	Pgjcvi_01784	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1971	1, 419	99	852	0
hypothetical protein	Pgjcvi_01785	PG JCVI SC001	TonB-dependent receptor plug domain-containing protein	PG TDC60	PGTDC60_1972	1, 682	100	1384.8	0
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_01786	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_1973	10, 737	99.5	1440.2	0
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_01786	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_1917	297, 569	34.7	162.9	4.60E-38
ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	Pgjcvi_01786	PG JCVI SC001	ABC transporter, ATP-binding protein, putative	PG W83	PG1176	12, 558	26.4	182.2	7.30E-44
hypothetical protein	Pgjcvi_01787	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1974	1, 161	92.5	287.7	0
Type IV secretory pathway, VirD4 components	Pgjcvi_01788	PG JCVI SC001	TraG family protein	PG TDC60	PGTDC60_1984	406, 655	97.2	471.9	0
Type IV secretory pathway, VirD4 components	Pgjcvi_01788	PG JCVI SC001	TraG family protein	PG W83	PG1490	406, 667	93.1	473.8	0
Type IV secretory pathway, VirD4 components	Pgjcvi_01788	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0579	105, 365	80.5	412.9	0
hypothetical protein	Pgjcvi_01789	PG JCVI SC001	TraG family protein	PG TDC60	PGTDC60_1984	1, 403	99	821.2	0
hypothetical protein	Pgjcvi_01789	PG JCVI SC001	TraG family protein	PG W83	PG1490	1, 403	98.3	815.8	0
hypothetical protein	Pgjcvi_01789	PG JCVI SC001	putative mobilization protein TraG family	PG ATCC 33277	PGN_0076	1, 403	73.4	632.9	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_01790	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1985	1, 426	98.1	837	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_01790	PG JCVI SC001	hypothetical protein	PG W83	PG1489	1, 426	97.4	829.7	0
Relaxase/Mobilisation nuclease domain.	Pgjcvi_01790	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0075	1, 406	39.5	271.9	0
hypothetical protein	Pgjcvi_01791	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1986	1, 133	99.2	269.2	0
hypothetical protein	Pgjcvi_01791	PG JCVI SC001	hypothetical protein	PG W83	PG1488	1, 133	97	261.2	0
hypothetical protein	Pgjcvi_01791	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0074	4, 137	42.5	100.5	5.10E-20
CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_01792	PG JCVI SC001	conjugative transposon protein TraA	PG TDC60	PGTDC60_1988	1, 269	99.6	533.5	0
CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_01792	PG JCVI SC001	conjugative transposon protein TraA	PG W83	PG1486	1, 269	98.9	530.4	0
CobQ/CobB/MinD/ParA nucleotide binding domain.	Pgjcvi_01792	PG JCVI SC001	putative conserved protein found in conjugate transposon TraA	PG ATCC 33277	PGN_0073	1, 259	35.4	179.1	2.30E-43
Protein of unknown function (DUF3408).	Pgjcvi_01793	PG JCVI SC001	conjugative transposon protein TraC	PG W83	PG1485	1, 127	98.4	246.9	0
Protein of unknown function (DUF3408).	Pgjcvi_01793	PG JCVI SC001	conjugative transposon protein TraC	PG TDC60	PGTDC60_1989	1, 127	98.4	247.7	0
hypothetical protein	Pgjcvi_01794	PG JCVI SC001	hypothetical protein	PG W83	PG1484	1, 234	98.3	451.4	0
hypothetical protein	Pgjcvi_01794	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1990	1, 234	97.9	451.8	0
hypothetical protein	Pgjcvi_01795	PG JCVI SC001	conjugative transposon protein TraE	PG W83	PG1483	7, 100	98.9	186.4	0
hypothetical protein	Pgjcvi_01795	PG JCVI SC001	conjugative transposon protein TraE	PG TDC60	PGTDC60_1991	7, 100	98.9	185.3	1.40E-45
hypothetical protein	Pgjcvi_01795	PG JCVI SC001	probable conserved transmembrane protein found in conjugate transposon TraE	PG ATCC 33277	PGN_0067	9, 99	86.8	157.9	1.90E-37
hypothetical protein	Pgjcvi_01796	PG JCVI SC001	conjugative transposon protein TraF	PG W83	PG1482	1, 111	99.1	229.2	0
hypothetical protein	Pgjcvi_01796	PG JCVI SC001	conjugative transposon protein TraF	PG TDC60	PGTDC60_1992	1, 111	99.1	228	0
hypothetical protein	Pgjcvi_01796	PG JCVI SC001	probable conserved transmembrane protein found in conjugate transposon TraF	PG ATCC 33277	PGN_0066	4, 101	65.3	142.9	7.50E-33
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_01797	PG JCVI SC001	conjugative transposon protein TraG	PG W83	PG1481	1, 840	98.7	1660.2	0
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_01797	PG JCVI SC001	conjugative transposon protein TraG	PG TDC60	PGTDC60_1993	1, 841	98.7	1666	0
Bacteroides conjugation system ATPase, TraG family	Pgjcvi_01797	PG JCVI SC001	conserved protein found in conjugate transposon TraG	PG ATCC 33277	PGN_0065	1, 830	69.9	1209.5	0
hypothetical protein	Pgjcvi_01798	PG JCVI SC001	conjugative transposon protein TraI	PG W83	PG1480	1, 209	100	414.1	0
hypothetical protein	Pgjcvi_01798	PG JCVI SC001	conjugative transposon protein TraI	PG TDC60	PGTDC60_1994	1, 209	99	408.3	0
hypothetical protein	Pgjcvi_01798	PG JCVI SC001	putative conserved protein found in conjugate transposon TraI	PG ATCC 33277	PGN_0064	1, 209	58.9	251.9	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_01799	PG JCVI SC001	conjugative transposon protein TraJ	PG TDC60	PGTDC60_1995	5, 346	98.8	673.7	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_01799	PG JCVI SC001	conjugative transposon protein TraJ	PG W83	PG1479	1, 368	96	709.9	0
Bacteroides conjugative transposon TraJ protein	Pgjcvi_01799	PG JCVI SC001	conserved transmembrane protein found in conjugate transposon TraJ	PG ATCC 33277	PGN_0063	4, 332	57.8	388.3	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_01800	PG JCVI SC001	conjugative transposon protein TraK	PG W83	PG1478	1, 207	100	408.3	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_01800	PG JCVI SC001	conjugative transposon protein TraK	PG TDC60	PGTDC60_1996	1, 207	99.5	407.9	0
Bacteroides conjugative transposon TraK protein	Pgjcvi_01800	PG JCVI SC001	putative conserved protein found in conjugate transposon TraK	PG ATCC 33277	PGN_0597	1, 207	66.7	300.1	0
hypothetical protein	Pgjcvi_01801	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1997	1, 95	97.9	191.4	0
hypothetical protein	Pgjcvi_01801	PG JCVI SC001	hypothetical protein	PG W83	PG1477	1, 95	94.7	186.4	0
Bacteroides conjugative transposon TraM protein	Pgjcvi_01802	PG JCVI SC001	conjugative transposon protein TraM	PG W83	PG1476	1, 453	98	870.5	0
Bacteroides conjugative transposon TraM protein	Pgjcvi_01802	PG JCVI SC001	conjugative transposon protein TraM	PG TDC60	PGTDC60_1998	1, 453	97.6	866.3	0
Bacteroides conjugative transposon TraM protein	Pgjcvi_01802	PG JCVI SC001	conserved protein found in conjugate transposon TraM	PG ATCC 33277	PGN_0060	17, 453	35.9	260	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_01803	PG JCVI SC001	conjugative transposon protein TraN	PG TDC60	PGTDC60_1999	1, 300	97.3	584.3	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_01803	PG JCVI SC001	conjugative transposon protein TraN	PG W83	PG1475	1, 341	95.9	651	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_01803	PG JCVI SC001	conserved protein found in conjugate transposon TraN	PG ATCC 33277	PGN_0594	133, 311	53.1	206.1	0
Bacteroides conjugative transposon TraN protein	Pgjcvi_01803	PG JCVI SC001	conserved protein found in conjugate transposon TraN	PG ATCC 33277	PGN_0594	1, 311	41.1	246.1	0
Conjugative transposon protein TraO.	Pgjcvi_01804	PG JCVI SC001	conjugative transposon protein TraO	PG W83	PG1474	3, 192	98.4	377.1	0
Conjugative transposon protein TraO.	Pgjcvi_01804	PG JCVI SC001	conjugative transposon protein TraO	PG TDC60	PGTDC60_2000	3, 192	96.8	372.1	0
Conjugative transposon protein TraO.	Pgjcvi_01804	PG JCVI SC001	putative conserved protein found in conjugate transposon TraO	PG ATCC 33277	PGN_0593	1, 190	34.4	110.2	9.20E-23
hypothetical protein	Pgjcvi_01805	PG JCVI SC001	conjugative transposon protein TraQ	PG TDC60	PGTDC60_2001	10, 152	95.8	283.5	0
hypothetical protein	Pgjcvi_01805	PG JCVI SC001	conjugative transposon protein TraQ	PG W83	PG1473	9, 151	93.7	273.1	0
hypothetical protein	Pgjcvi_01805	PG JCVI SC001	conserved protein found in conjugate transposon TraQ	PG ATCC 33277	PGN_1285	9, 150	51	161	3.50E-38

Predicted membrane protein	Pgjcvi_01807	PG JCVI SC001	hypothetical protein	PG W83	PG1471	1, 155	97.4	305.8	0
Predicted membrane protein	Pgjcvi_01807	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2014	1, 155	97.4	306.6	0
hypothetical protein	Pgjcvi_01808	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2016	1, 170	97.1	342	0
Methylase involved in ubiquinone/menaquinone biosynthesis	Pgjcvi_01809	PG JCVI SC001	methlytransferase, UbiE/COQ5 family	PG W83	PG1467	22, 202	99.4	368.6	0
Methylase involved in ubiquinone/menaquinone biosynthesis	Pgjcvi_01809	PG JCVI SC001	UbiE/COQ5 family methlytransferase	PG TDC60	PGTDC60_2017	22, 204	98.9	370.9	0
Putative protein-S-isoprenylcysteine methyltransferase	Pgjcvi_01810	PG JCVI SC001	hypothetical protein	PG W83	PG1466	1, 190	99.5	390.6	0
Putative protein-S-isoprenylcysteine methyltransferase	Pgjcvi_01810	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2018	1, 190	97.9	385.6	0
hypothetical protein	Pgjcvi_01811	PG JCVI SC001	hypothetical protein	PG W83	PG1465	1, 214	91.6	402.9	0
hypothetical protein	Pgjcvi_01811	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2019	1, 214	91.1	402.1	0
hypothetical protein	Pgjcvi_01812	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0589	1, 68	94.1	132.1	8.60E-30
hypothetical protein	Pgjcvi_01812	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1031	3, 75	75.3	114.8	1.40E-24
hypothetical protein	Pgjcvi_01812	PG JCVI SC001	hypothetical protein	PG W83	PG1470	11, 64	63	69.3	6.80E-11
hypothetical protein	Pgjcvi_01813	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1290	1, 84	77.4	147.5	2.30E-34
hypothetical protein	Pgjcvi_01814	PG JCVI SC001	conserved hypothetical protein related to phage	PG ATCC 33277	PGN_1291	1, 422	53.5	460.7	0
hypothetical protein	Pgjcvi_01814	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1032	1, 420	53.1	464.2	0
hypothetical protein	Pgjcvi_01815	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0851	1, 76	92.3	142.1	1.60E-32
hypothetical protein	Pgjcvi_01815	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1034	1, 136	57.6	167.2	4.70E-40
hypothetical protein	Pgjcvi_01816	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0849	1, 100	99	218	0
hypothetical protein	Pgjcvi_01816	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2020	1, 29	96.6	62.8	8.90E-09
hypothetical protein	Pgjcvi_01817	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0848	1, 93	97.8	190.3	0
hypothetical protein	Pgjcvi_01817	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2021	1, 93	97.8	189.5	0
hypothetical protein	Pgjcvi_01817	PG JCVI SC001	hypothetical protein	PG W83	PG1463	1, 93	96.8	189.1	0
hypothetical protein	Pgjcvi_01818	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0847	1, 75	98.7	144.8	1.30E-33
hypothetical protein	Pgjcvi_01818	PG JCVI SC001	hypothetical protein	PG W83	PG1462	1, 75	98.7	144.8	1.30E-33
hypothetical protein	Pgjcvi_01818	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2022	1, 75	98.7	144.8	1.30E-33
hypothetical protein	Pgjcvi_01819	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0846	1, 173	99.4	365.2	0
hypothetical protein	Pgjcvi_01819	PG JCVI SC001	hypothetical protein	PG W83	PG1461	1, 173	98.3	360.5	0
hypothetical protein	Pgjcvi_01819	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2023	1, 173	98.3	360.9	0
hypothetical protein	Pgjcvi_01820	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2024	1, 110	100	224.9	0
hypothetical protein	Pgjcvi_01820	PG JCVI SC001	hypothetical protein	PG W83	PG1460	1, 119	99.2	241.5	0
hypothetical protein	Pgjcvi_01820	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0845	1, 119	97.5	236.1	0
Domain of unknown function (DUF1896).	Pgjcvi_01821	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2026	1, 152	99.3	304.3	0
Domain of unknown function (DUF1896).	Pgjcvi_01821	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0844	1, 152	98.7	303.9	0
Domain of unknown function (DUF1896).	Pgjcvi_01821	PG JCVI SC001	hypothetical protein	PG W83	PG1458	1, 152	98.7	303.9	0
ORF6N domain.	Pgjcvi_01822	PG JCVI SC001	hypothetical protein	PG W83	PG1457	1, 155	98.7	303.5	0
ORF6N domain.	Pgjcvi_01822	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0843	1, 177	98.3	340.9	0
ORF6N domain.	Pgjcvi_01822	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2027	1, 177	98.3	340.9	0
Site-specific recombinase XerD	Pgjcvi_01823	PG JCVI SC001	integrase	PG TDC60	PGTDC60_2028	1, 410	98.5	800.4	0
Site-specific recombinase XerD	Pgjcvi_01823	PG JCVI SC001	integrase	PG W83	PG1435	1, 348	98	680.2	0
Site-specific recombinase XerD	Pgjcvi_01823	PG JCVI SC001	putative bacteriophage integrase	PG ATCC 33277	PGN_0094	1, 400	39.8	302.4	0
4-diphosphocytidyl-2-methyl-D-erithritol synthase	Pgjcvi_01825	PG JCVI SC001	putative 4-diphosphocytidyl-2C-methyl-D- erythritol synthase	PG ATCC 33277	PGN_0841	1, 222	100	454.1	0
4-diphosphocytidyl-2-methyl-D-erithritol synthase	Pgjcvi_01825	PG JCVI SC001	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	PG TDC60	PGTDC60_2029	1, 222	100	454.1	0
4-diphosphocytidyl-2-methyl-D-erithritol synthase	Pgjcvi_01825	PG JCVI SC001	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	PG W83	PG1434	1, 222	99.5	452.6	0
Exonuclease VII small subunit.	Pgjcvi_01826	PG JCVI SC001	hydrolase	PG W83	PG1433	1, 64	98.4	122.1	7.90E-27
Exonuclease VII small subunit.	Pgjcvi_01826	PG JCVI SC001	hydrolase	PG TDC60	PGTDC60_2030	1, 64	98.4	122.1	7.90E-27
Exonuclease VII small subunit.	Pgjcvi_01826	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0840	1, 64	96.9	119.4	5.10E-26
Tetratricopeptide repeat./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_01827	PG JCVI SC001	probable sensor histidine kinase	PG ATCC 33277	PGN_0904	11, 631	99.8	1196	0
Tetratricopeptide repeat./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_01827	PG JCVI SC001	sensor histidine kinase	PG W83	PG1432	1, 619	99.2	1191.4	0
Tetratricopeptide repeat./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	Pgjcvi_01827	PG JCVI SC001	sensor histidine kinase	PG TDC60	PGTDC60_2031	1, 602	98.8	1148.3	0
Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	Pgjcvi_01828	PG JCVI SC001	DNA-binding response regulator, LuxR family	PG W83	PG1431	1, 227	100	447.2	0
Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	Pgjcvi_01828	PG JCVI SC001	LuxR family DNA-binding response regulator	PG TDC60	PGTDC60_2032	1, 227	100	447.2	0
Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	Pgjcvi_01828	PG JCVI SC001	probable DNA-binding response regulator LuxR family	PG ATCC 33277	PGN_0903	1, 227	99.6	445.7	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01829	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_2033	1, 228	100	446.4	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01829	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0902	1, 228	99.6	444.5	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01829	PG JCVI SC001	TPR domain protein	PG W83	PG1430	1, 228	99.1	443.7	0
6,7-dimethyl-8-ribityllumazine synthase	Pgjcvi_01830	PG JCVI SC001	putative riboflavin synthase beta subunit	PG ATCC 33277	PGN_0901	1, 161	99.4	325.5	0
6,7-dimethyl-8-ribityllumazine synthase	Pgjcvi_01830	PG JCVI SC001	6,7-dimethyl-8-ribityllumazine synthase	PG TDC60	PGTDC60_2035	1, 161	99.4	327	0
6,7-dimethyl-8-ribityllumazine synthase	Pgjcvi_01830	PG JCVI SC001	riboflavin synthase subunit beta	PG W83	PG1428	1, 161	98.8	325.1	0
Por secretion system C-terminal sorting domain	Pgjcvi_01831	PG JCVI SC001	thiol protease/hemagglutinin PrtT precursor, putative	PG W83	PG1427	1, 843	98.6	1687.2	0
Por secretion system C-terminal sorting domain	Pgjcvi_01831	PG JCVI SC001	thiol protease/hemagglutinin PrtT precursor	PG TDC60	PGTDC60_2036	1, 843	98.5	1691.8	0
Por secretion system C-terminal sorting domain	Pgjcvi_01831	PG JCVI SC001	thiol protease	PG ATCC 33277	PGN_0900	1, 843	98.3	1688.3	0
Peptidylarginine deiminase and related enzymes	Pgjcvi_01832	PG JCVI SC001	probable peptidylarginine deiminase	PG ATCC 33277	PGN_0898	1, 556	98.9	1122.1	0
Peptidylarginine deiminase and related enzymes	Pgjcvi_01832	PG JCVI SC001	peptidylarginine deiminase	PG W83	PG1424	1, 556	98.9	1122.1	0
Peptidylarginine deiminase and related enzymes	Pgjcvi_01832	PG JCVI SC001	putative peptidylarginine deiminase	PG TDC60	PGTDC60_2039	1, 556	98.9	1122.1	0
D-alanyl-D-alanine carboxypeptidase, serine-type, PBP4 family	Pgjcvi_01833	PG JCVI SC001	D-alanyl-D-alanine carboxypeptidase	PG W83	PG1422	1, 510	99.6	1007.3	0
D-alanyl-D-alanine carboxypeptidase, serine-type, PBP4 family	Pgjcvi_01833	PG JCVI SC001	probable D-alanyl-D-alanine carboxypeptidase	PG ATCC 33277	PGN_0896	1, 500	99.4	986.9	0
D-alanyl-D-alanine carboxypeptidase, serine-type, PBP4 family	Pgjcvi_01833	PG JCVI SC001	D-alanyl-D-alanine carboxypeptidase	PG TDC60	PGTDC60_2040	1, 510	99.4	1005	0
hypothetical protein	Pgjcvi_01835	PG JCVI SC001	ferredoxin 4Fe-4S	PG ATCC 33277	PGN_0895	1, 56	100	123.6	2.40E-27
hypothetical protein	Pgjcvi_01835	PG JCVI SC001	ferredoxin, 4Fe-4S	PG W83	PG1421	1, 56	100	123.6	2.40E-27

hypothetical protein	Pgjcvi_01835	PG JCVI SC001	ferredoxin, 4Fe-4S	PG TDC60	PGTDC60_2041	1, 56	100	123.6	2.40E-27
DNA polymerase III, subunit gamma and tau	Pgjcvi_01836	PG JCVI SC001	DNA polymerase III, gamma and tau subunits	PG W83	PG1418	1, 602	99.8	1177.5	0
DNA polymerase III, subunit gamma and tau	Pgjcvi_01836	PG JCVI SC001	DNA polymerase III, gamma and tau subunits	PG ATCC 33277	PGN_0894	1, 602	99.5	1172.9	0
DNA polymerase III, subunit gamma and tau	Pgjcvi_01836	PG JCVI SC001	DNA polymerase III, gamma and tau subunits	PG TDC60	PGTDC60_2042	1, 602	99.3	1172.9	0
hydro-lyases, Fe-S type, tartrate/fumarate subfamily, alpha region/hydro-lyases, Fe-S type, tartrate/fumarate subfamily, beta region	Pgjcvi_01837	PG JCVI SC001	fumarate hydratase class I anaerobic	PG ATCC 33277	PGN_0893	1, 548	99.5	1109	0
hydro-lyases, Fe-S type, tartrate/fumarate subfamily, alpha region/hydro-lyases, Fe-S type, tartrate/fumarate subfamily, beta region	Pgjcvi_01837	PG JCVI SC001	fumarate hydratase class I, anaerobic	PG W83	PG1417	1, 548	99.5	1109	0
hydro-lyases, Fe-S type, tartrate/fumarate subfamily, alpha region/hydro-lyases, Fe-S type, tartrate/fumarate subfamily, beta region	Pgjcvi_01837	PG JCVI SC001	fumarate hydratase class I, anaerobic	PG TDC60	PGTDC60_2043	1, 548	99.5	1108.2	0
Dioxygenases related to 2-nitropropane dioxygenase	Pgjcvi_01838	PG JCVI SC001	dioxygenase	PG ATCC 33277	PGN_0891	1, 313	99.7	615.1	0
Dioxygenases related to 2-nitropropane dioxygenase	Pgjcvi_01838	PG JCVI SC001	enoyl-(acyl-carrier-protein) reductase II	PG TDC60	PGTDC60_2045	1, 313	99.4	612.8	0
Dioxygenases related to 2-nitropropane dioxygenase	Pgjcvi_01838	PG JCVI SC001	enoyl-(acyl-carrier-protein) reductase II	PG W83	PG1416	1, 313	99	609.8	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_01839	PG JCVI SC001	putative TonB-dependent outer membrane receptor protein	PG TDC60	PGTDC60_2046	1, 867	99.8	1770	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_01839	PG JCVI SC001	putative TonB-dependent outer membrane receptor protein	PG ATCC 33277	PGN_0890	1, 867	99.7	1767.7	0
Outer membrane receptor proteins, mostly Fe transport	Pgjcvi_01839	PG JCVI SC001	hypothetical protein	PG W83	PG1414	5, 871	99.7	1769.2	0
hypothetical protein	Pgjcvi_01840	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2049	1, 50	96	104.8	1.20E-21
Predicted permease	Pgjcvi_01843	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2050	11, 569	99.8	1089.3	0
Predicted permease	Pgjcvi_01843	PG JCVI SC001	potassium uptake protein TrkA, putative	PG W83	PG1411	3, 561	99.3	1083.2	0
Predicted permease	Pgjcvi_01843	PG JCVI SC001	potassium uptake protein TrkA	PG ATCC 33277	PGN_0889	3, 561	99.1	1079.7	0
hypothetical protein	Pgjcvi_01844	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2051	2, 172	99.4	350.9	0
hypothetical protein	Pgjcvi_01844	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0887	1, 129	99.2	262.3	0
hypothetical protein	Pgjcvi_01844	PG JCVI SC001	hypothetical protein	PG W83	PG1409	1, 130	99.2	265.8	0
cation diffusion facilitator family transporter	Pgjcvi_01845	PG JCVI SC001	heavy metal efflux pump, CzcD family	PG W83	PG1408	1, 321	99.7	652.9	0
cation diffusion facilitator family transporter	Pgjcvi_01845	PG JCVI SC001	CzcD family heavy metal efflux protein	PG TDC60	PGTDC60_2052	1, 276	99.6	546.6	0
cation diffusion facilitator family transporter	Pgjcvi_01845	PG JCVI SC001	putative cation efflux protein	PG ATCC 33277	PGN_0886	1, 321	99.4	652.5	0
Predicted flavin-nucleotide-binding protein	Pgjcvi_01846	PG JCVI SC001	nitroimidazole resistance protein, putative	PG W83	PG1407	1, 178	100	352.4	0
Predicted flavin-nucleotide-binding protein	Pgjcvi_01846	PG JCVI SC001	nitroimidazole resistance protein	PG TDC60	PGTDC60_2053	1, 171	97.7	330.9	0
Predicted flavin-nucleotide-binding protein	Pgjcvi_01846	PG JCVI SC001	probable nitroimidazole resistance protein	PG ATCC 33277	PGN_0885	1, 178	97.2	343.2	0
hypothetical protein	Pgjcvi_01847	PG JCVI SC001	organic solvent tolerance protein OstA	PG TDC60	PGTDC60_2055	1, 873	99.8	1791.5	0
hypothetical protein	Pgjcvi_01847	PG JCVI SC001	hypothetical protein	PG W83	PG1405	1, 951	99.5	1936.4	0
hypothetical protein	Pgjcvi_01847	PG JCVI SC001	organic solvent tolerance protein OstA	PG ATCC 33277	PGN_0884	1, 951	99.4	1934.1	0
Uncharacterized membrane protein (homolog of Drosophila rhomboid)	Pgjcvi_01848	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0883	1, 238	100	486.9	0
Uncharacterized membrane protein (homolog of Drosophila rhomboid)	Pgjcvi_01848	PG JCVI SC001	rhomboid family protein	PG W83	PG1404	1, 238	100	486.9	0
Uncharacterized membrane protein (homolog of Drosophila rhomboid)	Pgjcvi_01848	PG JCVI SC001	rhomboid family protein	PG TDC60	PGTDC60_2056	1, 240	99.2	482.6	0
Uncharacterized membrane protein (homolog of Drosophila rhomboid)	Pgjcvi_01849	PG JCVI SC001	rhomboid family protein	PG TDC60	PGTDC60_2057	1, 304	98.4	605.9	0
Uncharacterized membrane protein (homolog of Drosophila rhomboid)	Pgjcvi_01849	PG JCVI SC001	rhomboid family protein	PG W83	PG1403	1, 288	98.3	571.2	0
Uncharacterized membrane protein (homolog of Drosophila rhomboid)	Pgjcvi_01849	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0882	1, 288	97.6	570.5	0
Metal-dependent hydrolase	Pgjcvi_01850	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0881	1, 375	99.7	754.2	0
Metal-dependent hydrolase	Pgjcvi_01850	PG JCVI SC001	AP endonuclease domain protein	PG W83	PG1402	1, 310	99.7	632.9	0
Metal-dependent hydrolase	Pgjcvi_01850	PG JCVI SC001	AP endonuclease domain-containing protein	PG TDC60	PGTDC60_2058	1, 381	99.5	764.2	0
Tryptophanase	Pgjcvi_01851	PG JCVI SC001	tyrosine phenol-lyase	PG ATCC 33277	PGN_0880	1, 459	100	919.8	0
Tryptophanase	Pgjcvi_01851	PG JCVI SC001	beta-eliminating lyase	PG W83	PG1401	1, 459	100	919.8	0
Tryptophanase	Pgjcvi_01851	PG JCVI SC001	tryptophanase	PG TDC60	PGTDC60_2059	1, 459	99.6	917.5	0
AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)	Pgjcvi_01852	PG JCVI SC001	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	PG ATCC 33277	PGN_0865	1, 505	100	991.9	0
AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)	Pgjcvi_01852	PG JCVI SC001	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	PG W83	PG1397	4, 508	100	991.9	0
AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)	Pgjcvi_01852	PG JCVI SC001	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	PG TDC60	PGTDC60_2067	4, 508	99.4	987.3	0
cell shape determining protein, MreB/Mrl family	Pgjcvi_01853	PG JCVI SC001	cell shape-determining protein MreB	PG ATCC 33277	PGN_0866	1, 339	100	664.1	0
cell shape determining protein, MreB/Mrl family	Pgjcvi_01853	PG JCVI SC001	cell shape-determining protein MreB	PG W83	PG1396	1, 339	100	664.1	0
cell shape determining protein, MreB/Mrl family	Pgjcvi_01853	PG JCVI SC001	rod shape-determining protein MreB	PG TDC60	PGTDC60_2068	1, 339	100	664.1	0
Cell shape-determining protein	Pgjcvi_01854	PG JCVI SC001	probable cell shape-determining protein MreC	PG ATCC 33277	PGN_0867	1, 295	99.7	573.5	0
Cell shape-determining protein	Pgjcvi_01854	PG JCVI SC001	cell shape-determining protein MreC, putative	PG W83	PG1395	1, 295	99.7	573.5	0
Cell shape-determining protein	Pgjcvi_01854	PG JCVI SC001	rod shape-determining protein MreC	PG TDC60	PGTDC60_2069	1, 295	99	568.5	0
rod shape-determining protein MreD	Pgjcvi_01855	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0868	1, 172	100	335.9	0
rod shape-determining protein MreD	Pgjcvi_01855	PG JCVI SC001	hypothetical protein	PG W83	PG1394	1, 172	99.4	335.5	0
rod shape-determining protein MreD	Pgjcvi_01855	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2070	1, 172	98.8	334	0
penicillin-binding protein 2	Pgjcvi_01856	PG JCVI SC001	penicillin-binding protein 2, putative	PG W83	PG1393	1, 621	100	1267.7	0
penicillin-binding protein 2	Pgjcvi_01856	PG JCVI SC001	penicillin-binding protein 2	PG TDC60	PGTDC60_2071	1, 621	100	1267.7	0
penicillin-binding protein 2	Pgjcvi_01856	PG JCVI SC001	penicillin-binding protein 2	PG ATCC 33277	PGN_0869	1, 621	99.7	1261.5	0
Bacterial cell division membrane protein	Pgjcvi_01857	PG JCVI SC001	rod shape-determining protein RodA, putative	PG W83	PG1392	1, 485	99.8	956.1	0
Bacterial cell division membrane protein	Pgjcvi_01857	PG JCVI SC001	rod shape-determining protein RodA	PG TDC60	PGTDC60_2072	1, 485	99.8	956.1	0
Bacterial cell division membrane protein	Pgjcvi_01857	PG JCVI SC001	putative rod shape-determining protein RodA	PG ATCC 33277	PGN_0870	1, 485	99.6	954.5	0
hypothetical protein	Pgjcvi_01858	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2073	1, 371	99.7	738.8	0
hypothetical protein	Pgjcvi_01858	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0871	1, 403	98.8	793.5	0
hypothetical protein	Pgjcvi_01858	PG JCVI SC001	hypothetical protein	PG W83	PG1391	1, 403	98.8	793.1	0
DNA-binding protein, histone-like, putative	Pgjcvi_01859	PG JCVI SC001	DNA-binding protein histone-like family	PG TDC60	PGTDC60_2074	1, 152	100	299.3	0
DNA-binding protein, histone-like, putative	Pgjcvi_01859	PG JCVI SC001	DNA-binding protein histone-like family	PG ATCC 33277	PGN_0872	1, 152	99.3	297.4	0
DNA-binding protein, histone-like, putative	Pgjcvi_01859	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG1389	1, 152	99.3	297.7	0
Protein of unknown function (DUF3256).	Pgjcvi_01860	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2075	1, 236	100	469.5	0

Protein of unknown function (DUF3256).	Pgjcvi_01860	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0873	1, 236	99.6	468.4	0
Protein of unknown function (DUF3256).	Pgjcvi_01860	PG JCVI SC001	hypothetical protein	PG W83	PG1388	29, 264	99.2	466.8	0
hypothetical protein	Pgjcvi_01861	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2076	1, 298	99.7	570.9	0
hypothetical protein	Pgjcvi_01861	PG JCVI SC001	hypothetical protein	PG W83	PG1387	1, 308	99.4	586.6	0
hypothetical protein	Pgjcvi_01861	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0874	1, 308	98.7	580.9	0
DNA gyrase, A subunit	Pgjcvi_01862	PG JCVI SC001	DNA gyrase, A subunit	PG TDC60	PGTDC60_2077	1, 859	99.9	1679.1	0
DNA gyrase, A subunit	Pgjcvi_01862	PG JCVI SC001	DNA gyrase A subunit	PG ATCC 33277	PGN_0875	1, 859	99.7	1676.4	0
DNA gyrase, A subunit	Pgjcvi_01862	PG JCVI SC001	DNA gyrase, A subunit	PG W83	PG1386	1, 859	99.7	1676.8	0
Tetratricopeptide repeat.	Pgjcvi_01863	PG JCVI SC001	TPR domain protein	PG W83	PG1385	1, 400	100	803.1	0
Tetratricopeptide repeat.	Pgjcvi_01863	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_2078	1, 400	99.8	800.8	0
Tetratricopeptide repeat.	Pgjcvi_01863	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_0876	1, 400	99.5	798.9	0
Putative threonine efflux protein	Pgjcvi_01864	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0861	6, 217	100	425.6	0
Putative threonine efflux protein	Pgjcvi_01864	PG JCVI SC001	amino acid exporter, putative	PG W83	PG1383	1, 212	100	425.6	0
Putative threonine efflux protein	Pgjcvi_01864	PG JCVI SC001	amino acid exporter	PG TDC60	PGTDC60_2085	6, 217	99.1	420.6	0
Phosphate-selective porin O and P.	Pgjcvi_01865	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0860	1, 349	99.1	694.9	0
Phosphate-selective porin O and P.	Pgjcvi_01865	PG JCVI SC001	hypothetical protein	PG W83	PG1382	31, 379	99.1	694.1	0
Phosphate-selective porin O and P.	Pgjcvi_01865	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2086	31, 379	98.3	688.3	0
ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	Pgjcvi_01866	PG JCVI SC001	ABC transporter, permease protein	PG W83	PG1381	1, 249	100	481.1	0
ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	Pgjcvi_01866	PG JCVI SC001	ABC transporter permease	PG TDC60	PGTDC60_2087	1, 237	100	458	0
ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	Pgjcvi_01866	PG JCVI SC001	probable ABC transporter permease protein	PG ATCC 33277	PGN_0859	1, 249	98.4	476.1	0
ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	Pgjcvi_01867	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_2088	1, 232	100	461.5	0
ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	Pgjcvi_01867	PG JCVI SC001	probable ABC transporter ATP-binding protein	PG ATCC 33277	PGN_0858	1, 232	99.6	459.1	0
ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	Pgjcvi_01867	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG1380	1, 232	99.6	459.5	0
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	Pgjcvi_01868	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0857	1, 312	100	610.9	0
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	Pgjcvi_01868	PG JCVI SC001	ABC transporter, periplasmic substrate-binding protein	PG TDC60	PGTDC60_2089	1, 312	100	610.9	0
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	Pgjcvi_01868	PG JCVI SC001	ABC transporter, periplasmic substrate-binding protein, putative	PG W83	PG1379	1, 312	99.7	607.8	0
A/G-specific adenine glycosylase	Pgjcvi_01869	PG JCVI SC001	putative A/G-specific adenine glycosylase	PG ATCC 33277	PGN_0856	27, 407	99.7	785.4	0
A/G-specific adenine glycosylase	Pgjcvi_01869	PG JCVI SC001	A/G-specific adenine glycosylase	PG TDC60	PGTDC60_2090	1, 381	99.5	783.1	0
A/G-specific adenine glycosylase	Pgjcvi_01869	PG JCVI SC001	A/G-specific adenine glycosylase	PG W83	PG1378	27, 407	97.6	764.2	0
Por secretion system C-terminal sorting domain	Pgjcvi_01870	PG JCVI SC001	immunoreactive 47 kDa antigen PG97	PG TDC60	PGTDC60_2094	1, 428	99.8	861.3	0
Por secretion system C-terminal sorting domain	Pgjcvi_01870	PG JCVI SC001	immunoreactive 47 kDa antigen	PG ATCC 33277	PGN_0852	1, 428	99.5	860.1	0
Por secretion system C-terminal sorting domain	Pgjcvi_01870	PG JCVI SC001	immunoreactive 47 kDa antigen PG97	PG W83	PG1374	1, 428	98.8	852.8	0
hypothetical protein	Pgjcvi_01871	PG JCVI SC001	hypothetical protein	PG W83	PG1373	1, 91	96.7	181.8	1.30E-44
hypothetical protein	Pgjcvi_01871	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2095	1, 88	96.6	174.9	1.50E-42
hypothetical protein	Pgjcvi_01871	PG JCVI SC001	transposase in ISPg2	PG ATCC 33277	PGN_1160	1, 34	79.4	57.4	3.40E-07
WD40-like Beta Propeller Repeat.	Pgjcvi_01872	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2096	1, 473	99.6	922.9	0
WD40-like Beta Propeller Repeat.	Pgjcvi_01872	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1159	1, 473	98.7	917.1	0
WD40-like Beta Propeller Repeat.	Pgjcvi_01872	PG JCVI SC001	hypothetical protein	PG W83	PG1372	1, 473	98.1	912.1	0
Uridine phosphorylase	Pgjcvi_01873	PG JCVI SC001	putative purine nucleoside phosphorylase	PG ATCC 33277	PGN_1158	1, 292	99.7	580.1	0
Uridine phosphorylase	Pgjcvi_01873	PG JCVI SC001	phosphorylase family protein	PG W83	PG1371	1, 292	99.7	580.1	0
Uridine phosphorylase	Pgjcvi_01873	PG JCVI SC001	phosphorylase family protein	PG TDC60	PGTDC60_2097	1, 292	99.7	580.1	0
Lysyl-tRNA synthetase (class II)	Pgjcvi_01874	PG JCVI SC001	lysyl-tRNA synthetase	PG W83	PG1370	1, 194	99	383.6	0
Lysyl-tRNA synthetase (class II)	Pgjcvi_01874	PG JCVI SC001	lysyl-tRNA synthetase	PG TDC60	PGTDC60_2098	1, 194	99	383.6	0
Lysyl-tRNA synthetase (class II)	Pgjcvi_01874	PG JCVI SC001	lysyl-tRNA synthetase	PG ATCC 33277	PGN_1157	1, 194	98.5	380.6	0
Lysyl-tRNA synthetase (class II)	Pgjcvi_01875	PG JCVI SC001	lysyl-tRNA synthetase	PG ATCC 33277	PGN_1157	190, 578	99.5	789.3	0
Lysyl-tRNA synthetase (class II)	Pgjcvi_01875	PG JCVI SC001	lysyl-tRNA synthetase	PG W83	PG1370	190, 578	99.2	790.8	0
Lysyl-tRNA synthetase (class II)	Pgjcvi_01875	PG JCVI SC001	lysyl-tRNA synthetase	PG TDC60	PGTDC60_2098	190, 578	99	785.4	0
Glycerol-3-phosphate dehydrogenase	Pgjcvi_01876	PG JCVI SC001	glycerol-3-phosphate dehydrogenase	PG ATCC 33277	PGN_1156	1, 334	99.7	663.3	0
Glycerol-3-phosphate dehydrogenase	Pgjcvi_01876	PG JCVI SC001	glycerol-3-phosphate dehydrogenase (NAD(P)+)	PG W83	PG1369	1, 334	99.4	660.2	0
Glycerol-3-phosphate dehydrogenase	Pgjcvi_01876	PG JCVI SC001	glycerol-3-phosphate dehydrogenase (NAD(P)+)	PG TDC60	PGTDC60_2099	1, 334	99.4	660.2	0
Glucose-6-phosphate isomerase	Pgjcvi_01877	PG JCVI SC001	glucose-6-phosphate isomerase	PG W83	PG1368	1, 445	99.6	880.2	0
Glucose-6-phosphate isomerase	Pgjcvi_01877	PG JCVI SC001	glucose-6-phosphate isomerase	PG ATCC 33277	PGN_1155	1, 445	99.3	877.9	0
Glucose-6-phosphate isomerase	Pgjcvi_01877	PG JCVI SC001	glucose-6-phosphate isomerase	PG TDC60	PGTDC60_2100	1, 445	99.3	875.2	0
hypothetical protein	Pgjcvi_01878	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2101	1, 182	100	376.3	0
hypothetical protein	Pgjcvi_01878	PG JCVI SC001	hypothetical protein	PG W83	PG1367	1, 182	99.5	374	0
hypothetical protein	Pgjcvi_01878	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1154	1, 176	99.4	361.3	0
UDP-N-acetylglucosamine enolpyruvyl transferase	Pgjcvi_01879	PG JCVI SC001	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	PG W83	PG1366	1, 351	98.9	680.2	0
UDP-N-acetylglucosamine enolpyruvyl transferase	Pgjcvi_01879	PG JCVI SC001	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	PG ATCC 33277	PGN_1153	1, 351	98.6	678.3	0
UDP-N-acetylglucosamine enolpyruvyl transferase	Pgjcvi_01879	PG JCVI SC001	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	PG TDC60	PGTDC60_2102	1, 351	98.6	676.8	0
UDP-N-acetylglucosamine enolpyruvyl transferase	Pgjcvi_01880	PG JCVI SC001	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	PG ATCC 33277	PGN_1153	331, 434	100	201.4	0
UDP-N-acetylglucosamine enolpyruvyl transferase	Pgjcvi_01880	PG JCVI SC001	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	PG W83	PG1366	331, 434	100	201.4	0
UDP-N-acetylglucosamine enolpyruvyl transferase	Pgjcvi_01880	PG JCVI SC001	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	PG TDC60	PGTDC60_2102	331, 434	100	201.4	0
RimM protein, required for 16S rRNA processing	Pgjcvi_01881	PG JCVI SC001	probable 16S rRNA processing protein	PG ATCC 33277	PGN_1152	1, 136	99.3	273.5	0
RimM protein, required for 16S rRNA processing	Pgjcvi_01881	PG JCVI SC001	16S rRNA-processing protein RimM	PG TDC60	PGTDC60_2103	1, 136	99.3	273.5	0
RimM protein, required for 16S rRNA processing	Pgjcvi_01881	PG JCVI SC001	16S rRNA-processing protein	PG W83	PG1365	1, 136	97.8	268.9	0
1-deoxy-D-xylulose 5-phosphate reductoisomerase	Pgjcvi_01882	PG JCVI SC001	1-deoxy-D-xylulose-5-phosphate reductoisomerase	PG ATCC 33277	PGN_1151	1, 370	98.6	719.2	0
1-deoxy-D-xylulose 5-phosphate reductoisomerase	Pgjcvi_01882	PG JCVI SC001	1-deoxy-D-xylulose 5-phosphate reductoisomerase	PG W83	PG1364	1, 370	98.6	719.2	0
1-deoxy-D-xylulose 5-phosphate reductoisomerase	Pgjcvi_01882	PG JCVI SC001	1-deoxy-D-xylulose 5-phosphate reductoisomerase	PG TDC60	PGTDC60_2104	1, 370	98.6	719.2	0
Predicted N6-adenine-specific DNA methylase	Pgjcvi_01883	PG JCVI SC001	putative N6-adenine-specific DNA methylase	PG TDC60	PGTDC60_2107	1, 428	99.1	847.8	0
Predicted N6-adenine-specific DNA methylase	Pgjcvi_01883	PG JCVI SC001	hypothetical protein	PG W83	PG1362	1, 428	98.8	841.3	0
Predicted N6-adenine-specific DNA methylase	Pgjcvi_01883	PG JCVI SC001	putative N6-adenine-specific DNA methylase	PG ATCC 33277	PGN_1150	1, 441	96.6	847.4	0
hypothetical protein	Pgjcvi_01884	PG JCVI SC001	putative N6-adenine-specific DNA methylase	PG TDC60	PGTDC60_2107	417, 484	100	146.4	4.20E-34

hypothetical protein	Pgjcvi_01884	PG JCVI SC001	putative N6-adenine-specific DNA methylase	PG ATCC 33277	PGN_1150	417, 484	98.5	144.4	1.60E-33
hypothetical protein	Pgjcvi_01884	PG JCVI SC001	hypothetical protein	PG W83	PG1362	417, 484	97.1	141.4	1.30E-32
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01885	PG JCVI SC001	dipeptidyl aminopeptidase IV	PG TDC60	PGTDC60_2108	1, 617	98.6	1265	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01885	PG JCVI SC001	dipeptidyl aminopeptidase IV, putative	PG W83	PG1361	1, 617	98.4	1262.7	0
Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	Pgjcvi_01885	PG JCVI SC001	prolyl tripeptidase A	PG ATCC 33277	PGN_1149	1, 617	98.1	1258	0
phosphoribosylamine--glycine ligase	Pgjcvi_01887	PG JCVI SC001	phosphoribosylamine-glycine ligase	PG ATCC 33277	PGN_1148	1, 431	99.8	864	0
phosphoribosylamine--glycine ligase	Pgjcvi_01887	PG JCVI SC001	phosphoribosylamine--glycine ligase	PG W83	PG1360	1, 431	99.8	864	0
phosphoribosylamine--glycine ligase	Pgjcvi_01887	PG JCVI SC001	phosphoribosylamine--glycine ligase	PG TDC60	PGTDC60_2109	1, 431	99.8	864	0
hypothetical protein	Pgjcvi_01888	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2110	1, 278	98.6	549.7	0
hypothetical protein	Pgjcvi_01888	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1147	1, 323	90.7	587.8	0
hypothetical protein	Pgjcvi_01888	PG JCVI SC001	hypothetical protein	PG W83	PG1359	1, 323	90.1	582.4	0
Acetyltransferases, including N-acetylases of ribosomal proteins	Pgjcvi_01889	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1146	1, 226	98.7	467.6	0
Acetyltransferases, including N-acetylases of ribosomal proteins	Pgjcvi_01889	PG JCVI SC001	acetyltransferase, GNAT family	PG W83	PG1358	1, 226	98.7	467.6	0
Acetyltransferases, including N-acetylases of ribosomal proteins	Pgjcvi_01889	PG JCVI SC001	acetyltransferase	PG TDC60	PGTDC60_2112	1, 151	98	318.5	0
hypothetical protein	Pgjcvi_01890	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1145	1, 43	100	90.1	2.20E-17
hypothetical protein	Pgjcvi_01890	PG JCVI SC001	hypothetical protein	PG W83	PG1357	1, 43	100	90.1	2.20E-17
hypothetical protein	Pgjcvi_01890	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2113	1, 39	97.4	80.5	1.80E-14
hypothetical protein	Pgjcvi_01891	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1143	9, 141	100	262.7	0
hypothetical protein	Pgjcvi_01891	PG JCVI SC001	hypothetical protein	PG W83	PG1356	30, 162	100	262.7	0
hypothetical protein	Pgjcvi_01891	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2115	1, 133	100	262.7	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01892	PG JCVI SC001	acyltransferase	PG TDC60	PGTDC60_2116	2, 172	98.8	350.1	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01892	PG JCVI SC001	probable acetyltransferase	PG ATCC 33277	PGN_1142	12, 182	98.2	348.2	0
1-acyl-sn-glycerol-3-phosphate acyltransferase	Pgjcvi_01892	PG JCVI SC001	acyltransferase, putative	PG W83	PG1355	6, 176	98.2	347.8	0
hypothetical protein	Pgjcvi_01893	PG JCVI SC001	putative amidohydrolase	PG ATCC 33277	PGN_1141	156, 273	100	256.1	0
hypothetical protein	Pgjcvi_01893	PG JCVI SC001	hydrolase, carbon-nitrogen family	PG W83	PG1354	156, 273	100	256.1	0
hypothetical protein	Pgjcvi_01893	PG JCVI SC001	carbon-nitrogen family hydrolase	PG TDC60	PGTDC60_2117	156, 273	100	256.1	0
hypothetical protein	Pgjcvi_01894	PG JCVI SC001	putative orotate phosphoribosyltransferase	PG ATCC 33277	PGN_1140	1, 32	100	69.3	5.30E-11
hypothetical protein	Pgjcvi_01894	PG JCVI SC001	orotate phosphoribosyltransferase	PG W83	PG1353	1, 32	100	69.3	5.30E-11
hypothetical protein	Pgjcvi_01894	PG JCVI SC001	orotate phosphoribosyltransferase	PG TDC60	PGTDC60_2118	1, 32	100	69.3	5.30E-11
hypothetical protein	Pgjcvi_01895	PG JCVI SC001	putative orotate phosphoribosyltransferase	PG ATCC 33277	PGN_1140	128, 210	97.6	164.9	1.70E-39
hypothetical protein	Pgjcvi_01895	PG JCVI SC001	orotate phosphoribosyltransferase	PG TDC60	PGTDC60_2118	128, 210	97.6	164.9	1.70E-39
hypothetical protein	Pgjcvi_01895	PG JCVI SC001	orotate phosphoribosyltransferase	PG W83	PG1353	128, 210	96.4	161.8	1.50E-38
hypothetical protein	Pgjcvi_01896	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1139	1, 94	100	185.7	1.40E-45
hypothetical protein	Pgjcvi_01896	PG JCVI SC001	hypothetical protein	PG W83	PG1352	1, 94	100	185.7	1.40E-45
hypothetical protein	Pgjcvi_01896	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2119	1, 94	100	185.7	1.40E-45
hypothetical protein	Pgjcvi_01897	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1139	82, 137	100	115.2	8.40E-25
hypothetical protein	Pgjcvi_01897	PG JCVI SC001	hypothetical protein	PG W83	PG1352	82, 137	100	115.2	8.40E-25
hypothetical protein	Pgjcvi_01897	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2119	82, 137	100	115.2	8.40E-25
hypothetical protein	Pgjcvi_01898	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1138	9, 162	99.4	305.4	0
hypothetical protein	Pgjcvi_01898	PG JCVI SC001	hypothetical protein	PG W83	PG1351	15, 168	99.4	305.8	0
hypothetical protein	Pgjcvi_01898	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2120	1, 154	99.4	305.4	0
Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	Pgjcvi_01899	PG JCVI SC001	conserved hypothetical protein TIGR00147	PG W83	PG1348	21, 263	100	488.8	0
Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	Pgjcvi_01899	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1137	21, 263	99.6	486.1	0
Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase	Pgjcvi_01899	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2123	21, 263	99.6	486.1	0
hypothetical protein	Pgjcvi_01900	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1137	1, 38	100	79	4.60E-14
hypothetical protein	Pgjcvi_01900	PG JCVI SC001	conserved hypothetical protein TIGR00147	PG W83	PG1348	1, 38	100	79	4.60E-14
hypothetical protein	Pgjcvi_01900	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2123	1, 38	100	79	4.60E-14
7-cyano-7-deazaguanine reductase	Pgjcvi_01901	PG JCVI SC001	probable GTP-cyclohydrolase protein	PG ATCC 33277	PGN_1136	75, 154	100	171.8	1.10E-41
7-cyano-7-deazaguanine reductase	Pgjcvi_01901	PG JCVI SC001	hypothetical protein	PG W83	PG1347	75, 154	100	171.8	1.10E-41
7-cyano-7-deazaguanine reductase	Pgjcvi_01901	PG JCVI SC001	7-cyano-7-deazaguanine reductase	PG TDC60	PGTDC60_2124	75, 154	98.8	168.7	9.20E-41
hypothetical protein	Pgjcvi_01902	PG JCVI SC001	probable GTP-cyclohydrolase protein	PG ATCC 33277	PGN_1136	1, 60	100	131.7	1.40E-29
hypothetical protein	Pgjcvi_01902	PG JCVI SC001	hypothetical protein	PG W83	PG1347	1, 60	100	131.7	1.40E-29
hypothetical protein	Pgjcvi_01902	PG JCVI SC001	7-cyano-7-deazaguanine reductase	PG TDC60	PGTDC60_2124	1, 60	98.3	128.6	1.20E-28
Glycosyltransferase	Pgjcvi_01903	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG W83	PG1346	1, 423	99.5	844	0
Glycosyltransferase	Pgjcvi_01903	PG JCVI SC001	putative glycosyltransferase	PG ATCC 33277	PGN_1135	1, 423	97.9	831.2	0
Glycosyltransferase	Pgjcvi_01903	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG TDC60	PGTDC60_2125	1, 423	97.9	831.6	0
Glycosyltransferase	Pgjcvi_01904	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG W83	PG1345	1, 301	99.7	596.3	0
Glycosyltransferase	Pgjcvi_01904	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG TDC60	PGTDC60_2126	1, 301	98	588.6	0
Glycosyltransferase	Pgjcvi_01904	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1134	1, 301	97	580.9	0
Lipoate-protein ligase B	Pgjcvi_01905	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1131	431, 492	100	128.6	6.00E-28
Lipoate-protein ligase B	Pgjcvi_01905	PG JCVI SC001	lipoate-protein ligase B	PG W83	PG1343	431, 492	100	128.6	6.00E-28
Lipoate-protein ligase B	Pgjcvi_01905	PG JCVI SC001	lipoate-protein ligase B	PG W83	PG1343	1, 394	99.5	811.2	0
Lipoate-protein ligase B	Pgjcvi_01905	PG JCVI SC001	lipoate-protein ligase B	PG TDC60	PGTDC60_2128	1, 323	98.8	665.2	0
Lipoate-protein ligase B	Pgjcvi_01905	PG JCVI SC001	lipoate-protein ligase B	PG TDC60	PGTDC60_2128	360, 421	98.4	128.3	7.80E-28
Lipoate-protein ligase B	Pgjcvi_01905	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1131	1, 394	98.2	805.1	0
UDP-N-acetylenolpyruvoylglucosamine reductase	Pgjcvi_01906	PG JCVI SC001	putative UDP-N-acetylenolpyruvoylglucosamine reductase	PG ATCC 33277	PGN_1130	1, 338	100	688.3	0
UDP-N-acetylenolpyruvoylglucosamine reductase	Pgjcvi_01906	PG JCVI SC001	UDP-N-acetylenolpyruvoylglucosamine reductase	PG TDC60	PGTDC60_2130	1, 338	99.4	685.3	0
UDP-N-acetylenolpyruvoylglucosamine reductase	Pgjcvi_01906	PG JCVI SC001	UDP-N-acetylenolpyruvoylglucosamine reductase	PG W83	PG1342	1, 338	99.1	684.5	0
Cell division protein	Pgjcvi_01907	PG JCVI SC001	hypothetical protein	PG W83	PG1341	32, 184	100	294.3	0
Cell division protein	Pgjcvi_01907	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1129	4, 156	99.3	292.7	0
Cell division protein	Pgjcvi_01907	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2131	4, 156	99.3	292.4	0
Nucleotidyltransferase/DNA polymerase involved in DNA repair	Pgjcvi_01908	PG JCVI SC001	putative SOS mutagenesis and repair protein UmuC homolog	PG ATCC 33277	PGN_1127	1, 425	99.5	846.7	0

Nucleotidyltransferase/DNA polymerase involved in DNA repair	Pgjcvi_01908	PG JCVI SC001	umuC protein	PG TDC60	PGTDC60_2134	1, 432	99.5	859.4	0
Nucleotidyltransferase/DNA polymerase involved in DNA repair	Pgjcvi_01908	PG JCVI SC001	umuC protein	PG W83	PG1338	1, 432	98.8	851.3	0
SOS-response transcriptional repressors (RecA-mediated autopeptidases)	Pgjcvi_01909	PG JCVI SC001	umuD protein	PG TDC60	PGTDC60_2135	1, 141	100	292	0
SOS-response transcriptional repressors (RecA-mediated autopeptidases)	Pgjcvi_01909	PG JCVI SC001	umuD protein	PG W83	PG1337	1, 141	99.3	288.9	0
SOS-response transcriptional repressors (RecA-mediated autopeptidases)	Pgjcvi_01909	PG JCVI SC001	putative error-prone repair: SOS-response transcriptional repressor UmuD homolog	PG ATCC 33277	PGN_1126	1, 141	98.6	287	0
hypothetical protein	Pgjcvi_01910	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2136	4, 60	98.2	116.3	3.90E-25
Membrane protein implicated in regulation of membrane protease activity	Pgjcvi_01911	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1125	1, 154	99.4	303.1	0
Membrane protein implicated in regulation of membrane protease activity	Pgjcvi_01911	PG JCVI SC001	hypothetical protein	PG W83	PG1335	1, 154	99.4	303.1	0
Membrane protein implicated in regulation of membrane protease activity	Pgjcvi_01911	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2137	1, 154	99.4	303.1	0
Membrane protease subunits, stomatin/prohibitin homologs	Pgjcvi_01912	PG JCVI SC001	Band 7 protein	PG ATCC 33277	PGN_1124	1, 326	100	622.9	0
Membrane protease subunits, stomatin/prohibitin homologs	Pgjcvi_01912	PG JCVI SC001	band 7/Mec-2 family protein	PG W83	PG1334	1, 326	100	622.9	0
Membrane protease subunits, stomatin/prohibitin homologs	Pgjcvi_01912	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2138	1, 326	100	622.9	0
hypothetical protein	Pgjcvi_01913	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2139	1, 399	99.7	826.6	0
hypothetical protein	Pgjcvi_01913	PG JCVI SC001	hypothetical protein	PG W83	PG1333	1, 399	99	820.1	0
hypothetical protein	Pgjcvi_01913	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1123	1, 399	98.5	819.3	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	1, 335	100	639	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NAD(P) transhydrogenase subunit beta	PG TDC60	PGTDC60_2140	1, 335	100	639	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NAD(P) transhydrogenase, beta subunit	PG W83	PG1332	1, 335	99.1	634.8	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	784, 845	88.9	111.7	6.50E-23
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NAD(P) transhydrogenase, beta subunit	PG W83	PG1332	601, 662	88.9	111.7	6.50E-23
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NAD(P) transhydrogenase subunit beta	PG TDC60	PGTDC60_2140	601, 662	88.9	111.7	6.50E-23
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	484, 518	88.6	61.6	7.70E-08
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	667, 701	88.6	61.6	7.70E-08
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	418, 477	88.5	108.6	5.50E-22
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	601, 660	88.5	108.6	5.50E-22
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NAD(P) transhydrogenase, beta subunit	PG W83	PG1332	418, 477	88.5	108.6	5.50E-22
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NAD(P) transhydrogenase subunit beta	PG TDC60	PGTDC60_2140	418, 477	88.5	108.6	5.50E-22
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NAD(P) transhydrogenase, beta subunit	PG W83	PG1332	480, 518	84.6	62.4	4.50E-08
NAD/NADP transhydrogenase beta subunit	Pgjcvi_01914	PG JCVI SC001	NAD(P) transhydrogenase subunit beta	PG TDC60	PGTDC60_2140	480, 518	84.6	62.4	4.50E-08
NAD/NADP transhydrogenase alpha subunit	Pgjcvi_01915	PG JCVI SC001	probable NADPH-NAD transhydrogenase alpha subunit	PG ATCC 33277	PGN_1121	1, 104	100	202.2	0
NAD/NADP transhydrogenase alpha subunit	Pgjcvi_01915	PG JCVI SC001	putative NADPH-NAD transhydrogenase subunit alpha	PG TDC60	PGTDC60_2141	1, 104	100	202.2	0
NAD/NADP transhydrogenase alpha subunit	Pgjcvi_01916	PG JCVI SC001	putative NADPH-NAD transhydrogenase	PG ATCC 33277	PGN_1120	1, 385	100	754.2	0
NAD/NADP transhydrogenase alpha subunit	Pgjcvi_01916	PG JCVI SC001	putative NADPH-NAD transhydrogenase	PG TDC60	PGTDC60_2142	1, 376	99.7	735.3	0
large conductance mechanosensitive channel protein	Pgjcvi_01917	PG JCVI SC001	probable large conductance mechanosensitive channel protein	PG ATCC 33277	PGN_1119	1, 139	100	270.4	0
large conductance mechanosensitive channel protein	Pgjcvi_01917	PG JCVI SC001	large conductance mechanosensitive channel protein	PG W83	PG1330	1, 139	100	270.4	0
large conductance mechanosensitive channel protein	Pgjcvi_01917	PG JCVI SC001	large conductance mechanosensitive channel protein	PG TDC60	PGTDC60_2143	1, 139	100	270.4	0
Acyl-CoA synthetase (NDP forming)	Pgjcvi_01918	PG JCVI SC001	acetyl-CoA synthetase	PG ATCC 33277	PGN_1117	1, 685	99.9	1324.3	0
Acyl-CoA synthetase (NDP forming)	Pgjcvi_01918	PG JCVI SC001	CoA ligase family protein	PG W83	PG1328	1, 685	99.9	1323.1	0
Acyl-CoA synthetase (NDP forming)	Pgjcvi_01918	PG JCVI SC001	acetyl-CoA synthetase	PG TDC60	PGTDC60_2145	1, 685	99.9	1324.7	0
Aspartate/tyrosine/aromatic aminotransferase	Pgjcvi_01919	PG JCVI SC001	aminotransferase, putative	PG W83	PG1327	1, 436	99.8	878.2	0
Aspartate/tyrosine/aromatic aminotransferase	Pgjcvi_01919	PG JCVI SC001	aminotransferase	PG TDC60	PGTDC60_2146	1, 436	99.8	878.2	0
Aspartate/tyrosine/aromatic aminotransferase	Pgjcvi_01919	PG JCVI SC001	putative aminotransferase	PG ATCC 33277	PGN_1116	1, 436	99.5	875.2	0
hypothetical protein	Pgjcvi_01920	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2147	85, 186	98	202.2	0
hypothetical protein	Pgjcvi_01920	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1114	1, 102	97.1	201.4	0
hypothetical protein	Pgjcvi_01920	PG JCVI SC001	hypothetical protein	PG W83	PG1325	23, 124	94.1	198.7	0
crossover junction endodeoxyribonuclease RuvC	Pgjcvi_01921	PG JCVI SC001	Holliday junction resolvase	PG W83	PG1324	1, 189	100	379.8	0
crossover junction endodeoxyribonuclease RuvC	Pgjcvi_01921	PG JCVI SC001	putative crossover junction endodeoxyribonuclease RuvC	PG ATCC 33277	PGN_1113	1, 189	99.5	378.3	0
crossover junction endodeoxyribonuclease RuvC	Pgjcvi_01921	PG JCVI SC001	Holliday junction resolvase	PG TDC60	PGTDC60_2148	1, 189	99.5	378.3	0
Predicted ATPase related to phosphate starvation-inducible protein PhoH	Pgjcvi_01922	PG JCVI SC001	PhoH-like protein	PG ATCC 33277	PGN_1112	1, 444	99.8	868.2	0
Predicted ATPase related to phosphate starvation-inducible protein PhoH	Pgjcvi_01922	PG JCVI SC001	PhoH family protein	PG W83	PG1323	1, 444	99.8	868.2	0
Predicted ATPase related to phosphate starvation-inducible protein PhoH	Pgjcvi_01922	PG JCVI SC001	PhoH-like protein	PG TDC60	PGTDC60_2149	1, 444	99.8	868.2	0
Formyltetrahydrofolate synthetase	Pgjcvi_01923	PG JCVI SC001	formate-tetrahydrofolate ligase	PG ATCC 33277	PGN_1111	1, 555	100	1092.4	0
Formyltetrahydrofolate synthetase	Pgjcvi_01923	PG JCVI SC001	formate--tetrahydrofolate ligase	PG W83	PG1321	1, 555	100	1092.4	0
Formyltetrahydrofolate synthetase	Pgjcvi_01923	PG JCVI SC001	formate--tetrahydrofolate ligase	PG TDC60	PGTDC60_2150	1, 555	100	1092.4	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_01924	PG JCVI SC001	putative RNA polymerase ECF-type sigma factor	PG ATCC 33277	PGN_1108	1, 183	99.5	367.5	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_01924	PG JCVI SC001	RNA polymerase sigma-70 factor, ECF subfamily	PG W83	PG1318	1, 188	99.5	375.9	0
RNA polymerase sigma factor, sigma-70 family	Pgjcvi_01924	PG JCVI SC001	ECF subfamily RNA polymerase sigma factor	PG TDC60	PGTDC60_2157	1, 188	99.5	375.9	0
hypothetical protein	Pgjcvi_01925	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1107	1, 136	99.3	278.5	0
hypothetical protein	Pgjcvi_01925	PG JCVI SC001	hypothetical protein	PG W83	PG1317	1, 136	98.5	275.8	0
hypothetical protein	Pgjcvi_01925	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2158	1, 136	98.5	275.4	0
hypothetical protein	Pgjcvi_01926	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1106	1, 168	100	330.5	0
hypothetical protein	Pgjcvi_01926	PG JCVI SC001	hypothetical protein	PG W83	PG1316	1, 176	100	347.4	0
hypothetical protein	Pgjcvi_01926	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2159	1, 176	100	347.4	0
FKBP-type peptidyl-prolyl cis-trans isomerases 2	Pgjcvi_01927	PG JCVI SC001	probable FKBP-type peptidyl-prolyl cis-trans isomerase	PG ATCC 33277	PGN_1105	1, 190	98.9	395.6	0
FKBP-type peptidyl-prolyl cis-trans isomerases 2	Pgjcvi_01927	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase SlyD, FKBP-type	PG W83	PG1315	1, 190	98.4	394.4	0
FKBP-type peptidyl-prolyl cis-trans isomerases 2	Pgjcvi_01927	PG JCVI SC001	peptidyl-prolyl cis-trans isomerase SlyD, FKBP-type	PG TDC60	PGTDC60_2160	1, 190	98.4	394.4	0
chorismate synthase	Pgjcvi_01928	PG JCVI SC001	chorismate synthase	PG W83	PG1314	1, 368	99.5	734.6	0
chorismate synthase	Pgjcvi_01928	PG JCVI SC001	chorismate synthase	PG ATCC 33277	PGN_1104	1, 368	99.2	734.6	0
chorismate synthase	Pgjcvi_01928	PG JCVI SC001	chorismate synthase	PG TDC60	PGTDC60_2161	1, 368	98.6	726.5	0
Dipeptidase	Pgjcvi_01930	PG JCVI SC001	dipeptidase	PG ATCC 33277	PGN_1103	1, 552	99.8	1140.6	0
Dipeptidase	Pgjcvi_01930	PG JCVI SC001	dipeptidase-related protein	PG W83	PG1313	1, 552	99.8	1140.6	0
Dipeptidase	Pgjcvi_01930	PG JCVI SC001	dipeptidase	PG TDC60	PGTDC60_2162	1, 552	99.8	1140.6	0

Bacterial capsule synthesis protein PGA_cap.	Pgjcvi_01931	PG JCVI SC001	capA protein, putative	PG W83	PG1312	1, 395	100	796.2	0
Bacterial capsule synthesis protein PGA_cap.	Pgjcvi_01931	PG JCVI SC001	putative capA protein	PG TDC60	PGTDC60_2166	1, 375	100	758.8	0
Bacterial capsule synthesis protein PGA_cap.	Pgjcvi_01931	PG JCVI SC001	putative capsule biosynthesis protein CapA	PG ATCC 33277	PGN_1100	1, 375	99.7	755.7	0
phosphoesterase, MJ0936 family	Pgjcvi_01932	PG JCVI SC001	probable phosphoesterase	PG ATCC 33277	PGN_1099	1, 164	99.4	340.9	0
phosphoesterase, MJ0936 family	Pgjcvi_01932	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2167	1, 164	99.4	341.3	0
phosphoesterase, MJ0936 family	Pgjcvi_01932	PG JCVI SC001	hypothetical protein	PG W83	PG1311	25, 188	98.8	339.7	0
Predicted PP-loop superfamily ATPase	Pgjcvi_01933	PG JCVI SC001	probable succinoglycan biosynthesis regulator ExsB protein	PG ATCC 33277	PGN_1098	1, 190	100	382.5	0
Predicted PP-loop superfamily ATPase	Pgjcvi_01933	PG JCVI SC001	exsB protein	PG W83	PG1310	1, 190	100	382.5	0
Predicted PP-loop superfamily ATPase	Pgjcvi_01933	PG JCVI SC001	exsB protein	PG TDC60	PGTDC60_2168	1, 190	100	382.5	0
Protein of unknown function (DUF3298).	Pgjcvi_01934	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1097	1, 270	99.6	538.5	0
Protein of unknown function (DUF3298).	Pgjcvi_01934	PG JCVI SC001	hypothetical protein	PG W83	PG1308	1, 281	99.6	558.5	0
Protein of unknown function (DUF3298).	Pgjcvi_01934	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2169	1, 281	99.3	557	0
16S rRNA (guanine(527)-N(7))-methyltransferase GidB	Pgjcvi_01935	PG JCVI SC001	glucose-inhibited division protein B	PG ATCC 33277	PGN_1096	1, 224	99.1	447.2	0
16S rRNA (guanine(527)-N(7))-methyltransferase GidB	Pgjcvi_01935	PG JCVI SC001	16S rRNA methyltransferase GidB	PG TDC60	PGTDC60_2170	1, 224	99.1	447.2	0
16S rRNA (guanine(527)-N(7))-methyltransferase GidB	Pgjcvi_01935	PG JCVI SC001	glucose-inhibited division protein B	PG W83	PG1307	1, 221	98.6	440.7	0
Zn-dependent hydrolases, including glyoxylases	Pgjcvi_01936	PG JCVI SC001	metallo-beta-lactamase family protein	PG TDC60	PGTDC60_2171	1, 214	99.5	440.3	0
Zn-dependent hydrolases, including glyoxylases	Pgjcvi_01936	PG JCVI SC001	probable metallo-beta-lactamase	PG ATCC 33277	PGN_1095	1, 214	99.1	439.1	0
Zn-dependent hydrolases, including glyoxylases	Pgjcvi_01936	PG JCVI SC001	metallo-beta-lactamase family protein	PG W83	PG1306	1, 214	99.1	439.1	0
glycine dehydrogenase (decarboxylating)	Pgjcvi_01937	PG JCVI SC001	glycine dehydrogenase	PG ATCC 33277	PGN_1094	1, 955	99.6	1924.1	0
glycine dehydrogenase (decarboxylating)	Pgjcvi_01937	PG JCVI SC001	glycine dehydrogenase	PG TDC60	PGTDC60_2172	1, 955	99.5	1919.4	0
glycine dehydrogenase (decarboxylating)	Pgjcvi_01937	PG JCVI SC001	glycine dehydrogenase	PG W83	PG1305	1, 955	99.4	1920.6	0
Protein of unknown function (DUF3078).	Pgjcvi_01938	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1093	1, 443	99.1	879.8	0
Protein of unknown function (DUF3078).	Pgjcvi_01938	PG JCVI SC001	hypothetical protein	PG W83	PG1304	4, 446	98.4	874	0
Protein of unknown function (DUF3078).	Pgjcvi_01938	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2173	1, 388	97.7	759.6	0
PIF1 helicase.	Pgjcvi_01939	PG JCVI SC001	ATP-dependent exoDNAse alpha subunit	PG ATCC 33277	PGN_1092	1, 471	98.9	912.1	0
PIF1 helicase.	Pgjcvi_01939	PG JCVI SC001	helicase, putative	PG W83	PG1303	1, 471	98.9	914.1	0
PIF1 helicase.	Pgjcvi_01939	PG JCVI SC001	helicase	PG TDC60	PGTDC60_2174	1, 471	98.9	912.5	0
hypothetical protein	Pgjcvi_01940	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1091	1, 210	100	408.3	0
hypothetical protein	Pgjcvi_01940	PG JCVI SC001	hypothetical protein	PG W83	PG1302	23, 232	100	408.3	0
hypothetical protein	Pgjcvi_01940	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2175	1, 210	100	408.3	0
hypothetical protein	Pgjcvi_01941	PG JCVI SC001	hypothetical protein	PG W83	PG1301	22, 271	98.4	508.4	0
hypothetical protein	Pgjcvi_01941	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1090	22, 271	98	508.8	0
hypothetical protein	Pgjcvi_01941	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2176	22, 271	98	506.1	0
N6-adenine-specific methylase	Pgjcvi_01942	PG JCVI SC001	hypothetical protein	PG W83	PG1300	1, 179	99.4	365.2	0
N6-adenine-specific methylase	Pgjcvi_01942	PG JCVI SC001	probable methyltransferase	PG ATCC 33277	PGN_1089	1, 179	98.9	363.6	0
N6-adenine-specific methylase	Pgjcvi_01942	PG JCVI SC001	putative methyltransferase	PG TDC60	PGTDC60_2177	1, 179	98.3	359.4	0
hypothetical protein	Pgjcvi_01944	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0820	1, 27	96.3	53.9	1.70E-06
hypothetical protein	Pgjcvi_01944	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1810	56, 82	81.5	48.9	5.30E-05
Ribosomal protein S1	Pgjcvi_01945	PG JCVI SC001	30S ribosomal protein S1	PG ATCC 33277	PGN_1088	1, 599	100	1180.6	0
Ribosomal protein S1	Pgjcvi_01945	PG JCVI SC001	ribosomal protein S1	PG W83	PG1297	1, 599	100	1180.6	0
Ribosomal protein S1	Pgjcvi_01945	PG JCVI SC001	30S ribosomal protein S1	PG TDC60	PGTDC60_2180	1, 599	100	1180.6	0
hypothetical protein	Pgjcvi_01946	PG JCVI SC001	hypothetical protein	PG W83	PG1296	1, 151	100	304.3	0
hypothetical protein	Pgjcvi_01946	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1087	1, 151	99.3	301.6	0
hypothetical protein	Pgjcvi_01946	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2182	1, 151	98.7	298.9	0
hypothetical protein	Pgjcvi_01947	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1086	1, 61	100	123.2	3.40E-27
hypothetical protein	Pgjcvi_01947	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2183	1, 61	100	123.2	3.40E-27
ferrous iron transporter FeoB	Pgjcvi_01948	PG JCVI SC001	ferrous iron transport protein B	PG TDC60	PGTDC60_2184	30, 844	99.6	1607.8	0
ferrous iron transporter FeoB	Pgjcvi_01948	PG JCVI SC001	ferrous iron transport protein B	PG ATCC 33277	PGN_1085	30, 844	99.4	1604.3	0
ferrous iron transporter FeoB	Pgjcvi_01948	PG JCVI SC001	ferrous iron transport protein B	PG W83	PG1294	30, 844	99.4	1607	0
hypothetical protein	Pgjcvi_01949	PG JCVI SC001	hypothetical protein	PG W83	PG1291	3, 575	99.8	1162.5	0
hypothetical protein	Pgjcvi_01949	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2189	3, 575	99.7	1160.6	0
hypothetical protein	Pgjcvi_01949	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1081	1, 573	99.5	1159.1	0
branched-chain amino acid aminotransferase, group II	Pgjcvi_01950	PG JCVI SC001	branched-chain amino acid aminotransferase	PG TDC60	PGTDC60_2190	1, 339	100	691.8	0
branched-chain amino acid aminotransferase, group II	Pgjcvi_01950	PG JCVI SC001	branched-chain amino acid aminotransferase	PG ATCC 33277	PGN_1080	1, 339	99.7	690.6	0
branched-chain amino acid aminotransferase, group II	Pgjcvi_01950	PG JCVI SC001	branched-chain amino acid aminotransferase	PG W83	PG1290	1, 339	99.7	689.5	0
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_01951	PG JCVI SC001	GDP-fucose synthetase	PG W83	PG1289	1, 357	99.2	723.4	0
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_01951	PG JCVI SC001	GDP-fucose synthetase	PG ATCC 33277	PGN_1079	1, 357	98.9	722.6	0
Nucleoside-diphosphate-sugar epimerases	Pgjcvi_01951	PG JCVI SC001	GDP-fucose synthetase	PG TDC60	PGTDC60_2191	1, 357	98.9	718.8	0
GDP-mannose 4,6-dehydratase	Pgjcvi_01952	PG JCVI SC001	GDP-mannose 4,6-dehydratase	PG TDC60	PGTDC60_2192	1, 365	99.7	735.3	0
GDP-mannose 4,6-dehydratase	Pgjcvi_01952	PG JCVI SC001	GDP-mannose 4,6-dehydratase	PG ATCC 33277	PGN_1078	1, 365	99.5	733.4	0
GDP-mannose 4,6-dehydratase	Pgjcvi_01952	PG JCVI SC001	GDP-mannose 4,6-dehydratase	PG W83	PG1288	1, 361	99.2	724.5	0
Ferritin-like protein	Pgjcvi_01953	PG JCVI SC001	ferritin	PG ATCC 33277	PGN_0604	1, 160	100	318.9	0
Ferritin-like protein	Pgjcvi_01953	PG JCVI SC001	ferritin	PG W83	PG1286	1, 160	100	318.9	0
Ferritin-like protein	Pgjcvi_01953	PG JCVI SC001	ferritin	PG TDC60	PGTDC60_2193	1, 160	100	318.9	0
6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase	Pgjcvi_01954	PG JCVI SC001	glucosamine-6-phosphate deaminase	PG W83	PG1285	1, 655	100	1332	0
6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase	Pgjcvi_01954	PG JCVI SC001	glucosamine-6-phosphate isomerase	PG ATCC 33277	PGN_0606	1, 662	99.8	1342	0
6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase	Pgjcvi_01954	PG JCVI SC001	glucosamine-6-phosphate deaminase-like protein	PG TDC60	PGTDC60_2194	1, 655	99.8	1330.9	0
Peptidase S46.	Pgjcvi_01955	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2195	1, 720	99.3	1454.1	0
Peptidase S46.	Pgjcvi_01955	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0607	1, 720	99	1450.3	0
Peptidase S46.	Pgjcvi_01955	PG JCVI SC001	hypothetical protein	PG W83	PG1283	1, 720	98.6	1446	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01956	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0608	1, 151	98.7	308.1	0
Uncharacterized protein conserved in bacteria	Pgjcvi_01956	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2196	1, 151	98.7	308.5	0

Uncharacterized protein conserved in bacteria	Pgjcvi_01956	PG JCVI SC001	hypothetical protein	PG W83	PG1282	1, 151	98	307	0
Domain of unknown function (DUF2027)./Smr domain.	Pgjcvi_01957	PG JCVI SC001	putative DNA mismatch repair protein	PG TDC60	PGTDC60_2197	1, 374	100	756.5	0
Domain of unknown function (DUF2027)./Smr domain.	Pgjcvi_01957	PG JCVI SC001	probable DNA mismatch repair protein	PG ATCC 33277	PGN_0609	1, 374	99.7	754.6	0
Domain of unknown function (DUF2027)./Smr domain.	Pgjcvi_01957	PG JCVI SC001	hypothetical protein	PG W83	PG1281	14, 387	97.9	742.3	0
Uncharacterized conserved protein	Pgjcvi_01958	PG JCVI SC001	hypothetical protein	PG W83	PG1280	1, 415	100	844.3	0
Uncharacterized conserved protein	Pgjcvi_01958	PG JCVI SC001	conserved hypothetical protein with DUF1015 domain	PG ATCC 33277	PGN_0610	1, 415	99.8	842.8	0
Uncharacterized conserved protein	Pgjcvi_01958	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2198	1, 415	99.8	842.8	0
Phosphoglycerate dehydrogenase and related dehydrogenases	Pgjcvi_01959	PG JCVI SC001	D-isomer specific 2-hydroxyacid dehydrogenase family protein	PG W83	PG1279	1, 306	99.7	593.2	0
Phosphoglycerate dehydrogenase and related dehydrogenases	Pgjcvi_01959	PG JCVI SC001	D-isomer specific 2-hydroxyacid dehydrogenase family protein	PG TDC60	PGTDC60_2199	1, 306	99.7	593.2	0
Phosphoglycerate dehydrogenase and related dehydrogenases	Pgjcvi_01959	PG JCVI SC001	D-3-phosphoglycerate dehydrogenase	PG ATCC 33277	PGN_0611	1, 306	99.3	591.3	0
phosphoserine aminotransferase	Pgjcvi_01960	PG JCVI SC001	phosphoserine aminotransferase	PG TDC60	PGTDC60_2200	1, 360	100	718.4	0
phosphoserine aminotransferase	Pgjcvi_01960	PG JCVI SC001	phosphoserine aminotransferase	PG ATCC 33277	PGN_0612	1, 360	99.7	715.7	0
phosphoserine aminotransferase	Pgjcvi_01960	PG JCVI SC001	phosphoserine aminotransferase	PG W83	PG1278	1, 360	99.7	715.7	0
nucleotide sugar dehydrogenase	Pgjcvi_01961	PG JCVI SC001	UDP-glucose-6 dehydrogenase	PG TDC60	PGTDC60_2201	1, 421	99	835.1	0
nucleotide sugar dehydrogenase	Pgjcvi_01961	PG JCVI SC001	UDP-glucose-6 dehydrogenase, putative	PG W83	PG1277	1, 421	98.8	833.2	0
nucleotide sugar dehydrogenase	Pgjcvi_01961	PG JCVI SC001	UDP-glucose 6-dehydrogenase	PG ATCC 33277	PGN_0613	15, 435	98.6	827.4	0
ornithine aminotransferase	Pgjcvi_01962	PG JCVI SC001	ornithine aminotransferase	PG TDC60	PGTDC60_2206	1, 409	99.5	833.2	0
ornithine aminotransferase	Pgjcvi_01962	PG JCVI SC001	ornithine aminotransferase	PG ATCC 33277	PGN_1403	1, 409	99.3	831.2	0
ornithine aminotransferase	Pgjcvi_01962	PG JCVI SC001	acetylornithine aminotransferase, putative	PG W83	PG1271	1, 409	99.3	830.1	0
Uncharacterized protein conserved in bacteria containing a pentein-type domain	Pgjcvi_01963	PG JCVI SC001	hypothetical protein	PG W83	PG1270	1, 309	100	619	0
Uncharacterized protein conserved in bacteria containing a pentein-type domain	Pgjcvi_01963	PG JCVI SC001	putative amidinotransferase	PG ATCC 33277	PGN_1402	1, 309	99.7	616.7	0
Uncharacterized protein conserved in bacteria containing a pentein-type domain	Pgjcvi_01963	PG JCVI SC001	putative amidinotransferase	PG TDC60	PGTDC60_2207	1, 309	99.7	617.5	0
delta-1-pyrroline-5-carboxylate dehydrogenase, group 1	Pgjcvi_01964	PG JCVI SC001	delta-1-pyrroline-5-carboxylate dehydrogenase	PG W83	PG1269	1, 543	99.8	1098.6	0
delta-1-pyrroline-5-carboxylate dehydrogenase, group 1	Pgjcvi_01964	PG JCVI SC001	delta-1-pyrroline-5-carboxylate dehydrogenase	PG ATCC 33277	PGN_1401	1, 543	99.4	1092.4	0
delta-1-pyrroline-5-carboxylate dehydrogenase, group 1	Pgjcvi_01964	PG JCVI SC001	delta-1-pyrroline-5-carboxylate dehydrogenase	PG TDC60	PGTDC60_2208	1, 543	99.1	1090.5	0
hypothetical protein	Pgjcvi_01965	PG JCVI SC001	hypothetical protein	PG W83	PG1268	1, 32	100	69.7	4.40E-11
ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)	Pgjcvi_01966	PG JCVI SC001	UvrD/REP helicase domain protein	PG W83	PG2072	1, 1074	99.1	2109.7	0
ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)	Pgjcvi_01966	PG JCVI SC001	ATP-dependent helicase	PG ATCC 33277	PGN_2050	1, 1074	98.9	2103.2	0
ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)	Pgjcvi_01966	PG JCVI SC001	UvrD/REP helicase domain-containing protein	PG TDC60	PGTDC60_2212	1, 1074	98.9	2100.5	0
hypothetical protein	Pgjcvi_01967	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2051	26, 311	100	584.3	0
hypothetical protein	Pgjcvi_01967	PG JCVI SC001	hypothetical protein	PG W83	PG2071	26, 311	99.3	580.5	0
hypothetical protein	Pgjcvi_01967	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2213	1, 286	99.3	580.5	0
Phosphatidylglycerophosphate synthase	Pgjcvi_01968	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2052	1, 308	99.7	617.8	0
Phosphatidylglycerophosphate synthase	Pgjcvi_01968	PG JCVI SC001	hypothetical protein	PG W83	PG2070	1, 308	99.7	617.8	0
Phosphatidylglycerophosphate synthase	Pgjcvi_01968	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2214	1, 308	99.7	617.1	0
Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Pgjcvi_01969	PG JCVI SC001	oxidoreductase, short chain dehydrogenase/reductase family	PG W83	PG2069	1, 243	100	483.4	0
Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Pgjcvi_01969	PG JCVI SC001	short chain dehydrogenase/reductase family oxidoreductase	PG TDC60	PGTDC60_2215	1, 243	100	483.4	0
Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Pgjcvi_01969	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2053	1, 243	99.6	481.9	0
cytidyltransferase-related domain	Pgjcvi_01970	PG JCVI SC001	putative glycerol-3-phosphate cytidylyltransferase	PG ATCC 33277	PGN_2054	1, 152	100	310.8	0
cytidyltransferase-related domain	Pgjcvi_01970	PG JCVI SC001	glycerol-3-phosphate cytidylyltransferase	PG W83	PG2068	1, 152	100	310.8	0
cytidyltransferase-related domain	Pgjcvi_01970	PG JCVI SC001	glycerol-3-phosphate cytidylyltransferase	PG TDC60	PGTDC60_2216	1, 152	100	310.8	0
4-hydroxythreonine-4-phosphate dehydrogenase	Pgjcvi_01971	PG JCVI SC001	putative 4-hydroxythreonine-4-phosphate dehydrogenase	PG ATCC 33277	PGN_2055	1, 365	99.7	723	0
4-hydroxythreonine-4-phosphate dehydrogenase	Pgjcvi_01971	PG JCVI SC001	pyridoxal phosphate biosynthetic protein PdxA	PG W83	PG2067	1, 365	99.5	721.5	0
4-hydroxythreonine-4-phosphate dehydrogenase	Pgjcvi_01971	PG JCVI SC001	pyridoxal phosphate biosynthetic protein PdxA	PG TDC60	PGTDC60_2217	1, 365	99.5	722.6	0
hypothetical protein	Pgjcvi_01972	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_2218	1, 332	100	676	0
hypothetical protein	Pgjcvi_01972	PG JCVI SC001	lipoprotein, putative	PG W83	PG2066	1, 351	99.7	711.8	0
hypothetical protein	Pgjcvi_01972	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2056	1, 351	99.4	706.4	0
23S rRNA m2A2503 methyltransferase	Pgjcvi_01973	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2057	16, 352	99.4	674.1	0
23S rRNA m2A2503 methyltransferase	Pgjcvi_01973	PG JCVI SC001	conserved hypothetical protein TIGR00048	PG W83	PG2065	5, 341	99.1	672.5	0
23S rRNA m2A2503 methyltransferase	Pgjcvi_01973	PG JCVI SC001	ribosomal RNA large subunit methyltransferase N	PG TDC60	PGTDC60_2219	16, 352	99.1	672.5	0
histidyl-tRNA synthetase	Pgjcvi_01974	PG JCVI SC001	histidyl-tRNA synthetase	PG TDC60	PGTDC60_2221	10, 454	99.6	864.8	0
histidyl-tRNA synthetase	Pgjcvi_01974	PG JCVI SC001	histidyl-tRNA synthetase	PG W83	PG2062	10, 454	99.3	863.6	0
histidyl-tRNA synthetase	Pgjcvi_01974	PG JCVI SC001	histidyl-tRNA synthetase	PG ATCC 33277	PGN_2060	10, 454	99.1	862.1	0
Dihydrofolate reductase	Pgjcvi_01975	PG JCVI SC001	dihydrofolate reductase	PG TDC60	PGTDC60_2222	1, 162	100	328.2	0
Dihydrofolate reductase	Pgjcvi_01975	PG JCVI SC001	dihydrofolate reductase	PG W83	PG2061	1, 162	99.4	325.9	0
Dihydrofolate reductase	Pgjcvi_01975	PG JCVI SC001	probable dihydrofolate reductase	PG ATCC 33277	PGN_2061	1, 162	98.8	321.2	0
thymidylate synthase	Pgjcvi_01976	PG JCVI SC001	thymidylate synthase	PG ATCC 33277	PGN_2062	4, 267	100	555.8	0
thymidylate synthase	Pgjcvi_01976	PG JCVI SC001	thymidylate synthase	PG W83	PG2060	4, 267	100	555.8	0
thymidylate synthase	Pgjcvi_01976	PG JCVI SC001	thymidylate synthase	PG TDC60	PGTDC60_2223	4, 267	100	555.8	0
hypothetical protein	Pgjcvi_01977	PG JCVI SC001	transposase in ISPg1	PG ATCC 33277	PGN_0749	1, 37	97.3	74.3	2.20E-12
hypothetical protein	Pgjcvi_01977	PG JCVI SC001	ISPg1, transposase	PG W83	PG1906	1, 37	97.3	74.3	2.20E-12
hypothetical protein	Pgjcvi_01977	PG JCVI SC001	transposase in ISPg1	PG TDC60	PGTDC60_0178	1, 37	97.3	74.3	2.20E-12
Peptidase family M48.	Pgjcvi_01978	PG JCVI SC001	hypothetical protein	PG W83	PG2197	1, 265	99.6	511.5	0
Peptidase family M48.	Pgjcvi_01978	PG JCVI SC001	putative peptidase M48 family	PG TDC60	PGTDC60_2225	1, 265	99.6	511.5	0
Peptidase family M48.	Pgjcvi_01978	PG JCVI SC001	putative peptidase M48 family	PG ATCC 33277	PGN_2064	1, 265	98.9	508.8	0
hypothetical protein	Pgjcvi_01979	PG JCVI SC001	putative Lys- and Rgp- gingipain domain protein	PG TDC60	PGTDC60_2226	1, 293	100	582	0

hypothetical protein	Pgjcvi_01979	PG JCVI SC001	putative Lys- and Rgp- gingipain domain protein	PG ATCC 33277	PGN_2065	1, 293	99.3	578.6	0
hypothetical protein	Pgjcvi_01979	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	858, 944	56.3	97.4	9.50E-19
hypothetical protein	Pgjcvi_01979	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1323, 1408	51.2	87	1.30E-15
hypothetical protein	Pgjcvi_01979	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1572, 1669	43.9	78.2	6.00E-13
hypothetical protein	Pgjcvi_01979	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1513, 1706	33	97.1	1.20E-18
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01980	PG JCVI SC001	ABC transporter, ATP-binding protein, putative	PG W83	PG2199	1, 645	100	1269.2	0
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01980	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_2227	1, 645	100	1269.2	0
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01980	PG JCVI SC001	putative ABC transporter ATP-binding protein	PG ATCC 33277	PGN_2066	1, 645	99.7	1266.1	0
Tetratricopeptide repeat.	Pgjcvi_01981	PG JCVI SC001	TPR domain protein	PG W83	PG2200	1, 695	99.9	1349.3	0
Tetratricopeptide repeat.	Pgjcvi_01981	PG JCVI SC001	TPR domain-containing protein	PG TDC60	PGTDC60_2228	1, 695	99.9	1349.3	0
Tetratricopeptide repeat.	Pgjcvi_01981	PG JCVI SC001	TPR domain protein	PG ATCC 33277	PGN_2067	1, 695	99.4	1345.5	0
peptide deformylase	Pgjcvi_01982	PG JCVI SC001	peptide deformylase	PG W83	PG2201	1, 189	100	386	0
peptide deformylase	Pgjcvi_01982	PG JCVI SC001	peptide deformylase	PG TDC60	PGTDC60_2229	1, 225	100	457.2	0
peptide deformylase	Pgjcvi_01982	PG JCVI SC001	putative peptide deformylase	PG ATCC 33277	PGN_2068	1, 189	98.9	382.9	0
Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis)	Pgjcvi_01983	PG JCVI SC001	probable endonuclease	PG ATCC 33277	PGN_2069	1, 150	100	297	0
Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis)	Pgjcvi_01983	PG JCVI SC001	Holliday junction resolvase-like protein	PG W83	PG2202	1, 138	100	272.7	0
Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis)	Pgjcvi_01983	PG JCVI SC001	Holliday junction resolvase-like protein	PG TDC60	PGTDC60_2230	1, 150	100	297	0
Large extracellular alpha-helical protein	Pgjcvi_01984	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2231	2, 1908	97.6	3710.2	0
Large extracellular alpha-helical protein	Pgjcvi_01984	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2070	1, 1888	96.9	3638.6	0
Large extracellular alpha-helical protein	Pgjcvi_01984	PG JCVI SC001	hypothetical protein	PG W83	PG2204	2, 1908	96.9	3679	0
2-dehydropantoate 2-reductase	Pgjcvi_01985	PG JCVI SC001	probable ketopantoate reductase ApbA/PanE	PG ATCC 33277	PGN_2071	1, 314	100	624.4	0
2-dehydropantoate 2-reductase	Pgjcvi_01985	PG JCVI SC001	2-dehydropantoate 2-reductase	PG W83	PG2205	1, 314	99.7	622.9	0
2-dehydropantoate 2-reductase	Pgjcvi_01985	PG JCVI SC001	2-dehydropantoate 2-reductase	PG TDC60	PGTDC60_2232	1, 314	99.7	622.9	0
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01986	PG JCVI SC001	ABC transporter ATP-binding protein	PG ATCC 33277	PGN_2072	1, 538	100	1073.9	0
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01986	PG JCVI SC001	ABC transporter, ATP-binding protein	PG W83	PG2206	1, 538	100	1073.9	0
ATPase components of ABC transporters with duplicated ATPase domains	Pgjcvi_01986	PG JCVI SC001	ABC transporter ATP-binding protein	PG TDC60	PGTDC60_2233	1, 538	99.6	1071.2	0
3-beta hydroxysteroid dehydrogenase/isomerase family.	Pgjcvi_01987	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2073	1, 339	100	682.2	0
3-beta hydroxysteroid dehydrogenase/isomerase family.	Pgjcvi_01987	PG JCVI SC001	hypothetical protein	PG W83	PG2207	1, 339	99.7	681.8	0
3-beta hydroxysteroid dehydrogenase/isomerase family.	Pgjcvi_01987	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2234	1, 339	99.4	679.5	0
Predicted membrane protein	Pgjcvi_01988	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2074	1, 84	100	157.9	1.70E-37
Predicted membrane protein	Pgjcvi_01988	PG JCVI SC001	hypothetical protein	PG W83	PG2209	1, 84	100	157.9	1.70E-37
Predicted membrane protein	Pgjcvi_01988	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2236	1, 84	100	157.9	1.70E-37
excinuclease ABC, A subunit	Pgjcvi_01989	PG JCVI SC001	excinuclease ABC, A subunit	PG W83	PG2210	1, 952	99.4	1891.7	0
excinuclease ABC, A subunit	Pgjcvi_01989	PG JCVI SC001	excinuclease ABC, A subunit	PG TDC60	PGTDC60_2237	1, 952	99.4	1889	0
excinuclease ABC, A subunit	Pgjcvi_01989	PG JCVI SC001	excinuclease ABC A subunit	PG ATCC 33277	PGN_2075	1, 953	99.3	1887.5	0
NAD(P)H-nitrite reductase	Pgjcvi_01993	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2077	1, 60	100	125.2	8.70E-28
NAD(P)H-nitrite reductase	Pgjcvi_01993	PG JCVI SC001	nitrite reductase-related protein	PG W83	PG2213	1, 60	100	125.2	8.70E-28
NAD(P)H-nitrite reductase	Pgjcvi_01993	PG JCVI SC001	nitrite reductase-like protein	PG TDC60	PGTDC60_2239	1, 60	100	125.2	8.70E-28
Protein of unknown function (DUF2851).	Pgjcvi_01994	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2078	1, 424	98.6	856.3	0
Protein of unknown function (DUF2851).	Pgjcvi_01994	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2240	1, 424	98.6	855.9	0
Protein of unknown function (DUF2851).	Pgjcvi_01994	PG JCVI SC001	hypothetical protein	PG W83	PG2214	1, 424	98.3	853.2	0
Mannose-1-phosphate guanylyltransferase	Pgjcvi_01995	PG JCVI SC001	mannose-1-phosphate guanylyltransferase	PG W83	PG2215	1, 361	99.7	732.3	0
Mannose-1-phosphate guanylyltransferase	Pgjcvi_01995	PG JCVI SC001	mannose-1-phosphate guanylyltransferase	PG TDC60	PGTDC60_2241	1, 361	99.7	733.8	0
Mannose-1-phosphate guanylyltransferase	Pgjcvi_01995	PG JCVI SC001	mannose-1-phosphate guanylyltransferase	PG ATCC 33277	PGN_2079	1, 361	99.4	731.1	0
The GLUG motif.	Pgjcvi_01996	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2242	1, 474	100	960.7	0
The GLUG motif.	Pgjcvi_01996	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_2080	73, 576	99.6	1013.1	0
The GLUG motif.	Pgjcvi_01996	PG JCVI SC001	hypothetical protein	PG W83	PG2216	73, 576	99.4	1011.5	0
1-deoxy-D-xylulose-5-phosphate synthase	Pgjcvi_01997	PG JCVI SC001	1-deoxy-D-xylulose-5-phosphate synthase	PG W83	PG2217	2, 634	99.7	1280.4	0
1-deoxy-D-xylulose-5-phosphate synthase	Pgjcvi_01997	PG JCVI SC001	1-deoxy-D-xylulose 5-phosphate synthase	PG ATCC 33277	PGN_2081	2, 634	99.5	1280	0
1-deoxy-D-xylulose-5-phosphate synthase	Pgjcvi_01997	PG JCVI SC001	1-deoxy-D-xylulose-5-phosphate synthase	PG TDC60	PGTDC60_2243	2, 634	99.4	1278.5	0
K+ transport systems, NAD-binding component	Pgjcvi_01998	PG JCVI SC001	potassium uptake protein TrkA	PG W83	PG2218	1, 446	100	875.5	0
K+ transport systems, NAD-binding component	Pgjcvi_01998	PG JCVI SC001	potassium transporter peripheral membrane component	PG TDC60	PGTDC60_2244	1, 446	100	875.5	0
K+ transport systems, NAD-binding component	Pgjcvi_01998	PG JCVI SC001	putative potassium uptake protein TrkA	PG ATCC 33277	PGN_2082	1, 446	99.8	873.6	0
Trk-type K+ transport systems, membrane components	Pgjcvi_01999	PG JCVI SC001	potassium uptake protein TrkH	PG W83	PG2219	1, 487	100	975.7	0
Trk-type K+ transport systems, membrane components	Pgjcvi_01999	PG JCVI SC001	potassium uptake protein TrkH	PG TDC60	PGTDC60_2245	1, 487	99.6	971.5	0
Trk-type K+ transport systems, membrane components	Pgjcvi_01999	PG JCVI SC001	potassium uptake protein TrkH	PG ATCC 33277	PGN_2083	1, 487	99.4	971.1	0
Uncharacterized protein (competence- and mitomycin-induced)	Pgjcvi_02004	PG JCVI SC001	conserved hypothetical protein with competence-damaged protein domain	PG ATCC 33277	PGN_0392	2, 56	49.1	62	2.80E-08
Uncharacterized protein (competence- and mitomycin-induced)	Pgjcvi_02004	PG JCVI SC001	competence/damage-inducible protein CinA domain protein	PG W83	PG1725	2, 56	49.1	62	2.80E-08
Uncharacterized protein (competence- and mitomycin-induced)	Pgjcvi_02004	PG JCVI SC001	competence/damage inducible protein CinA	PG TDC60	PGTDC60_0575	2, 56	49.1	61.2	4.80E-08
16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	Pgjcvi_02005	PG JCVI SC001	S4 domain protein	PG W83	PG1156	1, 150	100	303.1	0
16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	Pgjcvi_02005	PG JCVI SC001	S4 domain-containing protein	PG TDC60	PGTDC60_1066	1, 150	100	303.1	0
16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	Pgjcvi_02005	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1256	1, 150	99.3	300.8	0
ADP-heptose:LPS heptosyltransferase	Pgjcvi_02006	PG JCVI SC001	putative heptosyltransferase	PG ATCC 33277	PGN_1255	1, 351	100	709.5	0
ADP-heptose:LPS heptosyltransferase	Pgjcvi_02006	PG JCVI SC001	ADP-heptose--LPS heptosyltransferase, putative	PG W83	PG1155	1, 296	100	603.2	0
ADP-heptose:LPS heptosyltransferase	Pgjcvi_02006	PG JCVI SC001	ADP-heptose--LPS heptosyltransferase	PG TDC60	PGTDC60_1065	1, 335	99.7	678.3	0
hypothetical protein	Pgjcvi_02007	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1254	1, 201	99.5	409.8	0
hypothetical protein	Pgjcvi_02007	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1064	1, 201	98.5	406.8	0
hypothetical protein	Pgjcvi_02008	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1063	1, 138	99.3	290	0
hypothetical protein	Pgjcvi_02008	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1253	1, 138	98.6	288.9	0

Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family	Pgjcvi_02009	PG JCVI SC001	alcohol dehydrogenase, iron-containing	PG W83	PG1151	1, 382	100	766.9	0
Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family	Pgjcvi_02009	PG JCVI SC001	iron-containing alcohol dehydrogenase	PG ATCC 33277	PGN_1252	1, 382	99.7	763.8	0
Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family	Pgjcvi_02009	PG JCVI SC001	alcohol dehydrogenase, iron-containing	PG TDC60	PGTDC60_1062	1, 382	99.7	766.5	0
Glycosyltransferase	Pgjcvi_02010	PG JCVI SC001	probable glycosyltransferase	PG ATCC 33277	PGN_1251	14, 375	99.2	713	0
Glycosyltransferase	Pgjcvi_02010	PG JCVI SC001	glycosyl transferase, group 1 family protein	PG W83	PG1149	14, 375	99.2	713	0
Glycosyltransferase	Pgjcvi_02010	PG JCVI SC001	putative glycosyltransferase	PG TDC60	PGTDC60_1060	1, 362	99.2	711.4	0
hypothetical protein	Pgjcvi_02011	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1059	1, 72	98.6	156.8	3.30E-37
hypothetical protein	Pgjcvi_02011	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1250	1, 72	94.4	149.1	6.80E-35
Helicase conserved C-terminal domain./SNF2 family N-terminal domain.	Pgjcvi_02013	PG JCVI SC001	putative DNA methylase	PG ATCC 33277	PGN_0086	1094, 1828	95.5	1381.7	0
Helicase conserved C-terminal domain./SNF2 family N-terminal domain.	Pgjcvi_02013	PG JCVI SC001	DNA methylase	PG TDC60	PGTDC60_0992	1096, 1830	92.5	1342.4	0
Helicase conserved C-terminal domain./SNF2 family N-terminal domain.	Pgjcvi_02013	PG JCVI SC001	hypothetical protein	PG W83	PG1500	52, 715	69.5	922.5	0
Type IV secretory pathway, VirD4 components	Pgjcvi_02015	PG JCVI SC001	putative mobilization protein TraG family	PG ATCC 33277	PGN_0076	299, 508	100	431.8	0
Type IV secretory pathway, VirD4 components	Pgjcvi_02015	PG JCVI SC001	TraG family protein	PG TDC60	PGTDC60_1006	300, 509	100	431.8	0
Type IV secretory pathway, VirD4 components	Pgjcvi_02015	PG JCVI SC001	TraG family protein	PG W83	PG1490	299, 507	86.6	376.3	0
methylmalonyl-CoA mutase C-terminal domain/methylmalonyl-CoA mutase N-terminal domain	Pgjcvi_02019	PG JCVI SC001	methylmalonyl-CoA mutase large subunit	PG ATCC 33277	PGN_0456	1, 715	100	1419.8	0
methylmalonyl-CoA mutase C-terminal domain/methylmalonyl-CoA mutase N-terminal domain	Pgjcvi_02019	PG JCVI SC001	methylmalonyl-CoA mutase	PG TDC60	PGTDC60_0641	1, 715	100	1419.8	0
methylmalonyl-CoA mutase C-terminal domain/methylmalonyl-CoA mutase N-terminal domain	Pgjcvi_02019	PG JCVI SC001	methylmalonyl-CoA mutase	PG W83	PG1657	1, 715	99.9	1416.7	0
methylmalonyl-CoA mutase, heterodimeric type, beta chain	Pgjcvi_02020	PG JCVI SC001	methylmalonyl-CoA mutase small subunit	PG ATCC 33277	PGN_0457	1, 618	99.8	1230.7	0
methylmalonyl-CoA mutase, heterodimeric type, beta chain	Pgjcvi_02020	PG JCVI SC001	methylmalonyl-CoA mutase, small subunit	PG W83	PG1656	1, 618	99.8	1230.7	0
methylmalonyl-CoA mutase, heterodimeric type, beta chain	Pgjcvi_02020	PG JCVI SC001	methylmalonyl-CoA mutase, small subunit	PG TDC60	PGTDC60_0642	1, 618	99.8	1230.3	0
Por secretion system C-terminal sorting domain	Pgjcvi_02021	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0458	10, 508	99.4	1030.4	0
Por secretion system C-terminal sorting domain	Pgjcvi_02021	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0643	1, 490	99.4	1014.6	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	797, 1056	100	545.8	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1249, 1508	100	545.8	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	836, 1095	100	545.8	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1288, 1547	100	545.8	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	856, 1119	98.1	539.3	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1312, 1575	98.1	538.5	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1768, 2031	98.1	538.5	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1701, 1957	88.2	477.2	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	348, 604	87.5	468	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2224, 2480	87.4	473.4	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	407, 663	87.2	466.1	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1740, 1996	85.9	465.3	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	391, 643	72.5	369.8	0
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	161, 392	38	136.3	1.90E-30
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	102, 333	37.9	137.5	8.30E-31
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	145, 376	37.9	136.7	1.40E-30
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	668, 823	35.8	95.9	2.80E-18
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	688, 843	35.2	93.6	1.40E-17
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1144, 1299	35.2	93.6	1.40E-17
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1600, 1755	35.2	93.6	1.40E-17
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2056, 2211	35.2	94	1.10E-17
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	629, 784	35.2	94	1.10E-17
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1081, 1236	35.2	94.4	8.10E-18
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1533, 1688	35.2	94	1.10E-17
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1120, 1275	35.2	93.6	1.40E-17
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1572, 1727	35.2	94	1.10E-17
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2493, 2578	34.8	55.8	3.20E-06
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1970, 2055	34.8	55.8	3.20E-06
Cleaved Adhesin Domain.	Pgjcvi_02022	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	2009, 2094	34.8	55.8	3.20E-06
Methylmalonyl-CoA mutase, N-terminal domain/subunit	Pgjcvi_02025	PG JCVI SC001	methylmalonyl-CoA mutase large subunit	PG ATCC 33277	PGN_0456	1, 715	100	1419.8	0
Methylmalonyl-CoA mutase, N-terminal domain/subunit	Pgjcvi_02025	PG JCVI SC001	methylmalonyl-CoA mutase	PG TDC60	PGTDC60_0641	1, 715	100	1419.8	0
Methylmalonyl-CoA mutase, N-terminal domain/subunit	Pgjcvi_02025	PG JCVI SC001	methylmalonyl-CoA mutase	PG W83	PG1657	1, 715	99.9	1416.7	0
methylmalonyl-CoA mutase, heterodimeric type, beta chain	Pgjcvi_02026	PG JCVI SC001	methylmalonyl-CoA mutase small subunit	PG ATCC 33277	PGN_0457	1, 618	99.8	1230.7	0
methylmalonyl-CoA mutase, heterodimeric type, beta chain	Pgjcvi_02026	PG JCVI SC001	methylmalonyl-CoA mutase, small subunit	PG W83	PG1656	1, 618	99.8	1230.7	0
methylmalonyl-CoA mutase, heterodimeric type, beta chain	Pgjcvi_02026	PG JCVI SC001	methylmalonyl-CoA mutase, small subunit	PG TDC60	PGTDC60_0642	1, 618	99.8	1230.3	0
Por secretion system C-terminal sorting domain	Pgjcvi_02027	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0458	10, 508	99.4	1030.4	0
Por secretion system C-terminal sorting domain	Pgjcvi_02027	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0643	1, 490	99.4	1014.6	0
Transposase and inactivated derivatives, IS5 family	Pgjcvi_02028	PG JCVI SC001	transposase in ISPg1	PG ATCC 33277	PGN_0605	231, 329	96	195.7	0
Transposase and inactivated derivatives, IS5 family	Pgjcvi_02028	PG JCVI SC001	transposase in ISPg1	PG TDC60	PGTDC60_1933	231, 329	96	195.7	0
Transposase and inactivated derivatives, IS5 family	Pgjcvi_02028	PG JCVI SC001	ISPg1, transposase	PG W83	PG0549	231, 329	93.9	190.7	0
Homologues of TraJ from Bacteroides conjugative transposon.	Pgjcvi_02029	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0105	1, 77	94.8	149.8	5.90E-35
Homologues of TraJ from Bacteroides conjugative transposon.	Pgjcvi_02029	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1347	1, 74	93.2	142.9	7.20E-33
Homologues of TraJ from Bacteroides conjugative transposon.	Pgjcvi_02029	PG JCVI SC001	hypothetical protein	PG W83	PG1787	1, 105	88.7	192.6	0
Site-specific recombinase XerD	Pgjcvi_02030	PG JCVI SC001	integrase	PG TDC60	PGTDC60_2028	236, 365	71.8	189.1	0
Site-specific recombinase XerD	Pgjcvi_02030	PG JCVI SC001	integrase	PG W83	PG1435	236, 348	68.4	158.3	2.30E-37
Site-specific recombinase XerD	Pgjcvi_02030	PG JCVI SC001	putative bacteriophage integrase	PG ATCC 33277	PGN_0094	243, 367	48.4	123.6	6.30E-27
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	743, 877	97.8	276.2	0

Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1199, 1333	97.8	276.2	0
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1655, 1789	97.8	276.2	0
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2111, 2245	97.8	276.2	0
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1197, 1331	97.8	276.2	0
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1175, 1309	97.8	276.2	0
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	723, 857	96.3	272.7	0
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1627, 1761	95.6	269.6	0
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1021, 1148	41.9	96.7	7.90E-19
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	547, 674	41.9	96.7	7.90E-19
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2383, 2507	38.6	94.4	3.90E-18
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1899, 2023	38.6	94.7	3.00E-18
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	566, 694	37	89.4	1.30E-16
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1022, 1150	37	89.4	1.30E-16
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1478, 1606	37	89.4	1.30E-16
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1934, 2062	36.3	87.8	3.70E-16
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	998, 1126	36.3	87.8	3.70E-16
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	1450, 1578	36.3	87.8	3.70E-16
Cleaved Adhesin Domain.	Pgjcvi_02032	PG JCVI SC001	hemagglutinin protein HagA	PG TDC60	PGTDC60_0058	275, 404	35.8	80.5	5.90E-14
hypothetical protein	Pgjcvi_02033	PG JCVI SC001	putative mobilization protein TraG family	PG ATCC 33277	PGN_0076	153, 297	99.3	310.1	0
hypothetical protein	Pgjcvi_02033	PG JCVI SC001	TraG family protein	PG TDC60	PGTDC60_1006	154, 298	98.6	308.1	0
hypothetical protein	Pgjcvi_02033	PG JCVI SC001	TraG family protein	PG W83	PG1490	153, 308	79.5	266.9	0
DNA adenine methylase (dam)	Pgjcvi_02035	PG JCVI SC001	putative adenine-specific DNA methyltransferase	PG ATCC 33277	PGN_1903	1, 279	100	570.5	0
hypothetical protein	Pgjcvi_02036	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1902	1, 246	99.6	493	0
hypothetical protein	Pgjcvi_02037	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1900	1, 41	97.6	87	2.10E-16
hypothetical protein	Pgjcvi_02039	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1821	1, 45	97.8	96.7	7.20E-19
hypothetical protein	Pgjcvi_02039	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0161	1, 45	95.6	95.5	1.60E-18
hypothetical protein	Pgjcvi_02040	PG JCVI SC001	hypothetical protein	PG W83	PG1893	36, 257	95.5	420.6	0
hypothetical protein	Pgjcvi_02040	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1823	36, 257	94.6	416.4	0
hypothetical protein	Pgjcvi_02041	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0152	1739, 1934	45.7	173.3	1.80E-41
hypothetical protein	Pgjcvi_02041	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1818	1725, 1969	43.3	176	2.80E-42
hypothetical protein	Pgjcvi_02043	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0050	261, 424	90.9	303.1	0
hypothetical protein	Pgjcvi_02043	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1032	261, 424	90.9	305.8	0
hypothetical protein	Pgjcvi_02044	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0051	1, 84	91.7	163.7	3.10E-39
hypothetical protein	Pgjcvi_02045	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0052	1, 76	89.5	142.1	8.80E-33
hypothetical protein	Pgjcvi_02045	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1031	3, 78	86.8	139	7.40E-32
hypothetical protein	Pgjcvi_02045	PG JCVI SC001	hypothetical protein	PG W83	PG1470	11, 62	50	55.1	1.40E-06
hypothetical protein	Pgjcvi_02046	PG JCVI SC001	hemagglutinin protein HagC	PG ATCC 33277	PGN_1906	80, 350	98.2	520.4	0
hypothetical protein	Pgjcvi_02046	PG JCVI SC001	hemagglutinin protein HagB	PG W83	PG1972	103, 373	98.2	520.4	0
hypothetical protein	Pgjcvi_02046	PG JCVI SC001	hemagglutinin protein HagB	PG TDC60	PGTDC60_0245	80, 350	98.2	520.4	0
Prolyl oligopeptidase family.	Pgjcvi_02047	PG JCVI SC001	prolyl tripeptidase A	PG ATCC 33277	PGN_1149	608, 732	100	269.2	0
Prolyl oligopeptidase family.	Pgjcvi_02047	PG JCVI SC001	dipeptidyl aminopeptidase IV, putative	PG W83	PG1361	608, 732	100	269.2	0
Prolyl oligopeptidase family.	Pgjcvi_02047	PG JCVI SC001	dipeptidyl aminopeptidase IV	PG TDC60	PGTDC60_2108	608, 732	99.2	266.9	0
phosphoribosylamine--glycine ligase	Pgjcvi_02048	PG JCVI SC001	phosphoribosylamine-glycine ligase	PG ATCC 33277	PGN_1148	1, 431	99.8	864	0
phosphoribosylamine--glycine ligase	Pgjcvi_02048	PG JCVI SC001	phosphoribosylamine--glycine ligase	PG W83	PG1360	1, 431	99.8	864	0
phosphoribosylamine--glycine ligase	Pgjcvi_02048	PG JCVI SC001	phosphoribosylamine--glycine ligase	PG TDC60	PGTDC60_2109	1, 431	99.8	864	0
hypothetical protein	Pgjcvi_02049	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_2110	1, 191	99.5	387.1	0
hypothetical protein	Pgjcvi_02049	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1147	1, 212	99.1	422.5	0
hypothetical protein	Pgjcvi_02049	PG JCVI SC001	hypothetical protein	PG W83	PG1359	1, 212	99.1	422.5	0
Transposase DDE domain.	Pgjcvi_02050	PG JCVI SC001	ISPg4, transposase	PG W83	PG1658	1, 210	99.5	428.3	0
Phage-related lysozyme (muraminidase)	Pgjcvi_02053	PG JCVI SC001	probable lysozyme	PG ATCC 33277	PGN_1286	5, 171	78.4	270	0
Phage-related lysozyme (muraminidase)	Pgjcvi_02053	PG JCVI SC001	lysozyme-related protein	PG W83	PG1441	1, 55	78.2	94	6.20E-18
Phage-related lysozyme (muraminidase)	Pgjcvi_02053	PG JCVI SC001	putative lysozyme	PG TDC60	PGTDC60_1028	1, 97	76.3	151.8	2.50E-35
hypothetical protein	Pgjcvi_02054	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1032	1, 239	91.6	468	0
hypothetical protein	Pgjcvi_02054	PG JCVI SC001	conserved hypothetical protein related to phage	PG ATCC 33277	PGN_1291	1, 239	91.2	467.6	0
Predicted spermidine synthase with an N-terminal membrane domain	Pgjcvi_02056	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0075	18, 370	89.2	642.1	0
Predicted spermidine synthase with an N-terminal membrane domain	Pgjcvi_02056	PG JCVI SC001	mobilization protein	PG TDC60	PGTDC60_1007	6, 372	83.2	628.6	0
Predicted spermidine synthase with an N-terminal membrane domain	Pgjcvi_02056	PG JCVI SC001	hypothetical protein	PG W83	PG1489	11, 346	43.3	261.5	0
Transposase DDE domain.	Pgjcvi_02059	PG JCVI SC001	transposase in ISPg3	PG TDC60	PGTDC60_1233	1, 155	100	319.3	0
Transposase DDE domain.	Pgjcvi_02059	PG JCVI SC001	transposase in ISPg3	PG ATCC 33277	PGN_1006	1, 300	99.7	613.2	0
Transposase DDE domain.	Pgjcvi_02059	PG JCVI SC001	ISPg3, transposase	PG W83	PG0798	1, 300	99.3	611.7	0
Phage integrase family.	Pgjcvi_02064	PG JCVI SC001	integrase	PG TDC60	PGTDC60_2028	249, 365	71.2	171.4	6.10E-41
Phage integrase family.	Pgjcvi_02064	PG JCVI SC001	integrase	PG W83	PG1435	249, 348	67.3	141	8.80E-32
Phage integrase family.	Pgjcvi_02064	PG JCVI SC001	putative bacteriophage integrase	PG ATCC 33277	PGN_0094	249, 367	46.7	112.1	4.40E-23
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG ATCC 33277	PGN_1728	1331, 1671	98.8	699.5	0
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	1291, 1631	55.9	331.6	0
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1314, 1654	55.6	329.7	0
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG ATCC 33277	PGN_1728	1152, 1389	47.2	200.7	0
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1135, 1372	46.8	197.6	0
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	1112, 1349	46.8	198	0
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	843, 1144	42.9	211.1	0
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	862, 1167	42.4	209.5	0
Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG ATCC 33277	PGN_1728	883, 1184	42.2	209.1	0

Cleaved Adhesin Domain.	Pgjcvi_02066	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG ATCC 33277	PGN_1728	683, 962	33.3	119.8	2.40E-25
translation elongation factor P	Pgjcvi_02067	PG JCVI SC001	probable elongation factor P	PG ATCC 33277	PGN_0616	1, 188	100	384	0
translation elongation factor P	Pgjcvi_02067	PG JCVI SC001	elongation factor P	PG W83	PG0568	1, 188	100	384	0
translation elongation factor P	Pgjcvi_02067	PG JCVI SC001	elongation factor P	PG TDC60	PGTDC60_1693	1, 188	100	384	0
L-lactate transport	Pgjcvi_02076	PG JCVI SC001	L-lactate permease	PG W83	PG1340	1, 516	100	971.5	0
L-lactate transport	Pgjcvi_02076	PG JCVI SC001	L-lactate permease	PG TDC60	PGTDC60_2132	1, 516	99.6	966.8	0
L-lactate transport	Pgjcvi_02076	PG JCVI SC001	L-lactate permease	PG ATCC 33277	PGN_1128	1, 516	99.2	964.1	0
hypothetical protein	Pgjcvi_02077	PG JCVI SC001	lipoprotein, putative	PG W83	PG0183	1, 1746	98.6	3491	0
hypothetical protein	Pgjcvi_02077	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0291	662, 770	60.7	143.7	7.20E-32
hypothetical protein	Pgjcvi_02077	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0454	775, 881	57.4	132.9	1.30E-28
hypothetical protein	Pgjcvi_02078	PG JCVI SC001	von Willebrand factor type A domain protein	PG W83	PG0182	1079, 1226	99.3	297	0
hypothetical protein	Pgjcvi_02078	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0291	1079, 1227	56.4	153.3	7.40E-36
hypothetical protein	Pgjcvi_02078	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0454	1190, 1338	56.4	152.9	9.70E-36
Predicted exporters of the RND superfamily	Pgjcvi_02079	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1920	1, 801	99.9	1575.5	0
Predicted exporters of the RND superfamily	Pgjcvi_02079	PG JCVI SC001	hypothetical protein	PG W83	PG1180	1, 801	99.6	1572.8	0
Predicted exporters of the RND superfamily	Pgjcvi_02079	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1155	1, 801	99.6	1573.9	0
Transcriptional regulator	Pgjcvi_02080	PG JCVI SC001	putative TetR family transcriptional regulator	PG ATCC 33277	PGN_0945	17, 215	100	399.1	0
Transcriptional regulator	Pgjcvi_02080	PG JCVI SC001	transcriptional regulator, tetR family	PG W83	PG1181	1, 199	100	399.1	0
Transcriptional regulator	Pgjcvi_02080	PG JCVI SC001	TetR family transcriptional regulator	PG TDC60	PGTDC60_1156	1, 199	99	396	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_02081	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	330, 445	100	238.4	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_02081	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	513, 628	100	238.4	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_02081	PG JCVI SC001	NADPH-NAD transhydrogenase beta subunit	PG ATCC 33277	PGN_1122	696, 811	100	238.4	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_02081	PG JCVI SC001	NAD(P) transhydrogenase, beta subunit	PG W83	PG1332	330, 445	100	238.4	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_02081	PG JCVI SC001	NAD(P) transhydrogenase, beta subunit	PG W83	PG1332	513, 628	100	238.4	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_02081	PG JCVI SC001	NAD(P) transhydrogenase subunit beta	PG TDC60	PGTDC60_2140	330, 445	99.1	236.5	0
NAD/NADP transhydrogenase beta subunit	Pgjcvi_02081	PG JCVI SC001	NAD(P) transhydrogenase subunit beta	PG TDC60	PGTDC60_2140	513, 628	99.1	236.5	0
hypothetical protein	Pgjcvi_02093	PG JCVI SC001	integrase	PG TDC60	PGTDC60_2028	1, 253	45.5	238	0
hypothetical protein	Pgjcvi_02093	PG JCVI SC001	integrase	PG W83	PG1435	1, 253	45.1	235.7	0
hypothetical protein	Pgjcvi_02093	PG JCVI SC001	putative bacteriophage integrase	PG ATCC 33277	PGN_0094	1, 252	32.8	154.1	9.20E-36
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	898, 1150	99.2	521.2	0
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	901, 1153	99.2	521.2	0
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	882, 1130	98.8	514.2	0
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	648, 692	48.9	45.8	0.0043
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	651, 695	48.9	45.8	0.0043
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	1139, 1323	39.6	123.2	2.10E-26
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1142, 1326	39.6	123.6	1.60E-26
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	1119, 1303	39.6	123.2	2.10E-26
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG TDC60	PGTDC60_0300	1335, 1564	27.8	60.8	1.30E-07
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	arginine-specific cysteine proteinase RgpA	PG ATCC 33277	PGN_1970	1355, 1584	27	58.5	6.40E-07
Zn-dependent protease with chaperone function	Pgjcvi_02094	PG JCVI SC001	hemagglutinin protein HagE	PG W83	PG2024	1358, 1620	26	61.2	9.90E-08
DNA-binding protein, histone-like, putative	Pgjcvi_02095	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG0853	1, 139	100	271.2	0
DNA-binding protein, histone-like, putative	Pgjcvi_02095	PG JCVI SC001	histone-like family DNA-binding protein	PG TDC60	PGTDC60_1254	1, 63	92.1	111.3	3.80E-23
Bacterial DNA-binding protein.	Pgjcvi_02098	PG JCVI SC001	DNA-binding protein, histone-like family	PG W83	PG0853	1, 129	100	252.3	0
Bacterial DNA-binding protein.	Pgjcvi_02098	PG JCVI SC001	histone-like family DNA-binding protein	PG TDC60	PGTDC60_1254	1, 53	90.6	92.4	1.70E-17
L-lactate permease	Pgjcvi_02099	PG JCVI SC001	L-lactate permease	PG W83	PG1340	1, 516	100	971.5	0
L-lactate permease	Pgjcvi_02099	PG JCVI SC001	L-lactate permease	PG TDC60	PGTDC60_2132	1, 516	99.6	966.8	0
L-lactate permease	Pgjcvi_02099	PG JCVI SC001	L-lactate permease	PG ATCC 33277	PGN_1128	1, 516	99.2	964.1	0
hypothetical protein	Pgjcvi_02101	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0090	1, 117	92.3	221.9	0
hypothetical protein	Pgjcvi_02101	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0990	1, 117	83.8	208.4	0
hypothetical protein	Pgjcvi_02102	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0091	1, 92	100	189.9	0
hypothetical protein	Pgjcvi_02102	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_0989	1, 92	95.7	180.6	2.70E-44
Predicted site-specific integrase-resolvase	Pgjcvi_02103	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0092	4, 103	99	203.4	0
Predicted site-specific integrase-resolvase	Pgjcvi_02103	PG JCVI SC001	DNA binding domain, excisionase family	PG TDC60	PGTDC60_0988	1, 100	92	191.8	0
Predicted site-specific integrase-resolvase	Pgjcvi_02103	PG JCVI SC001	hypothetical protein	PG W83	PG0546	15, 64	52	60.1	5.80E-08
hypothetical protein	Pgjcvi_02104	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_0093	1, 121	93.4	230.7	0
hypothetical protein	Pgjcvi_02104	PG JCVI SC001	putative lipoprotein	PG TDC60	PGTDC60_0987	1, 120	88.3	224.2	0
hypothetical protein	Pgjcvi_02104	PG JCVI SC001	lipoprotein, putative	PG W83	PG0821	1, 120	63.3	153.7	4.60E-36
Site-specific recombinase XerD	Pgjcvi_02105	PG JCVI SC001	putative bacteriophage integrase	PG ATCC 33277	PGN_0094	104, 411	99	627.1	0
Site-specific recombinase XerD	Pgjcvi_02105	PG JCVI SC001	putative bacteriophage integrase	PG TDC60	PGTDC60_0986	104, 411	92.9	585.9	0
Site-specific recombinase XerD	Pgjcvi_02105	PG JCVI SC001	integrase	PG W83	PG1113	106, 398	40.9	228.8	0
hypothetical protein	Pgjcvi_02107	PG JCVI SC001	alginate O-acetyltransferase	PG TDC60	PGTDC60_1161	425, 505	98.8	160.6	3.60E-38
hypothetical protein	Pgjcvi_02107	PG JCVI SC001	alginate O-acetyltransferase	PG ATCC 33277	PGN_0943	431, 511	97.5	159.5	7.90E-38
hypothetical protein	Pgjcvi_02107	PG JCVI SC001	alginate O-acetyltransferase, putative	PG W83	PG1184	431, 511	97.5	158.3	1.80E-37
hypothetical protein	Pgjcvi_02109	PG JCVI SC001	excinuclease ABC B subunit	PG ATCC 33277	PGN_1585	331, 433	71.8	159.8	1.60E-37
hypothetical protein	Pgjcvi_02109	PG JCVI SC001	excinuclease ABC subunit B	PG W83	PG0380	331, 433	71.8	159.8	1.60E-37
hypothetical protein	Pgjcvi_02109	PG JCVI SC001	excinuclease ABC, B subunit	PG TDC60	PGTDC60_1495	331, 433	71.8	159.8	1.60E-37
Transposase DDE domain.	Pgjcvi_02112	PG JCVI SC001	partial transposase in ISPg1	PG ATCC 33277	PGN_0967	69, 141	89	136.7	4.20E-31
Transposase DDE domain.	Pgjcvi_02112	PG JCVI SC001	ISPg1, transposase	PG W83	PG1177	289, 356	66.2	96.7	4.80E-19
Transposase DDE domain.	Pgjcvi_02112	PG JCVI SC001	transposase in ISPg1	PG TDC60	PGTDC60_0916	289, 356	66.2	94.7	1.80E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2468, 2578	98.2	223.8	0
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1945, 2055	98.2	223.8	0
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	1573, 1683	97.3	222.2	0

Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	1124, 1163	60	50.1	6.70E-05
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	651, 709	55.7	63.5	5.90E-09
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1107, 1165	55.7	63.5	5.90E-09
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1563, 1621	55.7	63.5	5.90E-09
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	592, 650	55.7	63.5	5.90E-09
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1044, 1102	55.7	63.5	5.90E-09
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1496, 1554	55.7	63.5	5.90E-09
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2019, 2077	54.1	62	1.70E-08
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	831, 921	48.4	92.8	9.10E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1287, 1377	48.4	92.8	9.10E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	1743, 1833	48.4	92.8	9.10E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	772, 862	48.4	92.8	9.10E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1224, 1314	48.4	92.8	9.10E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	1676, 1791	44.8	94.7	2.40E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	1304, 1419	44.8	95.1	1.80E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	2199, 2314	44	93.2	6.90E-18
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG W83	PG1837	327, 430	36.5	73.9	4.40E-12
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	hemagglutinin protein HagA	PG ATCC 33277	PGN_1733	386, 489	34.6	68.9	1.40E-10
Cleaved Adhesin Domain.	Pgjcvi_02114	PG JCVI SC001	lysine-specific cysteine proteinase Kgp	PG TDC60	PGTDC60_1418	876, 960	29.4	48.9	0.00015
hypothetical protein	Pgjcvi_02116	PG JCVI SC001	putative DNA polymerase III epsilon chain	PG ATCC 33277	PGN_1785	85, 249	49.7	166.8	7.60E-40
hypothetical protein	Pgjcvi_02116	PG JCVI SC001	exonuclease	PG W83	PG1852	85, 249	49.7	166.8	7.60E-40
hypothetical protein	Pgjcvi_02116	PG JCVI SC001	putative DNA polymerase III epsilon chain	PG TDC60	PGTDC60_0115	85, 249	49.7	166.8	7.60E-40
Predicted exporters of the RND superfamily	Pgjcvi_02121	PG JCVI SC001	hypothetical protein	PG ATCC 33277	PGN_1920	1, 801	99.9	1575.5	0
Predicted exporters of the RND superfamily	Pgjcvi_02121	PG JCVI SC001	hypothetical protein	PG W83	PG1180	1, 801	99.6	1572.8	0
Predicted exporters of the RND superfamily	Pgjcvi_02121	PG JCVI SC001	hypothetical protein	PG TDC60	PGTDC60_1155	1, 801	99.6	1573.9	0
Transcriptional regulator	Pgjcvi_02122	PG JCVI SC001	putative TetR family transcriptional regulator	PG ATCC 33277	PGN_0945	17, 215	100	399.1	0
Transcriptional regulator	Pgjcvi_02122	PG JCVI SC001	transcriptional regulator, tetR family	PG W83	PG1181	1, 199	100	399.1	0
Transcriptional regulator	Pgjcvi_02122	PG JCVI SC001	TetR family transcriptional regulator	PG TDC60	PGTDC60_1156	1, 199	99	396	0
hypothetical protein	Pgjcvi_02123	PG JCVI SC001	alginate O-acetyltransferase, putative	PG W83	PG1184	455, 511	98.2	110.9	1.60E-23
hypothetical protein	Pgjcvi_02123	PG JCVI SC001	alginate O-acetyltransferase	PG TDC60	PGTDC60_1161	449, 505	98.2	111.3	1.20E-23
hypothetical protein	Pgjcvi_02123	PG JCVI SC001	alginate O-acetyltransferase	PG ATCC 33277	PGN_0943	455, 511	96.5	110.2	2.80E-23