SI Table 1. Assessment of Genome Completeness

COG family	IMG gene object identifier	Conserved gene set
		Large subunit ribosomal proteins
COG0081	2062288324	Ribosomal protein L1
COG0244	2062347387	Ribosomal protein L10
COG0080	2062288323	Ribosomal protein L11
COG0102	Absent	Ribosomal protein L13
COG0093	2062418832	Ribosomal protein L14
COG0200	2062418826	Ribosomal protein L15
COG0197	2062418838	Ribosomal protein L16/L10E
COG0203	2062418836	Ribosomal protein L17
COG0256	2062418829	Ribosomal protein L18
COG0335	2062273558	Ribosomal protein L19
COG0090	2062418842	Ribosomal protein L2
COG0292	2062350539	Ribosomal protein L20
COG0261	2062142780	Ribosomal protein L21
COG0091	2062418840	Ribosomal protein L22
COG0089	2062138283	Ribosomal protein L23
COG0198	2062418834	Ribosomal protein L24
COG1825	2062269715	Ribosomal protein L25 (general stress protein Ctc)
COG0211	2062142779	Ribosomal protein L27
COG0227	Absent	Ribosomal protein L28
COG0255	2062418837	Ribosomal protein L29
COG0087	2062154483	Ribosomal protein L3
COG1841	2062335748	Ribosomal protein L30/L7E
COG0254	Absent	Ribosomal protein L31
COG0333	Absent	Ribosomal protein L32
COG0267	Absent	Ribosomal protein L33
COG0230	Absent	Ribosomal protein L34
COG0291	2062350538	Ribosomal protein L35

COG0257	Absent	Ribosomal protein L36
COG0088	2062138282	Ribosomal protein L4
COG0094	2062418833	Ribosomal protein L5
COG0097	2062418830	Ribosomal protein L6P/L9E
COG0222	2062288326	Ribosomal protein L7/L12
COG0359	2062209880	Ribosomal protein L9
		Small subunit ribosomal proteins
COG0539	Absent	Ribosomal protein S1
COG0051	2062192532	Ribosomal protein S10
COG0100	2062419497	Ribosomal protein S11
COG0048	2062276762	Ribosomal protein S12
COG0099	2062419496	Ribosomal protein S13
COG0199	2062418832	Ribosomal protein S14
COG0184	2062258759	Ribosomal protein S15P/S13E
COG0228	Absent	Ribosomal protein S16
COG0186	2062138291	Ribosomal protein S17
COG0238	2062209879	Ribosomal protein S18
COG0185	2062418841	Ribosomal protein S19
COG0052	2062164152	Ribosomal protein S2
COG0268	Absent	Ribosomal protein S20
COG0828	2062268357	Ribosomal protein S21
COG0092	2062418839	Ribosomal protein S3
COG0522	2062169304	Ribosomal protein S4 and related proteins
COG0098	2062177114	Ribosomal protein S5
COG0360	Absent	Ribosomal protein S6
COG0049	2062276763	Ribosomal protein S7
COG0096	2062177117	Ribosomal protein S8
COG0103	Absent	Ribosomal protein S9
		tRNA synthetases
COG0008	2062390201	Glutaminyl-tRNA synthetase
COG0008	2062286375	Glutamyl-tRNA synthetase

COG0013	2062169305	Alanyl-tRNA synthetase
COG0016	2062290278	Phenylalanyl-tRNA synthetase alpha subunit
COG0017	Absent	Aspartyl/asparaginyl-tRNA synthetases
COG0018	2062340978	Arginyl-tRNA synthetase
COG0060	2062428580	Isoleucyl-tRNA synthetase
COG0072	2062239745	Phenylalanyl-tRNA synthetase beta subunit
COG0124	2062378056	Histidyl-tRNA synthetase
COG0162	2062212472	Tyrosyl-tRNA synthetase
COG0172	2062213741	Seryl-tRNA synthetase/selenium transferase
COG0173	2062241044	Aspartyl-tRNA synthetase
COG0180	2062246669	Tryptophanyl-tRNA synthetase
COG0215	Absent	Cysteinyl-tRNA synthetase, class Ia
COG0215	2062359524	Cysteinyl-tRNA synthetase
COG0423	2062195145	Glycyl-tRNA synthetase (class II)
COG0441	Absent	Threonyl-tRNA synthetase, class IIa
COG0441	Absent	Threonyl-tRNA synthetase
COG0442	2062372294	Prolyl-tRNA synthetase
COG0495	2062281911	Leucyl-tRNA synthetase
COG0525	2062412400	Valyl-tRNA synthetase
COG0751	2062195145	Glycyl-tRNA synthetase, beta subunit
COG0752	Absent	Glycyl-tRNA synthetase, alpha subunit
COG1190	2062408438	Lysyl-tRNA synthetase (class II)
		Translation Initiation
COG0290	2062350536	Translation initiation factor 3 (IF-3)
COG0361	2062273562	Translation initiation factor 1 (IF-1)
COG0532	2062258762	Translation initiation factor 2 (IF-2; GTPase)
		Histidine biosynthesis
COG0040	Absent	ATP phosphoribosyltransferase
COG0079	2062292893	Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase
COG0106	2062379338	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase
COG0107	2062278039	Imidazoleglycerol-phosphate synthase

COG0118	2062108396	Glutamine amidotransferase
COG0131	2062278038	Imidazoleglycerol-phosphate dehydratase
COG0139	2062144792	Phosphoribosyl-AMP cyclohydrolase
COG0140	2062144792	Phosphoribosyl-ATP pyrophosphohydrolase
COG0141	2062292893	Histidinol dehydrogenase
COG0241	2062351198	Histidinol phosphatase and related phosphatases
COG0462	2062372297	Phosphoribosylpyrophosphate synthetase
		Chorismate biosynthesis
COG0082	2062271610	Chorismate synthase
COG0128	Absent	5-enolpyruvylshikimate-3-phosphate synthase
COG0169	2062122790	Shikimate 5-dehydrogenase
COG0337	2062281895	3-dehydroquinate synthetase
COG0703	Absent	Shikimate kinase
COG0710	2062137681	3-dehydroquinate dehydratase
COG0722	2062213736	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase
COG1605	2062245414	Chorismate mutase
		Threonine biosynthesis
COG0083	2062227476	Homoserine kinase
COG0136	2062404560	Aspartate-semialdehyde dehydrogenase
COG0460	2062318994	Homoserine dehydrogenase
COG0498	2062247978	Threonine synthase
COG0527	Absent	Aspartokinases
		Tryptophan biosynthesis
COG0133	2062376801	Tryptophan synthase beta chain
COG0134	2062290287	Indole-3-glycerol phosphate synthase
COG0135	2062125414	Phosphoribosylanthranilate isomerase
COG0147	Absent	Anthranilate/para-aminobenzoate synthases component I
COG0159	2062188126	Tryptophan synthase alpha chain
COG0512	2062338302	Anthranilate/para-aminobenzoate synthases component II
COG0547	2062322925	Anthranilate phosphoribosyltransferase
		CoA biosynthesis

COG0237	Absent	Dephospho-CoA kinase
COG0413	Absent	Ketopantoate hydroxymethyltransferase
COG0414	Absent	Panthothenate synthetase
COG0452	2062321607	Phosphopantothenoylcysteine synthetase/decarboxylase
COG0669	Absent	Phosphopantetheine adenylyltransferase
COG0853	Absent	Aspartate 1-decarboxylase
COG1072	Absent	Panthothenate kinase
COG1893	2062159636	Ketopantoate reductase
		FAD biosynthesis
COG0054	2062329407	Riboflavin synthase beta-chain
COG0108	2062140186	3,4-dihydroxy-2-butanone 4-phosphate synthase
COG0117	2062392754	Pyrimidine deaminase
COG0196	Absent	FAD synthase
COG0307	2062329407	Riboflavin synthase alpha chain
COG0807	2062140186	GTP cyclohydrolase II
COG1985	Absent	Pyrimidine reductase, riboflavin biosynthesis
		Isoprenoid biosynthesis
COG0245	Absent	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
COG0743	2062213770	1-deoxy-D-xylulose 5-phosphate reductoisomerase
COG1154	Absent	Deoxyxylulose-5-phosphate synthase
COG1211	2062124753	4-diphosphocytidyl-2-methyl-D-erithritol synthase
COG1947	2062412360	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synthase
COG0761	2062273564	Penicillin tolerance protein
COG0821	Absent	Enzyme involved in the deoxyxylulose pathway of isoprenoid biosynthesis
COG0020	2062334514	Undecaprenyl pyrophosphate synthase
		Purine biosynthesis
COG0015	2062334520	Adenylosuccinate lyase
COG0026	2062138909	Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)
COG0027	2062198978	Formate-dependent phosphoribosylglycinamide formyltransferase (GAR transformylase)
COG0034	2062358888	Glutamine phosphoribosylpyrophosphate amidotransferase
COG0041	Absent	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase

COG0046	2062198975	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
COG0047	2062198977	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain
COG0104	2062246668	Adenylosuccinate synthase
COG0138	2062390199	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)
COG0150	2062198977	Phosphoribosylaminoimidazole (AIR) synthetase
COG0151	2062198979	Phosphoribosylamine-glycine ligase
COG0152	Absent	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase
COG0299	2062198978	Folate-dependent phosphoribosylglycinamide formyltransferase PurN
COG0516	2062350527	IMP dehydrogenase/GMP reductase
COG0518	2062358888	GMP synthase - Glutamine amidotransferase domain
COG0519	Absent	GMP synthase, PP-ATPase domain/subunit
COG0563	2062236533	Adenylate kinase and related kinases
		Pyrimidine biosynthesis
COG0105	2062278040	Nucleoside diphosphate kinase
COG0167	Absent	Dihydroorotate dehydrogenase
COG0283	2062301236	Cytidylate kinase
COG0284	2062334517	Orotidine-5-phosphate decarboxylase
COG0418	2062224910	Dihydroorotase
COG0458	2062258111	Carbamoylphosphate synthase large subunit (split gene in MJ)
COG0461	2062351207	Orotate phosphoribosyltransferase
COG0504	2062379985	CTP synthase (UTP-ammonia lyase)
COG0505	Absent	Carbamoylphosphate synthase small subunit
COG0528	2062419482	Uridylate kinase
COG0540	2062288328	Aspartate carbamoyltransferase, catalytic chain
COG0125	2062310741	Thymidylate kinase
COG0207	2062318997	Thymidylate synthase
COG0717	Absent	Deoxycytidine deaminase
COG0756	Absent	dUTPase
		Protein translocase Sec
COG0201	2062418825	Preprotein translocase subunit SecY
COG0341	2062343500	Preprotein translocase subunit SecF

COG0342	2062343502	Preprotein translocase subunit SecD
COG0653	2062396646	Preprotein translocase subunit SecA (ATPase, RNA helicase)
COG0690	2062288320	Preprotein translocase subunit SecE
COG0706	2062184259	Preprotein translocase subunit YidC
COG1314	2062108388	Preprotein translocase subunit SecG
COG1862	2062343505	Preprotein translocase subunit YajC
COG1952	Absent	Preprotein translocase subunit SecB
		RNA polymerase subunits
COG0085	2062291019	DNA-directed RNA polymerase, beta subunit/140 kD subunit
COG0086	2062291018	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
COG0202	2062419498	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
COG0568	2062180322	DNA-directed RNA polymerase, sigma subunit RpoD
COG0568	Absent	DNA-directed RNA polymerase, sigma subunit RpoS
COG1758	Absent	DNA-directed RNA polymerase, subunit K/omega

SI Table 2. Abundance of core metabolimic pathway genes in GB-Sar324

Etner-Doudoroff Pathway

Gene Name	Gene No.	Contig	Plume	Background
Phosphogluconate Dehydratase	2062219032	c1346	66	6
	20622219033	c1346	68	11
2-Keto-3-deoxygluconate 6-phosphate aldolase	ND			

Glycolysis

Gene Name	Gene No.	Contig	Plume	Background
Glucose-6-phosphate isomerase	ND			
Fructose-1,6-bisphosphatase	2062190679	c5025	0	0
	2062198982	c770	47	3
6-phosphofructokinase	2062148697	c2991	106	12
fructose bisphosphate aldolase	2062142112	c685	52	19
	2062142113	c685	126	21
	2062143481	c1800	0	0
	2062171848	c1845	0	0
	2062171849	c1845	4	13
	2062171850	c1845	10	10
	2062324838	c423	20	2
	2062297385	c2046	40	0
	2062297386	c2046	98	29
triose phosphate isomerase	2062245413	c302	84	114
glyceraldehyde 3-phosphate dehydrogenase	2062195154	c3073	26	21
	2062195155	c3073	73	16
phosphoglycerate mutase	2062109680	c2922	17	3
	2062109681	c2922	48	10
enolase	2062312705	c2073	89	14
	2062312706	c2073	83	4
	2062373587	c4027	21	0
	2062373587	c4027	40	0

	2062373587	c4027	45	0
phosphoenolpyruvate synthetase	ND	ND	ND	ND
pyruvate kinase	2062143480	c1800	8	2
	2062265796	c562	40	16
	2062265796	c562	0	15
	2062265796	c562	0	0
	2062364012	c5355	65	7

Tricarboxylic Acid Cycle

Gene Name	Gene No.	Contig	Plume	Background
Pyruvate dehydrogenase	2062145448	c1805	89	6
	2062183609	c2440	31	9
	2062183610	c2440	50	14
	2062265799	c562	20	7
	2062290992	c1461	34	0
	2062290993	c1461	72	6
	2062290994	c1461	0	4
	2062317100	c1502	11	7
	2062346761	c457	52	5
Citrate synthase	2062167377	c187	9	0
	2062189403	c3060	14	4
	2062220989	c4400	133	6
	2062292236	c2620	0	0
Aconitase	2062286327	c904	64	10
	2062286328	c904	100	35
	2062286329	c904	13	10
Isocitrate dehydrogenase	2062196446	c1308	25	12
	2062342245	c11701	39	11
	2062342246	c11701	83	15
2-Oxogluterate dehydrogenase	2062407815	c5427	85	5
	2062407816	c5427	42	17

	2062407817	c5427	55	34
	2062407818	c5427	16	0
Succinyl-CoA synthetase	2062374218	c1040	70	9
Succinate dehydrogenase	2062159641	c1252	223	31
	2062159642	c1252	262	22
	2062159643	c1252	77	0
	2062159644	c1252	129	46
	2062205426	c4374	34	0
	2062205426	c4374	40	15
	2062205426	c4374	153	16
Fumarase	2062122134	c2339	15	0
	2062122134	c2339	116	12
Malate:quinone oxidoreductase	ND	ND	ND	ND
Malate dehydrogenase	2062392733	c529	0	0
	2062392734	c529	0	0
	2062272947	c5462	18	0

Glyoxylate Pathway

Gene Name	Gene No.	Contig	Plume	Background
Malate synthase	ND			
Malate dehydrogenase	See TCA			
Citrate Synthase	See TCA			
Aconitase	See TCA			
Isocitrate lyase	ND			

CBB/Pentose Phosphate

Gene Name	Gene No.	Contig	Plume	Background
Ribulose bisphosphate carboxylase oxidase	2062201587	c2828	53	9
	2062297384	c2046	69	18

Phosphoglycerate kinase	2062126053	c4229	0	0
	2062143478	c1800	0	0
	2062143479	c1800	22	10
	2062143480	c1800	8	2
	2062376159	c501	99	3
Glyceraldehyde 3-phosphate dehydrogenase	See Glycolysis			
Triosephosphate isomerase	2062245413	c302	84	114
Sedoheptulose bisphosphatase	ND			
Sedoheptulose-1,7-bisphosphate aldolase	2062142112	c685	52	19
	2062142113	c685	126	21
	2062198982	c770	47	3
	2062415655	c3541	50	13
Transketoaldolase	2062297387	c2046	21	0
	2062415657	c3541	87	16
	2062415658	c3541	114	16
Fructose bisphosphate aldolase	2062297385	c2046	98	29
	2062297386	c2046	40	0
	2062143481	c1800	0	0
Fructose bisphosphatase	See Glycolysis			
Pentose-5-phosphate 3-epimerase	2062222304	c1928	37	15
	2062201588	c2828	72	13
Phosphoribulokinase	2062112271	c2322	96	13
Ribose 5-phosphate isomerase	2062131204	c1209	12	24
	2062195153	c3073	0	40

Fatty Acid Beta Oxidation

Gene Name	Gene No.	Contig	Plume	Background
Acyl-CoA sythetase	2062131191	c1342	99	48
	2062131192	c1342	33	10
	2062209285	c3099	41	16

	2062242267	c387	69	30
	2062249887	c1398	66	13
	2062279979	c1668	40	10
	2062338314	c1537	54	28
	2062376158	c501	105	19
Long-Chain Acyl-CoA synthetase	2062190030	c3061	90	31
	2062224909	c1354	12	28
Acyl-CoA Dehydrogenase	2062108416	c5430	62	13
	2062164143	c183	121	39
	2062222301	c1928	36	9
	2062222302	c1928	84	12
	2062225592	c1355	90	13
	2062225593	c1355	51	9
	2062364013	c5355	109	18
	2062364014	c5355	0	0
	2062421433	c1164	109	11
	2062421434	c1164	39	18
Enoyl-CoA Hydratase	2062108414	c5430	39	4
	2062108415	c5430	41	9
	2062219666	c1347	46	12
	2062340257	c988	128	17
	2062364014	c5355	82	13
	2062364015	c5355	0	0
	2062421433	c1164	109	11
3-hydroxyacyl-CoA dehydrogenase	2062108416	c5430	62	13
	2062222301	c1928	36	9
	2062222302	c1928	84	12
	2062225592	c1355	90	13
	2062225593	c1355	51	9
3-ketoacyl-CoA thiolase	2062364013	c5355	109	18

C1 Carbon Metabolism

Gene Name	Gene No.	Contig	Plume	Background
Methanol Dehydrogenase	ND			
Methylenetetrahydrofolate reductase	2062171216	c193	13	193
Methylene tetrahydrofolate dehydrogenase	2062164159	c717	62	8
Methenyl tetrahydrofolate cyclohydrolase	2062164159	c717	62	8
Formyltetrahydrofolate synthetase	2062365296	c1680	80	18
formate-tetrahydrofolate ligase	2062386320	c582	16	8
Methylene tetrahydromethanopterin	ND			
Methenyltetrahyropterin cyclohydrolase	ND			
Formyltransferase hydrolase complex	2062265816	c1666	768	54
	2062265815	c1666	322	23
Formate dehydrogenase	2062142099	c151	2235	379
	2062142100	c151	4417	323

Serine Cycle

Gene Name	Gene No.	Contig	Plume	Background
Serine hydroxymethyltransferase	2062151908	c164	154	19
	2062151918	c698	61	10
	2062220945	c266	22	2
	2062280627	c2017	71	16
	2062280628	c2017	58	9
Serine-glyoxylate amiotransferase	2062401945	c2269	22	0
glycerate kinase	ND			
Enolase	See TCA			
Phosphoenolpyruvate carboxylase	ND			
Malate dehydrogenase	ND			
Malate thiokinase	ND			
Methylmalyl-CoA lyase	ND			
phosphoglycerate mutase	2062109680	c2922	17	3

	2062109681	c2922	48	10

SI Table 3. Annotation and Abundance of Genomic Bin Sar324

Illumina BWA Mapped Normalized Abundance

2062162882	239	38	8	c1004	hypothetical protein
2062187520	1100	647	136	c1004	TRAP-type mannitol/chloroaromatic compound transport system, periplasmic comp
2062207351	1028	50	25	c1004	TRAP-type mannitol/chloroaromatic compound transport system, small permease c
2062207352	962	138	3	c1007	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)(EC:1.1.1.262)
2062213746	329	170	0	c1007	dimethyladenosine transferase (EC 2.1.1.-)(EC:2.1.1.-)
2062213747	350	40	11	c1007	dimethyladenosine transferase (EC 2.1.1.-)(EC:2.1.1.-)
2062213757	128	23	0	c1007	hypothetical protein
2062217726	1019	485	55	c1007	RND family efflux transporter, MFP subunit
2062229412	884	1370	72	c1008	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homolo
2062246686	917	44	12	c1008	Dihydrodipicolinate synthase/N-acetylneuraminate lyase(EC:4.2.1.52)
2062246718	323	133	19	c1008	hypothetical protein
2062269713	59	0	0	c1008	hypothetical protein
2062269718	176	0	11	c1008	L-threonine aldolase (EC 4.1.2.5)(EC:4.1.2.5)
2062269719	338	15	24	c1008	Threonine aldolase(EC:4.1.2.5)
2062269720	530	42	2	c1008	Threonine aldolase(EC:4.1.2.5)
2062272268	1001	325	45	c1008	xanthine dehydrogenase, molybdenum binding subunit apoprotein (EC 1.17.1.4)
2062272269	593	7	3	c1009	ATP-dependent RNA helicase CsdA (EC 5.99.1.-)
2062284411	176	0	11	c1009	cold-shock DNA-binding protein family
2062284412	1379	36	5	c1009	Exodeoxyribonuclease I subunit C (EC 3.1.11.1)(EC:3.1.11.1)
2062288316	77	0	0	c1009	hypothetical protein
2062288317	920	212	89	c1010	cell division protein FtsA
2062288318	311	103	29	c1010	cell division protein FtsA
2062288319	1781	135	40	c1010	cell division protein FtsZ
2062288979	293	10	20	c1010	hypothetical protein
2062290327	224	18	13	c1010	hypothetical protein
2062301237	248	0	8	c1010	hypothetical protein
2062314589	1130	50	19	c1010	K+ transport systems, NAD-binding component
2062317129	1088	118	22	c1017	3-isopropylmalate dehydrogenase (EC 1.1.1.85)(EC:1.1.1.85)
2062317130	698	7	11	c1017	ABC-type multidrug transport system, ATPase and permease components(EC:3.6.

2062320340	548	11	5	c1017	ABC-type multidrug transport system, ATPase and permease components(EC:3.6.
2062333912	599	7	7	c1017	CDP-Glycerol:Poly(glycerophosphate) glycerophosphotransferase.
2062347390	140	0	0	c1017	Cysteinyl-tRNA synthetase(EC:6.1.1.16)
2062350535	59	0	0	c1017	hypothetical protein
2062358903	233	0	4	c1017	hypothetical protein
2062364616	314	10	0	c1017	hypothetical protein
2062365280	377	40	19	c1017	Mannose-6-phosphate isomerase
2062365281	821	45	29	c1017	Predicted sugar nucleotidyltransferases
2062142778	1355	37	10	c1021	Uncharacterized conserved protein
2062392735	521	58	8	c1021	5"-nucleotidase, C-terminal domain.
2062401925	1019	27	16	c1021	5"-nucleotidase/2",3"-cyclic phosphodiesterase and related esterases
2062401926	329	3	0	c1021	hypothetical protein
2062401927	239	25	4	c1021	hypothetical protein
2062401928	461	28	7	c1021	Rhodanese-related sulfurtransferase
2062213770	593	140	34	c1022	Uncharacterized protein conserved in bacteria
2062213771	704	185	45	c1022	Uncharacterized protein conserved in bacteria
2062246688	497	249	36	c1022	hypothetical protein
2062351211	224	27	22	c1022	hypothetical protein
2062358252	353	0	0	c1022	Predicted hydrolase of the alpha/beta-hydrolase fold
2062413008	623	26	8	c1022	Predicted hydrolase of the alpha/beta-hydrolase fold
2062156431	500	20	4	c1033	Cobyric acid synthase
2062159637	590	122	15	c1033	Predicted membrane protein
2062246672	221	0	0	c1033	cob(I)yrinic acid a,c-diamide adenosyltransferase (EC 2.5.1.17)
2062246673	797	503	31	c1033	cobalt transporter subunit CbtA (proposed)
2062247989	1352	29	1	c1033	Cobyrinic acid a,c-diamide synthase
2062247990	998	98	17	c1033	Cysteine synthase(EC:2.5.1.47)
2062274227	905	117	13	c1033	adenosylcobyric acid synthase (glutamine-hydrolysing) (EC 6.3.5.10)(EC:6.3.5.10)
2062310115	284	0	14	c1033	cob(I)yrinic acid a,c-diamide adenosyltransferase (EC 2.5.1.17)
2062246694	863	65	14	c1038	Predicted amidohydrolase(EC:3.5.1.53)
2062246695	905	124	10	c1038	protoheme IX farnesyltransferase(EC:2.5.1.-)
2062296742	725	32	18	c1038	Heme/copper-type cytochrome/quinol oxidases, subunit 2

2062367171	611	214	21	c1038	NADPH-dependent glutamate synthase beta chain and related oxidoreductases(EC
2062145443	875	70	9	c1040	succinyl-CoA synthetase (ADP-forming) alpha subunit (EC 6.2.1.5)(EC:6.2.1.5)
2062288314	515	49	91	c1040	hypothetical protein
2062340268	533	41	13	c1040	NADPH:quinone reductase and related Zn-dependent oxidoreductases
2062407815	476	4	6	c1040	NADPH:quinone reductase and related Zn-dependent oxidoreductases
2062407816	542	42	4	c1040	Metal-dependent hydrolase
2062108416	737	23	7	c1046	Uracil-DNA glycosylase
2062137681	566	224	28	c1046	Histidyl-tRNA synthetase(EC:6.1.1.21)
2062198346	296	57	10	c1046	histidyl-tRNA synthetase (EC 6.1.1.21)(EC:6.1.1.21)
2062216453	167	12	0	c1046	ATP-dependent protease HslVU (ClpYQ), ATPase subunit
2062222301	368	8	3	c1046	Putative Zn-dependent protease, contains TPR repeats
2062222302	485	12	8	c1046	Putative Zn-dependent protease, contains TPR repeats
2062238445	521	75	13	c1046	ATP dependent peptidase CodWX, CodW component. Threonine peptidase. MERO
2062246687	536	9	0	c1046	hypothetical protein
2062281250	332	24	27	c1046	Lipoprotein signal peptidase
2062281895	92	0	0	c1046	hypothetical protein
2062288338	365	8	8	c1046	ATP-dependent protease HslVU (ClpYQ), ATPase subunit
2062318992	596	102	23	c1046	Glutamyl-tRNA reductase(EC:1.2.1.70)
2062342186	347	9	12	c1046	Histidyl-tRNA synthetase(EC:6.1.1.21)
2062342853	401	32	7	c1046	Phosphatidylglycerophosphate synthase(EC:2.7.8.5)
2062413011	827	45	16	c1046	ATP-dependent protease HslVU (ClpYQ), ATPase subunit
2062124752	179	6	17	c1058	hypothetical protein
2062131218	446	56	58	c1058	Predicted sugar kinase
2062131219	557	14	2	c1058	hypothetical protein
2062131220	221	9	9	c1058	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
2062222975	443	27	7	c1058	hypothetical protein
2062222976	239	38	17	c1058	hypothetical protein
2062225592	782	179	14	c1058	conserved hypothetical protein TIGR00159
2062225593	692	12	0	c1058	Gram-negative bacterial tonB protein.
2062237844	368	22	8	c1058	Predicted sugar kinase
2062237845	812	73	16	c1058	membrane protease FtsH catalytic subunit (EC 3.4.24.-)(EC:3.4.24.-)

2062237846	959	86	49	c1058	membrane protease FtsH catalytic subunit (EC 3.4.24.-)(EC:3.4.24.-)
2062237847	689	20	1	c1058	Periplasmic component of the Tol biopolymer transport system
2062237848	695	124	16	c1058	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
2062278653	416	12	7	c1058	hypothetical protein
2062359516	632	44	9	c1058	Uncharacterized protein conserved in bacteria
2062414408	704	43	6	c1058	hypothetical protein
2062142776	911	40	2	c1064	glutaminyl-tRNA synthetase (EC 6.1.1.18)(EC:6.1.1.18)
2062142777	683	9	6	c1064	Glutathione S-transferase(EC:2.5.1.18)
2062164144	107	0	0	c1064	Uridine kinase
2062164146	209	0	0	c1064	glutaminyl-tRNA synthetase (EC 6.1.1.18)(EC:6.1.1.18)
2062184266	515	47	0	c1064	glutaminyl-tRNA synthetase (EC 6.1.1.18)
2062364013	782	41	14	c1064	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain i
2062414406	434	0	0	c1064	hypothetical protein
2062414407	476	19	11	c1064	Tetratricopeptide repeat.
2062124753	578	10	10	c1068	hypothetical protein
2062124754	158	0	0	c1068	hypothetical protein
2062140191	1445	19	8	c1068	ABC-type multidrug transport system, ATPase and permease components
2062164139	422	104	24	c1068	Pyrimidine deaminase(EC:3.5.4.26,EC:1.1.1.193)
2062195146	194	36	67	c1068	cold-shock DNA-binding protein family
2062195147	461	7	4	c1068	conserved hypothetical nucleotide-binding protein
2062227477	161	0	0	c1068	DNA primase (EC 2.7.7.-)(EC:2.7.7.-)
2062227478	212	38	5	c1068	Esterase/lipase
2062239094	233	4	0	c1068	hypothetical protein
2062269712	335	27	9	c1068	hypothetical protein
2062273564	668	9	4	c1068	Inactive homolog of metal-dependent proteases, putative molecular chaperone
2062353117	1400	56	15	c1068	transcriptional regulator
2062365296	992	32	17	c1068	Uncharacterized conserved protein
2062367169	182	0	0	c1068	ABC-type transport system involved in Fe-S cluster assembly, permease and ATPa
2062367170	440	27	7	c1068	ADP-ribose pyrophosphatase
2062405869	692	17	10	c1068	hypothetical protein
2062412360	368	5	14	c1068	hypothetical protein

2062148697	572	35	16	c1070	hypothetical protein
2062171216	1244	301	47	c1070	ABC-type branched-chain amino acid transport systems, periplasmic component
2062242871	305	0	7	c1070	Protein containing tetrapyrrole methyltransferase domain and MazG-like (predicted
2062278662	200	5	0	c1070	Choline dehydrogenase and related flavoproteins(EC:1.1.99.1)
2062281910	530	170	15	c1070	amino acid/amide ABC transporter ATP-binding protein 2, HAAT family (TC 3.A.1.4.-
2062300581	782	90	6	c1070	aspartate racemase(EC:5.1.1.13)
2062310745	527	101	8	c1070	MazG family protein(EC:3.6.1.19)
2062362068	728	88	25	c1070	Choline dehydrogenase and related flavoproteins
2062362069	590	39	27	c1070	hypothetical protein
2062396652	701	40	4	c1070	amino acid/amide ABC transporter membrane protein 2, HAAT family (TC 3.A.1.4.-)
2062396653	254	142	12	c1070	amino acid/amide ABC transporter membrane protein 2, HAAT family (TC 3.A.1.4.-)
2062135645	467	13	17	c1079	hypothetical protein
2062140201	527	6	6	c1079	hypothetical protein
2062235223	3998	64	15	c1079	glutamate synthase (NADH) large subunit (EC 1.4.1.14)(EC:1.4.1.14,EC:1.4.1.13)
2062236537	1427	33	11	c1079	Malic enzyme(EC:1.1.1.38)
2062242268	422	246	47	c1079	protein translocase, SecG subunit
2062283796	896	26	13	c1079	glutamate 5-kinase(EC:2.7.2.11)
2062323566	812	84	20	c1079	hypothetical protein
2062358886	1535	98	14	c1079	glutamate synthases, NADH/NADPH, small subunit
2062370969	143	0	0	c1079	Glutamine amidotransferases class-II.
2062107703	518	17	12	c10790	methionine-S-sulfoxide reductase(EC:1.8.4.11)
2062238463	1259	2	5	c10790	Uncharacterized enzyme of heme biosynthesis
2062335122	110	0	0	c10790	hypothetical protein
2062404580	791	20	5	c10790	DNA repair protein RecO
2062169303	539	100	11	c1081	methionine adenosyltransferase (EC 2.5.1.6)(EC:2.5.1.6)
2062187527	617	290	53	c1081	methionine adenosyltransferase (EC 2.5.1.6)(EC:2.5.1.6)
2062280618	929	82	14	c1081	cation diffusion facilitator family transporter
2062328741	620	66	3	c1081	Exonuclease VII, large subunit
2062328743	269	190	48	c1081	Phosphotransferase System HPr (HPr) Family
2062328744	236	42	4	c1081	Shikimate 5-dehydrogenase(EC:1.1.1.25)
2062328745	590	93	17	c1081	shikimate dehydrogenase (EC 1.1.1.25)(EC:1.1.1.25)

2062348683	611	151	7	c1081	hydroxyacylglutathione hydrolase(EC:3.1.2.6)
2062369666	140	7	0	c1081	hypothetical protein
2062412367	692	117	26	c1081	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)(EC:3.1.11.6)
2062348681	356	76	8	c10891	microcin-processing peptidase 2. Unknown type peptidase. MEROPS family U62
2062348682	152	53	0	c10891	microcin-processing peptidase 2. Unknown type peptidase. MEROPS family U62
2062369667	827	196	11	c10891	Predicted amidohydrolase(EC:3.5.5.1)
2062369668	884	27	11	c10891	Predicted membrane protein
2062109032	194	0	0	c1096	EamA-like transporter family.
2062109033	407	32	10	c1096	EamA-like transporter family.
2062370967	395	23	0	c1096	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenase
2062370968	482	6	2	c1096	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenase
2062372934	326	12	3	c1096	hypothetical protein
2062109034	167	108	48	c1117	hypothetical protein
2062154487	407	10	7	c1117	Thymidylate synthase complementing protein.
2062154488	452	2	18	c1117	Predicted alternative thymidylate synthase
2062154489	818	28	12	c1117	Predicted alternative thymidylate synthase
2062219038	578	22	5	c1117	Uncharacterized conserved protein
2062219039	473	36	11	c1117	Uncharacterized MobA-related protein
2062372932	131	0	0	c1117	hypothetical protein
2062372933	344	99	17	c1117	NADH dehydrogenase subunit I (EC 1.6.5.3)
2062392749	632	84	19	c1117	uracil phosphoribosyltransferase (EC 2.4.2.9)(EC:2.4.2.9)
2062154480	281	7	25	c1120	imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-)(EC:4.1.3.-)
2062172543	266	0	0	c1120	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) i
2062172544	473	13	4	c1120	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) i
2062207987	674	157	49	c1120	hypothetical protein
2062217725	794	13	8	c1120	Trans-aconitate methyltransferase
2062359521	371	11	3	c1120	hypothetical protein
2062359522	548	73	9	c1120	imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-)(EC:4.1.3.-)
2062154481	125	0	0	c1121	hypothetical protein
2062169300	386	10	0	c1121	Peptidase M15.
2062255617	191	0	0	c1121	hypothetical protein

2062308281	422	12	0	c1121	hypothetical protein
2062308282	248	16	8	c1121	hypothetical protein
2062326772	419	0	0	c1121	Plasmid maintenance system antidote protein
2062219050	2066	61	18	c1127	protein translocase subunit secA
2062219051	2537	56	16	c1127	valyl-tRNA synthetase
2062261893	233	4	4	c1127	hypothetical protein
2062291013	896	10	0	c1127	Predicted dehydrogenases and related proteins
2062291014	560	25	30	c1127	Preprotein translocase subunit SecA (ATPase, RNA helicase)
2062326773	374	13	0	c1127	hypothetical protein
2062169318	323	59	15	c1135	NifU homolog involved in Fe-S cluster formation
2062196435	494	111	20	c1135	Selenocysteine lyase(EC:4.4.1.16,EC:2.8.1.7)
2062219049	542	15	4	c1135	MoxR-like ATPases
2062260644	725	95	10	c1135	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family
2062291010	500	56	14	c1135	cysteine desulfurase (EC 2.8.1.7)(EC:2.8.1.7,EC:4.4.1.16)
2062291011	263	49	8	c1135	cysteine desulfurase (EC 2.8.1.7)(EC:4.4.1.16,EC:2.8.1.7)
2062169319	791	317	46	c11459	translation elongation factor 2 (EF-2/EF-G)(EC:3.6.5.3)
2062196436	806	311	25	c11459	translation elongation factor 2 (EF-2/EF-G)(EC:3.6.5.3)
2062242278	263	38	99	c11459	translation elongation factor 2 (EF-2/EF-G)(EC:3.6.5.3)
2062283160	608	893	82	c11459	translation elongation factor 1A (EF-1A/EF-Tu)(EC:3.6.5.3)
2062168693	194	5	0	c1149	hypothetical protein
2062169320	1115	163	18	c1149	chaperone protein DnaJ
2062260645	473	17	4	c1149	AIG2-like family.
2062283157	1958	102	29	c1149	chaperone protein DnaK
2062283158	1121	25	10	c1149	heat shock gene repressor HrcA
2062283161	908	51	14	c1149	Aspartate/tyrosine/aromatic aminotransferase(EC:2.6.1.1)
2062324864	152	0	0	c1149	hypothetical protein
2062335123	803	50	14	c1149	hypothetical protein
2062392750	518	39	12	c1149	Molecular chaperone GrpE (heat shock protein)
2062169309	77	0	0	c1150	hypothetical protein
2062236538	440	141	36	c1150	hypothetical protein
2062399942	1958	23	11	c1150	selenocysteine-specific elongation factor SelB

2062422702	2342	24	8	c1150	ABC-type branched-chain amino acid transport systems, periplasmic component
2062158379	455	13	0	c1151	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062172541	1169	26	15	c1151	Predicted permease
2062399943	842	62	8	c1151	1-aminocyclopropane-1-carboxylate deaminase(EC:4.4.1.15)
2062404576	791	34	20	c1151	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosph
2062404579	122	0	0	c1151	hypothetical protein
2062292916	368	120	95	c1161	SSU ribosomal protein S13P
2062346751	1109	36	21	c1161	DNA-directed RNA polymerase subunit alpha (EC 2.7.7.6)(EC:2.7.7.6)
2062346755	872	317	47	c1161	protein translocase subunit secY/sec61 alpha
2062346756	395	63	53	c1161	SSU ribosomal protein S11P
2062422727	155	0	0	c1161	protein translocase subunit secY/sec61 alpha
2062326774	1856	39	18	c1164	Acyl-CoA dehydrogenases(EC:1.3.99.2)
2062326775	1028	42	7	c1164	Cell division protein FtsI/penicillin-binding protein 2(EC:2.4.1.129)
2062326776	287	139	35	c1164	Cell division protein FtsL.
2062346752	476	109	11	c1164	short chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)(
2062346753	920	39	11	c11701	Monomeric isocitrate dehydrogenase(EC:1.1.1.42)
2062346754	806	83	15	c11701	Monomeric isocitrate dehydrogenase(EC:1.1.1.42)
2062422728	203	0	0	c11701	Peptidase family M48.
2062422729	275	0	0	c11701	Peptidase family M48.
2062118235	185	0	0	c1182	hypothetical protein
2062274220	572	159	23	c1182	NADH dehydrogenase subunit B (EC 1.6.5.3)(EC:1.6.5.3)
2062274221	1226	95	16	c1182	NADH dehydrogenase subunit D (EC 1.6.5.3)(EC:1.6.5.3)
2062274222	1073	194	17	c1182	NADH:ubiquinone oxidoreductase subunit 1 (chain H)(EC:1.6.5.3)
2062274223	635	90	24	c1182	Pyridoxamine 5''-phosphate oxidase (EC 1.4.3.5)(EC:1.4.3.5)
2062342190	143	14	14	c1182	hypothetical protein
2062342191	290	24	0	c1182	hypothetical protein
2062372935	560	38	36	c1182	NADH (or F420H2) dehydrogenase, subunit C
2062124736	311	6	23	c1202	hypothetical protein
2062124737	404	47	45	c1202	hypothetical protein
2062124738	329	15	0	c1202	hypothetical protein
2062162290	290	7	0	c1202	Uncharacterized protein, similar to the N-terminal domain of Lon protease

2062209878	284	14	0	c1202	hypothetical protein
2062290292	419	19	0	c1202	Uncharacterized protein, similar to the N-terminal domain of Lon protease
2062290294	716	84	25	c1202	DNA repair photolyase
2062362076	803	10	11	c1202	Predicted choloylglycine hydrolase
2062131872	920	25	5	c1209	DNA-directed RNA polymerase subunit beta'' (EC 2.7.7.6)(EC:2.7.7.6)
2062131873	452	60	18	c1209	Predicted thioesterase
2062162289	1787	151	26	c1209	DNA-directed RNA polymerase subunit beta'' (EC 2.7.7.6)(EC:2.7.7.6)
2062269041	575	99	5	c1209	DNA-directed RNA polymerase subunit beta'' (EC 2.7.7.6)(EC:2.7.7.6)
2062269664	230	100	4	c1209	DNA-directed RNA polymerase subunit beta'' (EC 2.7.7.6)(EC:2.7.7.6)
2062343514	677	12	24	c1209	ribose-5-phosphate isomerase (EC 5.3.1.6)(EC:5.3.1.6)
2062362060	851	49	28	c1209	DNA-directed RNA polymerase subunit beta'' (EC 2.7.7.6)(EC:2.7.7.6)
2062164153	926	21	4	c1212	KR domain.(EC:2.3.1.94)
2062166136	743	52	7	c1212	hypothetical protein
2062261278	356	22	8	c1212	hypothetical protein(EC:2.3.1.94)
2062343515	128	0	0	c1212	hypothetical protein
2062365299	314	35	105	c1212	Phosphopantetheine attachment site.(EC:2.3.1.94)
2062273565	203	0	0	c1215	hypothetical protein
2062286327	116	0	0	c1215	hypothetical protein
2062286328	1091	29	10	c1215	Predicted Zn-dependent hydrolases of the beta-lactamase fold
2062286329	623	11	6	c1215	YceI-like domain.
2062373571	323	0	0	c1215	hypothetical protein
2062131191	233	0	0	c1226	hypothetical protein
2062131192	92	0	0	c1226	hypothetical protein
2062158373	212	61	57	c1226	ATP synthase delta (OSCP) subunit.
2062164143	263	61	11	c1226	ATP synthase F1 subcomplex gamma subunit(EC:3.6.3.14)
2062164145	1556	91	44	c1226	ATP synthase F1 subcomplex alpha subunit(EC:3.6.3.14)
2062180333	317	38	19	c1226	ATP synthase F1 subcomplex epsilon subunit(EC:3.6.3.14)
2062209285	158	13	0	c1226	hypothetical protein
2062249887	158	0	0	c1226	hypothetical protein
2062260646	749	44	16	c1226	ATPases involved in chromosome partitioning
2062260647	395	66	5	c1226	Dioxygenases related to 2-nitropropane dioxygenase

2062260648	569	54	53	c1226	F0F1-type ATP synthase, subunit b
2062279979	209	24	14	c1226	hypothetical protein
2062281889	344	70	12	c1226	hypothetical protein
2062294807	1394	159	26	c1226	ATP synthase F1 subcomplex beta subunit(EC:3.6.3.14)
2062319662	503	70	36	c1226	F0F1-type ATP synthase, subunit b
2062338314	155	0	0	c1226	hypothetical protein
2062376158	371	70	22	c1226	hypothetical protein
2062388928	422	57	21	c1226	Predicted membrane protein
2062388929	353	14	25	c1226	Predicted membrane protein
2062388930	149	0	0	c1226	hypothetical protein
2062421434	401	22	17	c1226	ATP synthase F1 subcomplex gamma subunit(EC:3.6.3.14)
2062131860	371	5	5	c1229	hypothetical protein
2062157101	245	16	0	c1229	hypothetical protein
2062186880	371	46	11	c1229	RNA polymerase-binding protein DksA
2062200298	389	57	33	c1229	phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)/phosphoribosyl-AMP cyclohyd
2062261281	185	16	32	c1229	Co-chaperonin GroES (HSP10)
2062343513	1667	227	75	c1229	chaperonin GroL
2062369046	1499	55	32	c1229	Lysyl-tRNA synthetase (class II)(EC:6.1.1.6)
2062420780	563	75	36	c1229	isovaleryl-CoA dehydrogenase (EC 1.3.99.10)(EC:1.3.99.10)
2062200296	1508	0	3	c1242	ERCC4-like helicases(EC:3.6.1.-)
2062220970	275	0	0	c1242	Parvulin-like peptidyl-prolyl isomerase(EC:5.2.1.8)
2062290328	479	6	8	c1242	TATA binding protein of transcription factor TFIID
2062290329	218	5	0	c1242	Transcription initiation factor IIB (TFIIB)
2062290330	113	0	0	c1242	Transcription initiation factor IIB (TFIIB)
2062326781	191	5	0	c1242	Transcription initiation factor IIB (TFIIB)
2062358218	239	0	0	c1242	hypothetical protein
2062365293	110	0	0	c1242	hypothetical protein
2062365294	209	0	0	c1242	hypothetical protein
2062369057	155	0	6	c1242	Transcription initiation factor IIB (TFIIB)
2062236533	1007	38	22	c1246	Secreted/periplasmic Zn-dependent peptidases, insulinase-like
2062246668	770	8	1	c1246	Secreted/periplasmic Zn-dependent peptidases, insulinase-like

2062249250	1088	13	21	c1246	hypothetical protein
2062294170	317	16	13	c1246	hypothetical protein
2062296740	530	72	15	c1246	Phosphoglycerate dehydrogenase and related dehydrogenases(EC:1.1.1.81,EC:1.
2062334520	623	29	8	c1246	Transposase.
2062355701	488	2	2	c1246	hypothetical protein
2062149987	140	29	7	c1252	hypothetical protein
2062193194	371	129	46	c1252	succinate dehydrogenase subunit B (EC 1.3.5.1)(EC:1.3.99.1)
2062196441	779	157	18	c1252	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catecho
2062196442	1517	80	22	c1252	Gamma-glutamyltransferase(EC:2.3.2.2)
2062205429	236	21	4	c1252	hypothetical protein
2062205430	749	63	21	c1252	hypothetical protein
2062220960	155	0	71	c1252	ketopantoate reductase (EC 1.1.1.169)
2062280630	98	0	0	c1252	hypothetical protein
2062392753	455	77	0	c1252	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit(EC:1.3.99.1)
2062396013	773	223	31	c1252	succinate dehydrogenase subunit A (EC 1.3.5.1)(EC:1.3.99.1)
2062396014	545	262	22	c1252	succinate dehydrogenase subunit A (EC 1.3.5.1)(EC:1.3.99.1)
2062207361	266	4	8	c1253	hypothetical protein
2062207362	1568	31	15	c1253	Predicted exporters of the RND superfamily
2062299961	977	12	14	c1253	Predicted exporters of the RND superfamily
2062207360	530	4	11	c12546	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
2062242277	104	0	0	c12546	hypothetical protein
2062299958	689	3	0	c12546	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
2062299962	200	0	10	c12546	ATP-dependent Clp protease ATP-binding subunit ClpX (EC 3.4.21.92)
2062326777	329	3	0	c12546	Protein of unknown function (DUF790).
2062338315	191	0	0	c12546	hypothetical protein
2062353742	122	0	0	c12546	ATP-dependent protease Clp, ATPase subunit
2062371628	581	34	3	c12546	ATP-dependent Clp protease proteolytic subunit ClpP (EC 3.4.21.92)(EC:3.4.21.92
2062224258	653	126	37	c1262	hypothetical protein
2062345498	365	74	22	c1262	hypothetical protein
2062390199	503	278	8	c1262	Acetyltransferase (GNAT) family.
2062411705	248	48	65	c1262	hypothetical protein

2062131189	650	92	20	c1274	Uncharacterised protein family (UPF0104).
2062169305	872	81	33	c1274	Deacetylases, including yeast histone deacetylase and acetoin utilization protein
2062169306	152	0	0	c1274	hypothetical protein
2062169307	875	22	14	c1274	ATP-dependent DNA ligase(EC:6.5.1.1)
2062169308	203	0	0	c1274	hypothetical protein
2062207353	518	31	12	c1274	Type II secretory pathway, prepilin signal peptidase PulO and related peptidases
2062269685	371	38	32	c1274	Uncharacterised protein family (UPF0104).
2062198976	377	11	8	c1275	hypothetical protein
2062207363	473	6	11	c1275	general secretion pathway protein G
2062216438	176	4688	636	c1275	hypothetical protein
2062246678	782	27	26	c1275	Uncharacterized protein conserved in bacteria
2062246680	338	12	18	c1275	hypothetical protein
2062246681	215	0	23	c1275	hypothetical protein
2062314587	941	131	54	c1275	ATPases involved in chromosome partitioning
2062343510	77	0	0	c1275	hypothetical protein
2062394081	383	178	34	c1275	hypothetical protein
2062190029	71	0	0	c1294	hypothetical protein
2062299312	182	0	0	c1294	hypothetical protein
2062343507	767	73	8	c1294	FAD/FMN-containing dehydrogenases
2062343508	335	9	12	c1294	export-related chaperone CsaA
2062343509	968	46	4	c1294	FAD/FMN-containing dehydrogenases
2062395374	1175	34	15	c1294	Fe-S oxidoreductase
2062107702	1589	30	19	c1295	ATPases with chaperone activity, ATP-binding subunit
2062180338	503	8	26	c1295	ATPases with chaperone activity, ATP-binding subunit
2062299309	473	19	2	c1295	Molecular chaperone (small heat shock protein)
2062299310	182	22	0	c1295	tryptophan synthase, alpha chain (EC 4.2.1.20)(EC:4.2.1.20)
2062299313	380	0	0	c1295	ATPases with chaperone activity, ATP-binding subunit
2062107704	716	18	0	c13018	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and ex
2062107705	86	0	0	c13018	DNA polymerase I (EC 2.7.7.7)(EC:2.7.7.7)
2062387639	1718	59	2	c13018	arginyl-tRNA synthetase (EC 6.1.1.19)(EC:6.1.1.19)
2062195797	167	0	12	c1302	hypothetical protein

2062299308	728	477	19	c1302	Predicted methyltransferase
2062299311	512	504	45	c1302	Disulfide bond formation protein DsbB
2062387638	407	42	0	c1302	Short-chain alcohol dehydrogenase of unknown specificity
2062151906	593	13	37	c1308	ADP-glucose pyrophosphorylase(EC:2.7.7.27)
2062224256	362	11	14	c1308	Glycogen synthase
2062224257	686	25	12	c1308	Monomeric isocitrate dehydrogenase(EC:1.1.1.42)
2062224259	323	46	3	c1308	CBS domain.
2062224260	1304	62	15	c1308	Chloride channel protein EriC
2062248014	656	21	9	c1308	Predicted permease
2062344218	650	22	8	c1308	ADP-glucose pyrophosphorylase(EC:2.7.7.27)
2062171852	170	0	0	c1312	hypothetical protein
2062234571	344	20	3	c1312	hypothetical protein
2062248013	608	15	3	c1312	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having D
2062261285	227	31	26	c1312	hypothetical protein
2062322925	131	0	15	c1312	Isopropylmalate/homocitrate/citramalate synthases(EC:2.3.1.182)
2062338302	872	9	5	c1312	N-acetylmuramoyl-L-alanine amidase
2062401947	455	48	31	c1312	hypothetical protein
2062401948	626	18	8	c1312	hypothetical protein
2062112947	656	53	27	c1323	NAD-dependent aldehyde dehydrogenases(EC:1.2.1.3)
2062219036	695	19	7	c1323	Site-specific recombinase XerD
2062248011	545	165	40	c1323	NAD-dependent aldehyde dehydrogenases(EC:1.2.1.3)
2062340274	959	147	8	c1323	NAD-dependent aldehyde dehydrogenases(EC:1.2.1.3)
2062340275	926	50	13	c1323	ribokinase(EC:2.7.1.15)
2062388292	893	30	8	c1323	deoxyribose-phosphate aldolase(EC:4.1.2.4)
2062332642	665	2	0	c1330	DNA polymerase III, alpha subunit
2062392740	86	0	0	c1330	hypothetical protein
2062403885	911	3	4	c1330	DNA polymerase III, alpha subunit(EC:2.7.7.7)
2062413007	1241	96	9	c1330	threonine synthase(EC:4.2.3.1)
2062273561	590	80	8	c134	Uncharacterized protein conserved in bacteria
2062308276	305	13	0	c134	succinate semialdehyde dehydrogenase (EC 1.2.1.16)(EC:1.2.1.16)
2062308277	890	119	36	c134	Uncharacterized protein conserved in bacteria

2062308278	212	24	19	c134	ThiS family.
2062343525	1070	96	24	c134	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binc
2062343526	1031	202	53	c134	Uncharacterized protein conserved in bacteria
2062345527	605	99	48	c134	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II(EC:6.2.1.3)
2062387015	1394	72	12	c134	NAD-dependent aldehyde dehydrogenases
2062387016	1043	100	28	c134	Nitrate/nitrite transporter
2062387017	203	0	0	c134	NADPH:quinone reductase and related Zn-dependent oxidoreductases(EC:1.6.5.5
2062400645	1940	109	21	c134	Aldehyde:ferredoxin oxidoreductase(EC:1.2.7.5)
2062400646	563	14	23	c134	hypothetical protein
2062423332	836	33	10	c134	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II
2062136340	719	132	10	c1346	ABC-type multidrug transport system, ATPase and permease components
2062265106	1037	68	11	c1346	Dihydroxyacid dehydratase/phosphogluconate dehydratase(EC:4.2.1.9)
2062273560	509	57	37	c1346	Arabinose efflux permease
2062280656	473	108	13	c1346	UTP-hexose-1-phosphate uridylyltransferase (EC 2.7.7.10)/UDP-glucose-hexose-1-
2062300579	842	52	6	c1346	Cyanate permease
2062325509	470	66	6	c1346	Dihydroxyacid dehydratase/phosphogluconate dehydratase(EC:4.2.1.9)
2062340978	731	127	25	c1346	ABC-type multidrug transport system, ATPase and permease components
2062351199	164	12	0	c1346	hypothetical protein
2062358240	515	87	21	c1346	EamA-like transporter family.
2062415642	809	41	15	c1346	Galactokinase
2062415643	395	56	15	c1346	Galactokinase
2062415644	761	81	5	c1346	Gluconolactonase
2062248619	884	3	2	c1347	Isoleucyl-tRNA synthetase(EC:6.1.1.5)
2062248621	1109	17	5	c1347	Isoleucyl-tRNA synthetase (EC 6.1.1.5)(EC:6.1.1.5)
2062252432	431	46	12	c1347	Enoyl-CoA hydratase/carnithine racemase
2062280657	239	8	8	c1347	hypothetical protein
2062340919	728	12	7	c1347	Isoleucyl-tRNA synthetase (EC 6.1.1.5)(EC:6.1.1.5)
2062340920	236	8	4	c1347	Isoleucyl-tRNA synthetase (EC 6.1.1.5)
2062422709	206	0	0	c1347	hypothetical protein
2062107701	422	104	14	c1349	Trimethylamine:corrinoid methyltransferase
2062202207	1178	76	20	c1349	Trimethylamine:corrinoid methyltransferase

2062288328	533	4	26	c1349	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
2062288329	734	22	1	c1349	Glutamine synthetase(EC:6.3.1.2)
2062241043	398	146	15	c1354	Dihydroorotase and related cyclic amidohydrolases
2062241044	287	17	21	c1354	Transposase domain (DUF772).
2062252433	383	117	5	c1354	transposase, IS4 family
2062281888	674	175	53	c1354	Uncharacterized protein conserved in bacteria
2062317099	1502	4	10	c1354	hypothetical protein
2062317732	239	38	4	c1354	hypothetical protein
2062317733	326	12	28	c1354	Long-chain acyl-CoA synthetases (AMP-forming)(EC:6.2.1.3)
2062319661	944	161	16	c1354	Dihydroorotase and related cyclic amidohydrolases(EC:3.5.2.3)
2062404560	992	115	27	c1354	Delta-aminolevulinic acid dehydratase(EC:4.2.1.24)
2062411697	362	28	8	c1354	SpoVT / AbrB like domain.
2062118208	341	29	0	c1355	Cytochrome c556
2062118209	476	40	32	c1355	Flp pilus assembly protein TadD, contains TPR repeats
2062118210	848	103	15	c1355	Cytochrome c, mono- and diheme variants
2062129909	1205	80	18	c1355	beta-ketoadipyl CoA thiolase
2062299980	353	28	6	c1355	O-acetylhomoserine sulfhydrolase (EC 2.5.1.49)(EC:2.5.1.49)
2062299981	827	85	17	c1355	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)(EC:3.
2062299982	545	103	28	c1355	Protein of unknown function (DUF1185).
2062324862	455	51	9	c1355	3-hydroxyacyl-CoA dehydrogenase(EC:1.1.1.157)
2062324863	1040	90	13	c1355	3-hydroxyacyl-CoA dehydrogenase(EC:1.1.1.157)
2062378051	308	110	10	c1355	conserved hypothetical protein
2062142128	689	30	12	c1375	ABC-type antimicrobial peptide transport system, ATPase component(EC:3.6.3.-)
2062142130	143	35	0	c1375	hypothetical protein
2062142133	902	181	35	c1375	NAD/FAD-utilizing enzyme apparently involved in cell division
2062355056	1187	13	10	c1375	hypothetical protein
2062355059	566	28	9	c1375	Short-chain alcohol dehydrogenase of unknown specificity
2062362072	734	8	10	c1375	ABC-type transport system, involved in lipoprotein release, permease component
2062362073	641	50	31	c1375	Adenylate kinase (EC 2.7.4.3)(EC:2.7.4.3)
2062142131	632	22	14	c1377	glucosamine-6-phosphate isomerase(EC:3.5.99.6)
2062142132	1286	17	3	c1377	N-acetyl-beta-hexosaminidase

2062142134	443	14	14	c1377	2,4-dienoyl-CoA reductase (EC 1.3.1.34)(EC:1.3.1.34)
2062155789	1040	107	16	c1377	Proline racemase
2062355058	1094	101	13	c1377	N-acetylglucosamine-6-phosphate deacetylase
2062116217	1163	32	12	c1378	spermidine/putrescine ABC transporter ATP-binding subunit
2062183619	1043	294	40	c1378	Spermidine/putrescine-binding periplasmic protein
2062193160	383	34	10	c1378	4-carboxymuconolactone decarboxylase (EC 4.1.1.44)(EC:4.1.1.44)
2062213753	257	233	31	c1378	Uncharacterized conserved protein
2062213754	638	88	17	c1378	Uncharacterized conserved protein
2062225652	524	153	4	c1378	Uncharacterized protein involved in propionate catabolism
2062174467	434	28	7	c1386	Chromosome segregation ATPases
2062183618	410	20	5	c1386	7-cyano-7-deazaguanine reductase(EC:1.7.1.13)
2062213755	824	12	5	c1386	Chromosome segregation ATPases
2062225651	1682	17	11	c1386	Chromosome segregation ATPases
2062199631	737	19	18	c1397	Adenylate cyclase, family 3 (some proteins contain HAMP domain)
2062225653	263	0	8	c1397	Methylase of chemotaxis methyl-accepting proteins
2062238460	710	35	8	c1397	Chemotaxis response regulator containing a CheY-like receiver domain and a meth
2062238461	239	13	8	c1397	Chemotaxis protein histidine kinase and related kinases(EC:2.7.13.3)
2062238462	551	38	4	c1397	Chemotaxis signal transduction protein
2062258116	353	23	0	c1397	hypothetical protein
2062260028	1472	23	19	c1397	Chemotaxis protein histidine kinase and related kinases
2062299983	269	0	0	c1397	hypothetical protein
2062340977	419	17	17	c1397	Chemotaxis protein histidine kinase and related kinases(EC:2.7.13.3)
2062378052	212	5	5	c1397	Methylase of chemotaxis methyl-accepting proteins(EC:2.1.1.80)
2062378053	347	20	3	c1397	Response regulators consisting of a CheY-like receiver domain and a winged-helix
2062378054	299	27	0	c1397	STAS domain.
2062116220	1025	459	31	c1398	TRAP-type mannitol/chloroaromatic compound transport system, periplasmic comp
2062116221	599	28	12	c1398	UDP-N-acetylmuramate-alanine ligase
2062280633	116	0	0	c1398	L-glutamine synthetase (EC 6.3.1.2)(EC:6.3.1.2)
2062401941	773	254	26	c1398	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062401943	1418	66	13	c1398	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II
2062116222	2363	53	5	c14	assimilatory nitrite reductase (NAD(P)H) large subunit precursor (EC 1.7.1.4)(EC:1

2062116223	275	91	11	c14	Formate/nitrite family of transporters
2062213750	101	168	10	c14	hypothetical protein
2062213751	479	8	8	c1420	Fructose-2,6-bisphosphatase
2062213752	1001	30	6	c1420	hypothetical protein
2062258115	773	109	12	c1420	Spermidine synthase
2062258117	716	78	18	c1420	UDP-glucose pyrophosphorylase(EC:2.7.7.9)
2062258118	1175	4	14	c1420	Uncharacterized protein conserved in bacteria
2062119537	395	56	0	c1421	cobalamin-5''-phosphate synthase (EC 2.7.8.26)
2062169301	290	7	10	c1421	Predicted membrane protein
2062224266	353	14	25	c1421	arsenate reductase (glutaredoxin)
2062288310	374	32	11	c1421	Cobalamin-5-phosphate synthase
2062340924	1559	25	6	c1421	Cytosine deaminase and related metal-dependent hydrolases(EC:3.5.99.3)
2062340925	266	162	34	c1421	hypothetical protein
2062340926	461	20	9	c1421	MoxR-like ATPases
2062348679	326	28	12	c1421	Predicted membrane protein
2062354382	1130	424	39	c1421	Ca2+/Na+ antiporter
2062388926	947	45	15	c1421	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase(EC:2.4.2.
2062142141	488	10	8	c1426	pantetheine-phosphate adenylyltransferase, bacterial(EC:2.7.7.3)
2062155790	410	0	10	c1426	RNA polymerase, sigma 54 subunit, RpoN/SigL
2062175137	548	95	9	c1426	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin
2062188122	722	25	6	c1426	tryptophan synthase, alpha chain (EC 4.2.1.20)(EC:4.2.1.20)
2062199630	146	7	0	c1426	PspA/IM30 family.
2062217727	341	6	0	c1426	PspA/IM30 family.
2062249880	551	13	15	c1426	hypothetical protein
2062249882	200	255	35	c1426	hypothetical protein
2062261279	161	62	37	c1426	Rdx family.
2062298039	488	27	16	c1426	DNA mismatch repair protein MutS
2062348680	2321	20	9	c1426	DNA mismatch repair protein MutS
2062350550	245	4	16	c1426	hypothetical protein
2062358899	218	60	14	c1426	ribosomal protein S21
2062392105	890	33	8	c1426	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog

2062392106	380	5	5	c1426	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog
2062118237	1070	30	17	c1433	SAM dependent carboxyl methyltransferase.
2062188123	1412	15	5	c1433	Exoribonuclease R
2062188124	443	7	2	c1433	hypothetical protein
2062193158	551	9	11	c1433	hypothetical protein
2062193159	125	0	0	c1433	hypothetical protein
2062290985	1394	70	16	c1433	NAD/NADP transhydrogenase beta subunit(EC:1.6.1.2)
2062319666	1592	15	13	c1433	NAD(P) transhydrogenase, alpha subunit
2062193192	446	13	2	c1435	1-deoxy-D-xylulose-5-phosphate synthase (EC 2.2.1.7)
2062213749	59	0	0	c1435	hypothetical protein
2062222286	77	0	0	c1435	hypothetical protein
2062239744	1847	11	14	c1435	hypothetical protein
2062111604	188	27	27	c1457	hypothetical protein
2062145444	113	0	0	c1457	hypothetical protein
2062213748	392	41	18	c1457	Cupin domain.
2062258762	548	99	11	c1457	Predicted thiamine-pyrophosphate-binding protein
2062273562	293	65	3	c1457	hypothetical protein
2062280615	212	9	9	c1457	hypothetical protein
2062323582	971	14	10	c1457	hypothetical protein
2062350536	740	51	7	c1457	Putative protein-S-isoprenylcysteine methyltransferase
2062350537	359	72	22	c1457	Thiamine pyrophosphate-requiring enzymes
2062388932	563	87	43	c1457	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase(EC:4.1.2.-)
2062124755	920	36	2	c146	L-aspartate oxidase (EC 1.4.3.16)(EC:1.4.3.16)
2062124756	557	23	4	c146	peptide deformylase (EC 3.5.1.88)
2062167369	1250	30	6	c146	Predicted exporters of the RND superfamily
2062167371	959	51	6	c146	IMP cyclohydrolase/phosphoribosylaminoimidazolecarboxamide formyltransferase (
2062183617	227	31	0	c146	Factor for inversion stimulation Fis, transcriptional activator
2062342207	512	14	4	c146	L-aspartate oxidase (EC 1.4.3.16)(EC:1.4.3.16)
2062378081	971	27	5	c146	tRNA-U20-dihydrouridine synthase(EC:1.-)
2062212468	224	0	4	c1461	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062225591	692	13	3	c1461	hypothetical protein

2062235221	683	6	7	c1461	hypothetical protein
2062310734	263	34	0	c1461	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062362736	530	72	6	c1461	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062198348	437	53	5	c1464	Cytochrome c553
2062212467	632	152	6	c1464	Cytochrome c553
2062220301	698	186	32	c1464	Cytochrome c553(EC:1.9.3.1)
2062220302	899	92	18	c1464	ABC-type uncharacterized transport system, permease component
2062258124	494	22	8	c1464	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes
2062258125	341	53	15	c1464	Cytochrome c553(EC:1.9.3.1)
2062365942	92	0	0	c1464	hypothetical protein
2062365943	608	20	3	c1464	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes
2062365944	476	57	11	c1464	Cytochrome c553
2062388281	2045	198	23	c1464	vacuolar-type H(+)-translocating pyrophosphatase(EC:3.6.1.1)
2062148690	221	23	9	c1466	hypothetical protein
2062220984	158	6	0	c1466	hypothetical protein
2062220985	200	5	0	c1466	hypothetical protein
2062235226	209	10	0	c1466	hypothetical protein
2062292240	623	32	29	c1466	hypothetical protein
2062292241	254	28	0	c1466	hypothetical protein
2062331985	209	0	5	c1466	Helix-turn-helix.
2062332640	2495	9	8	c1466	Organic solvent tolerance protein OstA
2062333913	323	22	3	c1466	Predicted acyl-CoA transferases/carnitine dehydratase
2062335767	509	10	14	c1466	Staphylococcal nuclease homologue.
2062369669	632	51	3	c1466	Predicted acyl-CoA transferases/carnitine dehydratase(EC:5.1.99.4)
2062376165	443	45	14	c1466	Acyl dehydratase
2062193176	1109	19	14	c1502	Aspartate/tyrosine/aromatic aminotransferase(EC:2.6.1.-)
2062265112	1409	11	7	c1502	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062294793	386	78	21	c1502	Dihydropteroate synthase and related enzymes(EC:2.5.1.15)
2062323578	872	18	7	c1502	hypothetical protein
2062203468	2792	2235	379	c151	formate dehydrogenase alpha subunit (EC 1.2.1.2)(EC:1.2.1.2)
2062223003	299	0	20	c151	Uncharacterized protein conserved in bacteria

2062248622	269	115	7	c151	Polysulphide reductase, NrfD.
2062258109	743	8	20	c151	Uncharacterized protein conserved in bacteria
2062261284	1649	78	30	c151	hypothetical protein
2062269684	248	198	101	c151	hypothetical protein
2062281906	719	353	78	c151	Formate-dependent nitrite reductase, membrane component
2062290988	740	84	26	c151	Heterodisulfide reductase, subunit A and related polyferredoxins
2062305097	647	4417	323	c151	Fe-S-cluster-containing hydrogenase components 1(EC:1.2.1.2)
2062314586	125	344	0	c151	hypothetical protein
2062412399	515	25	29	c151	hypothetical protein
2062413015	221	5	0	c151	MORN repeat.
2062258110	467	9	0	c15130	hypothetical protein(EC:6.1.1.5)
2062258111	278	0	4	c15130	Isoleucyl-tRNA synthetase (EC 6.1.1.5)(EC:6.1.1.5)
2062267713	503	6	4	c15130	Isoleucyl-tRNA synthetase (EC 6.1.1.5)(EC:6.1.1.5)
2062324848	671	30	6	c15130	Isoleucyl-tRNA synthetase(EC:6.1.1.5)
2062425291	725	39	11	c15130	Isoleucyl-tRNA synthetase (EC 6.1.1.5)
2062112276	404	12	0	c1515	methionine-R-sulfoxide reductase(EC:1.8.4.12)
2062195798	659	82	5	c1515	Nucleoside 2-deoxyribosyltransferase
2062242273	419	38	0	c1515	conserved hypothetical protein TIGR00149
2062242274	521	67	25	c1515	ABC-type transport system involved in cytochrome c biogenesis, permease compor
2062242275	1112	22	6	c1515	Outer membrane protein
2062267714	380	113	32	c1515	CTP synthase (EC 6.3.4.2)(EC:6.3.4.2)
2062267715	290	24	59	c1515	Cytochrome c-type biogenesis protein CcmE
2062267716	515	0	4	c1515	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (EC 6.3.5.-)
2062267717	413	22	10	c1515	Signal transduction histidine kinase involved in nitrogen fixation and metabolism reg
2062267718	1481	43	14	c1515	Signal transduction histidine kinase involved in nitrogen fixation and metabolism reg
2062324843	308	13	10	c1515	Signal transduction histidine kinase involved in nitrogen fixation and metabolism reg
2062324845	935	70	16	c1515	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (EC 6.3.5.-)(EC:6.3.5
2062324846	203	69	64	c1515	Cytochrome c-type biogenesis protein CcmE
2062324847	536	88	15	c1515	hypothetical protein
2062112942	119	25	8	c152	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)(EC:1.1.1.100)
2062122785	431	12	0	c152	Cytosine/adenosine deaminases

2062156429	929	400	8	c152	[Acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39)(EC:2.3.1.39)
2062167374	650	105	3	c152	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)(EC:1.1.1.100)
2062172542	284	32	0	c152	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family(EC:5.2.1.8,EC:5.
2062175813	212	57	0	c152	UDP-2,3-diacylglucosamine hydrolase (EC 3.6.1.-)(EC:3.6.1.-)
2062196444	254	75	0	c152	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family(EC:5.2.1.8)
2062249881	152	0	0	c152	hypothetical protein
2062334497	311	119	0	c152	LSU ribosomal protein L21P
2062334498	257	78	8	c152	LSU ribosomal protein L27P
2062180972	143	0	0	c1522	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)(EC:2.7.7.6)
2062180973	1109	72	19	c1522	DNA-directed RNA polymerase subunit beta'' (EC 2.7.7.6)(EC:2.7.7.6)
2062355040	512	137	16	c1522	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)(EC:2.7.7.6)
2062355041	1040	195	36	c1522	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)(EC:2.7.7.6)
2062359518	566	293	72	c1522	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)(EC:2.7.7.6)
2062180970	164	0	18	c1526	NifU homolog involved in Fe-S cluster formation
2062187486	425	24	99	c1526	hypothetical protein
2062193172	371	0	5	c1526	hypothetical protein
2062299938	185	11	0	c1526	hypothetical protein
2062319665	155	0	0	c1526	NifU homolog involved in Fe-S cluster formation
2062340269	200	55	20	c1526	hypothetical protein
2062355042	188	0	16	c1526	hypothetical protein
2062411698	926	31	18	c1526	Thioredoxin-like proteins and domains
2062411699	392	43	18	c1526	Uncharacterized conserved protein
2062421435	206	5	10	c1526	hypothetical protein
2062421436	512	4	0	c1526	Biotin carboxylase
2062107695	749	8	11	c1528	Uncharacterized protein conserved in bacteria containing thioredoxin-like domain
2062107697	569	14	28	c1528	Uncharacterized conserved protein
2062144795	335	21	9	c1528	flagellar motor switch protein FliN
2062193190	539	56	11	c1528	Type II secretory pathway, pullulanase PulA and related glycosidases
2062196443	530	60	9	c1528	Type II secretory pathway, pullulanase PulA and related glycosidases
2062249251	191	10	5	c1528	hypothetical protein
2062249252	140	0	0	c1528	hypothetical protein

2062249253	686	32	16	c1528	isoamylase
2062249254	1052	48	18	c1528	S-adenosylmethionine:tRNA ribosyltransferase-isomerase(EC:5.-)
2062249255	332	30	12	c1528	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal domain
2062242868	935	34	12	c1531	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain(
2062245414	215	70	19	c1531	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062271610	422	17	7	c1531	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062271611	137	0	0	c1531	hypothetical protein
2062350551	404	5	5	c1531	Phosphoserine aminotransferase(EC:2.6.1.52)
2062350552	323	25	0	c1531	Pyridoxal phosphate biosynthesis protein
2062242869	1451	54	28	c1537	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II(EC:6.2.1.-)
2062242870	329	179	15	c1537	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs
2062283797	1133	69	12	c1537	Glycine cleavage system T protein (aminomethyltransferase)
2062292894	107	0	0	c1537	hypothetical protein
2062144794	1466	213	23	c1546	NADH dehydrogenase subunit L (EC 1.6.5.3)
2062167377	500	14	0	c1546	methionyl-tRNA synthetase (EC 6.1.1.10)(EC:6.1.1.10)
2062189403	149	13	13	c1546	hypothetical protein
2062220989	77	0	0	c1546	hypothetical protein
2062224261	431	14	0	c1546	NADH dehydrogenase subunit L (EC 1.6.5.3)(EC:1.6.5.3)
2062292236	116	0	0	c1546	hypothetical protein(EC:4.2.1.-)
2062292895	269	37	0	c1546	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)(EC:4.2.1.-)
2062319670	518	14	6	c1546	methionyl-tRNA synthetase (EC 6.1.1.10)(EC:6.1.1.10)
2062369048	389	10	0	c1546	Outer membrane protein (OmpH-like).
2062369049	236	8	8	c1546	Predicted RNA-binding protein containing KH domain, possibly ribosomal protein
2062392730	299	10	0	c1546	glutamyl-tRNA(Gln) and/or aspartyl-tRNA(Asn) amidotransferase, C subunit
2062167407	464	13	11	c1547	cold-shock DNA-binding protein family
2062167408	938	86	4	c1547	Glycine/D-amino acid oxidases (deaminating)
2062241035	821	49	4	c1547	hypothetical protein
2062265109	188	5	16	c1547	Predicted Zn-dependent proteases and their inactivated homologs
2062265110	989	58	25	c1547	Predicted ornithine cyclodeaminase, mu-crystallin homolog(EC:4.3.1.12)
2062288980	1064	16	18	c1547	argininosuccinate synthase
2062288981	164	0	0	c1547	argininosuccinate synthase (EC 6.3.4.5)(EC:6.3.4.5)

2062420779	812	107	26	c1547	microcin-processing peptidase 2. Unknown type peptidase. MEROPS family U62
2062119536	374	0	3	c1551	hypothetical protein
2062335167	1265	81	59	c1551	Uncharacterized protein related to the periplasmic component of the Tol biopolymer
2062369042	2093	82	9	c1551	Periplasmic protease
2062369044	185	5	0	c1551	hypothetical protein
2062369047	599	18	13	c1551	hypothetical protein
2062108417	164	0	0	c1552	hypothetical protein
2062133117	389	0	0	c1552	tRNA splicing endonuclease(EC:3.1.27.9)
2062162900	1286	2	2	c1552	transporter, CPA2 family (2.A.37)
2062255618	344	32	29	c1552	LSU ribosomal protein L10AE
2062299956	73	0	0	c1552	(tRNA)
2062299957	491	2	0	c1552	hypothetical protein
2062343524	644	3	0	c1552	hypothetical protein
2062354381	119	0	0	c1552	hypothetical protein(EC:3.1.27.9)
2062392751	215	5	9	c1552	LSU ribosomal protein L10AE
2062154485	1199	239	30	c1558	Xaa-Pro aminopeptidase(EC:3.5.3.3)
2062225595	173	243	6	c1558	hypothetical protein
2062260025	68	0	0	c1558	hypothetical protein
2062301235	305	66	20	c1558	Zn-dependent dipeptidase, microsomal dipeptidase homolog
2062324870	1034	43	15	c1558	IMP dehydrogenase/GMP reductase(EC:1.7.1.7)
2062386968	743	19	1	c1558	Protein of unknown function (DUF3726).
2062392743	728	3	0	c1558	hypothetical protein
2062413001	920	107	7	c1558	hypothetical protein
2062418870	461	41	9	c1558	Predicted phosphoribosyltransferases
2062112272	1994	23	6	c1565	Adenylate cyclase, family 3 (some proteins contain HAMP domain)
2062142121	548	2	5	c1565	hypothetical protein
2062154479	299	57	17	c1565	Predicted permease
2062334499	845	21	8	c1565	hypothetical protein
2062422730	140	7	0	c1565	hypothetical protein
2062224265	84	24	0	c1570	(tRNA)
2062234576	953	4	2	c1570	Zn-dependent oligopeptidases(EC:3.4.24.70)

2062324871	425	16	5	c1570	methionyl-tRNA synthetase (EC 6.1.1.10)(EC:6.1.1.10)
2062372929	734	74	26	c1570	ATPases involved in chromosome partitioning
2062372930	1208	22	7	c1570	methionyl-tRNA synthetase (EC 6.1.1.10)(EC:6.1.1.10)
2062379985	233	9	0	c1570	oligopeptidase A (EC:3.4.24.70). Metallo peptidase. MEROPS family M03A(EC:3.4
2062412363	194	5	0	c1570	methionyl-tRNA synthetase (EC 6.1.1.10)(EC:6.1.1.10)
2062134412	1556	21	6	c1578	Uncharacterized conserved protein
2062219037	233	86	34	c1578	ATP synthase F0 subcomplex A subunit(EC:3.6.3.14)
2062223000	374	21	0	c1578	hypothetical protein
2062244142	815	173	18	c1578	propionyl-CoA synthetase (EC 6.2.1.17)(EC:6.2.1.17)
2062288339	1928	121	16	c1578	acetyl-coenzyme A synthetase (EC 6.2.1.1)(EC:6.2.1.1)
2062325515	347	337	66	c1578	ATP synthase F0 subcomplex C subunit(EC:3.6.3.14)
2062325516	386	197	8	c1578	F0F1-type ATP synthase, subunit a
2062126049	458	15	0	c1581	Phosphate transport regulator (distant homolog of PhoU)
2062128585	905	109	43	c1581	Dihydrodipicolinate synthase/N-acetylneuraminate lyase(EC:4.2.1.52)
2062156439	1346	103	22	c1581	Glycine/D-amino acid oxidases (deaminating)
2062414409	902	333	72	c1581	hypothetical protein
2062207986	485	8	6	c1593	DnaJ-class molecular chaperone with C-terminal Zn finger domain
2062292909	1400	47	11	c1593	ABC-type Fe3+ transport system, permease component
2062292910	383	86	5	c1593	D-alanyl-D-alanine carboxypeptidase
2062301236	617	36	6	c1593	hypothetical protein
2062359524	170	0	0	c1593	hypothetical protein
2062362782	620	32	13	c1593	hypothetical protein
2062362783	407	15	7	c1593	hypothetical protein
2062369045	809	40	9	c1593	D-alanyl-D-alanine carboxypeptidase(EC:3.4.16.4)
2062392738	632	25	11	c1593	orotidine 5''-phosphate decarboxylase, subfamily 2
2062402554	968	31	11	c1593	ABC transporter periplasmic binding protein, thiB subfamily
2062402555	290	41	0	c1593	ABC-type Fe3+ transport system, permease component
2062124773	446	123	7	c1595	ABC-type Mn2+/Zn2+ transport systems, permease components
2062209886	269	26	7	c1595	ABC-type Zn2+ transport system, periplasmic component/surface adhesin
2062225598	497	8	12	c1595	Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory anc
2062234572	377	127	72	c1595	ABC-type Mn2+/Zn2+ transport systems, permease components

2062280629	794	38	3	c1595	ABC-type Mn/Zn transport systems, ATPase component(EC:3.6.3.-)
2062290295	290	10	0	c1595	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases(EC:1.3.99.22)
2062323568	794	4	14	c1595	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases(EC:1.3.99.22)
2062324865	302	7	7	c1595	hypothetical protein
2062324866	518	8	8	c1595	Uncharacterized protein conserved in bacteria
2062225596	488	94	10	c1619	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family(EC:5.2.1.8)
2062278660	1226	85	15	c1619	DNA gyrase subunit A (EC 5.99.1.3)
2062292911	851	72	19	c1619	DNA gyrase subunit A (EC 5.99.1.3)(EC:5.99.1.3)
2062292912	458	22	2	c1619	hypothetical protein
2062292913	407	140	22	c1619	Ferredoxin
2062292914	350	37	29	c1619	Iron-sulfur cluster assembly accessory protein
2062292915	299	10	20	c1619	hypothetical protein
2062395377	566	23	11	c1619	Peroxiredoxin
2062395378	254	398	55	c1619	Predicted transcriptional regulator, BolA superfamily
2062113630	233	4	0	c1621	hypothetical protein
2062142775	716	95	22	c1621	hypothetical protein
2062149988	1223	49	7	c1621	Putative Zn-dependent protease, contains TPR repeats
2062174463	260	38	31	c1621	Zn-ribbon protein, possibly nucleic acid-binding
2062190679	884	55	17	c1621	Threonine dehydratase(EC:4.3.1.19)
2062220957	317	66	13	c1621	hypothetical protein
2062241042	365	3	22	c1621	hypothetical protein
2062265107	143	105	0	c1621	hypothetical protein
2062337065	167	48	24	c1621	Anthranilate/para-aminobenzoate synthases component II(EC:4.1.3.27)
2062337066	509	65	22	c1621	Biopolymer transport proteins
2062370971	344	84	41	c1621	hypothetical protein
2062370972	482	39	19	c1621	hypothetical protein
2062124748	1406	10	6	c1622	hypothetical protein
2062142111	560	30	14	c1622	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases(EC:6.2.1.16)
2062157103	431	14	9	c1622	hypothetical protein
2062183611	587	31	12	c1622	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
2062249888	578	14	12	c1622	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases(EC:6.2.1.16)

2062335136	233	0	13	c1622	ATPase components of ABC transporters with duplicated ATPase domains
2062423331	281	28	39	c1622	Bacterial nucleoid DNA-binding protein
2062161598	809	135	22	c164	aminomethyltransferase (EC 2.1.2.10)(EC:2.1.2.10)
2062198320	545	108	29	c164	methylmalonate-semialdehyde dehydrogenase [acylating] (EC 1.2.1.27)(EC:1.2.1.2
2062202842	950	198	12	c164	methylmalonate-semialdehyde dehydrogenase [acylating] (EC 1.2.1.27)(EC:1.2.1.2
2062204763	560	16	0	c164	NADH:ubiquinone oxidoreductase subunit 2 (chain N)
2062224912	203	44	30	c164	hypothetical protein
2062267711	200	70	10	c164	hypothetical protein
2062273563	605	51	2	c164	NADH dehydrogenase subunit N (EC 1.6.5.3)(EC:1.6.5.3)
2062278663	389	183	23	c164	prepilin-type N-terminal cleavage/methylation domain
2062308269	446	114	45	c164	NADH:ubiquinone oxidoreductase subunit 2 (chain N)
2062335137	1289	154	19	c164	Glycine/serine hydroxymethyltransferase
2062340276	1307	35	6	c164	hypothetical protein
2062350533	425	136	52	c164	hypothetical protein
2062142112	2690	202	24	c1646	FAD/FMN-containing dehydrogenases
2062142113	1622	24	0	c1646	gamma-glutamyltranspeptidase
2062290280	89	0	0	c1646	hypothetical protein
2062292886	410	10	10	c1646	Uncharacterized conserved protein
2062292887	893	7	10	c1646	riboflavin kinase/FMN adenylyltransferase(EC:2.7.7.2,EC:2.7.1.26)
2062193170	188	5	5	c16488	hypothetical protein
2062327446	536	9	0	c16488	Gamma-glutamyl phosphate reductase(EC:1.2.1.41)
2062353746	776	17	6	c16488	Outer membrane protein/protective antigen OMA87
2062363989	392	23	13	c16488	Outer membrane protein/protective antigen OMA87
2062413004	776	3	5	c16488	glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41)(EC:2.7.2.11,EC:1.2.1.41,
2062145446	65	0	0	c1656	hypothetical protein
2062145447	554	14	25	c1656	hypothetical protein
2062224911	2309	34	6	c1656	phosphoenolpyruvate-protein phosphotransferase
2062388917	1061	36	17	c1656	DNA polymerase III, delta subunit
2062394078	314	57	6	c1656	NADH:flavin oxidoreductases, Old Yellow Enzyme family
2062190682	83	0	0	c1666	hypothetical protein
2062224910	734	322	23	c1666	formylmethanofuran dehydrogenase subunit C(EC:1.2.99.5)

2062317097	887	768	54	c1666	formylmethanofuran-tetrahydromethanopterin formyltransferase (EC 2.3.1.101)
2062388918	530	30	8	c1666	hypothetical protein
2062219032	944	93	30	c1668	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)(EC:2.5.1.7)
2062219033	248	101	73	c1668	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)(EC:2.5.1.7)
2062261290	1544	40	10	c1668	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II
2062367173	245	0	0	c1668	hypothetical protein
2062413010	854	26	15	c1668	small GTP-binding protein domain
2062142145	1106	0	2	c1678	Peptidase family M50.
2062265805	809	0	2	c1678	hypothetical protein
2062281254	230	0	0	c1678	Orotate phosphoribosyltransferase(EC:2.4.2.10)
2062353118	497	0	0	c1678	[SSU ribosomal protein S18P]-alanine acetyltransferase (EC 2.3.1.128)(EC:2.3.1.1
2062353119	281	0	0	c1678	hypothetical protein
2062358250	746	3	0	c1678	hypothetical protein
2062188759	548	51	5	c1680	5,10-methenyltetrahydrofolate synthetase
2062191919	365	55	8	c1680	hypothetical protein
2062220948	1289	171	21	c1680	O-acetylhomoserine sulfhydrolase (EC 2.5.1.49)(EC:2.5.1.49)
2062220949	497	121	24	c1680	O-acetylhomoserine sulfhydrolase (EC 2.5.1.49)(EC:2.5.1.49)
2062260022	437	23	7	c1680	Acetyltransferases
2062260023	611	33	15	c1680	adenosylhomocysteinase (EC 3.3.1.1)(EC:3.3.1.1)
2062288315	803	17	12	c1680	adenosylhomocysteinase (EC 3.3.1.1)(EC:3.3.1.1)
2062322914	257	0	0	c1680	hypothetical protein
2062322915	788	80	18	c1680	hypothetical protein
2062327448	77	0	0	c1680	hypothetical protein
2062386969	221	5	0	c1680	hypothetical protein
2062386970	1028	157	33	c1680	K+-dependent Na+/Ca+ exchanger related-protein
2062150613	317	47	0	c1686	Xaa-Pro aminopeptidase
2062202211	386	21	3	c1686	dihydroneopterin aldolase
2062268361	1313	35	12	c1686	Glycine/D-amino acid oxidases (deaminating)
2062268362	491	37	8	c1686	Uncharacterized conserved protein
2062327447	1166	174	17	c1686	amidohydrolase(EC:3.5.1.32)
2062150614	935	9	2	c1687	hypothetical protein

2062183612	74	0	0	c1687	hypothetical protein
2062209271	140	0	0	c1687	translation elongation factor P (EF-P)
2062340979	368	22	0	c1687	MoxR-like ATPases(EC:3.6.3.-)
2062371625	875	13	2	c1687	Uncharacterized conserved protein (some members contain a von Willebrand factor
2062396654	260	19	0	c1687	MoxR-like ATPases(EC:3.6.3.-)
2062396655	239	8	8	c1687	MoxR-like ATPases(EC:3.6.3.-)
2062193187	257	4	0	c1690	hypothetical protein
2062201578	1109	16	7	c1690	hypothetical protein
2062209272	443	11	0	c1690	DNA polymerase I - 3''-5'' exonuclease and polymerase domains
2062220951	1343	25	8	c1690	DNA polymerase I - 3''-5'' exonuclease and polymerase domains(EC:2.7.7.7)
2062350553	194	5	10	c1690	hypothetical protein
2062371626	305	23	7	c1690	5''-3'' exonuclease (including N-terminal domain of PolI)
2062371627	566	19	12	c1690	5''-3'' exonuclease (including N-terminal domain of PolI)(EC:2.7.7.7)
2062126021	248	20	4	c1699	protease FtsH subunit HflK(EC:3.4.-)
2062193188	254	0	0	c1699	ATP-dependent protease HslVU (ClpYQ), ATPase subunit
2062255615	641	0	0	c1699	Membrane protease subunits, stomatin/prohibitin homologs(EC:3.4.-)
2062329392	239	54	0	c1699	ATP-dependent protease HslVU (ClpYQ), peptidase subunit
2062365304	251	20	0	c1699	HslV component of HslUV peptidase. Threonine peptidase. MEROPS family T01B
2062392741	938	11	1	c1699	heat shock protein HslVU, ATPase subunit HslU
2062236547	506	836	43	c17037	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)(EC:4.2.1.60)
2062287059	665	1030	30	c17037	3-oxoacyl-[acyl-carrier-protein] synthase I (EC 2.3.1.41)(EC:2.3.1.41)
2062342185	950	213	20	c17037	Cystathionine beta-lyases/cystathionine gamma-synthases(EC:2.5.1.-)
2062358234	68	0	0	c17037	hypothetical protein(EC:2.5.1.-)
2062373594	377	244	24	c17037	3-oxoacyl-[acyl-carrier-protein] synthase I (EC 2.3.1.41)(EC:2.3.1.41)
2062135644	413	65	46	c171	Flagellar hook-associated protein
2062158374	683	78	9	c171	16S rRNA methyltransferase GidB(EC:2.1.-)
2062201595	305	0	0	c171	Cystathionine beta-lyases/cystathionine gamma-synthases
2062201597	299	23	3	c171	Enzyme related to GTP cyclohydrolase I
2062220956	230	48	70	c171	carbon storage regulator (csrA)
2062268351	1301	52	12	c171	flagellar hook-associated protein 3
2062268352	218	9	9	c171	hypothetical protein

2062272945	512	92	35	c171	exodeoxyribonuclease III (xth)(EC:3.1.11.2)
2062272946	242	4	0	c171	Exonuclease III(EC:3.1.11.2)
2062291019	395	76	5	c171	hypothetical protein
2062291020	572	201	51	c171	segregation and condensation protein B
2062294174	503	22	20	c171	Uncharacterized protein conserved in bacteria
2062419498	200	15	30	c171	hypothetical protein
2062131206	551	27	9	c1718	hypothetical protein
2062131207	434	198	46	c1718	hypothetical protein
2062131208	92	0	0	c1718	hypothetical protein
2062131209	200	10	25	c1718	hypothetical protein
2062131210	755	8	0	c1718	Predicted dehydrogenase
2062183589	512	14	23	c1718	Protein of unknown function (DUF3015).
2062291018	341	59	9	c1718	Predicted dehydrogenase
2062296084	668	57	13	c1718	Uncharacterized conserved protein
2062328730	449	29	18	c1718	Protein of unknown function (DUF3015).
2062328731	1427	87	34	c1718	2[4Fe-4S] protein, putative
2062328732	236	25	13	c1718	Capsular polysaccharide biosynthesis protein
2062328733	1622	82	20	c1718	dihydroxyacid dehydratase (EC 4.2.1.9)(EC:4.2.1.9)
2062328734	1046	78	39	c1718	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)
2062365305	287	31	10	c1718	Sigma 54 modulation protein / S30EA ribosomal protein.
2062126695	758	91	26	c172	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062151913	668	139	3	c172	EamA-like transporter family.
2062199629	1511	64	13	c172	Superfamily II DNA and RNA helicases(EC:3.6.1.-)
2062212464	737	115	26	c172	Short-chain dehydrogenases of various substrate specificities
2062278659	497	8	6	c172	Uncharacterized protein conserved in bacteria
2062296739	236	0	4	c172	Intracellular septation protein A
2062321615	221	0	0	c172	hypothetical protein
2062335124	398	25	5	c172	Predicted lactoylglutathione lyase
2062370975	1058	43	5	c172	adenosine deaminase(EC:3.5.4.4)
2062157102	392	41	18	c1722	glycine cleavage system H protein
2062198343	503	40	22	c1722	Arylsulfatase A and related enzymes

2062209883	683	117	26	c1722	Arylsulfatase A and related enzymes
2062219035	311	35	0	c1722	hypothetical protein
2062222974	275	22	7	c1722	hypothetical protein
2062222978	413	34	22	c1722	Molybdopterin converting factor, large subunit
2062246691	353	40	11	c1722	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain(
2062413017	431	9	12	c1722	Arylsulfatase A and related enzymes
2062248012	884	60	42	c1738	carbamoyl-phosphate synthase small subunit(EC:6.3.5.5)
2062271620	329	12	15	c1738	Flagellar motor switch protein
2062271621	1319	14	3	c1738	hypothetical protein
2062290286	635	39	2	c1738	Lysophospholipase L1 and related esterases(EC:3.1.1.5,EC:3.1.2.-)
2062294787	1217	7	7	c1738	Superfamily I DNA and RNA helicases(EC:3.6.1.-)
2062296743	392	15	0	c1748	hypothetical protein
2062386308	1271	59	12	c1748	Uncharacterized conserved protein
2062209895	719	38	0	c1755	GTP-binding protein HflX (EC 3.1.5.-)
2062209896	581	43	0	c1755	GTP-binding protein HflX (EC 3.1.5.-)
2062352507	641	148	11	c1755	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062352508	74	14	0	c1755	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062352509	584	26	10	c1755	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062386309	587	34	3	c1755	ATP-dependent Clp protease ATP-binding subunit ClpX (EC 3.4.21.92)
2062386319	983	54	6	c1755	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062180967	101	0	0	c1757	hypothetical protein
2062219047	572	42	10	c1757	hypothetical protein
2062228732	347	40	32	c1757	hypothetical protein(EC:2.9.1.-)
2062312705	236	25	0	c1757	Nucleoside-diphosphate-sugar epimerases(EC:4.2.1.46)
2062373587	773	28	16	c1757	Nucleoside-diphosphate-sugar epimerases(EC:4.2.1.46)
2062373588	701	111	23	c1757	Predicted ATPase(EC:2.9.1.-)
2062373589	1037	130	31	c1757	RecA protein
2062108414	149	0	0	c1771	hypothetical protein
2062108415	194	41	5	c1771	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)(
2062152597	284	14	0	c1771	imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-)(EC:4.1.3.-)
2062156438	929	36	5	c1771	hypothetical protein

2062172545	575	57	17	c1771	Predicted sugar kinase
2062219666	971	54	10	c1771	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)(
2062288312	239	46	4	c1771	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)(
2062340257	527	6	6	c1771	hypothetical protein
2062392746	719	36	13	c1771	yjeF N-terminal region
2062198321	746	8	13	c1782	Methylase involved in ubiquinone/menaquinone biosynthesis
2062207349	215	47	19	c1782	Sortase and related acyltransferases(EC:2.3.1.183)
2062207350	233	9	0	c1782	Sortase and related acyltransferases(EC:2.3.1.183)
2062219048	623	0	26	c1782	Glutathione S-transferase, N-terminal domain.
2062229409	413	41	15	c1795	ABC-type antimicrobial peptide transport system, ATPase component
2062229410	506	49	32	c1795	Gamma-glutamyl phosphate reductase(EC:1.2.1.41)
2062299947	392	10	3	c1795	Outer membrane protein/protective antigen OMA87
2062319697	2009	8	7	c1795	outer membrane protein assembly complex, YaeT protein
2062220963	842	133	19	c18	Prephenate dehydratase
2062220964	767	37	12	c18	Protein related to penicillin acylase
2062229407	284	32	46	c18	ACT domain.(EC:1.1.1.95)
2062229408	1469	24	5	c18	DNA topoisomerase IV subunit A (EC 5.99.1.3)(EC:5.99.1.-)
2062319696	116	0	0	c18	hypothetical protein
2062319698	503	8	12	c18	hypothetical protein
2062354380	1217	23	12	c18	PilZ domain.
2062122788	158	0	0	c1800	phosphoglycerate kinase (EC 2.7.2.3)(EC:2.7.2.3)
2062156432	1034	8	2	c1800	pyruvate kinase (EC 2.7.1.40)(EC:2.7.1.40)
2062156433	269	0	0	c1800	fructose-bisphosphate aldolase (EC 4.1.2.13)(EC:4.1.2.13)
2062213738	809	22	10	c1800	phosphoglycerate kinase (EC 2.7.2.3)(EC:2.7.2.3)
2062113632	1466	26	12	c1805	2,4-dienoyl-CoA reductase (EC 1.3.1.34)(EC:1.3.1.34)
2062113633	1067	155	27	c1805	bacterial peptide chain release factor 1 (bRF-1)
2062122787	695	63	27	c1805	dihydrolipoamide dehydrogenase (EC 1.8.1.4)(EC:1.8.1.4)
2062124113	1325	69	43	c1805	transcription termination factor Rho
2062149991	1136	33	58	c1805	dihydrolipoamide dehydrogenase (EC 1.8.1.4)(EC:1.8.1.4)
2062272266	1325	89	6	c1805	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase
2062138908	800	3	1	c1813	Truncated, possibly inactive, lysyl-tRNA synthetase (class II)(EC:6.1.1.6)

2062142126	239	0	0	c1813	translation elongation factor P (EF-P)
2062142127	473	11	2	c1813	Truncated, possibly inactive, lysyl-tRNA synthetase (class II)
2062186872	212	28	61	c1813	hypothetical protein
2062355057	242	8	29	c1813	hypothetical protein
2062362071	182	0	0	c1813	hypothetical protein
2062129924	410	0	0	c1814	DNA or RNA helicases of superfamily II
2062186868	62	0	0	c1814	hypothetical protein
2062186870	476	67	0	c1814	Major capsid protein Gp23.
2062188752	410	5	0	c1814	Recombination, repair and ssDNA binding protein UvsY.
2062249895	311	26	0	c1814	T4-like virus tail tube protein gp19.
2062343506	950	5	0	c1814	DNA or RNA helicases of superfamily II
2062186871	329	12	30	c1819	hypothetical protein
2062249892	233	26	26	c1819	hypothetical protein
2062249893	662	113	62	c1819	LSU ribosomal protein L3P
2062249896	857	123	12	c1819	ABC-type multidrug transport system, ATPase component
2062278672	410	5	7	c1819	O-6-methylguanine DNA methyltransferase(EC:2.1.1.63)
2062286372	470	143	19	c1819	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/
2062286373	491	98	26	c1819	hypothetical protein
2062290318	1004	85	37	c1819	putative NAD(P)H quinone oxidoreductase, PIG3 family
2062296081	401	42	22	c1819	ABC-type molybdenum transport system, ATPase component/photorepair protein P
2062325504	1058	3	2	c1819	ABC-type molybdenum transport system, ATPase component/photorepair protein P
2062325505	1481	49	14	c1819	ABC-type multidrug transport system, ATPase and permease components
2062345533	1109	44	10	c1819	ABC-type multidrug transport system, permease component
2062363984	827	7	19	c1819	conserved hypothetical protein TIGR00247
2062126029	230	35	26	c183	hypothetical protein
2062126048	1319	121	39	c183	Acyl-CoA dehydrogenases
2062142100	956	44	15	c183	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)(EC:1.17.1.2)
2062183616	1112	182	70	c183	ribosomal protein S2, bacterial type
2062192573	554	29	11	c183	Xanthosine triphosphate pyrophosphatase
2062225649	563	34	20	c183	ribosome recycling factor
2062225650	776	108	23	c183	translation elongation factor Ts

2062229415	437	27	2	c183	Acetyltransferases
2062245415	422	19	7	c183	Uncharacterized conserved protein
2062278670	1199	133	48	c183	3-oxoacyl-[acyl-carrier-protein] synthase II (EC 2.3.1.41)(EC:2.3.1.179)
2062347378	167	18	24	c183	hypothetical protein
2062361454	812	143	21	c183	3-oxoacyl-(acyl-carrier-protein) reductase(EC:1.1.1.100)
2062363982	659	65	39	c183	uridylate kinase (EC 2.7.4.22)(EC:2.7.4.22)
2062376155	122	57	131	c183	hypothetical protein
2062379982	1049	300	33	c183	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine
2062386975	224	49	27	c183	acyl carrier protein
2062112944	80	0	0	c1845	fructose-bisphosphate aldolase (EC 4.1.2.13)(EC:4.1.2.13)
2062112945	224	4	13	c1845	fructose-bisphosphate aldolase (EC 4.1.2.13)(EC:4.1.2.13)
2062288306	2870	210	49	c1845	Anaerobic dehydrogenases, typically selenocysteine-containing(EC:1.2.7.-)
2062387013	674	108	61	c1845	hypothetical protein
2062387014	395	10	10	c1845	fructose-bisphosphate aldolase (EC 4.1.2.13)(EC:4.1.2.13)
2062118205	173	0	0	c1869	hypothetical protein
2062118206	329	21	15	c1869	Uncharacterized protein conserved in bacteria
2062118207	62	0	0	c1869	hypothetical protein
2062321616	467	0	2	c1869	hypothetical protein
2062321617	281	25	32	c1869	hypothetical protein
2062321618	437	9	5	c1869	Lactoylglutathione lyase and related lyases(EC:4.4.1.5)
2062321619	1037	33	13	c1869	hypothetical protein
2062363983	479	77	6	c1869	adenosylhomocysteinase (EC 3.3.1.1)(EC:3.3.1.1)
2062161601	215	9	0	c187	Citrate synthase(EC:2.3.3.1)
2062184263	599	10	3	c187	Bacterial type II/III secretion system short domain.
2062184264	902	43	7	c187	CARDB.
2062184265	227	22	35	c187	Bacterial type II and III secretion system protein.
2062192571	110	0	0	c187	hypothetical protein
2062192574	821	27	12	c187	Type II secretory pathway, component PulD
2062321620	353	3	0	c187	hypothetical protein
2062345532	872	24	6	c187	Uncharacterized conserved protein
2062345535	398	13	30	c187	Protein affecting phage T7 exclusion by the F plasmid

2062112949	1814	53	15	c1872	GTP-binding protein LepA
2062156427	689	123	20	c1872	Dioxygenases related to 2-nitropropane dioxygenase
2062156428	401	342	32	c1872	FAD/FMN-containing dehydrogenases
2062192570	176	23	0	c1872	hypothetical protein
2062269667	1010	64	20	c1872	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily
2062269668	641	28	20	c1872	Lauroyl/myristoyl acyltransferase
2062342184	1577	136	22	c1872	Predicted integral membrane protein
2062345537	212	5	0	c1872	hypothetical protein
2062189402	437	21	32	c188	hypothetical protein
2062208677	653	86	46	c188	hypothetical protein
2062269665	407	84	39	c188	Glycosyltransferases involved in cell wall biogenesis
2062269666	251	12	4	c188	hypothetical protein
2062342183	449	4	11	c188	hypothetical protein
2062372273	545	61	15	c188	hypothetical protein
2062396012	629	17	16	c188	Protein of unknown function (DUF1239).
2062193193	1253	52	9	c1883	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT
2062201592	149	20	0	c1883	hypothetical protein
2062220961	158	0	0	c1883	hypothetical protein
2062258122	281	25	11	c1883	Predicted Co/Zn/Cd cation transporters
2062333283	725	34	8	c1883	Glycyl-tRNA synthetase, beta subunit
2062425292	335	33	18	c1883	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT
2062184262	272	59	33	c1884	carbohydrate ABC transporter substrate-binding protein, CUT1 family (TC 3.A.1.1.-)
2062191912	245	53	20	c1884	Fructosamine-3-kinase
2062191913	158	6	0	c1884	hypothetical protein
2062191914	491	26	24	c1884	protein tyrosine phosphatase
2062256928	782	5	3	c1884	Tryptophan 2,3-dioxygenase (EC 1.13.11.11)(EC:1.13.11.11)
2062372271	1199	1509	83	c1884	amino acid/amide ABC transporter substrate-binding protein, HAAT family (TC 3.A.1
2062290981	158	114	0	c1894	hypothetical protein
2062290983	260	235	23	c1894	hypothetical protein
2062290984	503	46	16	c1894	Methionine synthase II (cobalamin-independent)(EC:2.1.1.14)
2062290986	770	265	108	c1894	Uncharacterized protein conserved in bacteria

2062290987	515	19	8	c1913	hypothetical protein
2062342187	368	22	0	c1913	hypothetical protein
2062342188	911	50	5	c1913	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
2062376179	602	32	7	c1913	recombination protein RecR
2062388941	557	20	23	c1913	Tyrosyl-tRNA synthetase(EC:6.1.1.1)
2062112948	590	36	14	c1918	monosaccharide ABC transporter ATP-binding protein, CUT2 family (TC 3.A.1.2.-)(I
2062118213	953	472	61	c1918	monosaccharide ABC transporter substrate-binding protein, CUT2 family (TC 3.A.1.
2062225597	203	5	5	c1918	monosaccharide ABC transporter ATP-binding protein, CUT2 family (TC 3.A.1.2.-)(I
2062261286	224	40	13	c1918	Transcriptional regulators
2062296086	1124	272	29	c1918	monosaccharide ABC transporter membrane protein, CUT2 family (TC 3.A.1.2.-)
2062340270	278	0	4	c1918	Transcriptional regulators
2062340271	239	8	0	c1918	Transcriptional regulators
2062388942	758	94	13	c1918	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase(EC:4.1.2.-)
2062142120	680	203	69	c1925	Biopolymer transport proteins
2062151914	392	71	10	c1925	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
2062158382	407	39	10	c1925	hypothetical protein
2062158383	407	20	17	c1925	hypothetical protein
2062193191	422	14	19	c1925	Biopolymer transport protein
2062245452	1499	137	16	c1925	microcin-processing peptidase 2. Unknown type peptidase. MEROPS family U62
2062344219	1127	43	27	c1925	lipid-A-disaccharide synthase(EC:2.4.1.182)
2062129910	548	44	29	c1926	Lactate dehydrogenase and related dehydrogenases(EC:1.1.1.26)
2062142099	65	0	0	c1926	hypothetical protein
2062142102	248	145	16	c1926	hypothetical protein
2062250507	134	0	0	c1926	NAD-dependent aldehyde dehydrogenases(EC:1.2.1.3)
2062265815	416	60	14	c1926	NAD-dependent aldehyde dehydrogenases(EC:1.2.1.3)
2062265816	419	26	12	c1926	Protein of unknown function (DUF1049).
2062386320	206	15	5	c1926	hypothetical protein
2062195793	224	4	0	c19264	hypothetical protein
2062198978	581	5	3	c19264	hypothetical protein
2062198982	245	8	0	c19264	Nucleoside-diphosphate-sugar epimerases
2062264455	398	13	0	c19264	Predicted phosphatase/phosphohexomutase

2062415655	455	77	11	c19264	Predicted nucleoside-diphosphate sugar epimerase
2062143481	749	84	12	c1928	3-hydroxyacyl-CoA dehydrogenase
2062171848	176	28	0	c1928	hypothetical protein
2062171849	152	0	0	c1928	hypothetical protein
2062171850	755	42	12	c1928	Predicted permeases
2062297385	1118	20	9	c1928	Protein of unknown function (DUF971)./Taurine catabolism dioxygenase TauD, TfdA
2062297386	776	37	15	c1928	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases
2062324838	590	14	3	c1928	Transcriptional regulator
2062338306	449	36	9	c1928	3-hydroxyacyl-CoA dehydrogenase
2062122134	443	172	34	c193	Glycine/D-amino acid oxidases (deaminating)(EC:1.5.99.2)
2062122135	869	13	153	c193	5,10-methylenetetrahydrofolate reductase(EC:1.5.1.20)
2062219041	1538	153	22	c193	Trimethylamine:corrinoid methyltransferase
2062219042	2063	56	48	c193	Uncharacterized metal-binding protein
2062122129	110	0	0	c1936	hypothetical protein
2062140198	635	6	0	c1936	hypothetical protein
2062346758	266	0	0	c1936	hypothetical protein
2062364655	146	0	0	c1936	hypothetical protein
2062372276	1136	15	0	c1936	Major capsid protein Gp23.
2062420788	119	8	8	c1936	hypothetical protein
2062129927	158	19	0	c1948	hypothetical protein
2062159638	257	0	0	c1948	hypothetical protein
2062330036	887	68	11	c1948	Membrane protease subunits, stomatin/prohibitin homologs
2062372275	374	35	16	c1948	hypothetical protein
2062175134	890	36	13	c1959	carbohydrate ABC transporter membrane protein 2, CUT1 family (TC 3.A.1.1.-)
2062235227	818	533	82	c1959	carbohydrate ABC transporter substrate-binding protein, CUT1 family (TC 3.A.1.1.-)
2062330037	842	78	2	c1959	carbohydrate ABC transporter membrane protein 1, CUT1 family (TC 3.A.1.1.-)
2062108390	266	4	8	c1971	Uncharacterized protein conserved in bacteria
2062195788	311	16	32	c1971	Predicted methylated DNA-protein cysteine methyltransferase
2062195789	737	35	15	c1971	Site-specific recombinases, DNA invertase Pin homologs
2062219034	863	21	1	c1971	hypothetical protein
2062238448	245	16	0	c1971	transcriptional regulator, GntR family

2062269686	458	31	22	c1971	Transcriptional regulators
2062286367	755	163	23	c1971	Fe-S oxidoreductase
2062290290	317	79	9	c1971	FAD/FMN-containing dehydrogenases
2062290291	1481	50	19	c1971	FAD/FMN-containing dehydrogenases(EC:1.1.3.15)
2062326768	683	28	7	c1971	Fe-S oxidoreductase
2062393384	329	18	9	c1971	Uncharacterized protein conserved in bacteria
2062108395	416	139	24	c1973	Methionyl-tRNA formyltransferase
2062118239	1244	244	34	c1973	formyl-CoA transferase(EC:2.8.3.16)
2062118240	62	0	0	c1973	hypothetical protein
2062177106	1739	291	69	c1973	Thiamine pyrophosphate-requiring enzymes (EC:2.2.1.6)
2062273559	275	0	44	c1973	Methionyl-tRNA formyltransferase(EC:2.1.2.9)
2062177107	320	0	0	c1986	hypothetical protein
2062177108	398	0	0	c1986	hypothetical protein
2062177109	137	0	0	c1986	hypothetical protein
2062177110	512	0	4	c1986	hypothetical protein
2062265802	248	0	0	c1986	hypothetical protein
2062358247	389	0	0	c1986	Predicted endonuclease distantly related to archaeal Holliday junction resolvase an
2062108394	72	0	0	c2006	(tRNA)
2062108396	380	179	13	c2006	RNA methyltransferase, RsmE family
2062198329	245	392	0	c2006	Uncharacterized protein conserved in bacteria
2062258120	560	21	25	c2006	hypothetical protein
2062258121	152	211	112	c2006	hypothetical protein
2062278034	776	30	10	c2006	Nuclease subunit of the excinuclease complex
2062278035	275	33	18	c2006	Nuclease subunit of the excinuclease complex
2062358248	57	0	0	c2006	(tRNA)
2062364656	809	17	12	c2006	Nuclease subunit of the excinuclease complex
2062177104	503	117	16	c201	glutamate synthase (NADPH) GltB3 subunit (EC 1.4.1.13)
2062177105	338	420	36	c201	glutamate synthase (NADPH) GltB3 subunit (EC 1.4.1.13)
2062220967	1145	245	39	c201	Glutamine synthetase(EC:6.3.1.2)
2062221670	572	271	24	c201	Glycine cleavage system T protein (aminomethyltransferase)(EC:2.1.2.10)
2062221671	65	0	0	c201	hypothetical protein

2062221672	143	21	0	c201	L-glutamine synthetase (EC 6.3.1.2)(EC:6.3.1.2)
2062221673	1349	157	36	c201	Uncharacterized conserved protein(EC:2.1.2.10)
2062294187	374	115	11	c201	glutamate synthase (NADPH) GltB2 subunit (EC 1.4.1.13)(EC:1.4.1.14,EC:1.4.1.13
2062294188	311	74	10	c201	Glutamine synthetase(EC:6.3.1.2)
2062390203	296	186	27	c201	hypothetical protein
2062392107	935	164	19	c201	glutamate synthase (NADPH) GltB1 subunit (EC 1.4.1.13)
2062392108	815	454	49	c201	glutamate synthase (NADPH) GltB2 subunit (EC 1.4.1.13)(EC:1.4.1.13,EC:1.4.1.14
2062286375	128	0	0	c2017	hypothetical protein
2062317128	827	73	8	c2017	cytidyltransferase-related domain
2062319664	326	3	15	c2017	hypothetical protein
2062338304	260	15	8	c2017	Uncharacterized protein, similar to the N-terminal domain of Lon protease
2062342855	623	148	35	c2017	Protein-disulfide isomerase
2062378049	449	58	9	c2017	Glycine/serine hydroxymethyltransferase(EC:2.1.2.1)
2062390201	524	84	29	c2017	ADP-heptose synthase, bifunctional sugar kinase/adenylyltransferase
2062390202	209	0	0	c2017	ATP-dependent protease La (LON) domain.
2062408440	764	71	16	c2017	Glycine/serine hydroxymethyltransferase(EC:2.1.2.1)
2062132492	854	14	5	c2019	Methylase involved in ubiquinone/menaquinone biosynthesis
2062211825	515	21	16	c2019	NTP pyrophosphohydrolases including oxidative damage repair enzymes
2062269655	1589	21	3	c2019	methionine synthase (B12-dependent) (EC 2.1.1.13)(EC:2.1.1.13)
2062292889	908	8	0	c2019	hypothetical protein
2062390200	497	58	4	c2019	Uncharacterized protein conserved in bacteria
2062169940	614	0	10	c2021	hypothetical protein
2062195154	413	17	10	c2021	3-dehydroquinate synthetase
2062195155	266	0	15	c2021	Acyl-CoA-binding protein
2062300584	1499	67	17	c2021	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-bind
2062338305	836	291	22	c2021	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A (EC 6.3.5.-)(EC:6.3.5.
2062369055	887	289	17	c2021	ribosome small subunit-dependent GTPase A(EC:3.6.1.-)
2062387018	551	113	16	c2021	Putative transcriptional regulator
2062387019	485	52	6	c2021	hypothetical protein
2062224903	623	98	29	c2046	fructose-bisphosphate aldolase (EC 4.1.2.13)(EC:4.1.2.13)
2062246696	1310	69	18	c2046	ribulose 1,5-bisphosphate carboxylase large subunit (EC 4.1.1.39)(EC:4.1.1.39)

2062246697	425	40	0	c2046	fructose-bisphosphate aldolase (EC 4.1.2.13)(EC:4.1.2.13)
2062415645	326	21	0	c2046	transketolase (EC 2.2.1.1)(EC:2.2.1.1)
2062114276	1022	13	5	c2047	hypothetical protein
2062124114	398	48	18	c2047	hypothetical protein
2062164160	980	29	0	c2047	Mg-chelatase subunit ChlD
2062338313	794	10	11	c2047	Tetratricopeptide repeat.
2062352504	1040	5	7	c2047	von Willebrand factor type A domain.
2062177103	656	139	20	c2051	Coenzyme F390 synthetase(EC:6.2.1.30)
2062182971	458	17	2	c2051	hypothetical protein
2062182972	542	118	15	c2051	Coenzyme F390 synthetase
2062193183	317	9	6	c2051	hypothetical protein
2062373569	2435	79	9	c2051	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs
2062373575	512	70	0	c2051	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs
2062373576	704	24	0	c2051	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homolo
2062152620	560	0	7	c206	Nucleotide-binding protein implicated in inhibition of septum formation
2062199627	608	74	5	c206	Cell division protein FtsI/penicillin-binding protein 2
2062199628	1175	29	14	c206	Cell division protein FtsI/penicillin-binding protein 2(EC:2.4.1.129)
2062246690	407	17	22	c206	Cell shape-determining protein
2062343512	392	5	0	c206	endoribonuclease L-PSP
2062343529	248	16	0	c206	Homoserine dehydrogenase
2062352505	755	52	7	c206	Predicted xylanase/chitin deacetylase
2062363988	947	52	18	c206	Homoserine dehydrogenase(EC:1.1.1.3)
2062365275	605	41	3	c206	hypothetical protein
2062365276	869	51	23	c206	hypothetical protein
2062394080	179	28	0	c206	hypothetical protein
2062151908	494	8	4	c2068	Uncharacterized protein involved in biosynthesis of c-type cytochromes
2062151918	1358	49	16	c2068	Undecaprenyl-phosphate glucose phosphotransferase
2062171213	482	41	10	c2068	Integral membrane protein CcmA involved in cell shape determination
2062182970	173	6	0	c2068	hypothetical protein
2062273567	371	100	16	c2068	prepilin-type N-terminal cleavage/methylation domain
2062319699	332	30	12	c2068	hypothetical protein

2062352506	638	144	16	c2068	hypothetical protein
2062220945	1265	89	14	c2073	enolase (EC 4.2.1.11)(EC:4.2.1.11)
2062280627	752	16	8	c2073	hypothetical protein
2062280628	518	83	4	c2073	Uncharacterized membrane protein, putative virulence factor
2062148699	314	54	13	c2076	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation
2062148700	917	19	7	c2076	Predicted Rossmann fold nucleotide-binding protein
2062183629	833	14	10	c2076	Calcineurin-like phosphoesterase.
2062183630	446	0	0	c2076	alpha/beta hydrolase fold.
2062183631	82	0	0	c2076	(tRNA)
2062196440	314	0	0	c2076	hypothetical protein
2062306357	671	28	12	c2076	Uncharacterized protein involved in cation transport
2062326767	431	16	9	c2076	hypothetical protein
2062306358	2483	34	6	c208	hypothetical protein
2062116887	134	0	0	c2085	hypothetical protein
2062119542	272	29	0	c2085	hypothetical protein
2062168004	596	15	18	c2085	hypothetical protein
2062195145	191	0	0	c2085	N-acetylglutamate kinase (EC 2.7.2.8)(EC:2.7.2.8)
2062249885	1067	10	8	c2085	Soluble lytic murein transglycosylase and related regulatory proteins (some contain
2062269663	257	19	0	c2085	hypothetical protein
2062294794	287	0	0	c2085	O(6)-alkylguanine repair protein YbaZ
2062310746	72	0	0	c2085	(tRNA)
2062122131	560	16	4	c210	RecA/RadA recombinase
2062222283	155	0	0	c210	RecA/RadA recombinase
2062319667	1061	2	0	c210	radical SAM enzyme, Cfr family(EC:2.1.1.-)
2062358888	191	5	0	c210	hypothetical protein
2062358889	209	5	10	c210	DNA-directed RNA polymerase, subunit F (EC 2.7.7.6)(EC:2.7.7.6)
2062386953	299	27	30	c210	Ribosomal protein L21E
2062140186	200	0	0	c2106	hypothetical protein
2062187488	1748	53	6	c2106	hypothetical protein
2062290325	1181	55	17	c2106	BNR/Asp-box repeat.
2062290326	73	0	0	c2106	(tRNA)

2062116218	1070	57	14	c2109	branched chain amino acid aminotransferase apoenzyme (EC 2.6.1.42)(EC:2.6.1.4
2062116219	980	47	3	c2109	hypothetical protein
2062158380	464	52	11	c2109	hypothetical protein
2062188758	503	74	8	c2109	hypothetical protein
2062193178	161	6	19	c2109	hypothetical protein
2062198335	149	0	0	c2109	hypothetical protein
2062271616	212	14	9	c2109	hypothetical protein
2062300585	236	343	34	c2109	hypothetical protein
2062334501	299	194	13	c2109	YhhN-like protein.
2062422726	554	22	22	c2109	hypothetical protein
2062151919	932	197	80	c211	Flagellar capping protein
2062294803	2288	49	31	c211	Flagellar capping protein
2062305094	914	25	20	c211	membrane protein insertase, YidC/Oxa1 family, C-terminal domain
2062305095	116	17	0	c211	hypothetical protein
2062305096	797	21	25	c211	hypothetical protein
2062305098	1667	50	12	c211	Flagellin and related hook-associated proteins
2062401942	416	19	10	c211	flagellar biosynthetic protein FliS
2062411701	623	29	11	c211	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase
2062211207	461	9	22	c2125	hypothetical protein
2062212463	1109	44	2	c2125	Soluble lytic murein transglycosylase and related regulatory proteins (some contain
2062294171	737	5	3	c2125	hypothetical protein
2062305093	1109	106	17	c2125	alanine racemase(EC:5.1.1.1)
2062372923	227	26	4	c2125	hypothetical protein
2062131856	1559	153	31	c2130	ATPase components of various ABC-type transport systems, contain duplicated ATP
2062131857	254	55	0	c2130	ATPase components of various ABC-type transport systems, contain duplicated ATP
2062142105	722	116	22	c2130	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
2062247996	413	429	94	c2130	hypothetical protein
2062247997	371	11	0	c2130	hypothetical protein
2062276760	338	180	12	c2130	Metal-dependent hydrolase
2062276761	1628	61	21	c2130	putative hydrolase, CocE/NonD family
2062278656	581	71	12	c2130	Sulfite exporter TauE/SafE.

2062292893	320	75	16	c2130	Zn-dependent alcohol dehydrogenases, class III(EC:1.1.1.1,EC:1.1.1.284)
2062317132	1181	1229	87	c2130	ABC-type dipeptide transport system, periplasmic component
2062322905	242	91	17	c2130	hypothetical protein
2062325517	524	23	2	c2130	Transcriptional regulator
2062351198	323	19	40	c2130	Zn-dependent alcohol dehydrogenases, class III(EC:1.1.1.284,EC:1.1.1.1)
2062373579	956	241	25	c2130	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
2062229418	92	0	0	c2133	hypothetical protein
2062378056	158	0	13	c2133	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062378057	995	24	19	c2133	Nucleoside-diphosphate-sugar epimerases
2062378058	815	69	5	c2133	Short-chain dehydrogenases of various substrate specificities
2062142790	728	12	18	c2179	hypothetical protein
2062142791	1172	1	12	c2179	hypothetical protein
2062162881	110	0	0	c2179	hypothetical protein
2062180968	515	27	16	c2179	YeeE/YedE family (DUF395).
2062198322	584	101	10	c2179	YeeE/YedE family (DUF395).
2062288331	251	0	0	c2179	hypothetical protein
2062292898	218	5	0	c2179	hypothetical protein
2062292899	311	13	0	c2179	Predicted redox protein, regulator of disulfide bond formation
2062142786	1055	45	4	c2208	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily(E
2062180969	1115	100	12	c2208	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily
2062318994	470	49	11	c2208	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family
2062318995	545	62	13	c2208	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family
2062388919	359	253	22	c2208	Zn-dependent alcohol dehydrogenases, class III(EC:1.1.1.284,EC:1.2.1.66,EC:1.1.
2062401940	158	32	0	c2208	Zn-dependent alcohol dehydrogenases, class III
2062107696	191	37	0	c2236	MarC family integral membrane protein.
2062107698	407	86	12	c2236	Multiple antibiotic transporter
2062122786	422	71	21	c2236	hypothetical protein
2062175810	62	0	0	c2236	hypothetical protein
2062209874	371	8	0	c2236	hypothetical protein
2062322911	308	3	0	c2236	hypothetical protein
2062108389	299	50	0	c224	LSU ribosomal protein L23P

2062108392	149	27	13	c224	LSU ribosomal protein L2P
2062108393	512	2059	76	c224	LSU ribosomal protein L3P
2062111594	149	27	20	c224	LSU ribosomal protein L3P
2062111602	620	1035	56	c224	LSU ribosomal protein L4P
2062112275	311	80	0	c224	SSU ribosomal protein S10P
2062112938	1220	570	135	c224	translation elongation factor 1A (EF-1A/EF-Tu)(EC:3.6.5.3)
2062112939	830	370	24	c224	translation elongation factor 2 (EF-2/EF-G)(EC:3.6.5.3)
2062112943	176	523	6	c224	translation elongation factor 2 (EF-2/EF-G)(EC:3.6.5.3)
2062112954	527	0	4	c2243	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component
2062112956	179	0	0	c2243	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component(EC:3
2062112957	581	2	24	c2243	argininosuccinate synthase (EC 6.3.4.5)(EC:6.3.4.5)
2062113634	158	0	0	c2243	argininosuccinate synthase (EC 6.3.4.5)(EC:6.3.4.5)
2062114272	68	0	0	c2243	Arginosuccinate synthase.
2062116883	947	4	2	c2243	deoxyhypusine synthase (EC 2.5.1.46)(EC:2.5.1.46)
2062116884	182	5	5	c2243	hypothetical protein
2062116885	404	5	0	c2243	hypothetical protein
2062116886	158	0	0	c2243	hypothetical protein
2062117527	161	0	0	c2243	hypothetical protein
2062117533	461	2	0	c2243	L-2-aminoadipate N-acetyltransferase (EC 2.3.1.-)
2062118214	293	0	7	c2243	L-2-aminoadipate N-acetyltransferase (EC 2.3.1.-)
2062118215	545	2	7	c2243	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)/N2-acetyl-L-aminoad
2062118216	92	0	0	c2243	Uncharacterised BCR, YnfA/UPF0060 family.
2062118217	260	4	0	c2243	Uncharacterized conserved protein
2062118218	329	0	0	c2243	Uncharacterized conserved protein
2062118220	602	169	68	c225	ATP-dependent Clp protease ATP-binding subunit ClpA (EC 3.4.21.92)
2062119539	260	31	15	c225	ATPases with chaperone activity, ATP-binding subunit
2062119540	1133	232	30	c225	ATPases with chaperone activity, ATP-binding subunit
2062119543	332	36	0	c225	Branched-chain amino acid transport protein (AzlD).
2062119544	305	23	10	c225	Cell division protein ZapA.
2062119545	692	210	23	c225	dihydrodipicolinate reductase (EC 1.3.1.26)(EC:1.3.1.26)
2062120845	2945	79	13	c225	glycine dehydrogenase alpha subunit/glycine dehydrogenase (decarboxylating) bet

2062122130	1829	26	20	c225	GTP-binding protein TypA/BipA
2062122132	200	45	15	c225	hypothetical protein
2062122789	434	58	9	c225	hypothetical protein
2062123477	668	36	22	c225	hypothetical protein
2062123478	371	40	3	c225	hypothetical protein
2062123480	92	0	0	c225	hypothetical protein
2062123481	674	13	6	c225	hypothetical protein
2062124732	215	19	14	c225	hypothetical protein
2062124735	245	33	0	c225	hypothetical protein
2062124739	731	27	4	c225	hypothetical protein
2062124771	185	16	0	c225	hypothetical protein
2062125412	245	8	20	c225	hypothetical protein
2062125416	683	59	3	c225	NUDIX domain.
2062125417	671	63	3	c225	orotate phosphoribosyltransferase(EC:2.4.2.10)
2062125418	692	130	10	c225	Predicted branched-chain amino acid permease (azaleucine resistance)
2062126017	899	34	4	c225	ribosome biogenesis GTP-binding protein YlqF
2062126020	425	99	38	c225	RNA methyltransferase, RsmE family
2062126023	917	86	14	c225	Serine acetyltransferase
2062126024	782	170	58	c225	Site-specific recombinase XerD
2062126046	1169	133	29	c225	Type II secretory pathway, component PulF
2062126051	224	13	31	c225	Uncharacterized conserved protein
2062126052	1889	60	12	c225	VacB and RNase II family 3''-5'' exoribonucleases
2062126657	389	31	15	c225	Vitamin K epoxide reductase family.
2062126659	1349	107	13	c225	Zn-dependent hydrolases, including glyoxylases
2062126660	884	25	7	c2251	Arylsulfatase A and related enzymes
2062126664	896	134	28	c2251	DNA replication protein
2062126696	194	15	0	c2251	hypothetical protein
2062126697	329	9	12	c2251	hypothetical protein
2062126698	317	41	13	c2251	hypothetical protein
2062126699	224	4	0	c2251	hypothetical protein
2062126700	1028	162	6	c2251	N-acetyl-gamma-glutamyl-phosphate reductase, common form

2062127944	1304	67	17	c2252	DNA primase, catalytic core
2062128587	473	36	40	c2252	DnaB-like helicase N terminal domain.
2062128589	878	9	18	c2252	Sigma-70 factor, region 1.
2062129911	905	206	10	c2269	ammonium transporter
2062129925	116	9	17	c2269	ammonium transporter
2062129956	290	41	14	c2269	hypothetical protein
2062129957	515	210	33	c2269	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit(EC
2062129958	338	0	0	c2269	nitrogen regulatory protein P-II
2062131195	257	51	16	c2269	Oxaloacetate decarboxylase, gamma chain.
2062131217	257	0	8	c2269	Phytanoyl-CoA dioxygenase (PhyH).
2062131874	1793	121	23	c2269	Pyruvate/oxaloacetate carboxyltransferase(EC:6.4.1.1,EC:4.1.1.3)
2062132485	137	22	0	c2269	serine-glyoxylate aminotransferase apoenzyme (EC 2.6.1.45)(EC:2.6.1.45)
2062132486	737	137	7	c2269	sodium ion-translocating decarboxylase, beta subunit(EC:4.1.1.3)
2062134388	131	0	0	c2269	Threonine dehydratase(EC:4.3.1.19)
2062134389	869	52	12	c2274	aspartate semialdehyde dehydrogenase (EC 1.2.1.11)(EC:1.2.1.11)
2062134390	815	67	4	c2274	hypothetical protein
2062135646	329	0	15	c2274	hypothetical protein
2062135656	443	32	14	c2274	hypothetical protein
2062135657	1394	44	9	c2274	hypothetical protein
2062135658	476	0	0	c2316	ABC-type metal ion transport system, periplasmic component/surface adhesin
2062137678	722	0	0	c2316	ABC-type Mn/Zn transport systems, ATPase component(EC:3.6.3.-)
2062137679	818	0	0	c2316	ABC-type Mn2+/Zn2+ transport systems, permease components
2062137680	2453	1	0	c2316	Putative copper export protein
2062137682	812	344	43	c2322	carbohydrate ABC transporter substrate-binding protein, CUT1 family (TC 3.A.1.1.-)
2062138281	800	73	4	c2322	conserved hypothetical protein TIGR00259
2062142097	173	6	0	c2322	hypothetical protein
2062142098	653	72	14	c2322	Leucyl aminopeptidase (aminopeptidase T)(EC:3.4.11.-)
2062142103	434	9	23	c2322	Leucyl aminopeptidase (aminopeptidase T)(EC:3.4.11.-)
2062142104	1454	96	13	c2322	Ribulose kinase
2062142116	986	8	3	c2331	Glycosyltransferases, probably involved in cell wall biogenesis
2062142117	170	0	0	c2331	hypothetical protein

2062142118	149	0	0	c2331	hypothetical protein
2062142119	323	0	3	c2331	hypothetical protein
2062142122	1010	2	3	c2331	hypothetical protein
2062142123	647	116	12	c2339	fumarase (EC 4.2.1.2)
2062142125	131	15	0	c2339	fumarase (EC 4.2.1.2)(EC:4.2.1.2)
2062142129	266	0	0	c2339	Galactose mutarotase and related enzymes
2062142135	317	3	0	c2339	Gram-negative bacterial tonB protein.
2062142138	290	14	14	c2339	hypothetical protein
2062142139	281	36	11	c2339	hypothetical protein
2062142140	701	140	13	c2339	Site-specific recombinase XerD
2062142142	320	0	3	c2346	ferrochelatase (EC 4.99.1.1)(EC:4.99.1.1)
2062142143	974	15	2	c2346	Multidrug resistance efflux pump
2062142144	446	25	4	c2346	N-acetylglutamate synthase (EC 2.3.1.1)/glutamate N-acetyltransferase (EC 2.3.1.3
2062142774	200	10	0	c2346	N-acetylglutamate synthase (EC 2.3.1.1)/glutamate N-acetyltransferase (EC 2.3.1.3
2062142784	176	0	0	c2346	N-acetylglutamate synthase (N-acetylornithine aminotransferase)(EC:2.3.1.1,EC:2.
2062142785	299	0	7	c2346	Protoheme ferro-lyase (ferrochelatase)(EC:4.99.1.1)
2062142789	317	60	6	c2360	3-isopropylmalate dehydratase large subunit(EC:4.2.1.33,EC:4.2.1.35)
2062142792	1100	31	31	c2360	3-isopropylmalate dehydratase, large subunit (EC 4.2.1.33)(EC:4.2.1.35,EC:4.2.1.3
2062144797	398	20	8	c2360	3-isopropylmalate dehydratase, small subunit (EC 4.2.1.33)(EC:4.2.1.33,EC:4.2.1.3
2062144798	305	16	7	c2360	hypothetical protein
2062148687	572	105	26	c2361	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related de
2062148695	446	18	4	c2361	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related de
2062148696	164	6	0	c2361	hypothetical protein
2062148698	245	12	0	c2361	Uncharacterized membrane protein, putative virulence factor
2062149977	809	58	5	c2361	Uncharacterized membrane protein, putative virulence factor
2062149978	434	111	12	c2361	Uncharacterized membrane protein, putative virulence factor
2062149979	800	71	19	c2368	hypothetical protein
2062149990	1700	11	11	c2368	hypothetical protein
2062150615	272	11	0	c2368	hypothetical protein
2062151899	620	2	0	c2369	arginyl-tRNA synthetase (EC 6.1.1.19)(EC:6.1.1.19)
2062151907	392	13	0	c2369	phosphoglycolate phosphatase

2062151909	326	0	0	c2369	Predicted hydrolases of the HAD superfamily
2062151910	1118	2	3	c2369	small GTP-binding protein domain
2062151911	551	7	0	c239	Deoxycytidylate deaminase(EC:3.5.4.12)
2062151912	524	0	4	c239	hypothetical protein
2062151915	131	0	0	c239	replicative DNA polymerase I (EC 2.7.7.7)(EC:2.7.7.7)
2062151920	2051	1	1	c239	replicative DNA polymerase I (EC 2.7.7.7)(EC:2.7.7.7)
2062151921	338	6	0	c239	replicative DNA polymerase I (EC 2.7.7.7)(EC:2.7.7.7)
2062152595	311	0	0	c239	Uncharacterized conserved protein
2062152596	1352	0	7	c2401	ATP-dependent 26S proteasome regulatory subunit
2062152598	689	9	3	c2401	ATPases of the AAA+ class
2062152619	299	0	0	c2401	hypothetical protein
2062154482	329	0	0	c2401	Polyprenyltransferase (cytochrome oxidase assembly factor)(EC:2.5.1.-)
2062154484	281	0	0	c2401	translation elongation factor 1B (aEF-1B)
2062154486	518	4	0	c2430	CDP-diglyceride synthetase(EC:2.7.7.41)
2062155116	278	0	0	c2430	Hydantoinase/oxoprolinase.
2062155118	269	0	0	c2430	hypothetical protein
2062155120	257	0	0	c2430	hypothetical protein
2062155791	476	2	0	c2430	hypothetical protein
2062156434	392	10	5	c2430	hypothetical protein
2062156435	389	51	3	c2430	hypothetical protein
2062156436	1124	15	10	c2440	ATP-dependent Clp protease ATP-binding subunit ClpX (EC 3.4.21.92)
2062156441	581	48	12	c2440	ATP-dependent Clp protease proteolytic subunit ClpP (EC 3.4.21.92)(EC:3.4.21.92
2062156445	407	12	5	c2440	Bacterial trigger factor protein (TF) C-terminus.
2062156446	269	11	7	c2440	Dehydrogenases (flavoproteins)
2062157097	707	51	8	c2440	DNA or RNA helicases of superfamily II
2062158372	848	12	8	c2440	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
2062158375	191	26	21	c2440	hypothetical protein
2062158384	191	5	0	c2440	hypothetical protein
2062159634	452	31	9	c2440	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062159635	560	50	14	c2440	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062159639	776	15	4	c2440	Sugar kinases, ribokinase family

2062159640	1334	79	7	c2440	Uncharacterized conserved protein
2062160287	98	0	0	c2443	hypothetical protein
2062161602	1067	2	2	c2443	hypothetical protein
2062161603	1142	31	14	c2443	hypothetical protein
2062161604	1316	39	7	c2443	hypothetical protein
2062162879	890	20	9	c2443	Protein of unknown function (DUF2851).
2062162884	230	30	9	c2443	Protein of unknown function (DUF2851).
2062162885	70	0	0	c246	(tRNA)
2062164141	84	0	0	c246	(tRNA)
2062164142	1304	77	12	c246	Alcohol dehydrogenase, class IV
2062164148	374	29	16	c246	Eukaryotic glutathione synthase, ATP binding domain.
2062166133	935	34	12	c246	Eukaryotic glutathione synthase./Eukaryotic glutathione synthase, ATP binding dom
2062166134	122	0	0	c246	hypothetical protein
2062166135	89	0	0	c246	hypothetical protein
2062166746	539	13	22	c246	hypothetical protein
2062166748	407	7	12	c246	hypothetical protein
2062166751	401	75	5	c246	Protein of unknown function (DUF3604).
2062166752	1040	292	59	c246	rod shape-determining protein MreB
2062167373	830	8	4	c2464	23S rRNA m(2)A-2503 methyltransferase (EC 2.1.1.-)(EC:2.1.1.-)
2062167376	872	49	38	c2464	Biopolymer transport proteins
2062167998	362	28	6	c2464	DsrE/DsrF-like family.
2062168000	200	0	0	c2464	hypothetical protein
2062168001	257	4	8	c2464	Predicted Fe-S-cluster redox enzyme
2062168002	728	18	51	c2464	RNA polymerase sigma factor, sigma-70 family
2062168003	296	51	7	c247	hypothetical protein
2062168695	338	0	0	c247	methionyl-tRNA synthetase (EC 6.1.1.10)(EC:6.1.1.10)
2062169321	1526	55	12	c247	methionyl-tRNA synthetase C-terminal region/beta chain(EC:6.1.1.10)
2062169322	221	81	14	c247	NADH dehydrogenase subunit A (EC 1.6.5.3)(EC:1.6.5.3)
2062171851	542	11	2	c2472	CAAX amino terminal protease family.
2062172533	83	0	0	c2472	hypothetical protein
2062172538	257	12	0	c2472	hypothetical protein

2062172540	143	0	0	c2472	hypothetical protein
2062174462	719	86	7	c2472	leucyl/phenylalanyl-tRNA--protein transferase(EC:2.3.2.6)
2062174468	572	16	16	c2472	Sporulation related domain.
2062175135	176	0	0	c2472	Sporulation related domain.
2062175138	302	252	36	c2481	electron transport complex, RnfABCDGE type, B subunit
2062175139	1322	48	6	c2481	electron transport complex, RnfABCDGE type, C subunit
2062175140	161	43	0	c2481	hypothetical protein
2062175141	194	15	5	c2481	Predicted NADH:ubiquinone oxidoreductase, subunit RnfD
2062175142	440	32	0	c2481	Predicted NADH:ubiquinone oxidoreductase, subunit RnfD
2062175807	512	96	0	c2489	1-deoxy-D-xylulose 5-phosphate reductoisomerase
2062175808	758	67	9	c2489	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)(EC:1.1.1.267)
2062175809	62	0	0	c2489	hypothetical protein
2062175811	293	51	7	c2489	Predicted membrane-associated Zn-dependent proteases 1
2062175812	1034	54	15	c2489	Predicted membrane-associated Zn-dependent proteases 1
2062177101	305	7	0	c2489	Uncharacterized conserved protein
2062177111	296	3	0	c249	acetyl-coenzyme A synthetase (EC 6.2.1.1)
2062180320	446	49	7	c249	hydroxymethylpyrimidine synthase
2062180321	386	8	0	c249	hypothetical protein
2062180323	281	4	0	c249	hypothetical protein
2062180324	986	247	28	c249	porphobilinogen synthase (EC 4.2.1.24)(EC:4.2.1.24)
2062180325	72	0	0	c2494	(tRNA)
2062180327	929	10	2	c2494	ABC-type multidrug transport system, ATPase component
2062180331	1076	41	12	c2494	ATPases involved in chromosome partitioning
2062180332	257	19	8	c2494	hypothetical protein
2062180334	353	34	0	c2494	UDP-N-acetylmuramyl pentapeptide synthase
2062180335	581	71	26	c2497	ABC-type proline/glycine betaine transport system, permease component
2062180336	158	101	13	c2497	ABC-type proline/glycine betaine transport system, permease component
2062180971	986	294	30	c2497	ABC-type proline/glycine betaine transport systems, periplasmic components
2062180975	599	88	7	c2497	Endonuclease/Exonuclease/phosphatase family.
2062180977	902	79	7	c2497	Esterase/lipase(EC:3.1.1.-)
2062182261	533	81	8	c2514	Excinuclease ABC subunit A

2062183592	110	0	0	c2514	Excinuclease ABC subunit A
2062183613	1085	61	10	c2514	Excinuclease ATPase subunit
2062183615	1718	84	16	c2514	Excinuclease ATPase subunit
2062184260	836	11	26	c2514	Uncharacterized protein conserved in bacteria
2062184261	1289	53	10	c2536	ABC-type spermidine/putrescine transport system, permease component II
2062184931	959	173	20	c2536	agmatinase (EC 3.5.3.11)(EC:3.5.3.11)
2062184932	842	68	7	c2536	Methylase involved in ubiquinone/menaquinone biosynthesis
2062184933	122	0	0	c2545	hypothetical protein
2062184934	908	536	59	c2545	hypothetical protein
2062186867	686	19	9	c2545	hypothetical protein
2062186869	809	46	14	c2545	Uncharacterized Fe-S protein
2062186873	323	146	43	c2548	Ammonia permease
2062186874	971	196	28	c2548	ammonium transporter
2062186877	191	10	0	c2548	Antibiotic biosynthesis monooxygenase.
2062186878	815	92	5	c2548	EamA-like transporter family.
2062186879	569	40	16	c2548	Membrane protease subunits, stomatin/prohibitin homologs
2062187490	407	25	5	c2548	Predicted hydrolase (HAD superfamily)
2062187518	233	4	34	c256	exodeoxyribonuclease VII, small subunit(EC:3.1.11.6)
2062187519	437	16	14	c256	hypothetical protein
2062187521	878	11	8	c256	hypothetical protein
2062187524	347	20	6	c256	L-seryl-tRNA selenium transferase.
2062187526	503	121	16	c256	L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1)(EC:2.9.1.1)
2062188753	305	26	0	c256	Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains tl
2062188757	2054	17	7	c256	ribonuclease, Rne/Rng family
2062189401	209	5	0	c256	Shikimate kinase(EC:2.7.1.71)
2062190028	326	34	64	c256	Shikimate kinase(EC:2.7.1.71)
2062190035	443	7	9	c2583	alkylhydroperoxidase AhpD family core domain
2062190680	344	291	70	c2583	Calcineurin-like phosphoesterase.
2062190681	974	84	14	c2583	Glucose/sorbosone dehydrogenases
2062191908	200	40	10	c2583	Protein-L-isoaspartate carboxylmethyltransferase(EC:2.1.1.77)
2062191909	89	0	0	c2587	hypothetical protein

2062191915	1703	97	12	c2587	Trimethylamine:corrinoid methyltransferase
2062191920	1247	43	21	c2587	Xaa-Pro aminopeptidase
2062192569	530	4	6	c2598	glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41)(EC:1.2.1.41)
2062192572	479	8	0	c2598	glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41)(EC:1.2.1.41,EC:2.7.2.11,
2062193157	491	10	10	c2598	hypothetical protein
2062193164	1580	56	34	c2598	hypothetical protein
2062193167	533	92	21	c2598	imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-)(EC:2.4.2.-)
2062193168	479	111	15	c2598	imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)(EC:4.2.1.19)
2062193169	293	3	7	c2598	nucleoside diphosphate kinase (EC 2.7.4.6)(EC:2.7.4.6)
2062193173	314	13	6	c2612	hypothetical protein
2062193174	137	0	0	c2612	hypothetical protein
2062193180	1382	46	12	c2612	N-methylhydantoinase A/acetone carboxylase, beta subunit(EC:3.5.2.9)
2062193182	302	13	10	c2612	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides
2062193184	308	6	3	c2612	Uncharacterized protein conserved in bacteria
2062193186	518	6	12	c2612	Uncharacterized protein conserved in bacteria
2062193195	73	0	0	c2615	(tRNA)
2062195144	209	0	5	c2615	cob(II)yrinic acid a,c-diamide reductase (EC 1.16.8.1)
2062195148	344	3	0	c2615	cob(II)yrinic acid a,c-diamide reductase (EC 1.16.8.1)
2062195158	203	0	0	c2615	hypothetical protein
2062195786	488	4	4	c2615	hypothetical protein
2062195796	185	16	0	c2615	hypothetical protein
2062196433	236	21	0	c2615	hypothetical protein
2062196434	233	4	0	c2615	hypothetical protein
2062196437	278	0	0	c2615	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family(EC:5.2.1.8)
2062198323	530	0	4	c2615	Predicted flavoprotein(EC:1.5.1.29)
2062198324	86	0	0	c2617	(tRNA)
2062198325	515	43	4	c2617	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
2062198330	635	22	3	c2617	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase(EC:2.6.1.-)
2062198331	239	59	0	c2617	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase(EC:2.6.1.-)
2062198332	2069	69	19	c2617	Fe-S oxidoreductase
2062198333	233	0	21	c2617	GTP cyclohydrolase I

2062198336	383	26	13	c2617	GTP cyclohydrolase I (EC 3.5.4.16)
2062198337	614	42	2	c2617	hypothetical protein
2062198344	89	101	0	c2617	hypothetical protein
2062198974	407	113	20	c2617	hypothetical protein
2062200294	335	24	0	c2617	Predicted membrane protein
2062200295	647	26	15	c2617	Predicted membrane protein
2062200910	1043	86	7	c2617	Putative Zn-dependent protease, contains TPR repeats
2062200912	296	3	0	c2620	biotin carboxylase (EC 6.3.4.14)/acetyl-CoA carboxylase carboxyltransferase subun
2062201559	524	0	4	c2620	Biotin carboxylase(EC:6.4.1.2)
2062201560	191	0	0	c2620	citrate synthase (EC 2.3.3.1)(EC:2.3.3.1)
2062201562	353	17	8	c2620	Iron-sulfur cluster assembly accessory protein
2062201563	887	25	3	c2620	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)(EC:1.2.1.38)
2062201568	134	0	7	c2620	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)(EC:1.2.1.38)
2062201576	356	8	0	c2626	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catecho
2062201580	629	173	22	c2626	Adenylate cyclase, family 3 (some proteins contain HAMP domain)(EC:4.6.1.-)
2062201589	134	0	0	c2626	Domain of unknown function (DUF2024).
2062201591	791	223	28	c2626	EamA-like transporter family.
2062201593	533	15	8	c2626	hypothetical protein
2062201594	167	0	0	c2626	hypothetical protein
2062202209	155	26	0	c2626	hypothetical protein
2062202210	149	13	7	c2626	hypothetical protein
2062202843	341	44	6	c2626	hypothetical protein
2062203462	434	14	18	c266	DNA gyrase subunit B (EC 5.99.1.3)(EC:5.99.1.3)
2062203463	1028	25	15	c266	DNA gyrase subunit B (EC 5.99.1.3)(EC:5.99.1.3)
2062203467	1127	43	22	c266	DNA polymerase III, beta subunit(EC:2.7.7.7)
2062206019	578	22	2	c266	Glycine/serine hydroxymethyltransferase(EC:2.1.2.1)
2062206023	659	11	3	c266	hypothetical protein
2062207346	542	11	18	c266	hypothetical protein
2062207348	257	0	0	c266	hypothetical protein
2062207354	416	19	2	c266	Phosphopantetheinyl transferase component of siderophore synthetase
2062207356	914	11	10	c266	recF protein

2062207980	1376	133	25	c266	ribosome-associated GTPase EngA
2062207983	956	19	10	c266	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit(EC:5.99
2062208676	1007	153	36	c2679	bacterial peptide chain release factor 2 (bRF-2)
2062208678	1769	8	6	c2679	C-terminal peptidase (prc)
2062208679	410	10	2	c2679	hypothetical protein
2062208680	272	11	0	c2679	hypothetical protein
2062208681	659	6	3	c2679	hypothetical protein
2062209274	158	0	0	c2679	hypothetical protein
2062209286	485	31	4	c2679	Uncharacterized protein conserved in bacteria
2062209876	275	425	167	c268	Bacterial nucleoid DNA-binding protein
2062209877	485	31	0	c268	Gram-negative bacterial tonB protein.
2062209881	404	151	17	c268	hypothetical protein
2062209884	104	0	0	c268	hypothetical protein
2062209885	323	0	12	c268	hypothetical protein
2062209887	443	14	14	c268	hypothetical protein
2062209897	1361	24	13	c268	Periplasmic component of the Tol biopolymer transport system
2062211206	308	26	13	c268	Restriction endonuclease
2062211822	1196	146	23	c2688	ABC-type dipeptide transport system, periplasmic component
2062212461	836	72	8	c2688	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
2062212462	515	136	16	c2688	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
2062212465	356	48	20	c2688	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
2062212469	335	104	9	c2688	hypothetical protein
2062212474	689	15	9	c2688	L-aminopeptidase/D-esterase
2062212475	620	32	5	c2688	L-aminopeptidase/D-esterase
2062213740	383	8	8	c2689	Protein affecting phage T7 exclusion by the F plasmid
2062213743	830	292	25	c2689	riboflavin synthase, alpha subunit
2062213745	1571	8	10	c2689	Superfamily I DNA and RNA helicases(EC:3.6.1.-)
2062213766	413	15	5	c2689	uncharacterized domain 1
2062217724	191	10	5	c270	alanyl aminopeptidase. Metallo peptidase. MEROPS family M01(EC:3.4.11.2)
2062219040	488	25	12	c270	Aminopeptidase N
2062219665	1415	79	13	c270	aminopeptidase N, Escherichia coli type(EC:3.4.11.2)

2062219671	260	19	19	c270	Aminopeptidase N(EC:3.4.11.2)
2062220299	332	33	9	c270	Aminopeptidase N(EC:3.4.11.2)
2062220305	1157	90	15	c270	ATP-dependent RNA helicase CsdA (EC 5.99.1.-)
2062220953	194	5	0	c270	Co/Zn/Cd efflux system component
2062220954	2312	237	29	c270	copper-(or silver)-translocating P-type ATPase
2062220955	203	59	10	c270	hypothetical protein
2062220958	512	115	23	c270	hypothetical protein
2062220959	692	66	14	c270	Nitroreductase
2062220962	1364	74	9	c270	O-acetylhomoserine sulfhydrolase (EC 2.5.1.49)(EC:2.5.1.49)
2062220965	137	7	0	c2708	Bacterial type II secretion system protein G.
2062220966	182	0	0	c2708	hypothetical protein
2062220974	347	23	0	c2708	hypothetical protein
2062220975	1352	36	11	c2708	hypothetical protein
2062220976	251	16	12	c2708	hypothetical protein
2062221633	203	0	0	c2708	hypothetical protein
2062221634	407	52	7	c2708	prepilin-type N-terminal cleavage/methylation domain
2062222279	602	7	0	c2708	Pseudopilin GspJ.
2062222280	563	9	16	c2708	Putative translation factor (SUA5)
2062222284	953	161	17	c2725	Electron transfer flavoprotein, alpha subunit
2062222285	329	40	15	c2725	Electron transfer flavoprotein, beta subunit
2062222303	476	25	13	c2725	Electron transfer flavoprotein, beta subunit
2062222306	659	12	5	c2725	Glycine cleavage system T protein (aminomethyltransferase)
2062222977	986	101	24	c2725	Glycine/D-amino acid oxidases (deaminating)(EC:1.5.3.1)
2062223002	230	39	4	c2725	Glycine/D-amino acid oxidases (deaminating)(EC:1.5.3.1)
2062224263	893	18	7	c2753	2-keto-myo-inositol dehydratase (EC 4.2.1.44)(EC:4.2.1.44)
2062224264	1151	52	23	c2753	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (EC 3.7.1.-)(EC:3.7.1.-)
2062224905	425	66	35	c2753	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (EC 3.7.1.-)(EC:3.7.1.-)
2062224906	173	6	0	c2753	dihydroxyacid dehydratase (EC 4.2.1.9)(EC:4.2.1.9)
2062224914	224	0	0	c2753	hypothetical protein
2062224915	962	47	12	c2753	Predicted dehydrogenases and related proteins
2062225647	758	15	3	c2758	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase(EC:2.6.1.18)

2062225648	347	0	0	c2758	Glycerophosphoryl diester phosphodiesterase
2062226851	1484	27	4	c2758	methylmalonate-semialdehyde dehydrogenase [acylating] (EC 1.2.1.27)(EC:1.2.1.2
2062226852	281	4	0	c2763	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homolo
2062226854	2165	19	8	c2763	DNA polymerase III, alpha subunit
2062226855	287	42	17	c2763	DNA polymerase III, alpha subunit
2062226856	1397	54	9	c2763	DNA polymerase III, alpha subunit
2062227474	287	35	0	c2765	Acetyltransferases, including N-acetylases of ribosomal proteins
2062228731	650	17	6	c2765	Glycine cleavage system T protein (aminomethyltransferase)
2062228733	920	82	21	c2765	Glycine cleavage system T protein (aminomethyltransferase)
2062228738	479	146	13	c2765	Glycine cleavage system T protein (aminomethyltransferase)(EC:1.5.3.1)
2062228743	368	73	30	c2765	Heterodisulfide reductase, subunit A and related polyferredoxins
2062228744	65	0	0	c2765	hypothetical protein
2062228747	371	19	11	c2765	hypothetical protein
2062228749	128	8	0	c2765	hypothetical protein
2062229413	206	107	0	c2765	hypothetical protein
2062229414	200	10	10	c2765	hypothetical protein
2062231991	356	28	6	c2765	hypothetical protein
2062231993	290	14	7	c2765	Sarcosine oxidase delta subunit(EC:1.5.3.1)
2062231994	899	214	31	c2765	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase
2062231995	506	223	30	c2765	Thioredoxin reductase(EC:1.5.3.1)
2062233954	341	12	6	c2765	YtoQ family protein
2062233957	341	38	21	c2768	hypothetical protein
2062233958	101	0	0	c2768	hypothetical protein
2062234579	1001	110	64	c2768	NADH:flavin oxidoreductases, Old Yellow Enzyme family
2062234580	665	161	14	c2768	NADPH-dependent glutamate synthase beta chain and related oxidoreductases
2062234583	392	18	0	c277	endoribonuclease L-PSP
2062234585	119	0	0	c277	hypothetical protein
2062234586	134	7	0	c277	hypothetical protein
2062234588	689	6	6	c277	hypothetical protein
2062235217	509	31	28	c277	hypothetical protein
2062235218	866	81	18	c277	hypothetical protein

2062235219	155	77	6	c277	hypothetical protein
2062235220	92	0	0	c277	hypothetical protein
2062235222	884	79	19	c277	NADH:flavin oxidoreductases, Old Yellow Enzyme family
2062235230	947	8	6	c277	Peptidase family M48.
2062236534	335	6	12	c277	Phosphoribosyl-ATP pyrophosphohydrolase
2062236536	950	40	26	c277	Protein of unknown function (DUF1504).
2062236546	278	36	4	c277	Protein of unknown function (DUF1504).
2062237850	401	87	50	c277	Protein of unknown function (DUF1504).
2062238459	1640	623	48	c277	Protein of unknown function (DUF1504).
2062238464	500	90	26	c277	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binc
2062239743	920	73	29	c277	two component, sigma54 specific, transcriptional regulator, Fis family
2062240398	410	49	17	c277	Uncharacterized homolog of PrgY (pheromone shutdown protein)
2062240402	584	118	7	c277	Uncharacterized homolog of PrgY (pheromone shutdown protein)
2062240405	1463	45	14	c2772	Flagellin and related hook-associated proteins
2062240406	128	8	0	c2773	hypothetical protein
2062240407	296	115	47	c2773	hypothetical protein
2062241031	242	4	0	c2773	hypothetical protein
2062241037	1049	28	25	c2773	hypothetical protein
2062242266	1076	161	23	c2773	hypothetical protein
2062242891	269	0	4	c2773	hypothetical protein
2062242892	530	0	0	c2773	hypothetical protein
2062242893	707	48	14	c2773	NADPH:quinone reductase and related Zn-dependent oxidoreductases(EC:1.1.1.1
2062244143	1109	232	35	c2773	Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB)(EC:4.2.1.
2062244144	299	204	3	c2773	Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB)(EC:4.2.1.
2062245453	404	32	0	c2828	DNA topoisomerase IV subunit B (EC 5.99.1.3)(EC:5.99.1.-)
2062246676	668	27	9	c2828	DNA topoisomerase IV subunit B (EC 5.99.1.3)(EC:5.99.1.-)
2062246679	158	70	19	c2828	Flagellar motor switch/type III secretory pathway protein
2062246683	134	7	0	c2828	hypothetical protein
2062246684	788	49	15	c2828	hypothetical protein
2062246692	164	24	0	c2828	hypothetical protein
2062246698	116	0	0	c2828	hypothetical protein

2062246707	485	14	35	c2828	Response regulator containing a CheY-like receiver domain and an HTH DNA-bindi
2062246708	701	53	9	c2828	ribulose 1,5-bisphosphate carboxylase large subunit (EC 4.1.1.39)(EC:4.1.1.39)
2062246710	668	72	13	c2828	ribulose-5-phosphate 3-epimerase (EC 5.1.3.1)(EC:5.1.3.1)
2062246719	614	57	7	c2828	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit(EC:5.9
2062246720	1142	53	10	c2841	Glutamine synthetase(EC:6.3.1.11)
2062247981	191	0	0	c2841	Glutamine synthetase(EC:6.3.1.2)
2062247982	122	0	0	c2841	hypothetical protein
2062247983	170	0	6	c2841	hypothetical protein
2062247984	173	12	6	c2841	hypothetical protein
2062247985	317	6	0	c2841	Trimethylamine:corrinoid methyltransferase
2062247986	413	7	5	c2841	Trimethylamine:corrinoid methyltransferase
2062247987	311	23	13	c2856	hypothetical protein(EC:2.7.6.1)
2062247991	656	27	9	c2856	Phosphoribosylpyrophosphate synthetase
2062247993	1139	96	18	c2856	prolyl-tRNA synthetase (EC 6.1.1.15)(EC:6.1.1.15)
2062247994	356	11	0	c2856	prolyl-tRNA synthetase (EC 6.1.1.15)(EC:6.1.1.15)
2062247995	1097	40	5	c2861	methylmalonyl-CoA mutase (EC 5.4.99.2)(EC:5.4.99.2)
2062247998	986	64	7	c2861	methylmalonyl-CoA mutase metallochaperone MeaB(EC:2.7.-)
2062248616	251	16	16	c2861	Protein of unknown function (DUF861).
2062248617	614	59	7	c2862	ADP-heptose:LPS heptosyltransferase
2062248623	323	0	0	c2862	ADP-heptose:LPS heptosyltransferase
2062249244	926	15	8	c2862	Flagellar motor switch protein
2062249249	380	0	8	c2862	hypothetical protein
2062249878	857	21	12	c2862	Predicted Zn-dependent proteases and their inactivated homologs
2062249894	161	12	12	c2862	Putative modulator of DNA gyrase.
2062250505	353	14	23	c2868	ABC-type transport system, involved in lipoprotein release, permease component
2062254388	1133	27	12	c2868	ABC-type transport system, involved in lipoprotein release, permease component
2062254389	740	0	16	c2868	hypothetical protein
2062255613	176	45	11	c2868	hypothetical protein(EC:2.6.1.-)
2062255616	1109	53	11	c2868	iron-sulfur cluster binding protein, putative
2062255619	761	43	11	c2908	ABC-type uncharacterized transport system, ATPase component
2062256929	290	7	3	c2908	ABC-type uncharacterized transport system, permease component

2062258106	398	101	0	c2908	ABC-type uncharacterized transport system, permease component
2062258107	923	63	17	c2908	conserved protein of unknown function cotranscribed with Bmr (bmrU)
2062258112	659	33	3	c2908	haloacid dehalogenase superfamily, subfamily IA, variant 3
2062258119	101	10	0	c2908	hypothetical protein
2062260036	296	3	0	c2908	hypothetical protein
2062260037	428	56	9	c2908	Uncharacterized protein conserved in bacteria
2062260038	974	184	23	c2922	KpsF/GutQ family protein(EC:5.3.1.13)
2062260040	302	17	3	c2922	Phosphoglyceromutase(EC:5.4.2.1)
2062260041	866	48	10	c2922	Phosphoglyceromutase(EC:5.4.2.1)
2062261280	164	0	0	c2922	Predicted UDP-glucose 6-dehydrogenase(EC:1.1.1.22)
2062261283	275	4	15	c2922	Predicted UDP-glucose 6-dehydrogenase(EC:1.1.1.22)
2062261287	845	20	19	c2922	Predicted UDP-glucose 6-dehydrogenase(EC:1.1.1.22)
2062261288	452	223	13	c2922	Short-chain dehydrogenases of various substrate specificities
2062261289	1028	69	5	c2922	Tetrahydrodipicolinate N-succinyltransferase
2062261897	749	1	4	c2936	ABC-type Zn2+ transport system, periplasmic component/surface adhesin
2062261900	539	4	4	c2936	Bacterial NAD-glutamate dehydrogenase.
2062264452	956	44	14	c2936	glutamate dehydrogenase (NAD) (EC 1.4.1.2)(EC:1.4.1.2)
2062265111	194	0	21	c2936	glutamate dehydrogenase (NAD) (EC 1.4.1.2)(EC:1.4.1.2)
2062265795	401	0	22	c2936	NAD-specific glutamate dehydrogenase
2062265803	1175	14	4	c2936	NAD-specific glutamate dehydrogenase
2062265806	164	6	0	c294	Bacterial nucleoid DNA-binding protein
2062265814	200	5	0	c294	hypothetical protein
2062265817	2258	32	6	c294	phenylalanyl-tRNA synthetase beta subunit (EC 6.1.1.20)(EC:6.1.1.20)
2062265818	560	68	5	c294	phenylalanyl-tRNA synthetase, alpha subunit (EC 6.1.1.20)(EC:6.1.1.20)
2062265819	95	0	0	c294	phenylalanyl-tRNA synthetase, alpha subunit (EC 6.1.1.20)(EC:6.1.1.20)
2062265820	842	151	24	c2948	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenase
2062265823	458	28	22	c2948	4-diphosphocytidyl-2-methyl-D-erithritol synthase
2062268356	185	11	5	c2948	4-diphosphocytidyl-2-methyl-D-erithritol synthase(EC:2.7.7.60)
2062268359	776	18	6	c2948	Bacterial type II/III secretion system short domain.
2062268363	380	11	8	c2948	Bacterial type II/III secretion system short domain.
2062269040	128	0	16	c2948	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog

2062269671	947	89	18	c2948	NAD-dependent aldehyde dehydrogenases(EC:1.2.1.3)
2062269677	398	38	10	c2948	NAD-dependent aldehyde dehydrogenases(EC:1.2.1.3,EC:1.2.1.8)
2062269711	143	21	0	c2948	Short-chain alcohol dehydrogenase of unknown specificity(EC:1.1.1.100)
2062271607	92	0	0	c2949	hypothetical protein
2062271608	1181	4	9	c2949	hypothetical protein
2062271612	284	11	0	c2949	hypothetical protein
2062271613	224	31	0	c2949	hypothetical protein
2062271618	389	8	0	c2949	Phosphoribosylanthranilate isomerase
2062272261	212	5	0	c2949	phosphoribosylanthranilate isomerase (EC 5.3.1.24)(EC:5.3.1.24,EC:5.3.1.24,EC:4
2062272265	308	42	16	c2949	Uncharacterized conserved protein
2062272267	59	0	0	c2968	hypothetical protein
2062272273	416	488	41	c2968	LSU ribosomal protein L16P
2062272276	287	17	17	c2968	LSU ribosomal protein L23P
2062272277	617	120	49	c2968	LSU ribosomal protein L2P
2062272942	332	277	21	c2968	ribosomal protein L22, bacterial type
2062272943	194	46	5	c2968	ribosomal protein L29
2062272944	263	57	8	c2968	Ribosomal protein L4
2062273568	239	13	0	c2968	SSU ribosomal protein S17P
2062274225	281	43	60	c2968	SSU ribosomal protein S19P
2062274226	281	25	0	c2968	SSU ribosomal protein S3P
2062274228	407	64	17	c2968	SSU ribosomal protein S3P
2062277422	1193	106	12	c2991	6-phosphofructokinase (EC 2.7.1.11)(EC:2.7.1.11)
2062278036	179	346	34	c2991	BioY family.
2062278037	458	20	7	c2991	glycogen synthase (ADP-glucose)(EC:2.4.1.21)
2062278652	929	27	9	c2991	Glycogen synthase(EC:2.4.1.21)
2062278657	92	0	0	c2991	hypothetical protein
2062278665	464	86	0	c2991	hypothetical protein
2062278666	746	35	8	c2991	hypothetical protein
2062278671	86	0	0	c2991	hypothetical protein
2062278673	365	44	0	c2991	hypothetical protein(EC:1.5.99.8)
2062278674	1661	25	2	c2991	Proline dehydrogenase(EC:1.5.99.8)

2062279978	533	66	17	c2991	Thiamine pyrophosphate-requiring enzymes (EC:2.2.1.6)
2062280609	623	34	13	c2991	Thiamine pyrophosphate-requiring enzymes (EC:2.2.1.6)
2062280610	581	81	17	c2991	Thiamine pyrophosphate-requiring enzymes (EC:2.2.1.6)
2062280611	209	29	0	c2991	Uncharacterized conserved protein
2062280612	332	9	12	c30	Cyclic nucleotide-binding domain.
2062280616	200	20	10	c30	hypothetical protein
2062280617	317	13	0	c30	hypothetical protein
2062280626	845	49	7	c30	Mannose-1-phosphate guanylyltransferase
2062280632	458	35	13	c30	mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)/mannose-6-phosph
2062280650	248	32	16	c302	chorismate mutase domain of proteobacterial P-protein, clade 2(EC:4.2.1.51)
2062280652	509	31	24	c302	FKBP-type peptidyl-prolyl cis-trans isomerases 1(EC:5.2.1.8)
2062280655	902	12	9	c302	MoxR-like ATPases
2062280661	371	132	27	c302	protein translocase, SecG subunit
2062280662	752	84	114	c302	triosephosphate isomerase(EC:5.3.1.1)
2062281247	557	23	0	c3029	ABC-type spermidine/putrescine transport system, permease component I
2062281248	284	0	0	c3029	ABC-type spermidine/putrescine transport system, permease component II
2062281251	1124	138	13	c3029	ABC-type spermidine/putrescine transport systems, ATPase components
2062281257	311	26	26	c3029	hypothetical protein
2062281282	92	0	0	c3029	hypothetical protein
2062281283	707	45	30	c3029	Spermidine/putrescine-binding periplasmic protein
2062281892	73	96	0	c306	(tRNA)
2062281893	386	91	16	c306	[protein release factor]-glutamine N5-methyltransferase (EC 2.1.1.-)(EC:2.1.1.-)
2062281905	827	52	5	c306	1,4-Dihydroxy-2-naphthoate synthase (EC 4.1.3.36)(EC:4.1.3.36)
2062283155	890	64	15	c306	1,4-dihydroxy-2-naphtoate prenyltransferase (EC 2.5.1.-)(EC:2.5.1.-)
2062283159	1043	46	9	c306	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (EC 2.5.1.54)(EC:2.5.1.54
2062283798	203	5	0	c306	Adenylosuccinate lyase(EC:4.3.2.2)
2062284413	899	131	14	c306	amine acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine
2062286344	764	51	17	c306	amino acid ABC transporter ATP-binding protein, PAAT family (TC 3.A.1.3.-)(EC:3.6
2062286345	1196	151	28	c306	amino acid ABC transporter membrane protein 1, PAAT family (TC 3.A.1.3.-)
2062287061	887	44	3	c306	EamA-like transporter family.
2062288304	917	72	12	c306	Glycine/D-amino acid oxidases (deaminating)

2062288305	830	22	19	c306	hypothetical protein
2062288321	161	43	19	c306	hypothetical protein
2062288334	299	20	0	c306	hypothetical protein
2062288336	455	68	9	c306	hypothetical protein
2062288337	506	18	4	c306	hypothetical protein
2062288342	1016	1267	166	c306	L-glutamine-binding protein/L-glutamate-binding protein/L-aspartate-binding protein
2062288343	299	157	37	c306	LSU ribosomal protein L21P
2062288977	287	105	17	c306	LSU ribosomal protein L27P
2062288978	257	31	16	c306	Methylase of polypeptide chain release factors(EC:2.1.1.-)
2062288983	1454	30	9	c306	O-succinylbenzoate-CoA ligase
2062288984	1118	39	5	c306	o-succinylbenzoic acid (OSB) synthetase
2062288985	524	130	17	c306	Protein of unknown function (DUF3015).
2062290282	794	123	28	c306	tryptophanyl-tRNA synthetase (EC 6.1.1.2)(EC:6.1.1.2)
2062290285	455	51	4	c306	uncharacterized domain 1
2062290296	1292	14	4	c3060	citrate synthase (EC 2.3.3.1)(EC:2.3.3.1)
2062290297	821	94	43	c3060	Flagellar motor switch protein
2062290322	89	0	0	c3060	hypothetical protein
2062290323	647	20	11	c3060	Ornithine carbamoyltransferase(EC:2.1.3.3)
2062290324	788	84	18	c3061	amino acid/amide ABC transporter ATP-binding protein 1, HAAT family (TC 3.A.1.4.
2062290980	173	6	6	c3061	hypothetical protein
2062290982	1979	90	31	c3061	Long-chain acyl-CoA synthetases (AMP-forming)(EC:6.2.1.3)
2062290989	653	26	21	c3073	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
2062290990	317	73	16	c3073	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)(EC:1.2.1.12)
2062290991	302	7	7	c3073	hypothetical protein
2062291009	644	5	6	c3073	Major Facilitator Superfamily.
2062291012	908	22	24	c3073	Methylase involved in ubiquinone/menaquinone biosynthesis
2062291015	173	0	40	c3073	ribose-5-phosphate isomerase (EC 5.3.1.6)(EC:5.3.1.6)
2062292888	515	70	6	c308	2-isopropylmalate synthase (EC 2.3.3.13)(EC:2.3.3.13)
2062292892	212	52	9	c308	2-isopropylmalate synthase (EC 2.3.3.13)(EC:2.3.3.13)
2062292917	290	55	7	c308	hypothetical protein
2062294166	482	68	23	c308	hypothetical protein

2062294169	953	29	9	c308	hypothetical protein
2062294186	494	26	8	c308	hypothetical protein
2062294189	239	96	13	c308	hypothetical protein
2062294190	221	27	5	c308	hypothetical protein
2062294786	260	65	0	c308	hypothetical protein
2062294798	782	93	23	c308	Isopropylmalate/homocitrate/citramalate synthases(EC:2.3.3.13)
2062294799	383	16	0	c308	L-threonine synthase (EC 4.2.3.1)(EC:4.2.3.1)
2062294802	284	67	21	c308	L-threonine synthase (EC 4.2.3.1)(EC:4.2.3.1)
2062294805	1058	25	23	c308	Lauroyl/myristoyl acyltransferase
2062294808	1574	41	16	c3099	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II(EC:6.2.1.3)
2062294809	140	7	0	c3099	hypothetical protein
2062296080	281	96	28	c3099	Phosphohistidine phosphatase SixA(EC:3.1.3.-)
2062296082	233	77	0	c310	Asparaginase.
2062296083	1025	227	23	c310	aspartate carbamoyltransferase (EC 2.1.3.2)
2062296735	971	59	13	c310	Carbamate kinase(EC:2.7.2.2)
2062296736	296	3	0	c310	hypothetical protein
2062296737	341	44	0	c310	hypothetical protein
2062296738	407	39	10	c310	hypothetical protein
2062296741	560	143	25	c310	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D(EC:3.5.1.1)
2062298010	629	81	13	c310	Uncharacterized protein, possibly involved in glyoxylate utilization
2062298011	83	0	0	c3138	(tRNA)
2062298012	509	73	31	c3138	Ferredoxin
2062298013	902	0	0	c3138	Histidyl-tRNA synthetase(EC:6.1.1.21)
2062298019	131	15	0	c3138	hypothetical protein
2062298023	173	98	23	c3138	hypothetical protein
2062298034	518	6	2	c3138	replication factor C small subunit
2062298035	281	0	0	c3138	translation initiation factor 6 (aeIF-6)
2062298036	401	0	0	c3138	translation initiation factor 6 (aeIF-6)
2062298037	791	25	5	c3149	DNA repair protein RecO
2062298038	1226	3	4	c3149	hypothetical protein
2062298040	497	18	10	c3149	methionine-S-sulfoxide reductase(EC:1.8.4.11)

2062298041	242	4	4	c3151	ABC-type branched-chain amino acid transport systems, periplasmic component
2062299314	974	87	15	c3151	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I
2062299944	890	15	13	c3151	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I
2062299959	170	6	0	c3151	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I
2062299960	167	0	0	c3151	hypothetical protein
2062300580	74	0	0	c3151	hypothetical protein
2062300586	212	5	5	c3192	Acetyltransferase (GNAT) family.
2062301233	278	162	25	c3192	Acylphosphatases(EC:3.6.1.7)
2062301238	617	37	3	c3192	ATPases involved in chromosome partitioning
2062305091	740	0	3	c3192	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-d
2062305092	374	48	11	c3192	hypothetical protein
2062305101	170	0	0	c3192	hypothetical protein
2062305102	380	32	26	c3192	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binc
2062308275	1286	51	8	c3207	acetylornithine aminotransferase apoenzyme (EC 2.6.1.11)(EC:2.6.1.17,EC:2.6.1.1
2062308279	854	9	8	c3207	hypothetical protein
2062308280	1010	41	3	c3207	MoxR-like ATPases(EC:3.6.3.-)
2062308283	752	21	19	c3207	Predicted exporters of the RND superfamily
2062309527	911	4	3	c3207	Predicted exporters of the RND superfamily
2062309530	311	6	13	c3225	hypothetical protein
2062309531	347	26	0	c3225	Nitrate/nitrite transporter
2062310113	677	38	0	c3225	Nitrate/nitrite transporter
2062310116	638	0	3	c3225	RNAse G (EC 3.1.4.-)(EC:3.1.26.-)
2062310732	251	96	20	c323	ATP-dependent Lon protease, bacterial type(EC:3.4.21.53)
2062310733	686	70	35	c323	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062310735	1235	127	23	c323	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062310736	296	132	3	c323	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062310737	467	146	84	c323	Biopolymer transport protein
2062310738	728	166	47	c323	Biopolymer transport proteins
2062310740	554	54	14	c323	carbamoyl-phosphate synthase large subunit(EC:6.3.5.5)
2062310742	1664	41	11	c323	carbamoyl-phosphate synthase large subunit(EC:6.3.5.5)
2062310743	980	54	33	c323	Carbamoylphosphate synthase large subunit (split gene in MJ)

2062310747	284	14	4	c323	Flagellar motor switch/type III secretory pathway protein
2062312704	953	163	7	c323	glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)(EC:5.4.3.8)
2062314583	227	40	40	c323	glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)(EC:5.4.3.8)
2062314588	389	15	0	c323	hypothetical protein
2062316483	368	8	22	c323	hypothetical protein
2062316486	269	37	7	c323	hypothetical protein
2062317098	320	16	0	c323	hypothetical protein
2062317131	839	20	14	c323	Membrane carboxypeptidase/penicillin-binding protein(EC:2.4.1.-,EC:3.4.-)
2062317731	203	64	10	c323	mttA/Hcf106 family.
2062318354	368	1092	163	c323	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
2062318355	377	3	13	c323	R3H domain.
2062318357	749	52	9	c323	Uncharacterized conserved protein
2062318359	452	77	40	c323	Uncharacterized protein conserved in bacteria
2062318991	386	36	21	c3236	7-cyano-7-deazaguanine reductase(EC:1.7.1.13)
2062319669	2453	41	12	c3236	Chromosome segregation ATPases
2062319672	122	0	0	c3236	hypothetical protein
2062320337	83	0	0	c3237	(tRNA)
2062320338	72	0	0	c3237	(tRNA)
2062320339	254	0	0	c3237	hypothetical protein
2062320342	257	0	16	c3237	MORN repeat.
2062321606	215	23	23	c3237	Transposase.
2062321608	515	0	10	c3237	Uncharacterized protein conserved in bacteria
2062321611	542	9	22	c3237	Uncharacterized protein conserved in bacteria
2062321612	644	12	8	c3247	ABC-type proline/glycine betaine transport system, ATPase component(EC:3.6.3.3
2062321613	398	23	45	c3247	ABC-type proline/glycine betaine transport system, ATPase component(EC:3.6.3.3
2062321614	626	88	18	c3247	ABC-type proline/glycine betaine transport system, permease component
2062322904	1169	110	17	c3247	ABC-type proline/glycine betaine transport system, permease component
2062322916	182	27	0	c3247	hypothetical protein
2062322918	317	16	0	c3247	hypothetical protein
2062322924	158	184	0	c3247	hypothetical protein
2062322926	641	147	28	c328	ABC-type phosphate/phosphonate transport system, permease component

2062322927	257	553	70	c328	hypothetical protein
2062322929	713	398	36	c328	phosphate/phosphite/phosphonate ABC transporters, periplasmic binding protein
2062323579	776	62	46	c328	phosphonate ABC transporter, ATP-binding protein
2062323580	848	223	11	c328	phosphonate ABC transporter, permease protein PhnE
2062323583	935	2	4	c3321	Adenylosuccinate synthetase (EC 6.3.4.4)(EC:6.3.4.4)
2062323584	125	0	0	c3321	hypothetical protein
2062324839	272	0	0	c3321	hypothetical protein
2062324842	278	0	0	c3321	hypothetical protein
2062324844	164	0	0	c3321	NUDIX domain.
2062324849	785	0	3	c3321	orotidine-5''-phosphate decarboxylase (EC 4.1.1.23)(EC:4.1.1.23)
2062324850	254	0	0	c3321	Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)(EC:2.5.1.31)
2062324851	362	3	0	c3331	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase(EC:2.2.1.9)
2062324860	455	13	2	c3331	Apolipoprotein N-acyltransferase
2062325502	350	60	9	c3331	Apolipoprotein N-acyltransferase
2062325503	1148	55	20	c3331	cell division protein FtsW
2062326780	791	83	5	c3331	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062328115	2282	21	7	c3331	FOG: Ankyrin repeat
2062328116	911	63	10	c3331	FOG: Ankyrin repeat
2062328117	272	4	22	c3331	hypothetical protein
2062328742	815	37	7	c3331	hypothetical protein
2062329387	758	125	7	c3331	hypothetical protein
2062329388	911	55	5	c3331	MoxR-like ATPases
2062329390	71	42	0	c3354	(tRNA)
2062329393	353	68	62	c3354	bacterial translation initiation factor 3 (bIF-3)
2062329394	251	44	100	c3354	bacterial translation initiation factor 3 (bIF-3)
2062331980	236	8	0	c3354	hypothetical protein
2062331982	950	42	12	c3354	hypothetical protein
2062331983	368	90	27	c3354	LSU ribosomal protein L20P
2062331984	194	26	36	c3354	LSU ribosomal protein L35P
2062331986	422	73	9	c342	chorismate synthase (EC 4.2.3.5)(EC:4.2.3.5)
2062331987	680	79	16	c342	chorismate synthase (EC 4.2.3.5)(EC:4.2.3.5)

2062332638	293	27	24	c342	EamA-like transporter family.
2062332639	383	29	5	c342	EamA-like transporter family.
2062332641	1784	87	21	c342	Guanosine polyphosphate pyrophosphohydrolases/synthetases(EC:2.7.6.5)
2062332643	194	10	21	c342	hypothetical protein
2062332644	308	6	6	c342	hypothetical protein
2062332675	131	8	0	c342	hypothetical protein
2062333277	548	42	20	c342	hypothetical protein
2062333284	173	0	0	c342	hypothetical protein
2062333911	410	5	10	c342	NTP pyrophosphohydrolases including oxidative damage repair enzymes
2062333914	1430	119	20	c342	Trk-type K+ transport systems, membrane components
2062334496	401	12	5	c342	Uncharacterized conserved protein
2062334502	200	10	5	c342	Uncharacterized protein conserved in bacteria
2062334515	671	6	6	c342	Uncharacterized protein conserved in bacteria
2062334518	908	76	12	c3428	amino acid/amide ABC transporter membrane protein 1, HAAT family (TC 3.A.1.4.-)
2062334519	1250	119	52	c3428	amino acid/amide ABC transporter substrate-binding protein, HAAT family (TC 3.A.1
2062334523	74	0	0	c3428	hypothetical protein
2062334526	500	176	28	c344	glutamate synthase (NADH) small subunit (EC 1.4.1.14)(EC:1.4.1.13,EC:1.4.1.14)
2062335135	356	70	0	c344	LSU ribosomal protein L19P
2062335166	665	48	9	c344	Site-specific recombinase XerD
2062335168	437	0	0	c344	transcription elongation factor GreA
2062335744	1187	10	6	c3448	Glucose/sorbosone dehydrogenases
2062335749	593	8	0	c3448	Membrane-associated phospholipid phosphatase
2062335763	803	2	2	c3448	NAD-dependent DNA ligase (contains BRCT domain type II)
2062335764	248	8	8	c3497	Aminomethyltransferase folate-binding domain.
2062335765	605	88	5	c3497	folate-binding protein YgfZ
2062335768	1049	16	10	c3497	hypothetical protein
2062335769	581	33	0	c3497	inosine-5''-monophosphate dehydrogenase (EC 1.1.1.205)
2062335770	551	54	9	c3497	inosine-5''-monophosphate dehydrogenase (EC 1.1.1.205)(EC:1.1.1.205)
2062335771	380	42	18	c3500	1-acyl-sn-glycerol-3-phosphate acyltransferase
2062335772	671	9	1	c3500	Dimethyladenosine transferase (rRNA methylation)
2062337064	608	72	8	c3500	Glutamate synthase domain 2(EC:1.4.1.13,EC:1.4.1.14)

2062338307	1001	74	7	c3500	Glutamate synthase domain 2(EC:1.4.1.13,EC:1.4.1.14)
2062338312	203	10	10	c3500	hypothetical protein
2062339637	947	74	7	c3500	Molybdenum cofactor biosynthesis enzyme
2062339638	1496	14	9	c3500	Peptidase family S41.
2062340272	227	101	22	c3509	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)
2062340273	1091	10	5	c3509	Cytosine deaminase and related metal-dependent hydrolases
2062340277	323	19	25	c3509	Cytosine deaminase and related metal-dependent hydrolases(EC:3.5.3.13)
2062340922	779	0	5	c3509	N-formylglutamate amidohydrolase(EC:3.5.3.8,EC:3.5.1.68)
2062340923	224	0	0	c3509	transposase, IS4 family
2062342182	1667	27	6	c352	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases
2062342206	1640	88	57	c352	5''-nucleotidase/2'',3''-cyclic phosphodiesterase and related esterases
2062342208	704	80	38	c352	Cytochrome c, mono- and diheme variants
2062342212	467	64	30	c352	Desulfoferrodoxin.
2062342213	422	12	0	c352	Domain of unknown function DUF302.
2062342214	533	205	2	c352	Fe-S oxidoreductase
2062342851	770	188	6	c352	Fe-S-cluster-containing hydrogenase components 1
2062342852	1325	2	5	c352	Highly conserved protein containing a thioredoxin domain
2062343498	704	11	3	c352	hypothetical protein
2062343501	230	0	0	c352	hypothetical protein
2062343516	575	748	80	c352	hypothetical protein
2062343517	200	5	0	c352	hypothetical protein
2062343527	500	150	8	c352	hypothetical protein
2062344220	1160	123	15	c352	hypothetical protein
2062345495	113	0	0	c352	hypothetical protein
2062345496	2711	37	6	c352	Polyketide synthase modules and related proteins
2062345497	1088	108	8	c352	Polysulphide reductase(EC:1.2.7.-)
2062345524	215	0	0	c352	SmpA / OmlA family.
2062345525	353	25	6	c352	Sulphur oxidation protein SoxZ.
2062345526	419	0	5	c352	Thiol:disulfide interchange protein
2062345531	569	135	28	c352	Uncharacterized conserved protein
2062345534	515	97	0	c352	Uncharacterized conserved protein

2062345536	614	10	13	c352	Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory anc
2062345538	1025	145	56	c352	YeeE/YedE family (DUF395).
2062346757	614	50	13	c3541	Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisphosphatase and related protei
2062346759	893	114	16	c3541	transketolase (EC 2.2.1.1)
2062346763	1052	87	16	c3541	transketolase (EC 2.2.1.1)(EC:2.2.1.1)
2062346769	938	51	19	c3541	Uridine kinase
2062346770	281	36	7	c355	ABC-type branched-chain amino acid transport systems, periplasmic component
2062346771	317	6	0	c355	Bacterial regulatory protein, arsR family.
2062347376	239	21	4	c355	hypothetical protein
2062347377	659	17	8	c355	hypothetical protein
2062347379	842	55	12	c355	hypothetical protein
2062347380	323	133	12	c355	hypothetical protein
2062347381	254	12	0	c355	hypothetical protein
2062347384	218	14	5	c355	hypothetical protein
2062347389	941	176	20	c355	Predicted permeases
2062347392	1058	42	12	c355	Zn-dependent hydrolases, including glyoxylases
2062348678	518	58	17	c3572	bacterial translation initiation factor 2 (bIF-2)
2062348684	167	0	0	c3572	hypothetical protein
2062348685	149	7	0	c3572	Ribosome-binding factor A.
2062350520	1118	6	12	c3572	Translation initiation factor 2 (IF-2; GTPase)
2062350521	608	20	0	c3572	Translation initiation factor IF-2, N-terminal region.
2062350523	596	101	22	c3576	Cytosine/adenosine deaminases
2062350524	3407	47	9	c3576	Exonuclease V gamma subunit
2062350529	428	30	7	c3576	Exonuclease V gamma subunit
2062350530	341	62	0	c3576	hypothetical protein
2062350540	821	85	37	c3576	phosphonoacetaldehyde hydrolase(EC:3.11.1.1)
2062350541	932	58	21	c3576	Transcriptional regulator
2062350554	818	116	13	c3576	xanthine dehydrogenase accessory protein XdhC
2062351194	854	46	19	c359	ABC-type spermidine/putrescine transport system, permease component I
2062351200	674	85	16	c359	ABC-type spermidine/putrescine transport system, permease component II
2062351201	677	21	9	c359	ABC-type spermidine/putrescine transport systems, ATPase components

2062351202	485	6	0	c359	ABC-type spermidine/putrescine transport systems, ATPase components
2062351203	326	12	0	c359	hypothetical protein
2062351204	1340	239	88	c359	hypothetical protein
2062351208	683	10	4	c359	Transcriptional regulators
2062351209	1805	20	1	c3597	Exoribonuclease R(EC:3.1.13.1)
2062351212	257	241	12	c3597	Glycine cleavage system H protein (lipoate-binding)
2062353115	119	0	0	c3597	UDP-2,3-diacylglucosamine hydrolase (EC 3.6.1.-)(EC:3.6.1.-)
2062353747	194	0	0	c3597	UDP-2,3-diacylglucosamine hydrolase (EC 3.6.1.-)(EC:3.6.1.-)
2062353748	233	0	0	c3604	hypothetical protein
2062354383	920	77	7	c3604	Predicted integral membrane protein
2062355036	1022	5	6	c3604	Uncharacterized low-complexity proteins
2062355038	72	0	0	c366	(tRNA)
2062355039	81	0	0	c366	(tRNA)
2062355060	71	0	0	c366	(tRNA)
2062355698	72	42	0	c366	(tRNA)
2062355699	557	63	14	c366	2-nitropropane dioxygenase.
2062355700	296	98	17	c366	Aspartate carbamoyltransferase, catalytic chain(EC:2.1.3.2)
2062358217	425	49	21	c366	Aspartate carbamoyltransferase, catalytic chain(EC:2.1.3.2)
2062358222	260	46	19	c366	ATP-dependent Zn proteases(EC:3.4.24.-)
2062358230	497	42	20	c366	Dioxygenases related to 2-nitropropane dioxygenase(EC:1.13.12.16)
2062358236	782	139	19	c366	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)(EC:1.3.1.9)
2062358237	1610	80	42	c366	flagellar basal-body M-ring protein/flagellar hook-basal body protein (fliF)
2062358238	353	0	0	c366	Holliday junction DNA helicase subunit RuvB
2062358239	128	0	0	c366	hypothetical protein
2062358253	176	6	11	c366	hypothetical protein
2062358880	221	18	50	c366	hypothetical protein
2062358885	278	183	94	c366	hypothetical protein(EC:1.13.12.16)
2062358890	425	52	75	c366	LSU ribosomal protein L11P
2062359515	224	129	4	c366	LSU ribosomal protein L12P
2062359517	125	0	0	c366	LSU ribosomal protein L12P
2062359523	689	77	54	c366	LSU ribosomal protein L1P

2062359548	1205	316	36	c366	membrane protease FtsH catalytic subunit (EC 3.4.24.-)(EC:3.4.24.-)
2062361452	404	104	42	c366	membrane protease FtsH catalytic subunit (EC 3.4.24.-)(EC:3.4.24.-)
2062362066	590	364	20	c366	Phosphatidylserine decarboxylase(EC:4.1.1.65)
2062362067	1493	182	17	c366	Phosphatidylserine synthase
2062362074	188	53	5	c366	preprotein translocase, SecE subunit, bacterial
2062362712	1385	25	7	c366	putative efflux protein, MATE family
2062362713	524	132	27	c366	Ribosomal protein L10
2062362737	599	15	18	c366	transcription termination/antitermination factor NusG
2062362738	71	0	0	c3660	(tRNA)
2062362781	254	0	0	c3660	Histone-like transcription factor (CBF/NF-Y) and archaeal histone.
2062362784	98	0	0	c3660	hypothetical protein
2062362787	431	16	0	c3660	hypothetical protein
2062363981	227	0	0	c3660	hypothetical protein
2062363990	464	2	0	c3660	Mg-dependent DNase(EC:3.1.21.-)
2062364614	230	0	0	c3660	Mg-dependent DNase(EC:3.1.21.-)
2062364615	440	0	0	c3660	Plastocyanin
2062364657	293	0	7	c3660	Ribosomal protein S17E
2062365277	185	0	11	c3665	hypothetical protein
2062365292	206	0	0	c3665	hypothetical protein
2062365295	227	18	0	c3665	hypothetical protein
2062365297	89	0	0	c3665	hypothetical protein
2062365298	428	7	5	c3665	MORN repeat.
2062365303	575	122	14	c3665	Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding pr
2062367168	758	57	4	c3665	Short-chain alcohol dehydrogenase of unknown specificity
2062369036	596	15	3	c3666	Cobalamin biosynthesis protein CbiD
2062369665	215	19	9	c3666	Cobalamin biosynthesis protein CbiD
2062370965	167	0	36	c3666	Transcriptional regulator
2062370966	407	52	12	c3666	Transcriptional regulator
2062370970	776	76	14	c3666	uroporphyrinogen-III C-methyltransferase (EC 2.1.1.107)(EC:2.1.1.107)
2062370974	491	47	0	c3692	Glycine cleavage system T protein (aminomethyltransferase)(EC:1.5.99.1)
2062372272	800	48	4	c3692	Glycine/D-amino acid oxidases (deaminating)

2062372274	659	50	14	c3692	Glycine/D-amino acid oxidases (deaminating)(EC:1.5.99.1)
2062372278	836	12	8	c3692	Predicted choline kinase involved in LPS biosynthesis
2062372931	2024	51	17	c370	Acetyl-CoA carboxylase alpha subunit
2062373568	2411	39	9	c370	Acetyl/propionyl-CoA carboxylase, alpha subunit
2062373572	1907	40	10	c370	Cytochrome c biogenesis factor
2062373573	347	17	9	c370	diacylglycerol kinase (EC 2.7.1.107)(EC:2.7.1.107)
2062373577	725	72	4	c370	EamA-like transporter family.
2062373581	338	30	12	c370	Geranylgeranyl pyrophosphate synthase(EC:2.5.1.-)
2062373582	650	40	15	c370	Geranylgeranyl pyrophosphate synthase(EC:2.5.1.30)
2062373592	656	75	27	c370	hypothetical protein
2062373593	155	77	97	c370	hypothetical protein
2062374219	542	7	9	c370	hypothetical protein
2062374238	530	11	6	c370	hypothetical protein
2062374239	221	9	9	c370	hypothetical protein(EC:6.3.4.14)
2062374241	470	30	11	c370	Indole-3-glycerol phosphate synthase
2062374853	1610	30	40	c370	Metal-dependent hydrolases of the beta-lactamase superfamily III
2062374856	245	29	29	c370	Molybdopterin converting factor, small subunit
2062376149	401	10	5	c370	Phenylalanyl-tRNA synthetase beta subunit
2062376150	1427	18	10	c370	Phenylalanyl-tRNA synthetase beta subunit
2062376152	467	26	17	c370	Phosphoglycerate dehydrogenase and related dehydrogenases(EC:1.1.1.81,EC:1.
2062376154	779	49	28	c370	Purine nucleoside phosphorylase(EC:2.4.2.28)
2062376157	140	7	0	c370	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-bin
2062376160	197	5	46	c370	two component, sigma54 specific, transcriptional regulator, Fis family
2062376167	938	4	4	c3720	ATP-dependent DNA ligase(EC:6.5.1.1)
2062376798	614	10	10	c3720	ATPases involved in chromosome partitioning
2062376800	188	0	11	c3720	Domain of unknown function DUF302.
2062376803	413	73	7	c3720	Glycine/D-amino acid oxidases (deaminating)
2062376804	509	12	6	c3720	Glycine/D-amino acid oxidases (deaminating)
2062376805	581	40	2	c3720	Type II secretory pathway, prepilin signal peptidase PulO and related peptidases
2062376806	308	32	23	c3724	aspartate semialdehyde dehydrogenase (EC 1.2.1.11)(EC:1.2.1.11)
2062376807	692	10	13	c3724	DNA methylase.

2062378059	182	44	22	c3724	hypothetical protein
2062378061	707	41	25	c3724	hypothetical protein
2062378079	689	38	13	c3724	NAD/FAD-utilizing enzyme apparently involved in cell division
2062378080	152	0	0	c3724	NAD/FAD-utilizing enzyme apparently involved in cell division
2062378082	95	0	0	c3724	NAD/FAD-utilizing enzyme apparently involved in cell division
2062379336	872	102	31	c3724	Predicted membrane protein
2062379342	617	6	10	c3724	Uncharacterized protein conserved in bacteria
2062379995	119	8	0	c3732	hypothetical protein
2062379999	368	27	11	c3732	hypothetical protein
2062380000	482	12	8	c3732	Methylmalonyl-CoA mutase, N-terminal domain/subunit(EC:5.4.99.2)
2062380001	734	18	18	c3732	Methylmalonyl-CoA mutase, N-terminal domain/subunit(EC:5.4.99.2)
2062380002	635	35	3	c3732	Sua5/YciO/YrdC/YwlC family protein
2062386312	1109	10	17	c374	Chromosome segregation ATPases
2062386315	2372	43	18	c374	Chromosome segregation ATPases
2062386321	278	11	0	c374	diaminopimelate epimerase (EC 5.1.1.7)
2062386323	191	42	10	c374	diaminopimelate epimerase (EC 5.1.1.7)(EC:5.1.1.7)
2062386324	716	152	32	c374	glutaredoxin-related protein
2062386325	1295	123	29	c374	histidinol dehydrogenase (EC 1.1.1.23)
2062386954	617	26	3	c374	Holliday junction DNA helicase, RuvA subunit
2062386956	347	0	12	c374	Holliday junction endonuclease RuvC (EC 3.1.22.4)(EC:3.1.22.4)
2062386959	1619	12	8	c374	hypothetical protein
2062386960	158	0	19	c374	hypothetical protein
2062386962	248	20	4	c374	Iron-sulphur cluster biosynthesis.
2062386963	773	13	17	c374	Predicted metal-dependent hydrolase
2062386972	482	19	2	c374	single-strand binding protein
2062386977	590	14	17	c374	Uncharacterized conserved protein
2062387020	188	0	0	c374	Uncharacterized conserved protein
2062387637	626	455	50	c374	YGGT family.
2062388282	341	111	26	c376	Branched-chain amino acid transport protein (AzlD).
2062388283	938	18	9	c376	EamA-like transporter family.
2062388284	365	5	3	c376	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily.

2062388286	269	0	0	c376	hypothetical protein
2062388287	407	44	10	c376	Major Facilitator Superfamily.
2062388288	299	247	7	c376	Nitrile hydratase beta subunit.
2062388290	335	96	24	c376	Nitrile hydratase beta subunit.
2062388913	620	77	2	c376	Nitrile hydratase, alpha chain.(EC:4.2.1.84)
2062388914	734	45	15	c376	Predicted branched-chain amino acid permease (azaleucine resistance)
2062388915	401	7	22	c376	Uncharacterized protein conserved in bacteria
2062388916	554	0	0	c378	DnaJ-class molecular chaperone with C-terminal Zn finger domain
2062388927	524	4	0	c378	FAD/FMN-containing dehydrogenases(EC:1.1.2.4)
2062388931	227	18	0	c378	Flp pilus assembly protein TadD, contains TPR repeats
2062390197	227	0	0	c378	hypothetical protein
2062392729	1289	3	0	c378	hypothetical protein
2062392731	404	2	0	c378	hypothetical protein
2062392736	176	0	6	c378	transcriptional regulator, AsnC family
2062392742	73	0	0	c3807	(tRNA)
2062392745	1469	62	19	c3807	hypothetical protein
2062392747	908	62	13	c3807	hypothetical protein
2062392755	704	197	23	c3807	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
2062392756	1103	4	1	c3817	hypothetical protein
2062392757	323	0	0	c3817	hypothetical protein
2062394718	719	11	6	c3817	Transcription-repair coupling factor (superfamily II helicase)(EC:3.6.1.-)
2062394720	116	34	9	c3830	Ankyrin repeat.
2062396015	134	0	0	c3830	dihydroxyacid dehydratase (EC 4.2.1.9)(EC:4.2.1.9)
2062396648	248	81	20	c3830	FOG: Ankyrin repeat
2062396649	500	4	0	c3830	hypothetical protein
2062396650	905	9	4	c3830	hypothetical protein
2062396651	257	23	23	c3830	hypothetical protein
2062396656	1031	61	46	c384	Cell division septal protein
2062399355	299	50	3	c384	Excinuclease ABC subunit B
2062399356	329	12	0	c384	hypothetical protein
2062399944	377	16	21	c384	Integral membrane protein CcmA involved in cell shape determination

2062401921	458	22	22	c384	iojap-related protein
2062401922	1334	97	43	c384	Membrane proteins related to metalloendopeptidases
2062401924	371	84	30	c384	Predicted Fe-S oxidoreductase
2062401929	542	59	17	c384	Predicted Fe-S oxidoreductase
2062401930	533	71	30	c384	Predicted permeases
2062401951	374	45	0	c384	Predicted thioesterase
2062403884	800	63	1	c384	pseudouridylate synthase I(EC:5.4.99.12)
2062403886	470	26	17	c384	Septum formation initiator
2062404556	677	108	7	c384	thiamine pyrophosphokinase
2062404557	326	215	34	c384	thioredoxin
2062404558	1412	80	13	c384	Type II secretory pathway, ATPase PulE/Tfp pilus assembly pathway, ATPase PilB
2062404559	962	84	21	c384	UDP-N-acetylenolpyruvoylglucosamine reductase
2062404577	869	25	5	c384	Uncharacterized protein conserved in bacteria
2062404578	695	39	39	c386	5''-methylthioadenosine/S-adenosylhomocysteine nucleosidase(EC:3.2.2.9)
2062405830	860	17	15	c386	Arginyl-tRNA synthetase(EC:6.1.1.19)
2062405831	839	26	6	c386	Glycerophosphoryl diester phosphodiesterase
2062408442	2231	14	20	c386	Guanosine polyphosphate pyrophosphohydrolases/synthetases(EC:2.7.6.5)
2062411702	443	16	5	c386	hypothetical protein
2062411703	656	6	5	c386	hypothetical protein
2062411704	797	20	13	c386	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
2062412359	254	28	16	c386	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase(EC:2.4.1.227)
2062412365	230	9	0	c3862	CAAX amino terminal protease family.
2062412366	467	26	2	c3862	hypothetical protein
2062412398	719	19	11	c3862	leucyl/phenylalanyl-tRNA--protein transferase(EC:2.3.2.6)
2062412999	1010	38	39	c3862	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation
2062413002	467	9	6	c3862	Sporulation related domain.
2062413005	422	0	0	c3889	ATPase involved in DNA repair
2062413016	98	0	0	c3889	hypothetical protein
2062413018	326	0	0	c3889	hypothetical protein
2062413019	167	6	0	c3889	hypothetical protein
2062413023	722	1	0	c3889	hypothetical protein

2062415640	209	0	0	c3889	hypothetical protein
2062415646	170	0	0	c3889	hypothetical protein
2062416261	983	0	0	c3889	hypothetical protein
2062416262	662	50	15	c3935	Excinuclease ABC subunit A
2062416263	263	34	0	c3935	Excinuclease ATPase subunit
2062417556	443	79	16	c3935	Excinuclease ATPase subunit
2062417557	125	0	0	c3935	Glycine/D-amino acid oxidases (deaminating)(EC:1.5.99.1)
2062417560	386	13	5	c394	Glycosidases(EC:3.2.1.20)
2062418859	449	11	4	c394	Glycosidases(EC:3.2.1.20)
2062418860	1148	152	14	c394	maltose ABC transporter/trehalose ABC transporter membrane protein/sucrose ABC
2062418865	671	48	34	c394	maltose ABC transporter/trehalose ABC transporter membrane protein/sucrose ABC
2062418866	326	55	3	c394	maltose ABC transporter/trehalose ABC transporter membrane protein/sucrose ABC
2062418867	398	324	13	c394	maltose-binding protein/trehalose-binding protein/sucrose-binding protein
2062418869	536	392	32	c394	maltose-binding protein/trehalose-binding protein/sucrose-binding protein
2062418871	155	0	0	c3957	hypothetical protein
2062418873	92	0	0	c3957	hypothetical protein
2062419484	602	2	3	c3957	NADH dehydrogenase subunit B (EC 1.6.5.3)(EC:1.6.5.3)
2062419486	794	4	0	c3957	NADH dehydrogenase subunit D (EC 1.6.5.3)(EC:1.6.5.3)
2062420786	647	3	9	c3957	NADH-quinone oxidoreductase, E subunit(EC:1.6.5.3)
2062420787	395	18	0	c3957	NADH:ubiquinone oxidoreductase 27 kD subunit(EC:1.6.5.3)
2062124774	590	10	25	c401	hypothetical protein
2062132487	647	15	19	c401	thymidylate kinase
2062148689	164	0	0	c401	hypothetical protein
2062207357	203	0	0	c401	hypothetical protein
2062207358	713	7	11	c401	hypothetical protein
2062207359	437	34	9	c401	Peroxiredoxin
2062288313	191	10	0	c401	hypothetical protein
2062365282	221	5	5	c401	hypothetical protein
2062414410	323	15	59	c401	Uncharacterized protein conserved in bacteria
2062422703	470	136	21	c401	6,7-dimethyl-8-ribityllumazine synthase(EC:2.5.1.-)
2062422707	401	2	0	c401	Beta-propeller repeat.

2062422710	1817	67	37	c401	Glycosyltransferase
2062422725	653	3	17	c401	hypothetical protein
2062422731	248	8	0	c401	hypothetical protein
2062423336	887	33	25	c401	hypothetical protein
2062425290	866	7	8	c401	hypothetical protein
2062117528	1472	20	3	c4013	M6 family metalloprotease domain
2062126663	353	133	14	c4013	hypothetical protein
2062142114	284	25	14	c4013	Predicted GTPase
2062347385	272	125	0	c4013	Predicted GTPase
2062372296	401	102	20	c4013	hypothetical protein
2062399946	86	0	0	c4013	(tRNA)
2062129952	929	14	9	c4027	prolyl-tRNA synthetase (EC 6.1.1.15)(EC:6.1.1.15)
2062213744	425	40	0	c4027	enolase (EC 4.2.1.11)(EC:4.2.1.11)
2062269674	392	31	3	c4027	hypothetical protein
2062286371	353	45	0	c4027	enolase (EC 4.2.1.11)(EC:4.2.1.11)
2062286374	323	0	9	c4027	hypothetical protein
2062290293	827	11	8	c4027	Uncharacterized membrane protein (homolog of Drosophila rhomboid)
2062332681	674	18	0	c4027	DNA repair protein RecO
2062342854	140	21	0	c4027	enolase (EC 4.2.1.11)
2062428578	356	28	11	c4027	Septum formation initiator
2062124731	92	22	0	c4038	hypothetical protein
2062376166	896	194	4	c4038	Beta-glucosidase-related glycosidases(EC:3.2.1.52)
2062379340	1235	172	3	c4038	hypothetical protein
2062379341	152	26	0	c4038	hypothetical protein
2062138909	209	0	0	c4098	hypothetical protein
2062278038	563	0	0	c4098	Cyclic nucleotide-binding domain.
2062278039	1460	4	1	c4098	carbamoyl-phosphate synthase large subunit(EC:6.3.5.5)
2062350527	1103	10	0	c4098	K+ transport systems, NAD-binding component
2062126047	908	218	6	c41	Probable taurine catabolism dioxygenase
2062157099	1112	114	14	c41	NADPH-dependent glutamate synthase beta chain and related oxidoreductases
2062164157	371	151	22	c41	hypothetical protein

2062187489	230	13	0	c41	Predicted redox protein, regulator of disulfide bond formation
2062211821	824	61	5	c41	Predicted Fe-S-cluster oxidoreductase
2062219668	374	91	16	c41	Tetratricopeptide repeat.
2062219670	359	8	14	c41	sulfur relay protein TusD/DsrE(EC:2.8.1.-)
2062220988	407	20	5	c41	Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain)(EC:2.1.1.107,EC:4
2062224908	290	424	10	c41	Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits(EC:1.8.99.3
2062290287	812	706	27	c41	Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits(EC:1.8.99.3
2062292237	386	73	18	c41	sulfate adenylyltransferase (EC 2.7.7.4)(EC:2.7.7.4)
2062292890	266	49	0	c41	sulfur relay protein TusB/DsrH
2062294173	194	46	5	c41	hypothetical protein
2062299935	179	28	0	c41	hypothetical protein
2062299940	647	155	19	c41	Nitrate reductase gamma subunit
2062309528	185	54	27	c41	hypothetical protein
2062317730	491	22	4	c41	hypothetical protein
2062326769	1211	84	26	c41	Heterodisulfide reductase, subunit C
2062326770	1388	385	12	c41	hydrogenobyrinic acid a,c-diamide synthase (EC 6.3.5.9)/cobyrinate a,c-diamide sy
2062333279	374	5	19	c41	sulfur relay protein TusC/DsrF
2062344221	233	369	0	c41	hypothetical protein
2062344222	80	13	0	c41	hypothetical protein
2062386974	845	72	14	c41	sulfate adenylyltransferase (EC 2.7.7.4)(EC:2.7.7.4)
2062392744	899	166	19	c41	Anthranilate phosphoribosyltransferase
2062399945	1262	262	32	c41	sulfite reductase, dissimilatory-type alpha subunit(EC:1.8.99.3)
2062428582	335	206	15	c41	sulfur relay protein, TusE/DsrC/DsvC family(EC:2.8.1.-)
2062219667	248	32	24	c411	Integral membrane protein CcmA involved in cell shape determination
2062219669	704	23	1	c411	Aspartate/tyrosine/aromatic aminotransferase(EC:2.6.1.1)
2062325501	1301	81	35	c411	Superfamily I DNA and RNA helicases
2062428579	1082	23	13	c411	Superfamily I DNA and RNA helicases
2062428580	509	8	0	c411	Aspartate/tyrosine/aromatic aminotransferase(EC:2.6.1.1)
2062428581	161	0	0	c411	hypothetical protein
2062144791	1922	80	11	c413	N-methylhydantoinase A/acetone carboxylase, beta subunit
2062198338	149	20	7	c413	hypothetical protein

2062223001	524	63	4	c413	N-methylhydantoinase B/acetone carboxylase, alpha subunit
2062247988	287	42	10	c413	N-methylhydantoinase A/acetone carboxylase, beta subunit
2062252434	650	185	12	c413	TRAP-type C4-dicarboxylate transport system, small permease component
2062252436	1505	175	13	c413	Uncharacterized protein conserved in bacteria
2062252437	1211	52	3	c413	N-methylhydantoinase B/acetone carboxylase, alpha subunit(EC:3.5.2.9)
2062286368	299	0	3	c413	hypothetical protein
2062286369	284	99	18	c413	hypothetical protein
2062286370	482	91	8	c413	hypothetical protein
2062355037	611	116	10	c413	Protein of unknown function (DUF1446).
2062365300	1304	169	38	c413	TRAP transporter, DctM subunit
2062109686	272	55	37	c415	cell elongation-specific peptidoglycan biosynthesis regulator RodA
2062132488	326	31	3	c415	CMP-2-keto-3-deoxyoctulosonic acid synthetase(EC:2.7.7.38)
2062159636	842	70	13	c415	Bacterial cell division membrane protein
2062188755	239	0	4	c415	Phosphopantetheine attachment site.
2062248620	1379	32	11	c415	Uncharacterized conserved protein
2062260026	1124	29	20	c415	Acyl-CoA hydrolase
2062260027	1148	20	8	c415	Aspartate/tyrosine/aromatic aminotransferase
2062308273	1436	49	10	c415	glutamyl-tRNA synthetase, bacterial family(EC:6.1.1.24)
2062308274	1811	23	6	c415	GMP synthase (glutamine-hydrolyzing), N-terminal domain or A subunit(EC:6.3.5.2
2062326778	254	28	12	c415	hypothetical protein
2062326779	170	0	0	c415	hypothetical protein
2062328739	986	63	10	c415	pseudouridine synthase, RluA family(EC:5.4.99.12)
2062328740	515	31	8	c415	Sec-independent protein secretion pathway components
2062400647	224	13	0	c415	Predicted amidohydrolase
2062400648	404	10	0	c415	Predicted amidohydrolase
2062411740	650	12	28	c415	Thiopurine S-methyltransferase (TPMT).
2062138904	734	78	12	c4150	Arabinose efflux permease
2062138905	458	57	24	c4150	hypothetical protein
2062177100	119	0	0	c4150	hypothetical protein
2062198318	1295	103	12	c4150	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large t
2062198319	86	0	0	c4176	hypothetical protein

2062249889	803	57	31	c4176	hypothetical protein
2062363985	698	54	26	c4176	hypothetical protein
2062392109	962	36	85	c4176	Periplasmic component of the Tol biopolymer transport system
2062392110	284	28	28	c4176	WD40-like Beta Propeller Repeat.
2062112273	365	25	5	c420	Predicted ATPase related to phosphate starvation-inducible protein PhoH
2062112274	1007	52	3	c420	Predicted ATPase related to phosphate starvation-inducible protein PhoH
2062126658	509	47	8	c420	Flagellar biosynthesis pathway, component FliR
2062186875	233	279	9	c420	hypothetical protein
2062188756	173	104	0	c420	hypothetical protein
2062213741	1868	55	19	c420	flagellar biosynthesis protein FlhA
2062213742	1064	15	12	c420	flagellar biosynthetic protein FlhB
2062220977	545	61	9	c420	hypothetical protein
2062246677	389	10	72	c420	DnaK suppressor protein
2062247978	146	0	14	c420	hypothetical protein
2062247979	137	7	0	c420	hypothetical protein
2062247980	299	13	10	c420	hypothetical protein
2062281249	1253	119	22	c420	Phosphopantothenate-cysteine ligase (EC 6.3.2.5)/Phosphopantothenoylcysteine d
2062353744	215	51	14	c420	Flagellar GTP-binding protein
2062386318	242	21	0	c420	Flagellar biosynthesis pathway, component FliR
2062203464	173	0	0	c4229	hypothetical protein
2062220303	128	0	0	c4229	phosphoglycerate kinase (EC 2.7.2.3)(EC:2.7.2.3)
2062281903	182	0	0	c4229	hypothetical protein
2062281911	131	0	0	c4229	hypothetical protein
2062294167	863	0	0	c4229	Iron-regulated ABC transporter permease protein SufD
2062328118	443	2	5	c4229	SUF system FeS assembly protein, NifU family
2062329389	1190	2	3	c4229	cysteine desulfurase (EC 2.8.1.7)(EC:2.8.1.7,EC:4.4.1.16)
2062405836	317	0	0	c4229	Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases
2062177120	809	21	2	c423	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin
2062190030	404	5	2	c423	hypothetical protein
2062221674	362	30	14	c423	carbohydrate ABC transporter membrane protein 2, CUT1 family (TC 3.A.1.1.-)
2062224909	92	0	0	c423	hypothetical protein

2062242267	836	20	2	c423	fructose-bisphosphate aldolase (EC 4.1.2.13)(EC:4.1.2.13)
2062288323	167	0	0	c423	hypothetical protein
2062288326	683	3	15	c423	hypothetical protein
2062288327	1004	52	7	c423	myo-inositol 2-dehydrogenase (EC 1.1.1.18)
2062328119	749	120	24	c423	carbohydrate ABC transporter ATP-binding protein, CUT1 family (TC 3.A.1.1.-)
2062328120	653	61	8	c423	carbohydrate ABC transporter membrane protein 1, CUT1 family (TC 3.A.1.1.-)
2062328121	410	10	10	c423	carbohydrate ABC transporter membrane protein 2, CUT1 family (TC 3.A.1.1.-)
2062347387	158	13	0	c423	hypothetical protein
2062347388	170	6	12	c423	hypothetical protein
2062378060	1373	1047	86	c423	carbohydrate ABC transporter substrate-binding protein, CUT1 family (TC 3.A.1.1.-)
2062138283	806	73	22	c424	UDP-N-acetylmuramyl tripeptide synthase
2062138289	695	50	9	c424	FAD/FMN-containing dehydrogenases
2062142780	737	47	15	c424	Predicted deacylase
2062177113	2807	82	17	c424	cyanophycin synthetase(EC:6.-)
2062177124	596	62	5	c424	FAD/FMN-containing dehydrogenases(EC:1.1.2.4)
2062192536	146	7	0	c424	Uncharacterized conserved protein
2062246671	416	5	0	c424	Putative translation initiation inhibitor, yjgF family
2062246693	590	132	15	c424	hypothetical protein
2062273558	533	45	4	c424	Isopenicillin N synthase and related dioxygenases
2062288324	836	87	22	c424	N-acyl-D-aspartate/D-glutamate deacylase
2062350539	584	79	17	c424	N-acyl-D-aspartate/D-glutamate deacylase
2062418826	815	82	15	c424	cyanophycinase(EC:3.4.15.6)
2062418829	119	25	0	c424	hypothetical protein
2062418834	560	114	7	c424	Uncharacterized conserved protein
2062418835	1457	74	17	c424	Aromatic ring hydroxylase(EC:1.14.13.3)
2062418838	575	10	10	c424	Highly conserved protein containing a thioredoxin domain
2062418840	971	25	23	c424	UDP-N-acetylmuramyl pentapeptide synthase
2062138284	281	320	14	c426	ABC-type uncharacterized transport system, permease component
2062142779	824	249	32	c426	ABC-type oligopeptide transport system, periplasmic component
2062154483	3044	44	14	c426	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits(EC:1.2.7.8)
2062192533	257	51	0	c426	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits(EC:1.2.7.8)

2062192534	356	396	17	c426	L-alanine dehydrogenase (EC 1.4.1.1)(EC:1.4.1.1)
2062192535	719	323	36	c426	L-alanine dehydrogenase (EC 1.4.1.1)(EC:1.4.1.1)
2062192537	680	56	59	c426	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
2062246670	1097	100	19	c426	ABC-type uncharacterized transport system, permease component
2062269715	1073	14	15	c426	ABC-type oligopeptide transport system, periplasmic component
2062276769	1136	40	4	c426	PAP2 (acid phosphatase) superfamily protein
2062335748	209	14	0	c426	Glucan phosphorylase(EC:2.4.1.1)
2062350538	152	26	7	c426	hypothetical protein
2062418827	1232	15	9	c426	glycogen phosphorylase(EC:2.4.1.1)
2062418837	548	210	15	c426	ABC-type uncharacterized transport system, permease component
2062418842	419	79	12	c426	agmatinase (EC 3.5.3.11)(EC:3.5.3.11)
2062144793	1538	43	42	c4276	Parvulin-like peptidyl-prolyl isomerase
2062177118	935	31	6	c4276	ADP-glyceromanno-heptose 6-epimerase precursor (EC 5.1.3.20)(EC:5.1.3.20)
2062240399	167	18	12	c4276	Exonuclease V gamma subunit
2062418833	455	68	22	c4276	D-alpha,beta-D-heptose 7-phosphate 1-kinase/D-beta-D-heptose 1-phosphate ader
2062425289	242	21	0	c4276	hypothetical protein
2062150610	176	0	0	c4279	hypothetical protein
2062195157	965	830	55	c4279	TRAP transporter solute receptor, TAXI family
2062226853	821	100	7	c4279	Predicted acyl-CoA transferases/carnitine dehydratase
2062272947	1196	56	9	c4279	TRAP-type uncharacterized transport system, fused permease components
2062294795	1325	64	11	c4279	TRAP transporter, 4TM/12TM fusion protein
2062364617	284	32	14	c4279	Glycine/D-amino acid oxidases (deaminating)(EC:1.5.3.1)
2062108391	152	26	13	c431	hypothetical protein
2062306359	236	13	0	c431	hypothetical protein
2062306360	260	0	0	c431	hypothetical protein
2062306361	530	15	0	c431	hypothetical protein
2062306362	1136	59	46	c431	Leucyl aminopeptidase(EC:3.4.11.1)
2062306363	1097	30	17	c431	Mg/Co/Ni transporter MgtE (contains CBS domain)
2062392733	773	19	4	c431	DNA polymerase III, gamma/tau subunits(EC:2.7.7.7)
2062392734	158	0	0	c431	hypothetical protein
2062244140	761	30	4	c4333	glycogen branching enzyme (EC 2.4.1.18)

2062244141	1229	59	13	c4333	glycogen branching enzyme (EC 2.4.1.18)(EC:2.4.1.18)
2062359519	1250	14	7	c4333	glycogen phosphorylase(EC:2.4.1.1)
2062107700	1073	118	22	c4347	Protein of unknown function (DUF3341).
2062114274	767	201	60	c4347	quinol:cytochrome c oxidoreductase quinone-binding subunit 1(EC:1.2.7.-)
2062265822	269	93	33	c4347	hypothetical protein
2062258105	167	6	0	c4374	ADP-heptose:LPS heptosyltransferase
2062288308	821	50	9	c4374	ADP-heptose:LPS heptosyltransferase
2062288309	206	34	0	c4374	succinate dehydrogenase subunit A (EC 1.3.5.1)(EC:1.3.99.1)
2062386966	746	153	16	c4374	succinate dehydrogenase subunit B (EC 1.3.5.1)(EC:1.3.99.1)
2062386967	980	40	15	c4374	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit(EC:1.3.99.1)
2062184259	1244	15	15	c438	two component transcriptional regulator, winged helix family
2062187517	851	32	21	c438	Signal transduction histidine kinase
2062234573	1781	95	20	c438	Cation/multidrug efflux pump
2062234587	1322	57	17	c438	Cation/multidrug efflux pump
2062245450	710	10	6	c438	hypothetical protein
2062247999	614	168	23	c438	conserved hypothetical protein TIGR01777
2062248015	647	56	0	c438	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having D
2062269660	1166	192	53	c438	hypothetical protein
2062401939	314	105	6	c438	Predicted nucleoside-diphosphate sugar epimerase
2062290283	713	136	39	c439	Thiamine pyrophosphate-requiring enzymes(EC:2.3.3.15)
2062299936	1013	41	6	c439	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine pep
2062348675	476	71	21	c439	Domain of Unknown Function (DUF350).
2062374220	1085	187	18	c439	Thiamine pyrophosphate-requiring enzymes(EC:2.3.3.15)
2062393385	1322	45	17	c439	ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and pe
2062122793	170	0	0	c440	LSU ribosomal protein L30P
2062122794	866	2	6	c440	ornithine carbamoyltransferase (EC 2.1.3.3)(EC:2.1.3.3)
2062140190	128	0	0	c440	hypothetical protein
2062164159	65	0	0	c440	hypothetical protein
2062269661	758	9	18	c440	SSU ribosomal protein S5P
2062358219	482	17	6	c440	Ribosomal protein L18
2062200909	353	133	6	c4400	citrate synthase (EC 2.3.3.1)(EC:2.3.3.1)

2062236548	494	65	16	c4400	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)(EC:1.2.1.38)
2062281261	1262	1099	32	c4400	biotin carboxylase (EC 6.3.4.14)/acetyl-CoA carboxylase carboxyltransferase subun
2062318996	278	25	4	c4400	Iron-sulfur cluster assembly accessory protein
2062324859	104	10	0	c4400	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)(EC:1.2.1.38)
2062386316	80	13	0	c4400	Biotin-requiring enzyme.
2062207982	242	21	0	c443	hypothetical protein
2062250508	251	116	0	c443	Glutaredoxin and related proteins
2062250509	947	127	6	c443	glycerol 3-phosphate dehydrogenase (NAD(P)+) (EC 1.1.1.94)(EC:1.1.1.94)
2062260024	530	25	0	c443	Fructose-2,6-bisphosphatase
2062287060	425	186	12	c443	anthranilate synthase, component II (EC 4.1.3.27)(EC:4.1.3.27)
2062342857	419	24	10	c443	Rhodanese-related sulfurtransferase
2062342858	452	13	31	c4443	hypothetical protein
2062358900	980	11	4	c4443	hypothetical protein
2062358901	1484	44	3	c4443	hypothetical protein
2062132491	329	128	24	c450	ABC-type uncharacterized transport systems, ATPase components(EC:3.6.3.17)
2062151904	755	46	5	c450	Xanthine dehydrogenase, iron-sulfur cluster and FAD-binding subunit A
2062151905	596	55	39	c450	Xanthine dehydrogenase, molybdopterin-binding subunit B
2062187525	359	6	31	c450	Flagellin and related hook-associated proteins
2062195156	1391	32	18	c450	DNA replication and repair protein RadC
2062207981	974	56	18	c450	ABC-type uncharacterized transport systems, ATPase components(EC:3.6.3.17)
2062211824	917	205	19	c450	Flagellar motor component
2062242276	638	235	16	c450	Flagellar motor protein
2062246689	650	122	14	c450	Xanthine dehydrogenase, iron-sulfur cluster and FAD-binding subunit A
2062249245	896	7	15	c450	hypothetical protein
2062249246	275	0	51	c450	nucleoside ABC transporter ATP-binding protein
2062281260	1214	51	23	c450	Flagellin and related hook-associated proteins
2062358902	590	200	41	c450	23S rRNA methylase(EC:2.1.1.-)
2062369056	1358	31	16	c450	Xanthine dehydrogenase, molybdopterin-binding subunit B(EC:1.17.1.4)
2062126694	515	14	4	c452	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related de
2062142106	770	539	90	c452	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)
2062142107	1331	45	12	c452	FAD dependent oxidoreductase.

2062162878	872	216	32	c452	Prephenate dehydrogenase
2062162880	305	98	13	c452	Preprotein translocase subunit SecD
2062206020	686	26	25	c452	amino acid ABC transporter membrane protein 1, PAAT family (TC 3.A.1.3.-)
2062206021	692	191	10	c452	amino acid ABC transporter membrane protein 2, PAAT family (TC 3.A.1.3.-)
2062220304	293	65	14	c452	Preprotein translocase subunit YajC
2062269669	914	70	15	c452	Preprotein translocase subunit SecD
2062269670	668	66	6	c452	hypothetical protein
2062298022	137	7	0	c452	hypothetical protein
2062329391	359	64	22	c452	Preprotein translocase subunit SecD
2062330035	800	13	18	c452	hypothetical protein
2062335165	203	25	34	c452	hypothetical protein
2062339633	581	52	14	c452	Acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase.(EC:2.3.1.164)
2062343531	677	15	15	c452	protein translocase subunit secF
2062395371	707	99	35	c452	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related de
2062395372	779	1244	96	c452	amino acid ABC transporter ATP-binding protein, PAAT family (TC 3.A.1.3.-)(EC:3.6
2062411739	1127	37	21	c452	Glycine/D-amino acid oxidases (deaminating)
2062418230	1703	43	25	c452	Thioredoxin reductase
2062188125	1820	21	4	c4541	DNA-directed RNA polymerase subunit beta'' (EC 2.7.7.6)(EC:2.7.7.6)
2062418231	821	68	7	c4541	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)(EC:2.7.7.6)
2062418868	332	0	0	c4541	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)(EC:2.7.7.6)
2062196446	1109	52	5	c457	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062265804	329	18	0	c457	ABC-type uncharacterized transport system, permease component
2062281253	143	35	0	c457	hypothetical protein
2062290281	233	0	0	c457	hypothetical protein
2062301231	497	14	2	c457	ABC-type uncharacterized transport system, periplasmic component
2062301232	470	4	2	c457	ABC-type uncharacterized transport system, periplasmic component
2062342245	707	18	3	c457	Uncharacterized conserved protein(EC:1.16.1.1)
2062358249	509	28	0	c457	Galactose mutarotase and related enzymes
2062411700	569	28	4	c457	ABC-type uncharacterized transport system, ATPase component
2062413000	809	52	11	c457	Protein of unknown function, DUF547.
2062415641	266	11	0	c457	hypothetical protein

2062423334	332	120	12	c457	ABC-type uncharacterized transport system, permease component
2062423335	1073	33	5	c457	ABC-type uncharacterized transport system, permease component
2062142095	173	0	0	c458	hypothetical protein
2062166747	530	17	40	c458	Phosphomannomutase
2062216446	887	5	7	c458	hypothetical protein
2062216447	500	26	32	c458	hypothetical protein
2062216448	539	63	19	c458	hypothetical protein
2062216449	875	59	26	c458	hypothetical protein
2062342246	482	8	8	c458	FHA domain.
2062245416	68	0	0	c46	hypothetical protein
2062265115	710	134	7	c46	methionine adenosyltransferase (EC 2.5.1.6)(EC:2.5.1.6)
2062284414	1370	105	16	c46	adenosylhomocysteinase (EC 3.3.1.1)(EC:3.3.1.1)
2062269037	380	0	0	c464	urease, beta subunit(EC:3.5.1.5)
2062328123	248	0	0	c464	Urea amidohydrolase (urease) alpha subunit(EC:3.5.1.5)
2062340278	254	0	0	c464	Urease accessory protein UreE
2062394714	305	7	0	c464	urease, gamma subunit(EC:3.5.1.5)
2062394715	197	0	0	c464	urease. Metallo peptidase. MEROPS family M38
2062402558	1334	4	1	c464	urease, alpha subunit(EC:3.5.1.5)
2062126028	605	10	7	c4682	hypothetical protein
2062258123	1220	8	3	c4682	hypothetical protein
2062394716	791	5	3	c4682	Beta-propeller repeat.
2062265821	884	21	6	c4734	Flagellin and related hook-associated proteins
2062324841	608	36	25	c4734	Flagellin and related hook-associated proteins
2062126031	929	51	11	c476	Uncharacterized enzyme involved in pigment biosynthesis
2062126032	308	123	10	c476	Superfamily I DNA and RNA helicases(EC:3.6.1.-,EC:3.6.1.-)
2062126033	566	152	9	c476	Superfamily I DNA and RNA helicases
2062220986	242	8	17	c476	GMP synthase - Glutamine amidotransferase domain
2062220987	479	10	13	c476	GMP synthase - Glutamine amidotransferase domain(EC:6.3.5.2)
2062238447	443	7	9	c476	Predicted permeases
2062238449	2057	26	13	c476	AAA ATPase containing von Willebrand factor type A (vWA) domain
2062240400	764	43	14	c476	Signal recognition particle GTPase

2062240401	350	31	11	c476	signal recognition particle-docking protein FtsY
2062292238	275	4	29	c476	hypothetical protein
2062292239	116	9	0	c476	hypothetical protein
2062308268	452	53	20	c476	hypothetical protein
2062320343	758	42	4	c476	Superfamily I DNA and RNA helicases
2062358235	620	98	18	c476	Predicted permeases
2062198334	73	0	0	c4773	(tRNA)
2062216439	926	18	10	c4773	SPFH domain, Band 7 family protein
2062318350	446	25	2	c4773	Membrane protein implicated in regulation of membrane protease activity
2062318351	917	13	32	c4773	SPFH domain, Band 7 family protein
2062325511	158	0	0	c4773	hypothetical protein
2062325512	110	9	0	c4773	hypothetical protein
2062395376	401	105	35	c4773	hypothetical protein
2062216440	1070	32	10	c481	Acetyl/propionyl-CoA carboxylase, alpha subunit(EC:6.4.1.4)
2062216441	152	7	0	c481	NAD(FAD)-utilizing enzyme possibly involved in translation
2062286346	266	45	0	c481	NAD(FAD)-utilizing enzyme possibly involved in translation
2062318352	830	14	7	c481	NAD(FAD)-utilizing enzyme possibly involved in translation
2062318353	782	31	3	c481	Pyruvate-formate lyase-activating enzyme(EC:1.97.1.4)
2062124750	323	12	19	c4837	YCII-related domain.
2062131193	656	8	3	c4837	Sulfite exporter TauE/SafE.
2062401950	887	77	9	c4837	4-aminobutyrate aminotransferase and related aminotransferases(EC:2.6.1.19)
2062204764	770	27	25	c484	fagellar hook-basal body proteins
2062204765	1034	20	7	c484	flagella basal body P-ring formation protein FlgA
2062204766	788	30	16	c484	flagellar basal-body rod protein FlgG, Gram-negative bacteria
2062220971	326	28	0	c484	hypothetical protein
2062220972	299	37	13	c484	L-glutamine synthetase (EC 6.3.1.2)(EC:6.3.1.2)
2062118236	467	6	4	c4859	Peroxiredoxin
2062118238	305	23	10	c4859	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
2062124751	65	0	0	c4859	hypothetical protein
2062221628	80	0	0	c4859	hypothetical protein
2062221629	797	28	3	c4859	hypothetical protein

2062362061	374	8	19	c4859	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
2062362062	341	18	6	c4859	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
2062393386	611	124	13	c4859	hypothetical protein
2062202213	764	64	7	c4889	MazG family protein(EC:3.6.1.19)
2062202214	539	130	11	c4889	Response regulator consisting of a CheY-like receiver domain and a Fis-type HTH c
2062202215	698	226	30	c4889	Sugar kinases, ribokinase family(EC:2.7.1.20)
2062272264	371	59	0	c4889	hypothetical protein
2062362063	167	60	0	c4889	Glycine cleavage system H protein (lipoate-binding)
2062112953	557	50	13	c491	Predicted HD phosphohydrolase
2062112955	1097	17	9	c491	Protein of unknown function (DUF971)./Taurine catabolism dioxygenase TauD, TfdA
2062207979	803	29	11	c491	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin
2062236532	326	15	0	c491	hypothetical protein
2062272263	971	87	10	c491	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large t
2062334521	1064	71	8	c491	Putative NADP-dependent oxidoreductases(EC:1.6.5.5)
2062112952	1715	604	78	c492	ABC-type dipeptide transport system, periplasmic component
2062274217	788	89	14	c492	BNR/Asp-box repeat.
2062274219	785	183	17	c492	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
2062334524	1013	218	28	c492	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
2062358223	164	98	18	c492	hypothetical protein
2062359549	539	104	11	c492	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal domain
2062342849	434	5	5	c4985	hypothetical protein
2062359550	995	59	11	c4985	ABC-type spermidine/putrescine transport systems, ATPase components(EC:3.6.3.
2062359551	1427	155	22	c4985	type III secretion system ATPase, FliI/YscN (EC 3.6.3.15)(EC:3.6.3.14)
2062112951	902	37	10	c501	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
2062134414	263	4	8	c501	hypothetical protein
2062151901	482	10	12	c501	RDD family.
2062151902	287	0	0	c501	hypothetical protein
2062151903	920	15	20	c501	tRNA isopentenyltransferase (miaA)(EC:2.5.1.75)
2062201577	566	25	11	c501	hypothetical protein
2062207984	497	344	16	c501	FIST N domain.
2062207985	602	38	27	c501	tRNA-guanine transglycosylase (EC 2.4.2.29)(EC:2.4.2.29)

2062228734	2282	14	17	c501	hypothetical protein
2062274215	443	34	0	c501	tRNA-guanine transglycosylase (EC 2.4.2.29)(EC:2.4.2.29)
2062274216	530	2	4	c501	hypothetical protein
2062274218	1211	14	20	c501	tRNA-N(6)-(isopentenyl)adenosine-37 thiotransferase enzyme MiaB
2062322917	383	10	26	c501	Uncharacterized conserved protein
2062334522	1163	99	3	c501	phosphoglycerate kinase (EC 2.7.2.3)(EC:5.3.1.1,EC:2.7.2.3)
2062334525	389	5	5	c501	hypothetical protein
2062342848	1490	105	19	c501	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II(EC:6.2.1.-)
2062359552	371	5	8	c501	Biotin carboxyl carrier protein
2062372926	290	45	3	c501	Uncharacterized protein conserved in bacteria
2062374854	284	49	14	c501	Uncharacterized conserved protein
2062374855	197	41	20	c501	hypothetical protein
2062386311	815	23	13	c501	hypothetical protein(EC:6.3.4.14)
2062162899	206	0	0	c5025	D-fructose 1,6-bisphosphatase (EC 3.1.3.11)(EC:3.1.3.25)
2062332680	1064	2	3	c5025	dihydroxyacid dehydratase (EC 4.2.1.9)(EC:4.2.1.9)
2062339635	425	0	5	c5025	hypothetical protein
2062339636	227	0	0	c5025	hypothetical protein
2062131199	641	145	19	c5066	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
2062265108	341	23	3	c5066	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
2062331978	296	30	0	c5066	Uncharacterized protein conserved in bacteria
2062374216	341	147	29	c5066	hemimethylated DNA binding domain
2062374217	482	6	15	c5066	hypothetical protein
2062376799	524	103	11	c5066	Predicted dithiol-disulfide isomerase involved in polyketide biosynthesis
2062131198	920	46	7	c508	ParB-like nuclease domain.
2062277420	1037	857	62	c508	putative 2-aminoethylphosphonate ABC transport system, 1-aminoethylphosphonat
2062277421	1082	141	17	c508	putative 2-aminoethylphosphonate ABC transport system, ATP-binding protein comp
2062294790	1724	141	46	c508	putative 2-aminoethylphosphonate ABC transport system, permease protein
2062294791	386	36	13	c508	Uncharacterized protein conserved in bacteria
2062322928	878	35	27	c508	OstA-like protein.
2062331979	542	140	63	c508	CTP synthase (EC 6.3.4.2)(EC:6.3.4.2)
2062402557	425	125	14	c508	FKBP-type peptidyl-prolyl cis-trans isomerases 1

2062201565	128	0	0	c5109	3-isopropylmalate dehydratase, large subunit (EC 4.2.1.33)(EC:4.2.1.33,EC:4.2.1.3
2062224262	248	0	0	c5109	3-isopropylmalate dehydratase, large subunit (EC 4.2.1.33)(EC:4.2.1.33,EC:4.2.1.3
2062271617	341	0	0	c5109	hypothetical protein
2062281258	836	0	2	c5109	Uncharacterized conserved protein
2062294789	608	2	7	c5109	3-isopropylmalate dehydratase, large subunit (EC 4.2.1.33)(EC:4.2.1.33,EC:4.2.1.3
2062365279	341	0	6	c5109	3-isopropylmalate dehydratase, small subunit (EC 4.2.1.33)(EC:4.2.1.35,EC:4.2.1.3
2062401946	206	0	5	c5109	3-isopropylmalate dehydratase, large subunit (EC 4.2.1.33)(EC:4.2.1.33,EC:4.2.1.3
2062272270	1367	61	16	c5194	leucyl-tRNA synthetase (EC 6.1.1.4)(EC:6.1.1.4)
2062374240	893	29	1	c5194	5,10-methylenetetrahydrofolate reductase(EC:1.5.1.20)
2062140192	872	50	7	c522	phenylalanyl-tRNA synthetase beta subunit (EC 6.1.1.20)(EC:6.1.1.20)
2062140195	224	13	22	c522	hypothetical protein
2062164155	368	19	0	c522	hypothetical protein
2062164156	206	0	0	c522	hypothetical protein
2062272271	983	36	8	c522	Dihydrodipicolinate synthase/N-acetylneuraminate lyase(EC:4.2.1.52)
2062272272	1457	106	13	c522	dihydropyrimidinase (EC 3.5.2.2)(EC:3.5.2.2)
2062324861	653	205	35	c522	Hydantoin racemase
2062342189	422	14	2	c522	hypothetical protein
2062140193	1019	12	6	c528	ATPase involved in DNA repair
2062140194	563	2	34	c528	ATPase involved in DNA repair
2062164158	275	7	11	c528	L-glutamine synthetase (EC 6.3.1.2)(EC:6.3.1.2)
2062278040	1004	286	13	c528	L-glutamine synthetase (EC 6.3.1.2)(EC:6.3.1.2)
2062280649	1940	11	10	c528	Glutamine synthetase adenylyltransferase
2062280651	1022	37	7	c528	Glutamine synthetase adenylyltransferase
2062280653	545	81	18	c528	Protease subunit of ATP-dependent Clp proteases(EC:3.4.21.92)
2062117531	2024	58	8	c5285	DNA gyrase, A subunit(EC:5.99.1.3)
2062350532	254	102	0	c5285	Dienelactone hydrolase and related enzymes
2062399358	284	99	53	c5285	DNA gyrase subunit A (EC 5.99.1.3)(EC:5.99.1.3)
2062117532	98	0	0	c529	(tRNA)
2062140189	1001	2	0	c529	tRNA pseudouridine synthase B (EC 4.2.1.70)(EC:5.4.99.12)
2062154477	446	0	0	c529	hypothetical protein
2062180974	560	7	0	c529	Cytidylate kinase(EC:2.7.4.14)

2062193165	89	0	0	c529	hypothetical protein
2062195790	449	0	0	c529	Archaeal adenylate kinase(EC:2.7.4.3)
2062195791	374	0	0	c529	ChuX-like family.
2062224255	335	0	0	c529	Malate/lactate dehydrogenases
2062225589	536	0	0	c529	Malate/lactate dehydrogenases(EC:1.1.1.37)
2062334516	269	0	15	c529	hypothetical protein
2062365301	1298	11	3	c529	Predicted dehydrogenase
2062365302	632	9	0	c529	Predicted membrane protein
2062180328	263	19	8	c5334	F0F1-type ATP synthase, alpha subunit(EC:3.6.3.14)
2062246674	1400	71	6	c5334	ATP synthase F1 subcomplex beta subunit(EC:3.6.3.14)
2062246675	254	31	0	c5334	ATP synthase F1 subcomplex alpha subunit(EC:3.6.3.14)
2062320336	854	8	2	c5334	ATP synthase, F1 gamma subunit(EC:3.6.3.14,EC:3.6.3.14)
2062358905	86	12	0	c5334	hypothetical protein
2062169302	125	0	0	c5342	hypothetical protein
2062189404	641	14	3	c5342	Uncharacterized anaerobic dehydrogenase
2062294801	548	53	4	c5342	NADH dehydrogenase subunit L (EC 1.6.5.3)
2062333286	269	22	0	c5342	NADH dehydrogenase subunit J (EC 1.6.5.3)
2062335745	503	26	8	c5342	NADH dehydrogenase subunit L (EC 1.6.5.3)(EC:1.6.5.3)
2062369664	302	70	13	c5342	NADH dehydrogenase subunit K (EC 1.6.5.3)(EC:1.6.5.3)
2062193163	1142	109	18	c5355	3-ketoacyl-CoA thiolase (EC 2.3.1.16)(EC:2.3.1.16)
2062334517	245	0	0	c5355	short chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase (EC:5.1.2.3,E
2062351207	581	65	7	c5355	pyruvate kinase (EC 2.7.1.40)(EC:2.7.1.40)
2062370973	611	82	13	c5355	short chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase (EC:5.1.2.3,E
2062128588	530	55	34	c5427	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062305104	1238	42	17	c5427	2-oxoglutarate dehydrogenase complex dihydrolipoamide succinyltransferase (E2 c
2062324858	188	16	0	c5427	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062379984	554	85	5	c5427	2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and relat
2062212466	782	50	6	c5430	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase
2062220300	581	41	9	c5430	Enoyl-CoA hydratase/carnithine racemase
2062258126	230	39	4	c5430	Enoyl-CoA hydratase/carnithine racemase(EC:4.2.1.-)
2062342850	971	62	13	c5430	3-hydroxyacyl-CoA dehydrogenase(EC:1.1.1.157)

2062140199	248	0	0	c5462	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
2062140200	284	0	4	c5462	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
2062242269	536	19	4	c5462	hypothetical protein
2062364653	233	0	0	c5462	hypothetical protein
2062364654	971	0	5	c5462	hypothetical protein
2062401953	341	18	0	c5462	malate dehydrogenase (NAD) (EC 1.1.1.37)(EC:1.1.1.37)
2062126702	659	38	11	c547	haloacid dehalogenase superfamily, subfamily IA, variant 3
2062268360	401	12	0	c547	ABC-type uncharacterized transport system, ATPase component
2062294172	824	117	42	c547	Twin arginine targeting (Tat) protein translocase TatC
2062326771	1040	40	3	c547	FOG: WD40 repeat
2062374243	824	34	11	c547	FOG: WD40 repeat
2062379978	155	0	0	c547	hypothetical protein
2062138906	560	0	0	c549	Transcriptional regulator
2062142115	584	5	17	c549	ABC-type multidrug transport system, ATPase component
2062142782	326	991	52	c549	Uncharacterized conserved protein
2062149989	212	14	9	c549	ABC-type multidrug transport system, ATPase component
2062152599	1073	136	20	c549	ABC-type uncharacterized transport system involved in gliding motility, auxiliary com
2062156442	803	34	6	c549	CcmB protein.
2062156444	683	23	18	c549	Esterase/lipase
2062228745	986	37	6	c549	hypothetical protein
2062342243	365	178	30	c549	hypothetical protein
2062342244	821	106	9	c549	hypothetical protein
2062351210	1124	48	11	c549	Predicted exporters of the RND superfamily
2062358251	1283	34	2	c549	Predicted exporters of the RND superfamily
2062386322	764	5	9	c549	Protein of unknown function (DUF1329).
2062142781	74	0	0	c550	hypothetical protein
2062222282	722	3	6	c550	hypothetical protein
2062269656	227	198	9	c550	hypothetical protein
2062269657	1790	12	17	c550	RNA polymerase sigma factor RpoD, C-terminal domain/RNA polymerase sigma fac
2062269716	386	21	21	c550	hypothetical protein
2062269717	950	36	13	c550	hypothetical protein

2062288986	776	4	5	c550	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase(EC:2.3.1.1
2062290278	797	8	4	c550	Uncharacterized protein conserved in bacteria
2062290279	338	53	21	c550	Uncharacterized protein conserved in bacteria
2062310739	371	51	11	c550	hypothetical protein
2062346767	161	6	0	c550	hypothetical protein
2062365941	98	0	0	c550	hypothetical protein
2062386961	191	0	0	c550	hypothetical protein
2062386971	176	11	6	c550	amino acid/amide ABC transporter ATP-binding protein 2, HAAT family (TC 3.A.1.4.·
2062386976	1070	105	23	c550	Obg family GTPase CgtA
2062401923	383	138	81	c550	Uncharacterized protein affecting Mg2+/Co2+ transport
2062417558	221	50	9	c550	hypothetical protein
2062418861	1019	48	20	c550	phenylalanyl-tRNA synthetase, alpha subunit (EC 6.1.1.20)(EC:6.1.1.20)
2062420789	542	11	17	c550	hypothetical protein
2062180337	227	0	0	c551	hypothetical protein
2062239745	971	189	35	c551	cell division protein FtsZ
2062239746	323	9	12	c551	iron donor protein CyaY
2062239747	701	150	44	c551	Putative arginyl-tRNA:protein arginylyltransferase(EC:2.3.2.8)
2062388912	380	113	8	c551	GTP cyclohydrolase subunit MoaC
2062198328	59	0	0	c553	hypothetical protein
2062224907	338	89	18	c553	nitrogen regulatory protein P-II
2062234575	494	0	4	c553	Ribonuclease D
2062261896	398	3	5	c553	Response regulator containing a CheY-like receiver domain and a GGDEF domain
2062288311	1265	6	6	c553	Small-conductance mechanosensitive channel
2062363987	137	0	15	c553	hypothetical protein
2062369038	1586	6	10	c553	hypothetical protein
2062374242	296	7	0	c553	hypothetical protein
2062378050	941	12	14	c553	Site-specific recombinase XerD
2062403887	185	5	0	c553	hypothetical protein
2062142793	386	0	0	c5542	conserved hypothetical protein TIGR00149
2062155121	377	0	0	c5542	Predicted RNA-binding proteins
2062198326	293	0	7	c5542	hypothetical protein

2062198327	383	3	21	c5542	Mn-dependent transcriptional regulator
2062201579	413	5	12	c5542	hypothetical protein
2062288330	380	3	0	c5542	hypothetical protein
2062412364	164	6	0	c5542	hypothetical protein
2062126053	1670	128	23	c561	polyribonucleotide nucleotidyltransferase(EC:2.7.7.8)
2062143478	383	18	5	c561	ribosome-binding factor A
2062143479	269	7	0	c561	SSU ribosomal protein S15P
2062290298	1523	21	10	c561	bacterial translation initiation factor 2 (bIF-2)
2062376159	932	18	8	c561	tRNA pseudouridine 55 synthase
2062109680	260	15	0	c562	hypothetical protein
2062109681	527	11	2	c562	hypothetical protein
2062136342	173	0	0	c562	hypothetical protein
2062195787	200	0	15	c562	Pyruvate kinase
2062209287	947	53	16	c562	Molybdenum cofactor biosynthesis enzyme
2062231989	137	0	0	c562	pyruvate kinase (EC 2.7.1.40)(EC:2.7.1.40)
2062231990	1460	20	7	c562	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase
2062261894	875	187	21	c562	Thiamine pyrophosphate-requiring enzymes (EC:2.2.1.6)
2062261895	725	134	10	c562	Thiamine pyrophosphate-requiring enzymes (EC:2.2.1.6)
2062280660	362	14	3	c562	Dimethyladenosine transferase (rRNA methylation)
2062347375	980	40	16	c562	pyruvate kinase(EC:2.7.1.40)
2062422706	1082	193	32	c562	Glutamate synthase domain 2
2062113628	2075	80	23	c567	Adenylate cyclase, family 3 (some proteins contain HAMP domain)
2062132484	758	488	38	c567	hemolysin TlyA family protein
2062144792	680	346	44	c567	Integral membrane protein, interacts with FtsH
2062198979	872	34	14	c567	ParB-like partition proteins
2062198981	401	0	5	c567	Type II secretory pathway, component PulD
2062220952	146	14	0	c567	hypothetical protein
2062228735	185	0	0	c567	lipid-A-disaccharide kinase (EC 2.7.1.130)(EC:2.7.1.130)
2062319657	2195	231	32	c567	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)(EC:2.7.7.6)
2062321607	1133	101	26	c567	hypothetical protein
2062125413	428	19	23	c568	Cytidylate kinase

2062125414	320	9	13	c568	hypothetical protein
2062198975	782	24	3	c568	Molecular chaperone, HSP90 family
2062198977	668	6	1	c568	conserved hypothetical protein TIGR00255
2062198980	73	0	0	c568	(tRNA)
2062372297	230	4	13	c568	Uncharacterized stress-induced protein
2062379338	143	0	0	c568	hypothetical protein
2062379339	761	16	12	c568	Molecular chaperone, HSP90 family
2062126662	278	0	7	c573	GDP-D-mannose dehydratase
2062161599	215	14	0	c573	Predicted ATPase with chaperone activity
2062286325	644	26	14	c573	GDP-D-mannose dehydratase
2062335133	1322	142	13	c573	Mg chelatase-related protein
2062122792	164	0	12	c5753	adenosylhomocysteinase (EC 3.3.1.1)
2062158377	671	7	0	c5753	hypothetical protein
2062193189	515	21	8	c5753	adenosylhomocysteinase (EC 3.3.1.1)(EC:3.3.1.1)
2062337067	416	26	10	c5753	S-adenosylhomocysteine hydrolase(EC:3.3.1.1)
2062401954	749	8	0	c5753	hypothetical protein
2062124772	1079	16	10	c576	Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase(E
2062142101	563	16	0	c576	hypothetical protein
2062155792	443	16	9	c576	hypothetical protein
2062162883	125	0	0	c576	hypothetical protein
2062209875	521	23	27	c576	Transcription-repair coupling factor (superfamily II helicase)
2062241032	401	15	10	c576	transcription-repair coupling factor(EC:3.6.1.-)
2062241033	458	24	2	c576	transcription-repair coupling factor(EC:3.6.1.-)
2062241034	374	48	5	c576	transcription-repair coupling factor(EC:3.6.1.-)
2062241036	428	2	0	c576	Transcription-repair coupling factor (superfamily II helicase)
2062247992	137	0	0	c576	hypothetical protein
2062258758	116	0	26	c576	hypothetical protein
2062278651	290	3	0	c576	hypothetical protein
2062278669	968	7	11	c576	Transcription-repair coupling factor (superfamily II helicase)
2062386326	167	0	12	c576	AsnC family.
2062152615	467	32	6	c578	Glycine/D-amino acid oxidases (deaminating)

2062241038	73	0	0	c578	(tRNA)
2062241039	72	0	0	c578	(tRNA)
2062294804	371	259	100	c578	hypothetical protein
2062294806	467	19	2	c578	hypothetical protein(EC:1.2.7.3)
2062318997	968	12	25	c578	NTP pyrophosphohydrolases containing a Zn-finger, probably nucleic-acid-binding
2062323567	776	13	4	c578	Glycine/D-amino acid oxidases (deaminating)
2062358224	320	6	3	c578	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductas
2062358225	977	273	14	c578	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductas
2062376801	545	75	13	c578	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductas
2062376802	323	34	22	c578	Uncharacterized conserved protein
2062207364	599	112	38	c580	Flagellar motor switch protein
2062319658	1295	24	22	c580	Flagellar motor switch/type III secretory pathway protein
2062319659	350	49	0	c580	Gamma-glutamylcysteine synthetase
2062321609	233	99	4	c580	hypothetical protein
2062321610	194	0	10	c580	hypothetical protein
2062330034	632	16	6	c580	Zn-dependent proteases
2062372925	776	26	4	c580	Gamma-glutamylcysteine synthetase(EC:6.3.2.2)
2062418232	284	14	14	c580	hypothetical protein
2062117529	800	53	23	c582	hypothetical protein
2062126022	836	171	38	c582	NADH:flavin oxidoreductases, Old Yellow Enzyme family
2062182969	905	50	36	c582	Methionine synthase I, cobalamin-binding domain(EC:2.1.1.13)
2062193177	275	47	4	c582	hypothetical protein
2062195149	728	70	36	c582	Predicted cobalamin binding protein(EC:2.1.1.13)
2062294792	911	59	5	c582	L-serine ammonia-lyase (EC 4.3.1.17)(EC:4.3.1.17)
2062310114	488	10	0	c582	Serine dehydratase beta chain.(EC:4.3.1.17)
2062325510	1799	105	73	c582	Trimethylamine:corrinoid methyltransferase
2062335164	278	101	86	c582	EamA-like transporter family.
2062386313	695	12	6	c582	Protein of unknown function (DUF1638).
2062405833	524	84	71	c582	EamA-like transporter family.
2062405834	614	101	10	c582	EamA-like transporter family.
2062405835	257	16	8	c582	Formate-tetrahydrofolate ligase (EC 6.3.4.3)

2062227475	374	16	5	c5825	Uncharacterized protein conserved in bacteria
2062367172	374	11	21	c5825	Uncharacterized protein conserved in bacteria
2062392732	101	0	0	c5825	hypothetical protein
2062396644	275	4	4	c5825	Uncharacterized protein conserved in bacteria
2062413013	626	3	3	c5825	hypothetical protein
2062413014	179	0	6	c5825	hypothetical protein
2062138903	134	60	0	c5915	hypothetical protein
2062160288	203	10	0	c5915	hypothetical protein
2062160289	323	34	0	c5915	nucleoside ABC transporter membrane protein
2062172535	476	508	50	c5915	nucleoside ABC transporter membrane protein
2062172536	686	856	31	c5915	nucleoside-binding protein
2062211208	878	33	5	c5915	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases(EC:
2062260039	62	0	0	c5915	hypothetical protein
2062269038	353	249	25	c5915	Uncharacterized ABC-type transport system, periplasmic component/surface lipopr
2062420791	374	64	13	c5915	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases
2062198347	749	0	0	c600	Predicted ATPase, RNase L inhibitor (RLI) homolog
2062269039	134	0	0	c600	hypothetical protein
2062288982	458	0	0	c600	Predicted methyltransferase
2062299941	365	0	0	c600	Leucyl aminopeptidase(EC:3.4.11.1)
2062299942	224	0	0	c600	Predicted ATPase, RNase L inhibitor (RLI) homolog
2062322909	767	0	0	c600	Predicted ATPase, RNase L inhibitor (RLI) homolog
2062422701	230	0	0	c600	hypothetical protein
2062136341	197	234	10	c6018	MoxR-like ATPases
2062191911	167	0	0	c6018	hypothetical protein
2062248010	344	44	3	c6018	Lipoate synthase(EC:2.8.1.8)
2062362714	287	80	0	c6018	Lipoate synthase(EC:2.8.1.8)
2062362715	605	7	3	c6018	lipoate-protein ligase B(EC:2.3.1.181)
2062364612	98	0	0	c6018	hypothetical protein
2062364613	341	23	6	c6018	hypothetical protein
2062369040	263	8	0	c6018	Lipoate synthase(EC:2.8.1.8)
2062412998	284	21	0	c6018	Uncharacterized conserved protein

2062127943	962	17	23	c603	selenium donor protein
2062142136	731	7	0	c603	Truncated, possibly inactive, lysyl-tRNA synthetase (class II)
2062142137	416	0	2	c603	Truncated, possibly inactive, lysyl-tRNA synthetase (class II)(EC:6.1.1.6)
2062157105	233	9	4	c603	translation elongation factor 2 (EF-2/EF-G)
2062162901	560	7	9	c603	translation elongation factor P
2062188754	461	22	11	c603	transcription elongation factor GreA
2062212476	950	32	14	c603	Glutamyl- and glutaminyl-tRNA synthetases
2062225590	374	96	16	c603	Predicted thioesterase
2062376148	479	48	13	c603	hypothetical protein
2062202212	569	4	0	c6060	ATPase involved in DNA replication initiation
2062265113	299	0	0	c6060	chromosomal replication initiator protein DnaA
2062265114	353	0	0	c6060	chromosomal replication initiator protein DnaA
2062290320	1100	7	2	c6060	DNA polymerase III, beta subunit(EC:2.7.7.7)
2062290321	101	10	0	c6060	hypothetical protein
2062305100	896	11	15	c6082	Fe-S oxidoreductase
2062369043	203	34	10	c6082	hypothetical protein
2062392739	566	223	16	c6082	Transketolase, N-terminal subunit
2062413003	491	24	4	c6082	Uncharacterized protein conserved in bacteria
2062151917	515	0	8	c6106	NTP pyrophosphohydrolases including oxidative damage repair enzymes(EC:3.6.1
2062211826	644	0	0	c6106	Phosphate uptake regulator
2062213767	389	0	0	c6106	hypothetical protein
2062213768	314	0	0	c6106	hypothetical protein
2062292896	713	0	6	c6106	pantothenate kinase (EC 2.7.1.33)
2062418233	398	0	0	c6106	hypothetical protein
2062118219	938	35	14	c611	Xaa-Pro aminopeptidase
2062133121	377	21	21	c611	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synthase
2062191918	161	0	0	c611	hypothetical protein
2062209898	410	24	7	c611	Xaa-Pro aminopeptidase(EC:3.4.11.9)
2062249891	380	16	13	c611	Creatinase/Prolidase N-terminal domain.
2062405832	1592	128	28	c611	phosphoenolpyruvate carboxykinase (ATP)(EC:4.1.1.49)
2062209899	542	9	13	c612	conserved hypothetical integral membrane protein

2062211209	1826	93	13	c612	molybdopterin molybdochelatase
2062211210	350	94	0	c612	Predicted hydrolases of the HAD superfamily
2062334500	1421	25	4	c612	diguanylate cyclase (GGDEF) domain
2062343528	728	33	38	c612	hypothetical protein
2062386957	611	23	11	c612	Predicted membrane protein
2062399359	473	57	13	c612	hypothetical protein
2062196445	386	3	5	c616	replication restart DNA helicase PriA
2062386958	452	7	22	c616	hypothetical protein
2062418862	866	6	2	c616	hypothetical protein
2062418863	359	3	19	c616	hypothetical protein
2062418864	1613	22	4	c616	Primosomal protein N'' (replication factor Y) - superfamily II helicase
2062118211	878	23	17	c6172	hypothetical protein
2062222300	554	31	22	c6172	Methylase involved in ubiquinone/menaquinone biosynthesis(EC:2.1.1.17)
2062355697	458	50	4	c6172	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component
2062413006	86	0	0	c6172	hypothetical protein
2062269675	1406	0	1	c62	Phage integrase family.
2062280613	73	0	0	c62	(tRNA)
2062299931	83	0	0	c62	(tRNA)
2062340255	72	0	0	c62	(tRNA)
2062350526	347	12	0	c62	hypothetical protein
2062358883	74	0	0	c62	(tRNA)
2062358884	104	0	0	c62	hypothetical protein
2062399357	179	0	0	c62	hypothetical protein
2062420790	197	0	0	c62	hypothetical protein
2062423329	674	6	3	c62	hypothetical protein
2062124734	533	310	161	c620	ribosomal protein L6, bacterial type
2062131205	512	3367	102	c620	SSU ribosomal protein S5P
2062166750	887	771	62	c620	protein translocase subunit secY/sec61 alpha
2062241041	545	204	53	c620	LSU ribosomal protein L5P
2062281907	368	215	76	c620	LSU ribosomal protein L14P
2062288340	680	228	60	c620	SSU ribosomal protein S3P

2062299933	395	185	58	c620	SSU ribosomal protein S8P
2062314584	185	16	22	c620	LSU ribosomal protein L30P
2062314590	434	286	288	c620	LSU ribosomal protein L15P
2062318993	314	159	102	c620	LSU ribosomal protein L24P
2062322910	413	82	36	c620	LSU ribosomal protein L16P
2062332678	335	119	39	c620	LSU ribosomal protein L22P
2062342856	191	21	0	c620	LSU ribosomal protein L29P
2062359520	275	138	40	c620	SSU ribosomal protein S19P
2062379996	236	81	64	c620	LSU ribosomal protein L18P
2062386964	305	603	46	c620	SSU ribosomal protein S14P
2062386965	260	46	23	c620	SSU ribosomal protein S17P
2062418872	98	0	0	c620	LSU ribosomal protein L2P
2062213735	854	7	5	c6207	Pirin-related protein
2062281252	362	116	11	c6207	hypothetical protein
2062386973	599	142	13	c6207	Cytosine deaminase and related metal-dependent hydrolases(EC:3.5.4.-,EC:3.5.4.
2062408443	752	76	7	c6207	Cytosine deaminase and related metal-dependent hydrolases(EC:3.5.4.-,EC:3.5.4.
2062109682	221	41	14	c623	adenosylcobinamide-phosphate synthase (EC 6.3.1.10)(EC:6.3.1.10)
2062109683	158	6	0	c623	Cobalamin biosynthesis protein CobD/CbiB(EC:6.3.1.10)
2062109684	929	31	13	c623	Gamma-aminobutyrate permease and related permeases
2062134386	185	0	0	c623	hypothetical protein
2062151900	209	0	10	c623	RNAse PH (EC 2.7.7.56)(EC:2.7.7.56)
2062158376	791	33	10	c623	Predicted permeases
2062180976	545	55	15	c623	hypothetical protein
2062249883	146	0	0	c623	TrkA-C domain.
2062249884	284	7	0	c623	Valyl-tRNA synthetase(EC:6.1.1.9)
2062332676	413	51	10	c623	Prolipoprotein diacylglyceryltransferase
2062332677	428	40	9	c623	Prolipoprotein diacylglyceryltransferase
2062343499	530	19	21	c623	RNAse PH (EC 2.7.7.56)(EC:2.7.7.56)
2062343530	614	3	13	c623	periplasmic chaperone LolA
2062396016	920	17	4	c623	Predicted dehydrogenases and related proteins
2062309533	542	72	4	c6242	ABC-type antimicrobial peptide transport system, ATPase component(EC:3.6.3.-)

2062342209	275	0	0	c6242	ABC-type transport system, involved in lipoprotein release, permease component
2062343502	221	5	0	c6242	hypothetical protein
2062343503	209	5	10	c6242	hypothetical protein
2062343504	371	8	0	c6242	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
2062396646	191	5	0	c6242	ABC-type transport system, involved in lipoprotein release, permease component
2062148688	470	26	6	c625	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
2062162288	575	682	75	c625	TRAP-type mannitol/chloroaromatic compound transport system, small permease c
2062211823	200	155	20	c625	hypothetical protein
2062238446	578	0	14	c625	Predicted exporters of the RND superfamily
2062288320	1328	236	51	c625	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases(EC:
2062322919	731	4	0	c625	hypothetical protein
2062343505	392	15	0	c625	ABC-type transport system involved in resistance to organic solvents, auxiliary com
2062372294	647	17	17	c625	Surface lipoprotein
2062372295	1367	661	69	c625	TRAP-type mannitol/chloroaromatic compound transport system, large permease c
2062373595	554	3242	175	c625	TRAP-type mannitol/chloroaromatic compound transport system, periplasmic comp
2062416260	236	13	8	c625	hypothetical protein
2062420781	992	8	5	c625	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferases
2062420782	407	5	5	c625	Sulfatase.
2062234584	224	0	0	c6328	hypothetical protein
2062245451	164	0	12	c6328	hypothetical protein(EC:1.10.2.2)
2062269658	461	0	0	c6328	Plastocyanin
2062362077	1598	21	27	c6328	Cytochrome b subunit of the bc complex
2062107699	173	0	12	c6331	methylmalonyl-CoA mutase (EC 5.4.99.2)(EC:5.4.99.2)
2062112941	260	23	0	c6331	PAP2 superfamily.
2062167375	314	6	6	c6331	hypothetical protein
2062268364	320	53	13	c6331	Protein of unknown function (DUF3467).
2062269659	713	8	3	c6331	DnaJ-domain-containing proteins 1
2062316484	161	0	0	c6331	hypothetical protein
2062329406	113	0	0	c6331	hypothetical protein
2062392104	224	4	0	c6331	hypothetical protein
2062401938	362	6	14	c6331	hypothetical protein

2062135648	1514	76	32	c641	flagellar hook-associated protein FlgK
2062167999	482	102	10	c641	FlgN protein.
2062172534	545	0	0	c641	hypothetical protein
2062220973	248	69	8	c641	Flagellar basal-body P-ring protein
2062225594	728	304	21	c641	Flagellar basal-body P-ring protein
2062228739	1214	54	18	c641	Protein containing von Willebrand factor type A (vWA) domain
2062228740	1328	76	4	c641	putative efflux protein, MATE family
2062228741	230	35	26	c641	Rod binding protein
2062267712	260	27	15	c641	hypothetical protein
2062318356	131	8	0	c641	hypothetical protein
2062324840	296	0	20	c641	Anti-sigma-28 factor, FlgM.
2062369039	425	40	0	c641	Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily
2062184935	818	5	4	c6410	propionyl-CoA carboxylase carboxyltransferase subunit(EC:6.4.1.3)
2062228742	440	0	0	c6410	Acetyl/propionyl-CoA carboxylase, alpha subunit
2062386314	1484	0	3	c6410	Acetyl/propionyl-CoA carboxylase, alpha subunit(EC:6.4.1.2,EC:6.4.1.1)
2062184936	395	53	0	c6411	Competence protein.
2062234577	443	18	7	c6411	NADPH:quinone reductase and related Zn-dependent oxidoreductases
2062234578	1142	28	14	c6411	Predicted membrane metal-binding protein
2062246682	686	9	4	c6411	Type II secretory pathway, component PulC
2062126701	599	7	10	c649	Flagellar biosynthesis protein, FliO.
2062158378	632	6	5	c649	uridine kinase (EC 2.7.1.48)
2062190036	173	17	35	c649	Flagellar biosynthesis pathway, component FliQ
2062207355	803	10	24	c649	FOG: Ankyrin repeat
2062222305	254	4	8	c649	hypothetical protein
2062225646	791	9	13	c649	hypothetical protein
2062269654	530	9	9	c649	flagellar biosynthetic protein FliP
2062339634	425	19	7	c649	hypothetical protein
2062346760	827	33	25	c649	Predicted permeases
2062350525	596	0	13	c649	hypothetical protein
2062362786	1016	22	22	c649	hypothetical protein
2062369041	782	15	8	c649	Predicted N-acetylglucosaminyl transferase

2062395373	290	83	17	c649	hypothetical protein
2062411738	356	17	6	c649	ATP dependent PIM1 peptidase. Serine peptidase. MEROPS family S16(EC:3.4.21
2062413020	383	5	3	c649	ATP dependent PIM1 peptidase. Serine peptidase. MEROPS family S16(EC:3.4.21
2062413021	1784	16	10	c649	ATP dependent PIM1 peptidase. Serine peptidase. MEROPS family S16(EC:3.4.21
2062108388	233	9	21	c651	hypothetical protein
2062177112	446	13	16	c651	Glycosyltransferases involved in cell wall biogenesis
2062195794	545	57	22	c651	Sugar phosphate permease
2062245412	95	0	0	c651	hypothetical protein
2062280631	338	18	18	c651	Uncharacterized protein conserved in bacteria
2062343500	878	52	6	c651	Cobyric acid synthase
2062396647	668	39	10	c651	ATP:corrinoid adenosyltransferase(EC:2.5.1.17)
2062418825	236	8	0	c651	hypothetical protein
2062419494	197	30	10	c651	hypothetical protein
2062419495	128	23	23	c651	hypothetical protein
2062249879	380	61	29	c653	succinate semialdehyde dehydrogenase (EC 1.2.1.16)(EC:1.2.1.16)
2062269683	665	24	6	c653	hypothetical protein
2062126030	1316	8	7	c6588	folylpolyglutamate synthase/dihydrofolate synthase
2062319660	374	0	8	c6588	protease FtsH subunit HflC(EC:3.4.-)
2062342210	254	4	16	c6588	Membrane protease subunits, stomatin/prohibitin homologs(EC:3.4.-)
2062372924	404	42	12	c6588	hypothetical protein
2062231992	419	0	0	c662	hypothetical protein
2062268354	245	0	0	c662	hypothetical protein
2062268355	161	0	0	c662	hypothetical protein
2062290284	122	0	0	c662	hypothetical protein(EC:2.7.6.1)
2062299946	89	0	0	c662	hypothetical protein
2062379979	275	0	0	c662	L-lysine 2,3-aminomutase (EC 5.4.3.2)
2062379980	566	0	0	c662	Phosphoribosylpyrophosphate synthetase(EC:2.7.6.1)
2062379981	1040	0	9	c662	Small-conductance mechanosensitive channel
2062109035	500	8	4	c665	hypothetical protein
2062112940	557	18	11	c665	hypothetical protein
2062187487	1184	66	18	c665	cystathionine beta-lyase (EC 4.4.1.8)(EC:4.4.1.8)

2062227476	155	0	0	c665	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binc
2062288307	713	90	32	c665	outer membrane assembly lipoprotein YfiO
2062154478	701	512	30	c669	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit(EC:1.8.99.2)
2062317133	2147	243	16	c669	Heterodisulfide reductase, subunit A and related polyferredoxins(EC:1.8.98.1)
2062348686	437	442	34	c669	Adenosine-5''-phosphosulfate reductase beta subunit;.
2062369037	1289	424	29	c669	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit(EC:1.8.99.2)
2062396017	1253	95	30	c669	Heterodisulfide reductase, subunit A and related polyferredoxins(EC:1.8.98.1)
2062235224	401	0	0	c6709	ATP-dependent Lon protease, bacterial type
2062235225	527	21	9	c6709	Sulfite exporter TauE/SafE.
2062235231	230	0	0	c6709	ATP dependent PIM1 peptidase. Serine peptidase. MEROPS family S16(EC:3.4.21
2062281894	167	30	0	c6709	ATP dependent PIM1 peptidase. Serine peptidase. MEROPS family S16(EC:3.4.21
2062288335	326	3	6	c6709	ATP dependent PIM1 peptidase. Serine peptidase. MEROPS family S16(EC:3.4.21
2062290319	302	3	10	c6709	uridine kinase (EC 2.7.1.48)(EC:2.7.1.48)
2062325508	332	3	3	c6709	uridine kinase (EC 2.7.1.48)
2062342211	302	0	26	c6709	Sulfite exporter TauE/SafE.
2062134413	623	22	8	c671	segregation and condensation protein B
2062335138	488	25	37	c671	Uncharacterized protein conserved in bacteria
2062378062	275	40	7	c671	condensin subunit ScpA
2062378063	284	70	11	c671	Predicted metal-sulfur cluster biosynthetic enzyme
2062388285	854	53	13	c671	ribosomal large subunit pseudouridine synthase B (EC 5.4.99.-)(EC:5.4.99.12)
2062112950	587	24	0	c675	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog
2062143480	779	12	5	c675	Uncharacterized protein conserved in bacteria
2062265797	164	12	0	c675	Protein of unknown function (DUF1239).
2062273566	725	47	8	c675	ABC-type (unclassified) transport system, ATPase component(EC:3.6.3.-)
2062392754	158	0	0	c675	hypothetical protein
2062145448	422	50	5	c682	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)(EC:3.4.24.57)
2062183609	290	7	7	c682	Uncharacterized protein conserved in bacteria
2062265796	620	37	15	c682	Metal-dependent proteases with possible chaperone activity
2062265798	929	28	14	c682	3-oxoacyl-[acyl-carrier-protein] synthase III(EC:2.3.1.180)
2062317100	1010	30	16	c682	Serine hydrolase (FSH1).
2062362064	1556	5	19	c682	nucleoside ABC transporter ATP-binding protein(EC:3.6.3.17)

2062364012	1214	124	40	c682	GTP cyclohydrolase II (EC 3.5.4.25)/3,4-dihydroxy-2-butanone 4-phosphate synthas
2062365283	1091	54	28	c682	nucleoside ABC transporter membrane protein
2062365284	593	27	0	c682	nucleoside ABC transporter membrane protein
2062365285	392	125	15	c682	nucleoside ABC transporter membrane protein
2062413009	656	117	9	c682	riboflavin biosynthesis protein RibD(EC:3.5.4.26,EC:1.1.1.193)
2062117530	866	27	16	c685	Parvulin-like peptidyl-prolyl isomerase
2062183591	89	22	0	c685	hypothetical protein(EC:4.1.2.-)
2062183593	431	9	9	c685	Tetratricopeptide repeat.
2062183594	629	49	6	c685	Uncharacterized conserved protein
2062183610	623	91	18	c685	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/
2062190037	749	19	3	c685	hypothetical protein
2062220950	362	55	6	c685	Uncharacterized conserved protein
2062221630	605	79	10	c685	Uncharacterized conserved protein
2062258114	740	5	0	c685	hypothetical protein
2062265799	362	52	19	c685	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes(EC:4.1.2.-)
2062268358	449	100	13	c685	methylthioribose-1-phosphate isomerase (EC 5.3.1.23)(EC:5.3.1.23)
2062290992	428	126	21	c685	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes(EC:4.1.2.-)
2062290993	815	160	22	c685	FOG: HEAT repeat
2062290994	209	19	0	c685	hypothetical protein
2062346761	473	121	11	c685	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062376147	323	15	3	c685	methylthioribose-1-phosphate isomerase (EC 5.3.1.23)(EC:5.3.1.23)
2062401952	1361	60	27	c685	hypothetical protein
2062407817	551	15	7	c685	hypothetical protein
2062407818	311	3	10	c685	hypothetical protein
2062150612	227	101	79	c686	hypothetical protein
2062156447	1010	70	37	c686	hypothetical protein
2062156448	344	38	9	c686	hypothetical protein
2062202839	467	13	9	c686	UTP:GlnB (protein PII) uridylyltransferase
2062209882	2516	10	9	c686	UTP:GlnB (protein PII) uridylyltransferase
2062212473	890	121	3	c686	homoserine O-succinyltransferase (EC 2.3.1.46)(EC:2.3.1.46)
2062221631	485	85	16	c686	Holliday junction DNA helicase subunit RuvB

2062221632	593	74	10	c686	Holliday junction DNA helicase subunit RuvB
2062229411	503	4	6	c686	hypothetical protein
2062416259	344	6	0	c686	Phosphatidylserine synthase
2062114273	521	2	8	c6956	hypothetical protein
2062128586	578	0	3	c6956	tryptophanyl-tRNA synthetase (EC 6.1.1.2)(EC:6.1.1.2)
2062131190	350	0	6	c6956	tryptophanyl-tRNA synthetase (EC 6.1.1.2)(EC:6.1.1.2)
2062201564	587	0	3	c6956	hypothetical protein(EC:6.1.1.20)
2062201590	218	0	0	c6956	tryptophanyl-tRNA synthetase (EC 6.1.1.2)(EC:6.1.1.2)
2062202840	281	0	0	c6956	hypothetical protein
2062202841	263	0	0	c6956	hypothetical protein
2062156443	266	11	8	c698	DnaK suppressor protein
2062222281	557	5	0	c698	hypothetical protein
2062228736	818	5	4	c698	formamidopyrimidine-DNA glycosylase (fpg)
2062240404	950	62	8	c698	S-adenosyl-methyltransferase MraW
2062240408	326	49	0	c698	Predicted metal-dependent hydrolase
2062249248	503	16	4	c698	hypothetical protein
2062261282	1334	61	10	c698	Glycine/serine hydroxymethyltransferase(EC:2.1.2.1)
2062261899	398	0	8	c698	hypothetical protein
2062281890	428	30	49	c698	Helix-turn-helix.
2062286326	1253	8	1	c698	hypothetical protein
2062290289	143	0	0	c698	hypothetical protein
2062240403	1547	15	3	c7057	valyl-tRNA synthetase (EC 6.1.1.9)(EC:6.1.1.9)
2062281255	503	18	4	c7057	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-d
2062338303	290	3	3	c7057	hypothetical protein
2062362070	425	16	5	c7057	valyl-tRNA synthetase (EC 6.1.1.9)
2062129928	296	0	0	c706	hypothetical protein
2062140187	218	28	0	c706	hypothetical protein
2062201567	245	29	0	c706	Regulator of cell morphogenesis and NO signaling
2062204762	632	3	3	c706	PAS domain S-box
2062213739	350	0	11	c706	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binc
2062235228	1202	37	27	c706	Uncharacterized protein conserved in bacteria

2062255620	134	0	0	c706	hypothetical protein
2062269672	179	6	0	c706	Regulator of cell morphogenesis and NO signaling
2062329407	1049	4	7	c706	PAS domain S-box
2062131204	485	25	33	c713	hypothetical protein
2062133119	626	16	8	c713	phosphoserine phosphatase (EC 3.1.3.3)/phosphoserine:homoserine phosphotrans
2062195153	116	0	0	c713	hypothetical protein
2062235229	353	45	0	c713	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062269673	722	84	22	c713	rRNA methylase, putative, group 3(EC:2.1.1.-)
2062269714	1274	47	30	c713	hypothetical protein
2062419485	440	23	18	c713	Flagellar FliJ protein.
2062234581	452	44	0	c7168	Pyridine nucleotide-disulphide oxidoreductase.
2062234582	1301	102	10	c7168	NADH:flavin oxidoreductases, Old Yellow Enzyme family
2062288325	623	16	8	c7168	Cyclopropane fatty acid synthase and related methyltransferases(EC:2.1.1.103)
2062138286	296	0	0	c717	nucleoside ABC transporter ATP-binding protein(EC:3.6.3.17)
2062177115	890	62	8	c717	methenyltetrahydrofolate cyclohydrolase/5,10-methylenetetrahydrofolate dehydroge
2062177123	431	26	14	c717	Glycine cleavage system T protein (aminomethyltransferase)
2062177126	779	315	137	c717	nucleoside-binding protein
2062183590	473	0	6	c717	nucleoside ABC transporter ATP-binding protein(EC:3.6.3.17)
2062335746	773	67	22	c717	Inosine-uridine nucleoside N-ribohydrolase(EC:3.2.2.1)
2062138282	842	106	20	c724	alanyl-tRNA synthetase (EC 6.1.1.7)(EC:6.1.1.7)
2062138290	272	15	0	c724	ABC-type oligopeptide transport system, ATPase component
2062162877	716	207	35	c724	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal domain
2062164152	611	272	44	c724	ribosomal protein S4, bacterial/organelle type
2062177116	668	138	34	c724	alanyl-tRNA synthetase (EC 6.1.1.7)(EC:6.1.1.7)
2062177119	170	47	24	c724	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component
2062177122	833	61	26	c724	ABC-type transport system, involved in lipoprotein release, permease component
2062209880	377	74	13	c724	ATPase components of various ABC-type transport systems, contain duplicated AT
2062316487	755	25	24	c724	Alanyl-tRNA synthetase
2062418830	431	70	28	c724	Alanyl-tRNA synthetase(EC:6.1.1.7)
2062169304	419	26	2	c725	Rubrerythrin
2062193175	914	4	4	c725	Transcriptional regulator

2062268357	1340	14	7	c725	glycerol 3-phosphate dehydrogenase (quinone) subunit C (EC 1.1.5.3)(EC:1.1.5.3
2062111606	215	19	42	c736	ribosomal protein L16, bacterial/organelle
2062112271	341	53	62	c736	ribosomal protein L24, bacterial/organelle
2062164149	368	84	65	c736	LSU ribosomal protein L14P
2062180322	395	20	43	c736	SSU ribosomal protein S8P
2062193156	239	8	0	c736	SSU ribosomal protein S17P
2062201587	368	117	16	c736	ribosomal protein L18, bacterial type
2062201588	194	10	10	c736	ribosomal protein L29
2062220946	536	22	30	c736	LSU ribosomal protein L5P
2062222304	539	17	9	c736	ribosomal protein L6, bacterial type
2062258761	803	179	45	c736	protein translocase subunit secY/sec61 alpha
2062272274	653	52	14	c736	SSU ribosomal protein S3P
2062281891	212	90	14	c736	LSU ribosomal protein L16P
2062297384	332	166	3	c736	ribosomal protein L22, bacterial type
2062419483	290	66	17	c736	LSU ribosomal protein L15P
2062423333	500	172	64	c736	SSU ribosomal protein S5P
2062144796	92	0	0	c7372	glutaminyl-tRNA synthetase (EC 6.1.1.18)(EC:6.1.1.18)
2062198345	86	0	0	c7372	glutaminyl-tRNA synthetase (EC 6.1.1.18)
2062268353	380	0	0	c7372	glutaminyl-tRNA synthetase (EC 6.1.1.18)(EC:6.1.1.18)
2062277423	500	10	0	c7372	glutaminyl-tRNA synthetase (EC 6.1.1.18)(EC:6.1.1.18)
2062420783	971	4	0	c7372	lipopolysaccharide heptosyltransferase I(EC:2.4.-)
2062112946	1403	6	4	c7509	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamil
2062353116	554	7	4	c7509	hypothetical protein
2062420784	92	0	0	c7509	hypothetical protein
2062151916	191	0	0	c7521	glutamyl-tRNA synthetase (EC 6.1.1.17)(EC:6.1.1.17)
2062161600	437	11	0	c7521	farnesyl-diphosphate synthase (EC 2.5.1.10)/geranylgeranyl-diphosphate synthase
2062169939	179	6	0	c7521	GHMP kinases C terminal.(EC:2.7.1.36)
2062200297	287	0	0	c7521	hypothetical protein(EC:5.3.3.2)
2062207347	440	0	2	c7521	farnesyl-diphosphate synthase (EC 2.5.1.10)/geranylgeranyl-diphosphate synthase
2062272262	368	3	0	c7521	isopentenyl phosphate kinase (EC 2.7.4.-)
2062319668	398	0	8	c7521	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)(EC:5.3.3.2)

2062333282	212	0	0	c7521	hypothetical protein(EC:6.1.1.17)
2062373580	167	0	0	c7521	isopentenyl phosphate kinase (EC 2.7.4.-)
2062133118	923	196	21	c758	Flagellin and related hook-associated proteins
2062155115	443	25	16	c758	Flagellin and related hook-associated proteins
2062155117	1034	25	11	c758	Flagellin and related hook-associated proteins
2062156437	443	43	5	c758	hypothetical protein
2062193162	389	237	10	c758	Xaa-Pro aminopeptidase(EC:3.4.13.9)
2062299934	701	11	11	c758	small GTP-binding protein domain
2062373590	329	52	21	c758	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides
2062402556	224	4	27	c758	hypothetical protein
2062408444	416	24	12	c758	hypothetical protein
2062412368	635	277	25	c758	Predicted GTPase
2062122790	608	0	0	c7590	Putative Mg2+ and Co2+ transporter CorB
2062140188	86	0	0	c7590	(tRNA)
2062234574	221	14	0	c7590	Hemolysins and related proteins containing CBS domains
2062373574	245	8	0	c7590	hypothetical protein
2062386317	88	0	0	c7590	(tRNA)
2062401945	527	2	0	c7590	Glutamyl- and glutaminyl-tRNA synthetases
2062122791	467	62	19	c760	ADP-ribose pyrophosphatase
2062166749	446	4	2	c760	FOG: CBS domain
2062191921	296	7	27	c760	hypothetical protein
2062213736	275	4	11	c760	Bacterial nucleoid DNA-binding protein
2062213737	1328	71	27	c760	Chloride channel protein EriC
2062236535	512	14	4	c760	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)
2062364014	842	10	0	c760	DNA polymerase III, gamma/tau subunits
2062364015	407	5	7	c760	DNA polymerase III, gamma/tau subunits(EC:2.7.7.7)
2062421433	1025	49	35	c760	flagellar motor switch protein FliM
2062109687	185	0	0	c7648	hypothetical protein
2062124749	224	13	4	c7648	hypothetical protein
2062157100	617	83	8	c7648	methylmalonyl-CoA mutase metallochaperone MeaB(EC:2.7.-)
2062350531	665	38	17	c7648	NADPH:quinone reductase and related Zn-dependent oxidoreductases

2062365306	215	9	14	c7648	Protein of unknown function (DUF861).
2062413022	383	5	0	c7648	NADPH:quinone reductase and related Zn-dependent oxidoreductases
2062269662	1127	46	9	c765	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosug
2062324867	1334	43	31	c765	Phosphomannomutase
2062324868	551	20	15	c765	Nucleoside-diphosphate-sugar pyrophosphorylase
2062334495	680	129	28	c765	Nucleoside-diphosphate-sugar pyrophosphorylase
2062358881	719	33	25	c765	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosug
2062358882	686	10	10	c765	hypothetical protein
2062122133	626	16	6	c766	hypothetical protein
2062193171	110	9	0	c766	hypothetical protein
2062201566	542	22	4	c766	Xaa-Pro aminopeptidase(EC:3.4.11.-)
2062204761	677	16	4	c766	Xaa-Pro aminopeptidase(EC:3.4.13.9)
2062292897	635	27	8	c766	ABC-type spermidine/putrescine transport system, permease component II
2062322923	224	1232	13	c766	hypothetical protein
2062324869	653	34	9	c766	ABC-type spermidine/putrescine transport system, permease component I
2062126661	371	86	22	c769	hypothetical protein
2062136343	1421	130	47	c769	Glutamine synthetase
2062191910	1022	77	13	c769	Homoserine acetyltransferase(EC:2.3.1.31)
2062201561	404	92	7	c769	hypothetical protein
2062249899	386	23	8	c769	Ethanolamine utilization protein
2062273557	491	358	75	c769	Deoxycytidylate deaminase(EC:3.5.4.12)
2062278655	338	201	6	c769	L-glutamine synthetase (EC 6.3.1.2)(EC:6.3.1.2)
2062279980	368	79	5	c769	hypothetical protein
2062320341	362	50	6	c769	Phosphoglycerate dehydrogenase and related dehydrogenases
2062345494	662	272	30	c769	Phosphoglycerate dehydrogenase and related dehydrogenases
2062362785	113	0	0	c769	hypothetical protein
2062401949	1349	238	32	c769	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large t
2062422708	119	59	0	c769	L-glutamine synthetase (EC 6.3.1.2)(EC:6.3.1.2)
2062132489	575	47	5	c770	formyltetrahydrofolate-dependent phosphoribosylglycinamide formyltransferase (EC
2062132490	386	47	3	c770	Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisphosphatase and related protei
2062169323	578	35	0	c770	phosphoribosylamine--glycine ligase (EC 6.3.4.13)(EC:6.3.4.13)

2062187515	1055	38	6	c770	phosphoribosylaminoimidazole synthetase(EC:6.3.3.1)
2062187516	941	47	6	c770	phosphoribosylformylglycinamidine synthase subunit II (EC 6.3.5.3)(EC:6.3.5.3)
2062239090	401	15	12	c770	Phosphoribosylamine-glycine ligase(EC:6.3.4.13)
2062239091	320	16	3	c770	phosphoribosylamine--glycine ligase (EC 6.3.4.13)
2062240397	1175	116	25	c770	amidophosphoribosyltransferase (EC 2.4.2.14)(EC:2.4.2.14)
2062264454	83	24	0	c770	hypothetical protein
2062203465	398	13	10	c7701	Biopolymer transport protein
2062203466	407	7	0	c7701	Biopolymer transport protein
2062224913	872	16	0	c7701	Periplasmic protease
2062281904	617	204	15	c7701	Biopolymer transport proteins
2062192532	80	0	0	c7814	hypothetical protein
2062255614	413	5	5	c7814	Flagellar motor switch protein
2062276762	812	31	10	c7814	hypothetical protein
2062276768	386	0	0	c7814	hypothetical protein
2062419496	74	0	0	c7814	hypothetical protein
2062419497	899	46	17	c7814	hypothetical protein
2062138285	602	22	3	c783	hypothetical protein(EC:1.97.1.9)
2062138291	872	73	47	c783	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs
2062177121	1232	74	32	c783	amidase, hydantoinase/carbamoylase family(EC:3.5.1.87)
2062209879	983	40	7	c783	hypothetical protein(EC:1.97.1.9)
2062258759	800	96	19	c783	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs
2062418832	668	240	31	c783	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs
2062418836	392	23	0	c783	hypothetical protein(EC:1.97.1.9)
2062418841	869	123	20	c783	Predicted amidohydrolase
2062138287	863	6	1	c784	ABC-type multidrug transport system, ATPase and permease components(EC:3.6.
2062138288	1442	130	6	c784	cysteinyl-tRNA synthetase (EC 6.1.1.16)(EC:6.1.1.16)
2062177114	266	34	0	c784	NADH:ubiquinone oxidoreductase subunit 4 (chain M)(EC:1.6.5.3)
2062177125	212	19	0	c784	hypothetical protein
2062418839	1094	152	16	c784	NADH dehydrogenase subunit M (EC 1.6.5.3)(EC:1.6.5.3)
2062159641	194	15	0	c787	SSU ribosomal protein S18P
2062177117	446	22	0	c787	hypothetical protein

2062206022	491	43	59	c787	ribosomal protein L9
2062249247	1319	14	22	c787	replicative DNA helicase(EC:3.6.1.-)
2062276763	122	8	8	c787	hypothetical protein
2062294800	89	0	0	c787	hypothetical protein
2062335747	830	92	18	c787	Cytochrome C assembly protein.
2062418828	995	87	25	c787	EAL domain.
2062418831	452	100	13	c787	hypothetical protein
2062159642	614	62	21	c791	Glutathione S-transferase(EC:2.5.1.18)
2062159643	182	0	0	c791	Predicted metal-dependent hydrolase with the TIM-barrel fold
2062159644	785	3	3	c791	Ion transport protein.
2062205426	155	0	0	c791	hypothetical protein
2062205427	860	35	47	c791	Probable taurine catabolism dioxygenase(EC:1.14.11.17)
2062205428	806	12	7	c791	Methylase involved in ubiquinone/menaquinone biosynthesis
2062114275	359	354	81	c792	hypothetical protein
2062119538	842	59	43	c792	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
2062120846	209	167	10	c792	Domain of unknown function DUF21.
2062126050	473	21	8	c792	hypothetical protein
2062131187	839	67	18	c792	Hemolysins and related proteins containing CBS domains
2062131858	419	136	12	c792	Biopolymer transport protein
2062131859	740	85	43	c792	Biopolymer transport proteins
2062183620	191	5	52	c792	hypothetical protein
2062374218	497	20	4	c792	hypothetical protein
2062278661	323	0	0	c794	hypothetical protein(EC:5.2.1.8)
2062299984	683	45	20	c794	ATP-dependent Clp protease ATP-binding subunit ClpX (EC 3.4.21.92)
2062299985	581	26	7	c794	ATP-dependent Clp protease ATP-binding subunit ClpX (EC 3.4.21.92)
2062317734	1325	8	6	c794	trigger factor
2062322906	72	0	0	c794	(tRNA)
2062322907	80	0	0	c794	(tRNA)
2062322912	284	7	7	c794	hypothetical protein
2062322913	803	82	25	c794	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062322920	134	806	15	c794	bacterial nucleoid protein HU alpha subunit

2062322921	146	41	27	c794	Bacterial nucleoid DNA-binding protein
2062322922	1319	57	23	c794	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062348687	638	27	17	c794	ATP-dependent Clp protease proteolytic subunit ClpP (EC 3.4.21.92)(EC:3.4.21.92
2062405871	347	69	23	c794	ATP-dependent proteinase. Serine peptidase. MEROPS family S16(EC:3.4.21.53)
2062422705	73	0	0	c794	(tRNA)
2062317735	242	79	8	c797	Amidases related to nicotinamidase
2062329404	1367	79	37	c797	N-methylhydantoinase B/acetone carboxylase, alpha subunit(EC:3.5.2.14)
2062358877	605	36	5	c797	N-methylhydantoinase A/acetone carboxylase, beta subunit(EC:3.5.2.14)
2062358878	1439	38	7	c797	N-methylhydantoinase A/acetone carboxylase, beta subunit(EC:3.5.2.14)
2062150611	725	7	1	c8024	hypothetical protein
2062157104	311	84	0	c8024	hypothetical protein
2062358879	248	60	0	c8024	hypothetical protein
2062422704	665	60	9	c8024	hypothetical protein
2062425288	458	39	4	c8024	3-dehydroquinate dehydratase (EC 4.2.1.10)(EC:4.2.1.10)
2062109685	1418	35	4	c805	D-3-phosphoglycerate dehydrogenase(EC:1.1.1.95)
2062142124	245	0	4	c805	DNA topoisomerase IV subunit A (EC 5.99.1.3)(EC:5.99.1.-)
2062148692	608	16	13	c805	hypothetical protein
2062148693	203	0	5	c805	hypothetical protein
2062148694	233	64	21	c805	hypothetical protein
2062152600	959	46	17	c805	ADP-heptose:LPS heptosyltransferase
2062250506	131	0	0	c805	hypothetical protein
2062288341	149	0	0	c805	hypothetical protein
2062298020	656	128	21	c805	Exodeoxyribonuclease III (EC 3.1.11.2)
2062322908	128	0	0	c805	Exodeoxyribonuclease III (EC 3.1.11.2)(EC:3.1.11.2)
2062390198	314	0	3	c805	Flagellar motor switch/type III secretory pathway protein
2062265800	596	5	0	c806	hypothetical protein
2062265801	395	23	0	c806	hypothetical protein
2062278654	560	30	5	c806	Recombination protein MgsA
2062299932	347	14	0	c806	Recombination protein MgsA
2062299945	479	17	13	c806	UDP-glucose pyrophosphorylase(EC:2.7.7.9)
2062319671	380	34	21	c806	Recombination protein MgsA

2062335125	1214	26	12	c806	NAD-dependent DNA ligase (contains BRCT domain type II)
2062335126	833	16	4	c806	NAD-dependent DNA ligase (contains BRCT domain type II)(EC:6.5.1.2)
2062131188	830	53	17	c812	phosphate:acyl-[acyl carrier protein] acyltransferase(EC:2.3.1.15)
2062224904	134	0	0	c812	hypothetical protein
2062331981	311	68	32	c812	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits
2062343511	269	7	7	c812	Glycerophosphoryl diester phosphodiesterase(EC:3.1.4.46)
2062353743	764	25	8	c812	Thioredoxin-like proteins and domains
2062373578	422	40	14	c812	hypothetical protein
2062345528	989	144	34	c816	Predicted dehydrogenases and related proteins
2062345529	1787	37	12	c816	Putative homoserine kinase type II (protein kinase fold)
2062353745	506	75	4	c816	4-aminobutyrate aminotransferase and related aminotransferases
2062388291	416	50	5	c816	4-aminobutyrate aminotransferase and related aminotransferases
2062401944	341	67	6	c816	hypothetical protein
2062209273	467	36	15	c8167	Flagellar hook capping protein
2062310741	152	20	0	c8167	Flagellar hook protein FlgE
2062345530	257	16	0	c8167	Flagellar basal body rod protein
2062358226	653	25	21	c8167	Flagellar hook-length control protein
2062379337	317	35	25	c8167	hypothetical protein
2062411737	392	10	13	c8167	hypothetical protein
2062145445	710	10	17	c822	Pseudouridylate synthases, 23S RNA-specific(EC:5.4.99.12)
2062152601	308	6	0	c822	hypothetical protein
2062152602	494	0	4	c822	hypothetical protein
2062152603	344	12	9	c822	Phosphomannomutase
2062152604	785	28	9	c822	Phosphomannomutase(EC:5.4.2.2)
2062273556	317	3	6	c822	hypothetical protein
2062408441	230	13	0	c822	hypothetical protein
2062113629	719	49	6	c826	protease FtsH subunit HflC(EC:3.4.-)
2062167404	470	30	6	c826	Protein of unknown function (DUF3015).
2062167405	440	5	7	c826	Protein of unknown function (DUF3015).
2062169938	359	17	0	c826	Ribosomal protein L11 methylase
2062172537	233	26	9	c826	Ribosomal protein L11 methylase(EC:2.1.1.-)

2062222299	1139	21	11	c826	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase
2062254387	176	11	0	c826	hypothetical protein
2062288322	314	25	0	c826	Anaerobic dehydrogenases, typically selenocysteine-containing
2062351191	128	8	0	c826	CTP:phosphocholine cytidylyltransferase involved in choline phosphorylation for cel
2062351192	974	14	3	c826	Cytochrome c
2062351193	236	4	8	c826	hypothetical protein
2062351195	968	17	2	c826	Membrane protease subunits, stomatin/prohibitin homologs
2062351196	776	30	12	c826	Phosphatidylglycerophosphate synthase
2062351197	140	7	0	c826	hypothetical protein
2062216450	452	4	2	c827	hypothetical protein
2062216451	110	0	0	c827	hypothetical protein
2062216452	182	5	0	c827	hypothetical protein
2062249897	248	4	0	c827	hypothetical protein
2062249898	155	13	6	c827	hypothetical protein
2062274224	1100	17	16	c827	AAA ATPase containing von Willebrand factor type A (vWA) domain
2062283156	1208	2	3	c827	putative oxygen-independent coproporphyrinogen III oxidase
2062296085	65	0	0	c827	hypothetical protein
2062297387	437	0	9	c827	Putative transcriptional regulator, homolog of Bvg accessory factor(EC:2.7.1.33)
2062340256	1193	3	8	c827	General secretion pathway protein K.
2062348688	1124	12	6	c827	Beta-lactamase class A
2062361451	2765	178	58	c827	ribonucleoside-diphosphate reductase class II (EC 1.17.4.-)(EC:1.17.4.1)
2062392748	569	0	7	c827	Biotin-(acetyl-CoA carboxylase) ligase
2062415657	998	69	39	c827	ribonucleoside-diphosphate reductase class II (EC 1.17.4.-)(EC:1.17.4.1)
2062415658	260	50	4	c827	Putative transcriptional regulator, homolog of Bvg accessory factor
2062155788	773	153	48	c8331	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)
2062192529	590	136	14	c8331	LSU ribosomal protein L25P
2062192530	350	43	6	c8331	peptidyl-tRNA hydrolase (EC 3.1.1.29)(EC:3.1.1.29)
2062192531	71	99	0	c8331	(tRNA)
2062269721	81	0	0	c8331	(tRNA)
2062274269	218	23	9	c8331	Peptidyl-tRNA hydrolase(EC:3.1.1.29)
2062274270	968	265	26	c8331	ribose-phosphate pyrophosphokinase(EC:2.7.6.1)

2062274271	164	37	0	c8331	translation elongation factor 1A (EF-1A/EF-Tu)(EC:3.6.5.3)
2062274272	70	0	0	c8331	(tRNA)
2062276767	72	14	0	c8331	(tRNA)
2062408445	107	9	0	c8331	hypothetical protein
2062111603	458	22	9	c834	Soluble lytic murein transglycosylase and related regulatory proteins (some contain
2062111605	971	145	1	c834	Rhodanese-Like Protein
2062149974	236	110	8	c834	hypothetical protein
2062164151	461	17	4	c834	N-acetylglutamate kinase (EC 2.7.2.8)(EC:2.7.2.8)
2062229416	521	150	48	c834	Rhodanese-related sulfurtransferase
2062229417	398	204	28	c834	Rhodanese-related sulfurtransferase(EC:2.8.1.1)
2062276764	557	9	5	c834	hypothetical protein
2062276765	662	65	9	c834	hypothetical protein
2062276766	191	0	16	c834	hypothetical protein
2062394719	248	16	0	c834	LysM domain.
2062408439	278	4	0	c834	hypothetical protein
2062419481	377	5	5	c834	N-acetylglutamate kinase (EC 2.7.2.8)(EC:2.7.2.8)
2062152617	476	82	6	c835	precorrin-4 C11-methyltransferase (EC 2.1.1.133)(EC:2.1.1.133)
2062152618	1271	93	17	c835	precorrin-3 methyltransferase (EC 2.1.1.131)(EC:2.1.1.131)
2062155119	152	20	13	c835	hypothetical protein
2062224917	1433	33	20	c835	aspartyl-tRNA synthetase (EC 6.1.1.12)(EC:6.1.1.12)
2062224918	1064	126	8	c835	D-alanine--D-alanine ligase (EC 6.3.2.4)(EC:6.3.2.4)
2062249890	476	13	8	c835	Predicted rRNA methylase (SpoU class)
2062261898	677	123	10	c835	Cobalamin biosynthesis protein CbiG
2062284417	737	34	16	c835	precorrin-2 C20-methyltransferase(EC:2.1.1.130,EC:2.1.1.151)
2062318348	1094	209	16	c835	precorrin-6Y C5,15-methyltransferase (decarboxylating) (EC 2.1.1.132)(EC:2.1.1.1
2062318349	320	16	13	c835	precorrin-4 C11-methyltransferase (EC 2.1.1.133)(EC:2.1.1.133)
2062347391	350	11	9	c835	aspartate--tRNA(Asn) ligase (EC 6.1.1.23)(EC:6.1.1.12)
2062350519	818	94	21	c835	Uncharacterized conserved protein(EC:4.99.1.3)
2062395375	1058	63	9	c835	hypothetical protein
2062422711	665	126	17	c835	precorrin-8X methylmutase (EC 5.4.1.2)(EC:5.4.1.2)
2062350518	1676	32	4	c8355	hypothetical protein

2062422713	1046	27	2	c8355	hypothetical protein
2062152616	83	0	0	c837	hypothetical protein
2062171214	1115	3	7	c837	Outer membrane protein/protective antigen OMA87
2062213756	1778	69	30	c837	Long-chain acyl-CoA synthetases (AMP-forming)
2062422712	581	90	29	c837	ABC-type antimicrobial peptide transport system, ATPase component(EC:3.6.3.-)
2062220968	467	9	0	c843	2-methylthioadenine synthetase
2062220969	593	5	7	c843	2-methylthioadenine synthetase(EC:2.7.13.3)
2062272278	359	0	0	c843	Glycerophosphoryl diester phosphodiesterase family.(EC:3.1.4.46)
2062294191	749	3	3	c843	Glycerophosphoryl diester phosphodiesterase(EC:3.1.4.46)
2062294192	314	13	0	c843	hypothetical protein
2062386310	686	111	22	c843	LSU ribosomal protein L17P
2062245413	1784	72	6	c845	Highly conserved protein containing a thioredoxin domain
2062252435	599	0	3	c845	hypothetical protein
2062252438	575	9	3	c845	hypothetical protein
2062255612	281	0	11	c845	hypothetical protein
2062258760	611	110	8	c845	Membrane protease subunits, stomatin/prohibitin homologs
2062271615	467	36	0	c845	Highly conserved protein containing a thioredoxin domain
2062376151	236	8	0	c845	hypothetical protein
2062392737	500	0	10	c845	Polyferredoxin
2062420785	524	2	6	c845	hypothetical protein
2062138907	203	49	20	c848	hypothetical protein
2062149975	350	3	0	c848	prepilin-type N-terminal cleavage/methylation domain
2062149976	662	77	21	c848	protein-L-isoaspartate(D-aspartate) O-methyltransferase(EC:2.1.1.77)
2062347386	1289	44	12	c848	ATPase, P-type (transporting), HAD superfamily, subfamily IC
2062376153	161	0	0	c848	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily.(EC:4.4.1.5)
2062376163	578	66	14	c848	ATPase, P-type (transporting), HAD superfamily, subfamily IC
2062376164	815	38	7	c848	Cation transport ATPase
2062408438	527	9	17	c848	prepilin-type N-terminal cleavage/methylation domain
2062129953	626	35	13	c8487	Zn-dependent alcohol dehydrogenases
2062188126	353	0	0	c8487	Prephenate dehydratase(EC:4.2.1.51)
2062195795	473	0	4	c8487	Predicted RNA-binding protein (consists of S1 domain and a Zn-ribbon domain)

2062268365	158	0	0	c8487	Prephenate dehydratase(EC:4.2.1.51)
2062335134	95	0	0	c8487	hypothetical protein(EC:4.1.3.34)
2062408437	161	0	0	c8487	hypothetical protein
2062415647	548	15	24	c8487	NADPH:quinone reductase and related Zn-dependent oxidoreductases
2062129954	1151	29	6	c8496	Cobyrinic acid a,c-diamide synthase(EC:6.3.1.-,EC:6.3.5.9)
2062129955	503	85	12	c8496	hypothetical protein
2062158381	1076	100	21	c8496	Mg-chelatase subunit ChlI(EC:6.6.1.1)
2062246669	260	27	12	c8496	hypothetical protein
2062334494	809	33	7	c8496	Predicted ATPase with chaperone activity
2062162902	1295	618	69	c850	Kef-type K+ transport systems, membrane components
2062167370	1904	563	54	c850	Kef-type K+ transport systems, membrane components
2062193166	1043	12	12	c850	TrkA-N domain./Ion channel.
2062228737	848	57	17	c850	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases(EC:
2062290288	203	79	10	c850	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A (EC 6.3.5.-)(EC:6.3.5.
2062294168	575	268	38	c850	TrkA-N domain.
2062299937	1544	57	25	c850	K+ transport systems, NAD-binding component
2062168694	266	0	4	c8531	Threonine dehydrogenase and related Zn-dependent dehydrogenases(EC:1.1.1.14
2062174466	266	0	8	c8531	Archaeal/vacuolar-type H+-ATPase subunit F(EC:3.6.3.14)
2062199632	119	0	0	c8531	hypothetical protein
2062201596	203	0	0	c8531	Threonine dehydrogenase and related Zn-dependent dehydrogenases(EC:1.1.1.14
2062220947	419	5	0	c8531	Threonine dehydrogenase and related Zn-dependent dehydrogenases(EC:1.1.1.14
2062246721	62	0	0	c8531	hypothetical protein
2062333278	101	0	0	c8531	hypothetical protein
2062333280	299	30	0	c8531	hypothetical protein
2062124111	923	23	23	c855	Collagenase and related proteases
2062124112	1181	39	22	c855	DNA protecting protein DprA
2062142783	119	17	8	c855	hypothetical protein
2062212472	377	13	8	c855	ABC-type multidrug transport system, ATPase component
2062221627	245	12	24	c855	hypothetical protein
2062264456	941	13	0	c855	riboflavin kinase/FMN adenylyltransferase(EC:2.7.1.26,EC:2.7.7.2)
2062279981	1295	17	6	c855	tRNA nucleotidyltransferase/poly(A) polymerase

2062299939	455	53	13	c855	SsrA-binding protein
2062404581	572	3	12	c855	hypothetical protein
2062164147	185	11	0	c862	Kef-type potassium/proton antiporter, CPA2 family (TC 2.A.37.1)
2062217728	1538	56	10	c862	Kef-type potassium/proton antiporter, CPA2 family (TC 2.A.37.1)
2062249886	416	31	36	c862	Dioxygenases related to 2-nitropropane dioxygenase
2062279982	542	30	4	c862	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and ex
2062300582	128	8	8	c862	Conserved domain frequently associated with peptide methionine sulfoxide reducta
2062300583	413	63	31	c862	Dioxygenases related to 2-nitropropane dioxygenase
2062325513	686	23	3	c862	methionine-S-sulfoxide reductase(EC:1.8.4.12,EC:1.8.4.11,EC:1.8.4.11)
2062174464	344	81	23	c863	Acyl-CoA dehydrogenases(EC:1.3.99.3)
2062174465	755	127	21	c863	Acyl-CoA dehydrogenases(EC:1.3.99.3,EC:1.3.99.2)
2062280654	1970	115	16	c863	Acyl-CoA synthetase (NDP forming)(EC:6.2.1.1)
2062308271	653	251	12	c863	ABC-type spermidine/putrescine transport system, permease component II
2062325514	632	544	97	c863	ABC-type spermidine/putrescine transport system, permease component I
2062111595	341	41	12	c8640	Argininosuccinate lyase
2062123479	506	67	10	c8640	Argininosuccinate lyase(EC:4.3.2.1)
2062125415	530	40	4	c8640	flagellar basal-body rod protein FlgB
2062129926	449	76	67	c8640	flagellar basal-body rod protein FlgC
2062142108	728	78	3	c8640	glycerol 3-phosphate dehydrogenase (NAD(P)+) (EC 1.1.1.94)(EC:1.1.1.94)
2062142109	326	31	89	c8640	Glycerol-3-phosphate dehydrogenase
2062142110	386	60	5	c8640	hypothetical protein
2062359547	569	102	18	c8640	Argininosuccinate lyase
2062148691	287	3	0	c866	hypothetical protein
2062164154	977	17	0	c866	Retron-type reverse transcriptase
2062167372	227	9	0	c866	Transposase IS200 like.
2062172539	329	30	3	c87	hypothetical protein
2062183614	134	15	0	c87	hypothetical protein
2062193161	455	18	9	c87	Ribonucleotide reductase, alpha subunit
2062202838	572	10	0	c87	ribosome recycling factor
2062213769	149	0	0	c87	translation elongation factor Ts (EF-Ts)
2062237849	716	101	1	c87	uridylate kinase (EC 2.7.4.22)

2062239092	1100	45	13	c875	carbohydrate ABC transporter ATP-binding protein, CUT1 family (TC 3.A.1.1.-)
2062239093	755	89	8	c875	carbohydrate ABC transporter membrane protein 1, CUT1 family (TC 3.A.1.1.-)
2062258108	332	48	0	c875	carbohydrate ABC transporter membrane protein 2, CUT1 family (TC 3.A.1.1.-)
2062271619	548	29	0	c875	carbohydrate ABC transporter membrane protein 2, CUT1 family (TC 3.A.1.1.-)
2062278664	488	719	53	c875	carbohydrate ABC transporter substrate-binding protein, CUT1 family (TC 3.A.1.1.-)
2062278668	182	132	22	c875	carbohydrate ABC transporter substrate-binding protein, CUT1 family (TC 3.A.1.1.-)
2062292900	134	0	0	c875	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062292901	1166	184	15	c875	Protein of unknown function (DUF1479).
2062177102	638	69	28	c878	ribonuclease III, bacterial(EC:3.1.26.3)
2062241040	440	159	5	c878	ribosomal large subunit pseudouridine synthase B (EC 5.4.99.-)(EC:5.4.99.12)
2062246685	854	136	34	c878	signal peptidase I, bacterial type
2062308270	1304	27	15	c878	Acetylglutamate kinase
2062308272	269	7	26	c878	Flagellar motor component
2062316485	533	103	11	c878	Flagellar motor component
2062319663	638	36	38	c878	Flagellar motor protein
2062325506	656	55	8	c878	Flagellar motor protein
2062325507	233	21	0	c878	Glutaredoxin.
2062328122	992	68	17	c878	Glycosyltransferases involved in cell wall biogenesis
2062329405	839	41	10	c878	Uncharacterized low-complexity proteins
2062331977	467	64	11	c878	hypothetical protein
2062333281	356	163	8	c878	hypothetical protein
2062346762	431	5	5	c878	Protein of unknown function (DUF3501).
2062358228	131	8	0	c878	hypothetical protein(EC:5.4.99.12)
2062362065	470	89	17	c878	Membrane protease subunits, stomatin/prohibitin homologs
2062362075	875	231	19	c878	methionine aminopeptidase, type I (EC 3.4.11.18)
2062365278	479	4	4	c878	Mg-dependent DNase
2062376161	290	34	3	c878	Mg-dependent DNase(EC:3.1.21.-)
2062376162	296	355	37	c878	Peroxiredoxin
2062392752	134	37	0	c878	Peroxiredoxin(EC:1.11.1.15)
2062394079	1661	69	16	c878	Predicted polymerase, most proteins contain PALM domain, HD hydrolase domain
2062394717	218	9	9	c878	protease FtsH subunit HflK(EC:3.4.-)

2062413012	137	0	0	c878	protease FtsH subunit HflK(EC:3.4.-)
2062191916	590	17	7	c8809	L-aminopeptidase/D-esterase
2062286341	617	13	0	c8809	methyltransferase, FkbM family
2062287058	1226	188	111	c8809	TonB dependent receptor.
2062358887	563	5	0	c8809	Protein of unknown function (DUF3228).
2062127942	473	2	13	c883	Arginyl-tRNA synthetase(EC:6.1.1.19)
2062131869	482	52	4	c883	Glycine/sarcosine/betaine reductase selenoprotein B (GRDB).
2062131870	254	102	4	c883	hypothetical protein
2062131871	719	15	17	c883	pyridoxal phosphate enzyme, YggS family
2062228746	521	6	13	c883	Acetyltransferases, including N-acetylases of ribosomal proteins
2062228748	905	18	7	c883	Arginyl-tRNA synthetase
2062246709	1082	21	10	c883	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (EC 1.17.4.3)(EC:1.17.7.1)
2062269676	221	0	18	c883	bacterial translation initiation factor 1 (bIF-1)
2062373591	1319	15	8	c883	deoxyguanosinetriphosphate triphosphohydrolase, putative
2062119541	215	19	0	c884	NADH dehydrogenase subunit E (EC 1.6.5.3)(EC:1.6.5.3)
2062131194	968	170	35	c884	NADH dehydrogenase subunit F (EC 1.6.5.3)(EC:1.6.5.3)
2062131196	1661	74	15	c884	NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)
2062131197	344	52	3	c884	NADH:ubiquinone oxidoreductase subunit 6 (chain J)(EC:1.6.5.3)
2062133120	278	122	7	c884	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit
2062135647	506	6	2	c884	Transcriptional regulator
2062171215	128	39	0	c884	acetolactate synthase, large subunit (EC 2.2.1.6)(EC:2.2.1.6)
2062180329	491	75	20	c884	acetolactate synthase, small subunit (EC 2.2.1.6)(EC:2.2.1.6)
2062312706	650	154	6	c884	acetolactate synthase, large subunit (EC 2.2.1.6)(EC:2.2.1.6)
2062358229	875	86	13	c884	acetolactate synthase, large subunit (EC 2.2.1.6)(EC:2.2.1.6)
2062140185	1418	51	18	c889	Highly conserved protein containing a thioredoxin domain
2062142094	422	64	19	c889	Highly conserved protein containing a thioredoxin domain
2062142096	212	24	33	c889	LSU ribosomal protein L4P
2062156430	335	307	45	c889	SSU ribosomal protein S10P
2062156440	371	264	129	c889	SSU ribosomal protein S12P
2062157098	473	372	95	c889	SSU ribosomal protein S7P
2062175136	1199	553	138	c889	translation elongation factor 1A (EF-1A/EF-Tu)(EC:3.6.5.3)

2062180326	1079	528	100	c889	translation elongation factor 2 (EF-2/EF-G)(EC:3.6.5.3)
2062180330	425	544	75	c889	translation elongation factor 2 (EF-2/EF-G)(EC:3.6.5.3)
2062186876	587	1005	145	c889	translation elongation factor 2 (EF-2/EF-G)(EC:3.6.5.3)
2062200911	659	3	0	c8910	hypothetical protein
2062202208	152	0	0	c8910	hypothetical protein
2062211211	251	56	8	c8910	hypothetical protein
2062224916	284	0	0	c8910	hypothetical protein
2062229406	287	28	10	c8910	Uncharacterized conserved protein
2062233955	1394	34	4	c896	3-deoxy-D-manno-octulosonic-acid transferase(EC:2.-)
2062233956	563	39	9	c896	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis
2062233959	299	7	3	c896	hypothetical protein
2062249900	476	8	0	c896	hypothetical protein
2062249901	374	35	0	c896	hypothetical protein
2062258113	512	20	14	c896	LETM1-like protein.
2062264453	296	10	0	c896	Molybdopterin converting factor, small subunit
2062271609	572	3	0	c896	Predicted transcriptional regulators
2062271614	488	57	23	c896	Rhodanese-related sulfurtransferase
2062272275	839	64	10	c904	aconitase (EC 4.2.1.3)(EC:4.2.1.3)
2062281259	1442	100	35	c904	aconitase (EC 4.2.1.3)(EC:4.2.1.3)
2062284415	479	13	17	c904	aconitase (EC 4.2.1.3)(EC:4.2.1.3)
2062284416	947	27	13	c904	Phosphoserine aminotransferase(EC:2.6.1.52)
2062286342	551	103	25	c904	Restriction endonuclease
2062286343	1457	13	6	c913	Bacterial flagellin N-terminal helical region.
2062294788	644	37	11	c913	CAAX amino terminal protease family.
2062299943	782	13	5	c913	Flagellin and related hook-associated proteins
2062305099	458	72	0	c913	Flagellin and related hook-associated proteins
2062310744	887	30	18	c913	Flagellin and related hook-associated proteins
2062318358	350	0	11	c913	Flagellin and related hook-associated proteins
2062323581	1268	39	28	c913	Flagellin and related hook-associated proteins
2062340921	101	0	0	c913	hypothetical protein
2062361453	191	31	0	c913	hypothetical protein

2062362710	293	0	0	c913	hypothetical protein
2062333285	959	16	6	c92	Uncharacterized protein conserved in bacteria
2062362711	803	72	0	c92	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosph
2062372928	698	77	30	c92	Dehydrogenases with different specificities (related to short-chain alcohol dehydrog
2062376156	95	0	0	c92	hypothetical protein
2062379983	434	5	0	c92	Molecular chaperone, HSP90 family
2062386955	812	38	10	c92	Molecular chaperone, HSP90 family
2062422732	230	13	0	c92	Predicted phosphatases(EC:3.1.3.18)
2062423330	743	26	3	c92	RNA methyltransferase, TrmH family, group 1(EC:2.1.1.-)
2062239095	257	0	0	c924	hypothetical protein
2062309529	815	0	0	c924	hypothetical protein
2062314585	218	0	0	c924	hypothetical protein
2062346768	191	0	0	c924	hypothetical protein
2062126018	998	26	8	c926	amino acid/amide ABC transporter membrane protein 2, HAAT family (TC 3.A.1.4.-)
2062126019	1172	149	28	c926	amino acid/amide ABC transporter substrate-binding protein, HAAT family (TC 3.A.1
2062248618	170	41	0	c926	amino acid/amide ABC transporter membrane protein 1, HAAT family (TC 3.A.1.4.-)
2062278658	383	23	10	c926	amino acid/amide ABC transporter ATP-binding protein 2, HAAT family (TC 3.A.1.4.-
2062280634	65	15	0	c926	hypothetical protein
2062305103	737	94	5	c926	amino acid/amide ABC transporter ATP-binding protein 1, HAAT family (TC 3.A.1.4.-
2062372927	761	91	7	c926	amino acid/amide ABC transporter membrane protein 1, HAAT family (TC 3.A.1.4.-)
2062301234	1439	325	70	c9274	Flagellin and related hook-associated proteins
2062334514	83	0	0	c9274	hypothetical protein
2062118212	263	46	0	c934	Predicted membrane protein
2062299986	791	59	14	c934	Uncharacterized protein conserved in bacteria
2062299987	875	26	22	c934	Uncharacterized protein required for cytochrome oxidase assembly
2062309532	329	146	88	c934	caa(3)-type oxidase, subunit IV
2062350512	1082	482	41	c934	Heme/copper-type cytochrome/quinol oxidases, subunit 1(EC:1.9.3.1)
2062350513	152	0	0	c934	hypothetical protein
2062350514	137	0	0	c934	hypothetical protein
2062350515	779	96	37	c934	Heme/copper-type cytochrome/quinol oxidases, subunit 2
2062350516	662	270	48	c934	Heme/copper-type cytochrome/quinol oxidases, subunit 1

2062350517	236	17	4	c934	hypothetical protein
2062358227	626	534	62	c934	Heme/copper-type cytochrome/quinol oxidase, subunit 3
2062378055	575	99	26	c934	Heme/copper-type cytochrome/quinol oxidase, subunit 3(EC:1.9.3.1)
2062390196	131	8	0	c934	hypothetical protein
2062415656	1352	27	10	c934	Osmosensitive K+ channel histidine kinase
2062164150	371	27	3	c941	hypothetical protein
2062167406	707	82	14	c941	hypothetical protein
2062219043	986	39	3	c941	Predicted deacylase
2062419482	779	58	6	c941	1,4-dihydroxy-2-naphthoate octaprenyltransferase
2062142787	1226	321	51	c9497	fagellar hook-basal body proteins
2062142788	575	37	28	c9497	Flagellar hook capping protein
2062193179	266	38	83	c9497	Flagellar hook protein FlgE
2062292908	158	0	0	c9497	Flagellar hook-length control protein
2062396645	182	22	22	c9497	hypothetical protein
2062412400	326	0	15	c9497	hypothetical protein
2062412401	206	0	15	c9497	hypothetical protein
2062193185	428	47	23	c953	hypothetical protein
2062272279	806	0	0	c953	Uncharacterized conserved protein
2062298021	737	3	5	c953	proteasome subunit alpha 4 (EC:3.4.25.1)(EC:3.4.25.1)
2062417559	533	13	19	c953	Ribosomal protein L3
2062420792	149	0	0	c953	hypothetical protein
2062191917	398	13	5	c957	methionine-R-sulfoxide reductase(EC:1.8.4.12)
2062196438	422	5	2	c957	homoserine dehydrogenase (EC 1.1.1.3)(EC:1.1.1.3)
2062196439	1214	0	1	c957	Predicted alternative thymidylate synthase
2062350528	392	0	0	c957	Predicted RNA-binding protein (contains PUA domain)
2062394082	584	7	31	c957	20S proteasome, alpha and beta subunits(EC:3.4.25.1)
2062412361	515	0	0	c957	hypothetical protein
2062412362	608	0	7	c957	homoserine dehydrogenase (EC 1.1.1.3)(EC:1.1.1.3)
2062113631	479	29	10	c962	Cytochrome c biogenesis factor
2062342192	2609	49	8	c962	Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis
2062402553	662	9	8	c962	ABC-type antimicrobial peptide transport system, ATPase component

2062134387	161	56	31	c975	hypothetical protein
2062164140	254	83	0	c975	hypothetical protein
2062342193	1040	121	26	c975	Arabinose efflux permease
2062342194	353	93	6	c975	hypothetical protein
2062342195	596	233	15	c975	hypothetical protein
2062353741	1481	51	12	c975	BNR/Asp-box repeat.
2062405870	143	7	0	c975	hypothetical protein
2062278667	584	128	17	c988	Enoyl-CoA hydratase/carnithine racemase
2062292891	341	91	3	c988	Zn-dependent alcohol dehydrogenases, class III(EC:1.1.1.284,EC:1.1.1.1,EC:1.2.1
2062379997	986	80	5	c988	Predicted permeases
2062379998	335	113	3	c988	transcriptional regulator, ArsR family
2062124733	467	225	13	c989	Asparaginase(EC:3.5.1.1)
2062332679	677	62	22	c989	ATPase components of ABC transporters with duplicated ATPase domains
2062335766	365	433	8	c989	Asparaginase
2062340258	1682	44	24	c989	Uncharacterized protein conserved in bacteria
2062348676	1832	34	13	c989	hypothetical protein
2062348677	164	6	0	c989	hypothetical protein
2062373570	380	34	11	c989	ATPase components of ABC transporters with duplicated ATPase domains
2062400643	293	10	31	c989	ATPase components of ABC transporters with duplicated ATPase domains

IMG Gene ID	**Gene Length**	**Plume**	**Background**	**Contig**	**IMG Annotation**
2062193181	188	0	0	rep_c38584	hypothetical protein
2062280614	275	0	0	rep_c38584	hypothetical protein
2062350522	281	0	0	rep_c38584	cysteinyl-tRNA synthetase (EC 6.1.1.16)(EC:6.1.1.16)
2062358904	74	0	0	rep_c38584	hypothetical protein
2062372277	296	0	0	rep_c38584	Protein of unknown function (DUF432).
2062388289	824	0	0	rep_c38584	Small-conductance mechanosensitive channel
2062400644	233	0	0	rep_c38584	cysteinyl-tRNA synthetase (EC 6.1.1.16)(EC:6.1.1.16)