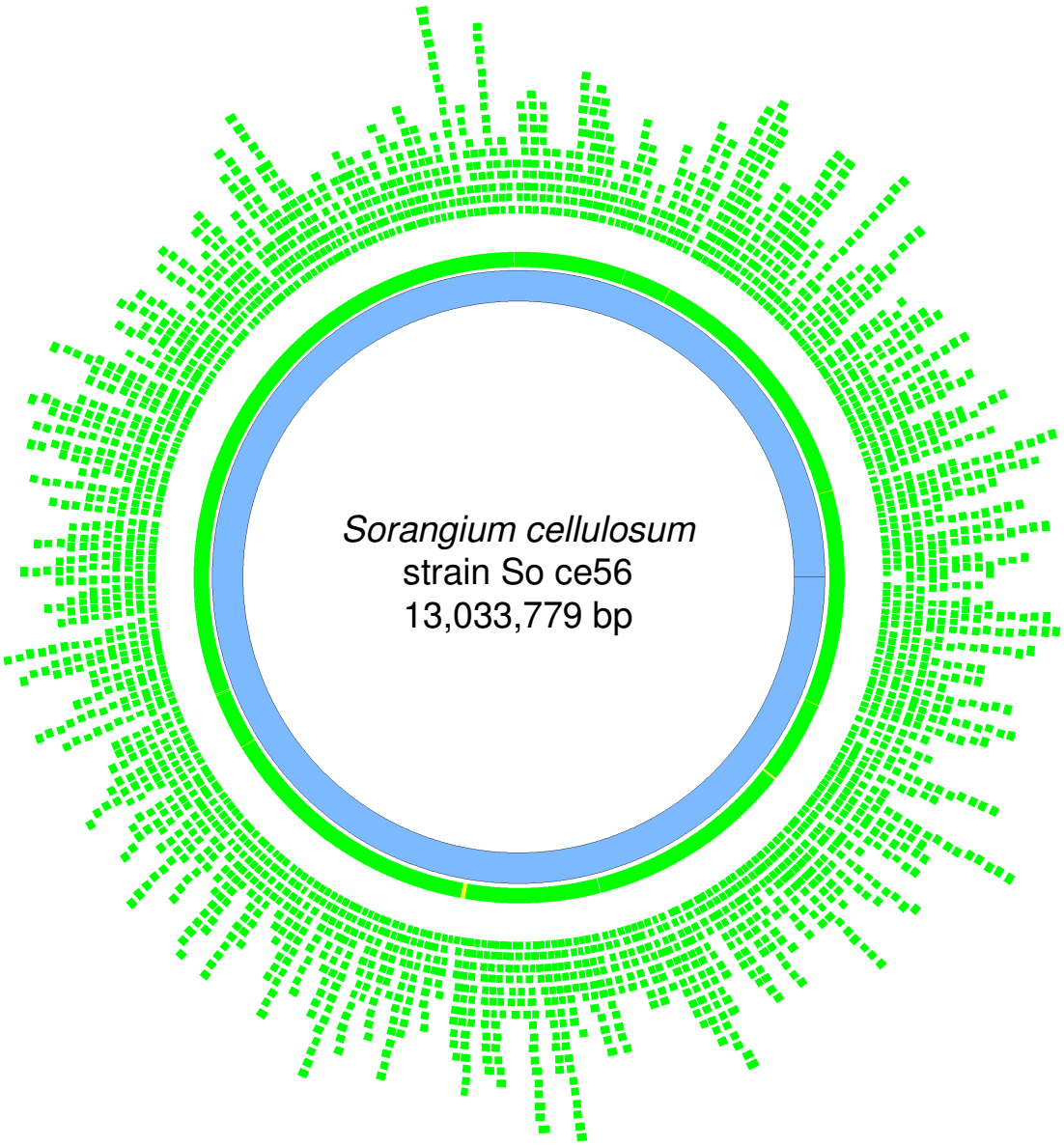
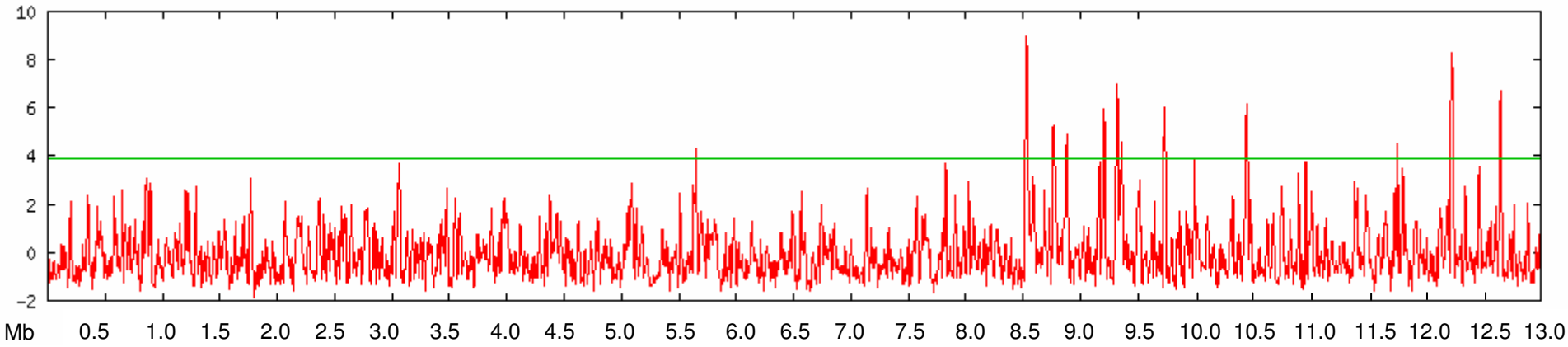
Supplementary Figure 1, Schneiker, *et al.*



Fosmid map of the *S. cellulosum* So ce56 chromosome.
To validate the assembly, fosmid end sequences were mapped onto the genome sequence by employing the BACCardI software[1]. Each green arc represents a single fosmid clone mapped onto the assembled sequence; circle 1: coverage of the *S. cellulosum* chromosome with fosmid clones (green: covered by more than two fosmids; yellow: covered by one fosmid).

Reference:
1. Bartels, D. *et al.* BACCardI – a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. *Bioinformatics* **21**, 853–859 (2005).

Supplementary Figure 2, Schneiker, *et al.*

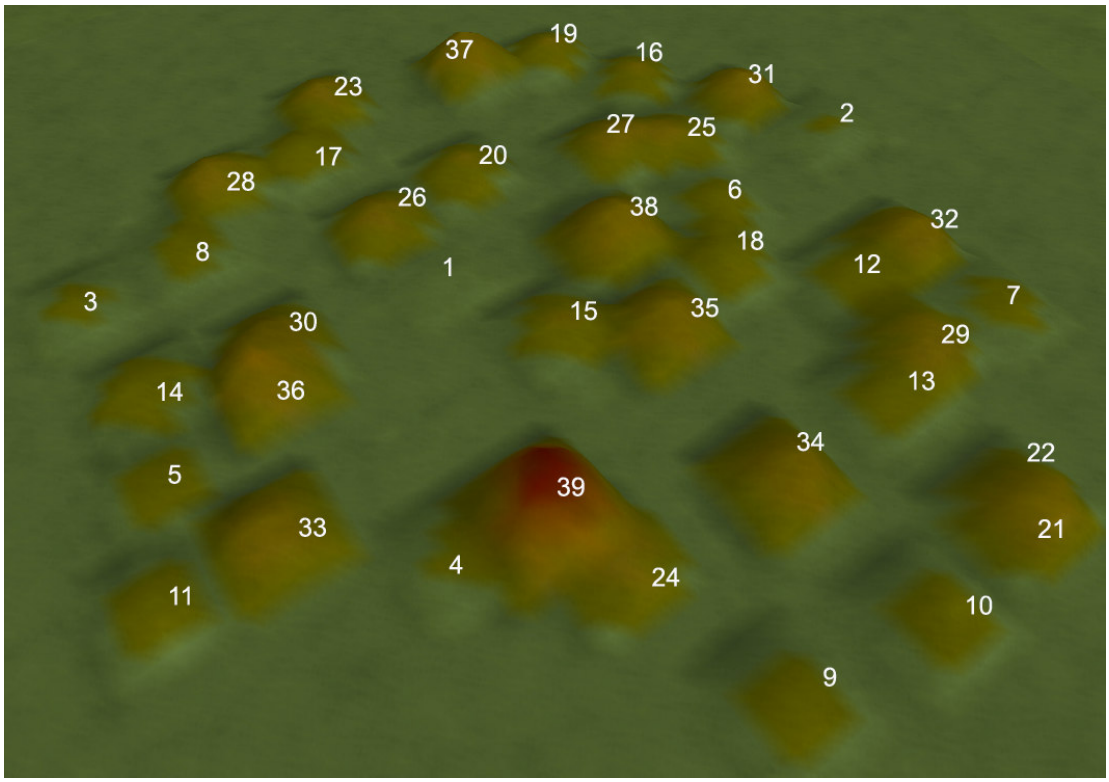


PAI-IDA analysis for detection of pathogenicity islands and anomalous gene clusters in the *S. cellulosum* genome. Analysis for anomalous gene clusters or putative pathogenicity islands in the genome was performed using the PAI-IDA program 1.1 (http://compbio.sibsnet.org/projects/pai-ida/) based on an iterative discriminant analysis[1]. The first two-thirds of the genome show a relatively uniform PAI-IDA pattern with only one score above the threshold, whereas the last third of the chromosome exhibits nine distinct peaks above the given threshold.

Reference:

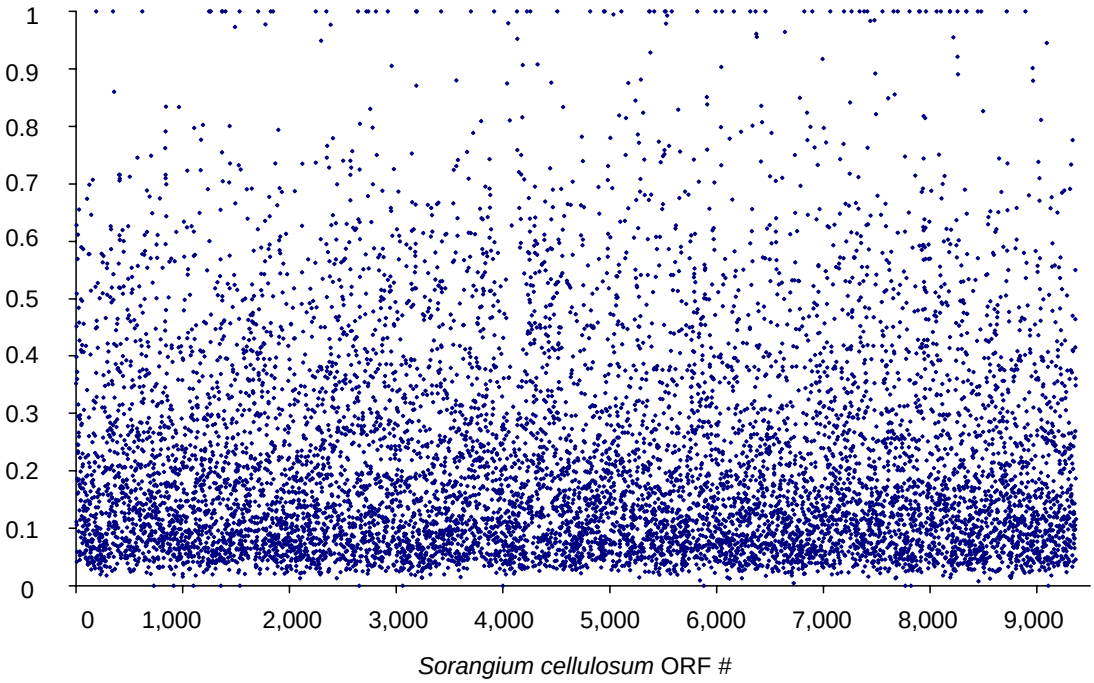
1. Tu,Q. & Ding, D.F. Detecting pathogenicity islands and anomalous gene clusters by iterative discriminant analysis. *FEMS Microbiol. Lett.* **221**, 269–275 (2003).

Supplementary Figure 3, Schneiker, *et al.*



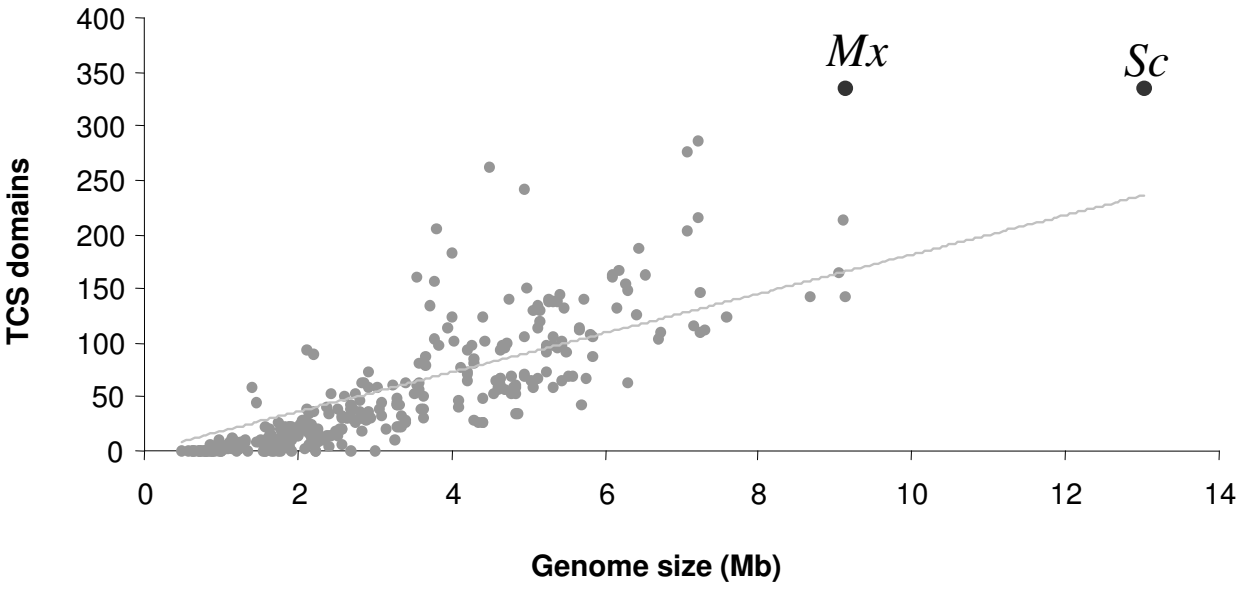
The phylogenomic map of *S. cellulosum* at lowest resolution with mountains labeled. Proteins were clustered using a combination of force-directed placement and multidimensional scaling into a total of 39 mountains, as visualized by *VxInsight*

Supplementary Figure 4, Schneiker, *et al.*



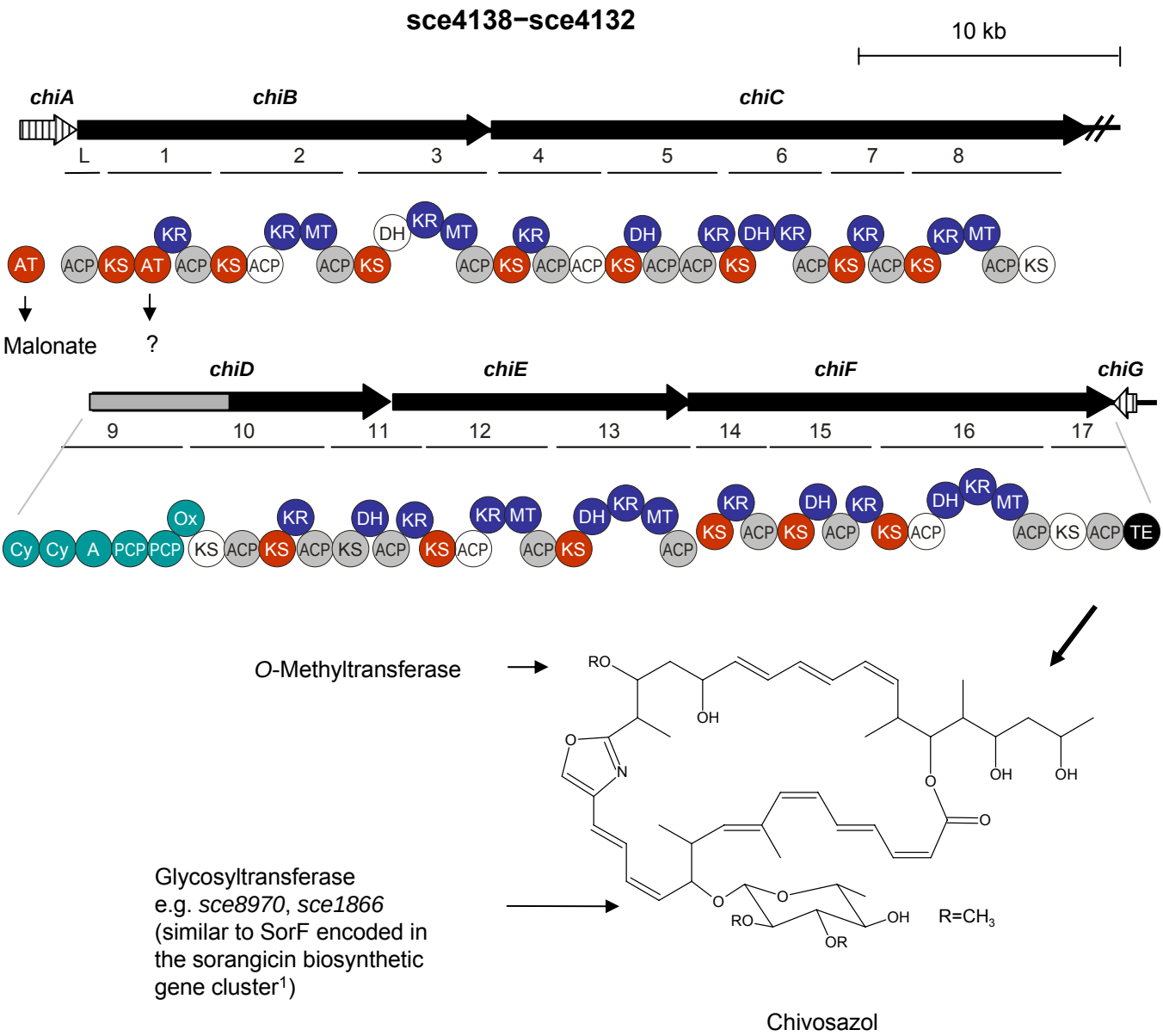
Degree of conservation among orthologs from *S. cellulosum* and *M. xanthus*. The conservation score is computed by dividing the score of the best cross-species BLAST hit by the score obtained when a BLAST is performed against the protein itself. The conservation score is roughly equivalent to amino acid identity, with 1.0 indicating 100% identity.

Supplementary Figure 5, Schneiker, *et al.*



TCS domains as a function of bacterial genome size. Numbers of receiver and transmitter domains encoded in a particular genome are plotted against the size of the genome. The trendline indicates all bacteria other than myxobacteria (316 completed genomes downloaded from Genbank). Mx, *Myxococcus xanthus*; Sc, *Sorangium cellulosum*.

Supplementary Figure 6, Schneiker, *et al.*



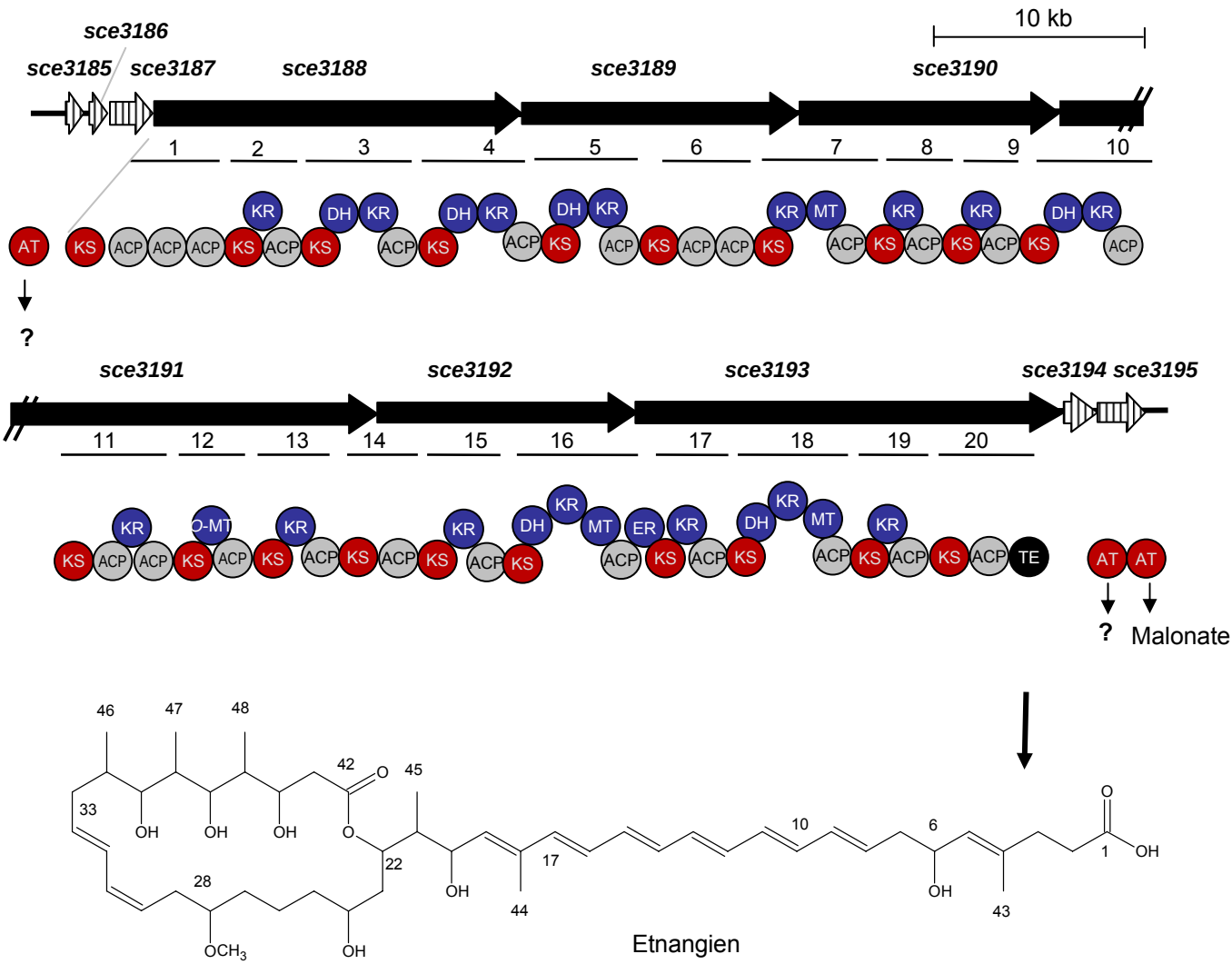
Domain organization of the proteins involved in the biosynthesis of chivosazol in *S. cellulosum*. This cluster belong to *trans*-AT family of biosynthetic clusters[2]. Substrate specificity could only be predicted for the *trans*-AT domain. Modules are depicted as lines. Domains proposed to be inactive are shown in white. CDSs encoding candidate proteins for modification of the core molecule are shown. Abbreviations are: AT, acyltransferase; ACP, acyl carrier protein; KS, ketosynthase; KR, ketoreductase; DH, dehydratase; MT, methyltransferase; TE, thioesterase; Cy, condensation/cyclization; A, adenylation; PCP, peptidyl carrier protein; Ox, oxidation. *chiA* encodes an acyltransferase, and *chiG,* a methyltransferase.

References:

1. Kopp, M. *et al.* SorF, a glycosyltransferase with promiscuous donor substrate specificity *in vitro*. *ChemBioChem.* **8**, 813−819 (2007).

2. Perlova, O., Gerth, K., Hans, A., Kaiser, O., & Müller, R. Identification and analysis of the chivosazol biosynthetic gene cluster from the myxobacterial model strain *Sorangium cellulosum* So ce56. *J. Biotechnol.* **121**, 174−191 (2006).

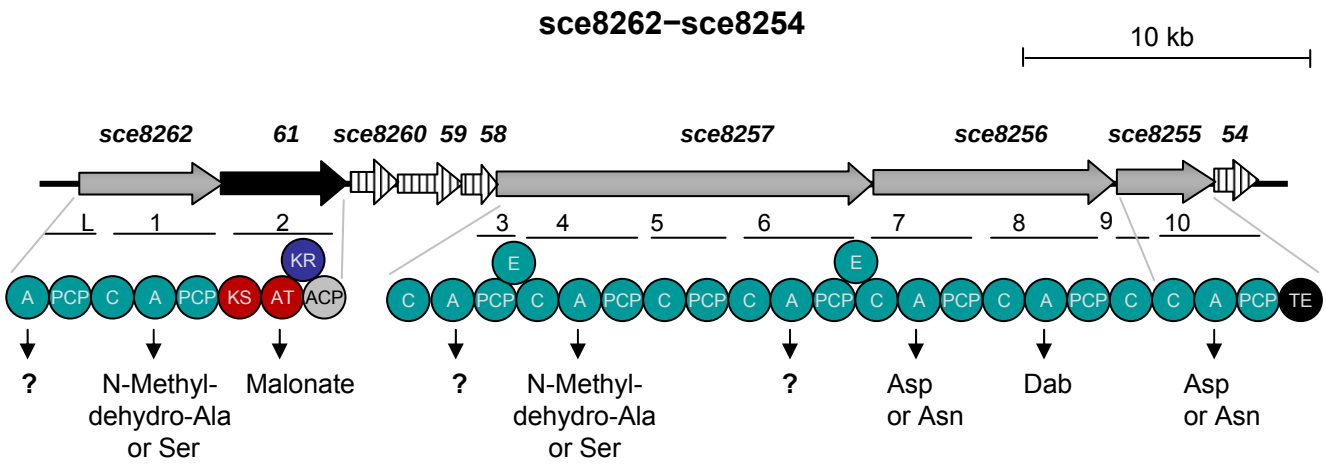
sce3185–sce3195



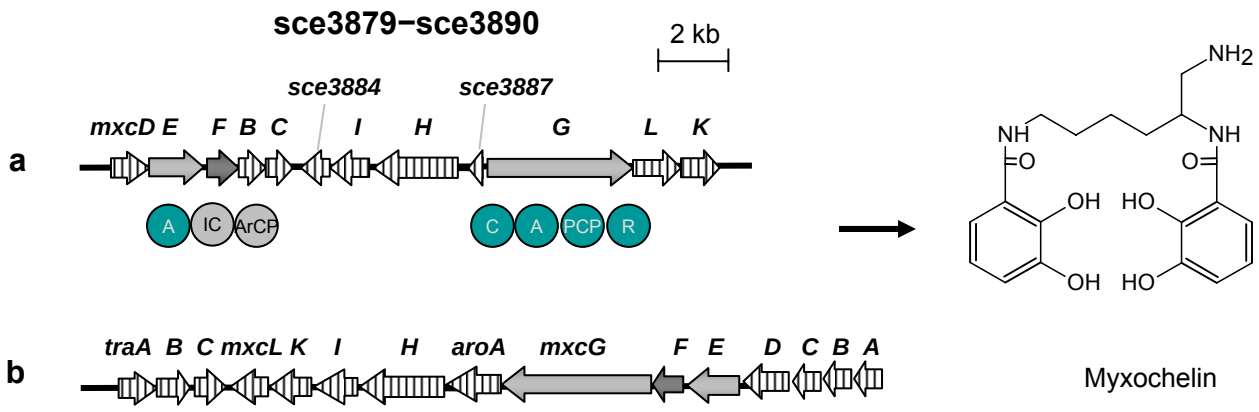
Domain organization of the PKS and NRPS multienzymes involved in biosynthesis of etnangien[1]. This cluster belong to *trans*-AT family of PKSs and includes split modules as well as missing and redundant domains. Because of significant deviations from "co-linearity"[2] it has not been posible to propose a biosynthetic pathway to this molecule. Abbreviations are: AT, acyltransferase; KS, ketosynthase; ACP, acyl carrier protein; KR, ketoreductase; DH, dehydratase; MT, methyltransferase; TE, thioesterase. PKS encoding genes are shown in black. The genes upstream of the PKSs encode: *sce3185*, hypothetical protein; *sce3186* (*fabD1*), malonyl CoA-acyl carrier protein transacylase; *sce3187* (*asnB1*), asparagine synthetase. The genes downstream of the PKSs encode: *sce3194*, multi antimicrobial extrusion protein MatE; *sce3195*, malonyl CoA-acyl carrier protein transacylase.

References:

1. Irschik, H., Schummer, D., Höfle, G., Reichenbach, H., Steinmetz, H. & Jansen, R. Etnangien, a macrolide-polyene antibiotic from *Sorangium cellulosum* that Inhibits nucleic acid polymerases. *J. Nat. Prod.* **70**, 1060–1063 (2007).
2. Müller, R. Don't classify polyketide synthases. *Chem. Biol.* **11**, 4−6 (2004).



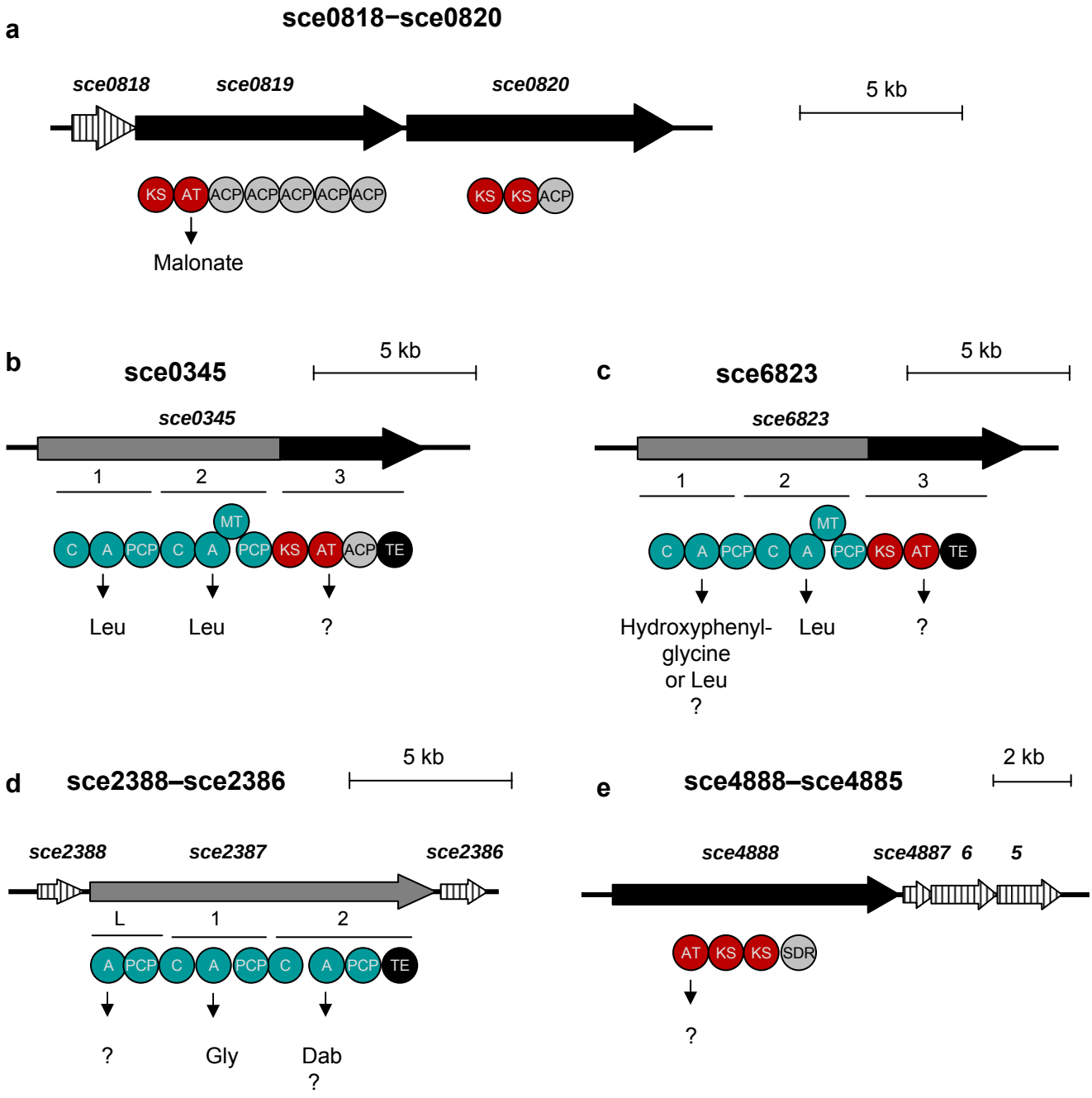
Analysis of the domain organization of the proteins encoded by the gene cluster sce8262−sce8254 potentially involved in the secondary metabolite biosynthesis. The substrate specificity could not be assigned for all A domains, and therefore the structure of the probable metabolite could not be predicted.
PKS-encoding genes are shown in black while NRPS-encoding genes are indicated in grey. A, adenylation domain; PCP, peptidyl carrier protein; C, condensation; E, epimerase; KS, ketosynthase; AT, acyltransferase; ACP, acyl carrier protein; KR, ketoreductase; TE, thioesterase. Additional non-PKS/NRPS genes in the biosynthetic gene cluster encode: sce8260, ABC transporter; sce8259, penicillin amidase; sce8258, regulatory protein; sce8254, diaminobutyrate-2-oxoglutarate transaminase. Dab, 2,4-diamino-butyric acid.



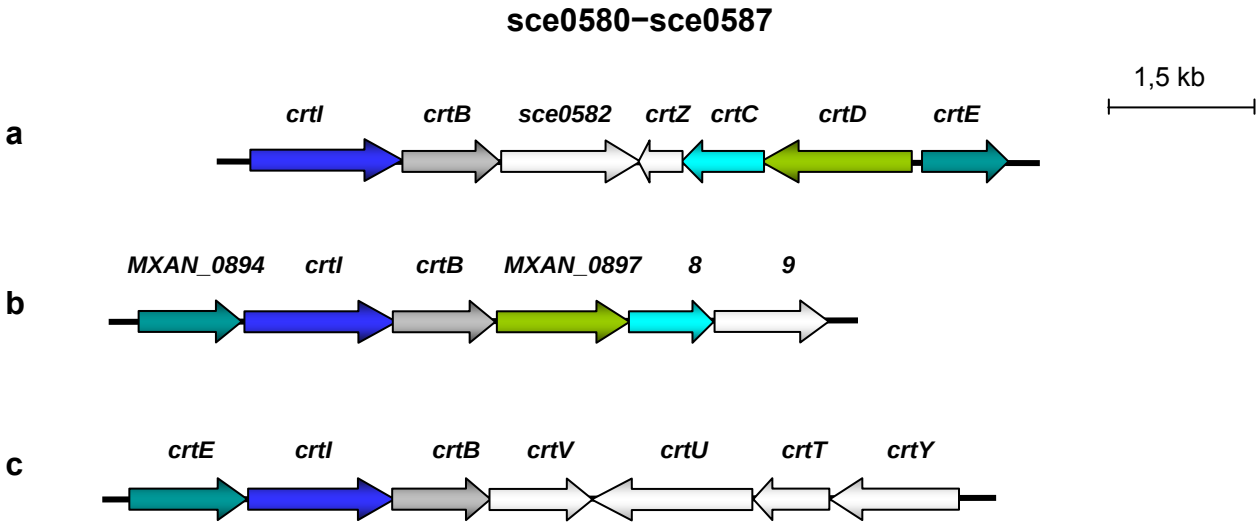
Protein domains which are known to be involved in myxochelin biosynthesis.
Comparison of the organization of the gene clusters in (a) *S. cellulosum* and (b) *Stigmatella aurantiaca,* and detailed analysis of the biosynthesis are described by Gaitatzis *et al.*[1] Abbreviations are: A, adenylation domain; IC, isochorismate lyase domain; ArCP, aryl carrier protein; C, condensation; PCP, peptidyl carrier protein; R, reductase domain. CDSs *sce3884* and *sce3887* encode hypothetical proteins.

References:

1. Gaitatzis, N., Kunze, B. & Müller, R. Novel insights into siderophore formation in myxobacteria. *ChemBioChem* **6**, 365−374 (2005).



Analysis of the domain organization of the proteins containing PKS and/or NRPS domains (a–e), and potentially involved in secondary metabolite biosynthesis. PKS-encoding genes are shown in black, while grey indicates the NRPS-encoding genes. Modules are depicted as lines. Abbreviations are: KS, ketosynthase; AT, acyltransferase; ACP, acyl carrier protein; C, condensation; A, adenylation; PCP, peptidyl carrier protein; MT, methyltransferase; TE, thioesterase; SDR, short-chain dehydrogenase/reductase. Genes located upstream and downstream encode: sce0818, putative dioxygenase; sce2388, putative ornithine cyclodeaminase; sce2386, hypothetical protein; sce4887, putative phosphopantetheinyl transferase; sce4886, 3-oxoacyl-[acyl-carrier-protein] reductase; sce4885, cytochrome P450. Dab, 2,4-diamino-butyric acid.



Genetic organization of the putative carotenoid biosynthetic loci in (a) *S. cellulosum*, (b) *M. xanthus* and (c) *Streptomyces coelicolor*. The data for *M. xanthus* were obtained from http://cmr.tigr.org/tigr-scripts/CMR/GenomePage.cgi?org=gmx, and for *S. coelicolor* from http://www.sanger.ac.uk/Projects/S_coelicolor/. The genes *crtI and crtB,* which are located adjacent to each other, were identified in all three genomes. In addition, *crtE* is shared among three clusters, but is located in a different position in *S. cellulosum*. Similar genes are indicated with the same color; genes without apparent homologues in other clusters are depicted in white. No proteins similar to CrtV, CrtU, CrtT and CrtY from *S. coelicolor* could be found in myxobacterial genomes. The putative gene products encoded by the analyzed clusters are listed in the table below:

Genome	CDS	Gene product	Additional similar CDSs
S. cellulosum	***crtI***	Phytoene dehydrogenase	*sce3350, sce0611, sce3770*
	crtB	Phytoene synthase	
	sce0582	Hypothetical protein	
	crtZ	ß-carotene hydroxylase	
	crtC	Hydroxyneurosporene dehydrogenase	
	crtD	Putative methoxyneurosporene dehydrogenase	
	crtE	Farnesyltranstransferase	*sce4204*
M. xanthus	***MXAN_0894***	Putative farnesyltranstransferase	*MXAN_4644*
	crtI	Phytoene desaturase	*MXAN_4052, MXAN_7517*
	crtB	Phytoene synthetase	
	MXAN_0897	Hydroxyneurosporene dehydrogenase	
	MXAN_0898	Neurosporene hydroxylase	
	MXAN_0899	Putative carotenoid biosynthesis protein	
S. coelicolor	***crtE***	Geranylgeranyl pyrophosphate synthase	
	crtI	Phytoene dehydrogenase	
	crtB	Phytoene synthase	
	crtV	Methylesterase	
	crtU	Dehydrogenase	
	crtT	Methyltransferase	
	crtY	Lycopene cyclase	

Supplementary Table1 List of paralogous gene families of *Sorangium cellulosum* . Comparison of all predicted genes of *S. cellulosum* was performed by using BlastP, applying an E-value threshold of 1E-30. The table below contains information about the overall number of families with paralogous genes, the number of CDS in each family, the dominant COG-number for each family, a counter for the occurrence of the dominant COG number and the percentage of the dominant COG-number for each family. In addition to this, a complete list of the name, start and stop positions, gene product, and gene name for each paralogous CDS is given, as well as the GO- and COG-numbers for each CDS.

Fam: 1	No. of CDS: 498	Dom. COG: 515	counter: 298 / 498	percentage: 59.84%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0002	5367	1450	Protein kinase		4674,5524,6468,4672	515
CDS	sce0022	33614	31725	Protein kinase		4672,4674,5524,6468	515
CDS	sce0038	52143	53348	Protein kinase		4672,4674,5524,6468	515
CDS	sce0042	59809	58445	Protein kinase		4672,4674,5524,6468	515
CDS	sce0060	85125	83602	Protein kinase		4672,4674,5524,6468	515
CDS	sce0182	245211	243952	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce0184	249602	246300	Protein kinase		4672,4674,5524,6468	515
CDS	sce0186	253391	250851	Two-component histidine kinase		7165,16301	2202
CDS	sce0195	262861	265218	Two-component sensor histidine kinase		7165,16301	642
CDS	sce0206	284289	280858	Two-component system sensor histidine kinase/response regulator, hybrid ('one-component system')		7165,16301	642
CDS	sce0220	298372	301281	Protein kinase		4672,4674,5524,6468	515
CDS	sce0224	306871	311031	Protein kinase		4674,5524,6468,4672	515
CDS	sce0230	319491	322157	WD-repeat protein			0
CDS	sce0284	405207	403381	Protein kinase		4672,4674,5524,6468	515
CDS	sce0312	441815	438678	Protein kinase		4672,4674,5524,6468	515
CDS	sce0336	475185	474094	Cytochrome c551 peroxidase precursor	ccpR	6118	1858
CDS	sce0344	483063	488123	Protein kinase		4672,4674,5524,6468	515
CDS	sce0350	505580	507451	Two-component sensor histidine kinase		7165,16301	642
CDS	sce0353	511253	512947	Protein kinase		4672,4674,5524,6468	515
CDS	sce0359	519682	521313	Protein kinase		4672,4674,5524,6468	515
CDS	sce0363	526688	528289	Protein kinase		4672,4674,5524,6468	515
CDS	sce0385	559173	557569	Two-component sensor histidine kinase		7165,16301	642
CDS	sce0401	580302	578491	Protein kinase		4672,4674,5524,6468	515
CDS	sce0419	608334	607066	Protein kinase		4672,4674,5524,6468	515
CDS	sce0428	618706	620928	Histidine kinase		7165,16301	642
CDS	sce0431	627196	623237	Protein kinase		4672,4674,5524,6468	515
CDS	sce0469	666769	667917	Protein kinase		4674,5524,6468,4672	515
CDS	sce0487	690730	692436	Protein kinase		4674,5524,6468,4672	515
CDS	sce0516	731757	733448	Two-component sensor histidine kinase		7165,16301	642
CDS	sce0531	753843	757301	Two-component hybrid sensor and regulator			642
CDS	sce0538	766404	769832	Protein kinase		4672,5524,6468,4674	515
CDS	sce0569	816217	818097	Protein kinase		4672,4674,5524,6468	515
CDS	sce0589	842203	844338	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce0619	886016	887482	Protein kinase		4672,4674,5524,6468	515
CDS	sce0624	893796	891040	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce0631	898829	900031	Protein kinase		4672,4674,5524,6468	515
CDS	sce0632	900031	902670	Protein kinase		4672,4674,5524,6468	515
CDS	sce0682	968480	971065	Protein kinase		4672,4674,5524,6468	515
CDS	sce0687	978859	974945	Protein kinase		4672,4674,5524,6468	515
CDS	sce0705	1005544	1004888	Anti-anti sigma factor protein			1366
CDS	sce0713	1012567	1016490	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce0723	1024469	1026379	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce0737	1040791	1041564	Anti-anti sigma factor protein			1366
CDS	sce0788	1104975	1109069	Ser/Thr protein kinase with adenylate/guanylate cyclase associated		4672,4674,5524,6468	515
CDS	sce0793	1115783	1114170	Two-component hisidine kinase		7165,16301	642
CDS	sce0794	1117870	1115909	Protein kinase		4672,4674,5524,6468	515
CDS	sce0817	1149891	1147312	Two-component hybrid histidine kinase		7165,16301	642

CDS	sce0827	1174959	1176353	Protein kinase		4672,4674,5524,6468	515
CDS	sce0828	1176390	1177547	Protein kinase		4672,4674,5524,6468	515
CDS	sce0848	1202204	1197987	Protein kinase		4672,4674,5524,6468	515
CDS	sce0850	1204741	1203224	Protein kinase		4672,4674,5524,6468	515
CDS	sce0855	1210649	1213477	Protein kinase		4672,4674,5524,6468	515
CDS	sce0919	1304685	1297507			6807	0
CDS	sce0921	1308788	1306224	Protein kinase		4672,4674,5524,6468	515
CDS	sce0929	1317084	1319423	Two-component hybrid sensor and regulator		7165,16301	2202
CDS	sce0932	1321611	1322903	Two-component sensor histidine kinase		7165,16301	642
CDS	sce0933	1323113	1324864	Protein kinase		4672,4674,5524,6468	515
CDS	sce0944	1339002	1337665	Protein kinase		4672,4674,5524,6468	515
CDS	sce0962	1362302	1364260	Two-component sensor histidine kinase		7165,16301	642
CDS	sce1013	1432746	1430947	Protein kinase		4672,4674,5524,6468	515
CDS	sce1019	1439405	1440859	Protein kinase		4672,4674,5524,6468	515
CDS	sce1026	1451821	1450313	Protein kinase		4672,4674,5524,6468	515
CDS	sce1043	1474160	1472679	Protein kinase		4672,4674,5524,6468	515
CDS	sce1066	1501380	1503665	Hypothetical protein			2319
CDS	sce1089	1528125	1529729	Protein kinase		4672,4674,5524,6468	515
CDS	sce1137	1586963	1588372	Two-component sensor histidine kinase		7165,16301	642
CDS	sce1173	1625051	1626700	Histidine kinase		7165,16301	642
CDS	sce1189	1648300	1650315	Two-component histidine kinase		7165,16301	642
CDS	sce1207	1670307	1669354	Protein kinase		4672,4674,5524,6468	515
CDS	sce1256	1742443	1737362	Protein kinase		4672,4674,5524,6468	515
CDS	sce1257	1742853	1743983	Protein kinase		4672,4674,5524,6468	515
CDS	sce1260	1746009	1748150	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce1263	1752547	1749944	Conserved hypothetical protein			2203
CDS	sce1275	1767296	1769323	Protein kinase		4672,4674,5524,6468	515
CDS	sce1296	1792509	1791511	Two-component sensor histidine kinase		7165,16301	642
CDS	sce1305	1804625	1803738	Protein kinase		4672,4674,5524,6468	515
CDS	sce1317	1818247	1819149	Putative positive regulator of sigma-B		4871,7165	2202
CDS	sce1346	1853124	1855973	Hybrid histidine kinase		7165,16301	642
CDS	sce1355	1868760	1871492	Sensor for high-affinity potassium transport system	kdpD	7165,16301	2205
CDS	sce1380	1903312	1901663	Protein kinase		4672,4674,5524,6468	515
CDS	sce1383	1905179	1907011	Two-component sensor histidine kinase		7165,16301	642
CDS	sce1401	1928148	1929404	Anti-anti-sigma factor protein		4871,7165	1366
CDS	sce1403	1930862	1932070	Anti-anti-sigma factor protein		4871,7165	1366
CDS	sce1408	1936949	1935489	Protein kinase		4672,4674,5524,6468	515
CDS	sce1474	2023594	2022341	Two-component sensor histidine kinase		7165,16301	642
CDS	sce1494	2046835	2040881	Protein kinase		4672,4674,5524,6468	515
CDS	sce1501	2059739	2057952	Putative adenylate/guanylate cyclase		4383,7242	2114
CDS	sce1504	2064088	2065599	Protein kinase		4674,5524,6468,4672	515
CDS	sce1552	2114658	2118560	Protein kinase		4672,4674,5524,6468	515
CDS	sce1587	2164683	2168420	Protein kinase		4672,4674,5524,6468	515
CDS	sce1598	2182589	2183515	Chemotaxis protein methyltransferase CheR	cheR1	6935,8757	1352
CDS	sce1602	2188229	2190742	Protein kinase		4674,5524,6468,4672	515
CDS	sce1603	2190997	2192673	Protein kinase		4672,4674,5524,6468	515
CDS	sce1604	2192679	2194703	Protein kinase		4674,5524,6468,4672	515
CDS	sce1609	2203385	2201781	Protein kinase		4672,4674,5524,6468	515
CDS	sce1617	2216105	2220103	Protein kinase		4672,4674,5524,6468	515
CDS	sce1654	2266447	2268597	Hypothetical membrane-associated protein			0
CDS	sce1716	2335606	2336568	Protein kinase		4672,4674,5524,6468	515
CDS	sce1725	2347458	2348867	Putative adenylate cyclase		4383,7242	2114
CDS	sce1730	2355830	2352735	Conserved hypothetical protein		6935,8757	1352
CDS	sce1742	2371846	2370197	Hybrid histidine kinase		7165,16301	642
CDS	sce1782	2419163	2420521	Positive regulator of sigma-B	rsbR1		2203
CDS	sce1794	2433017	2431572	Protein kinase		4672,4674,5524,6468	515
CDS	sce1800	2440308	2441822	Sensory box hybrid histidine kinase		7165,16301	642
CDS	sce1846	2499163	2503029	Protein kinase		4672,4674,5524,6468	515
CDS	sce1848	2507834	2510344	Protein kinase		4672,5524,6468,4674	515
CDS	sce1851	2514470	2512770	Protein kinase		4672,4674,5524,6468	515
CDS	sce1859	2526222	2520670	Protein kinase		4672,4674,5524,6468	515

CDS	sce1938	2629593	2627908	Two-component response regulator			784
CDS	sce1939	2632479	2629660	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce1949	2644574	2647816	Protein kinase		4672,4674,5524,6468	515
CDS	sce2026	2749040	2746704	Protein kinase		4672,4674,5524,6468	515
CDS	sce2056	2789247	2787817	Protein kinase		4672,4674,5524,6468	515
CDS	sce2235	3010906	3012954	Protein kinase		4672,4674,5524,6468	515
CDS	sce2236	3013025	3015148	Putative two-component system sensor kinase		7165,16301	642
CDS	sce2261	3048399	3047251	Sensor histidine kinase		7165,16301	642
CDS	sce2291	3092997	3091192	Protein kinase		4672,4674,5524,6468	515
CDS	sce2301	3103621	3102725	Conserved hypothetical protein		4871,7165	2202
CDS	sce2312	3115952	3114708	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce2313	3117564	3116062	Protein kinase		4672,4674,5524,6468	515
CDS	sce2326	3138239	3134217	Protein kinase		4672,4674,5524,6468	515
CDS	sce2353	3165579	3166454	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce2379	3196000	3197304	Protein kinase		4672,4674,5524,6468	515
CDS	sce2435	3278152	3277127	Putative sensor kinase		7165,16301	642
CDS	sce2461	3316354	3318570	Two-component system sensor protein		7165,16301	642
CDS	sce2466	3325600	3323834	Protein kinase		4672,4674,5524,6468	515
CDS	sce2470	3331383	3328543	Protein kinase		4672,4674,5524,6468	515
CDS	sce2506	3380039	3378489	Sensor histidine kinase		7165,16301	2202
CDS	sce2554	3448965	3447589	Two-component system sensor protein		7165,16301	642
CDS	sce2574	3474827	3472749	Protein kinase		4672,4674,5524,6468	515
CDS	sce2653	3586848	3590003	Two-component system sensor histidine kinase/response regulator, hybrid		7165,16301	642
CDS	sce2655	3593196	3590539	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce2661	3601370	3602200	Chemotaxis protein methyltransferase 2	cheR3	6935,8757	1352
CDS	sce2676	3624033	3629474	Protein kinase		4672,4674,5524,6468	515
CDS	sce2678	3631900	3629987	Two-component histidine kinase		7165,16301	2202
CDS	sce2679	3632086	3634188	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce2683	3640849	3640136	Hypothetical protein		5554	1262
CDS	sce2686	3650953	3644036	Hypothetical WD-repeat protein			2319
CDS	sce2695	3663598	3664530	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce2714	3683120	3682257	Positive regulator of sigma-B		4871,7165	2202
CDS	sce2727	3700026	3703034	Two-component system sensor protein		5215,6810,16020	591
CDS	sce2730	3711849	3707518	Protein kinase		4672,4674,5524,6468	515
CDS	sce2746	3739094	3744235	Protein kinase		4674,5524,6468,4672	515
CDS	sce2753	3755822	3751338	Protein kinase		4672,5524,6468,4674	515
CDS	sce2761	3763394	3765778	Two-component sensor histidine kinase		7165,16301	642
CDS	sce2767	3773346	3774239	Protein kinase		4674,5524,6468,4672	515
CDS	sce2798	3818343	3817147	Protein kinase		4672,4674,5524,6468	515
CDS	sce2815	3845148	3843616	Protein kinase		4672,4674,5524,6468	515
CDS	sce2822	3851224	3852177	Sensory transduction histidine kinase		7165,16301	642
CDS	sce2825	3853634	3855250	Protein kinase		4672,4674,5524,6468	515
CDS	sce2866	3909758	3911218	Protein kinase		4672,4674,5524,6468	515
CDS	sce2922	3995922	3997556	Protein kinase		4674,5524,6468,4672	515
CDS	sce2923	4001495	3997605	Protein kinase		4674,5524,6468,4672	515
CDS	sce2934	4018076	4021663	Protein kinase		4672,4674,5524,6468	515
CDS	sce2935	4023681	4021675	Positive regulator of sigma-B		4871,7165	2202
CDS	sce2937	4028627	4025082	Protein kinase		4672,4674,5524,6468	515
CDS	sce2947	4037677	4036181	Phosphate sensory box histidine kinase PhoR	phoR1	7165,16301	642
CDS	sce2953	4043147	4042155	Histidine kinase		7165,16301	642
CDS	sce2960	4053280	4056114	Protein kinase		4672,4674,5524,6468	515
CDS	sce2975	4075839	4077338	Putative membrane protein			0
CDS	sce3002	4115681	4117402	Protein kinase		4672,4674,5524,6468	515
CDS	sce3021	4140850	4143012	Protein kinase		4672,4674,5524,6468	515
CDS	sce3028	4150659	4148419	Protein kinase		4672,4674,5524,6468	515
CDS	sce3063	4196773	4195220	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce3080	4220513	4218603	Two-component histidine kinase	phoR2	7165,16301	642
CDS	sce3102	4245803	4244784	ABC-type sugar transport system, periplasmic component			1879

CDS	sce3108	4253421	4253837	Hypothetical protein		0
CDS	sce3109	4254022	4258065	Protein kinase	4672,4674,5524,6468	515
CDS	sce3119	4283329	4281737	Hypothetical protein		2319
CDS	sce3123	4291107	4286980	Protein kinase	4672,4674,5524,6468	515
CDS	sce3165	4349127	4351049	Conserved hypothetical protein		2203
CDS	sce3210	4482587	4487053	Hypothetical WD-repeat protein all2124.		2319
CDS	sce3211	4488579	4487533	Conserved hypothetical protein	6118	1858
CDS	sce3221	4503079	4507587	Protein kinase	4674,5524,6468,4672	515
CDS	sce3229	4515935	4519330	Protein kinase	4674,5524,6468,4672	515
CDS	sce3265	4574946	4573435	Sensor histidine kinase	7165,16301	642
CDS	sce3347	4679597	4683520	Protein kinase	4672,4674,5524,6468	515
CDS	sce3380	4723683	4722709	Anti-anti sigma factor protein	4871,7165	1366
CDS	sce3386	4729784	4732738	Protein kinase	4674,5524,6468,4672	515
CDS	sce3393	4743961	4745586	Protein kinase	4672,4674,5524,6468	515
CDS	sce3423	4778457	4776664	Sensory box histidine kinase similar to PhoR	7165,16301	5002
CDS	sce3428	4784714	4786243	Protein kinase	4672,4674,5524,6468	515
CDS	sce3469	4840282	4844541	Protein kinase	4672,4674,5524,6468	515
CDS	sce3490	4869400	4871292	Protein kinase	4672,4674,5524,6468	515
CDS	sce3493	4873844	4878322	Protein kinase	4672,4674,5524,6468	515
CDS	sce3496	4879831	4880439	Hypothetical protein predicted by Glimmer/Critica		0
CDS	sce3497	4880639	4886734	Protein kinase	4672,4674,5524,6468	515
CDS	sce3502	4890963	4891883	Truncated anti-anti sigma factor protein	4871,7165	1366
CDS	sce3504	4892256	4893929	Anti-anti sigma factor protein	4871,7165	1366
CDS	sce3507	4900639	4897124	Two-component hybrid sensor and regulator	7165,16301	642
CDS	sce3538	4944783	4946432	Protein kinase	4672,4674,5524,6468	515
CDS	sce3562	4978448	4980256	Protein kinase	4672,4674,5524,6468	515
CDS	sce3589	5021582	5020146	Protein kinase	4672,4674,5524,6468	515
CDS	sce3598	5036183	5034546	Sensory box histidine kinase/response regulator hybrid	7165,16301	642
CDS	sce3613	5056200	5054851	Positive regulator of sigma-B activity	rsbR2	1366
CDS	sce3621	5066873	5068429	Protein kinase	4672,4674,5524,6468	515
CDS	sce3623	5071499	5076667	Conserved hypothetical protein		2319
CDS	sce3630	5080728	5084609	WD-repeat protein		2319
CDS	sce3632	5090549	5086644	Protein kinase	4672,4674,5524,6468	515
CDS	sce3649	5113961	5110872	Two-component response regulator		745
CDS	sce3650	5115543	5114143	Protein kinase	4672,4674,5524,6468	515
CDS	sce3671	5141338	5139710	Protein kinase	4672,4674,5524,6468	515
CDS	sce3683	5151619	5153022	Protein kinase	4672,4674,5524,6468	515
CDS	sce3704	5176668	5175352	Two-component hybrid sensor and regulator	7165,16301	642
CDS	sce3720	5196420	5194879	Protein kinase	4672,4674,5524,6468	515
CDS	sce3737	5219369	5217714	Protein kinase	4672,4674,5524,6468	515
CDS	sce3766	5246647	5248290	Protein kinase	4672,4674,5524,6468	515
CDS	sce3781	5269762	5268491	Protein kinase	4672,4674,5524,6468	515
CDS	sce3799	5291672	5293063	Protein kinase	4672,4674,5524,6468	515
CDS	sce3803	5299449	5296579	Putative ATP/GTP-binding protein		457
CDS	sce3804	5300658	5299597	Putative ATP/GTP-binding protein		0
CDS	sce3805	5302199	5300700	Conserved hypothetical protein	3677,5677,6342	0
CDS	sce3806	5302081	5303367	Conserved hypothetical protein	5554	1262
CDS	sce3829	5328374	5326809	Protein kinase	4672,4674,5524,6468	515
CDS	sce3850	5352837	5357309	Protein kinase	4674,5524,6468,4672	515
CDS	sce3907	5433994	5435676	Protein kinase	4672,4674,5524,6468	515
CDS	sce3940	5479507	5477309	Sensory box histidine kinase/response regulator hybrid	7165,16301	642
CDS	sce3942	5482326	5483828	Protein kinase	4672,4674,5524,6468	515
CDS	sce3944	5485187	5487043	Protein kinase	4672,4674,5524,6468	515
CDS	sce3947	5490175	5488745	Protein kinase	4672,4674,5524,6468	515
CDS	sce3955	5499745	5497889	Protein kinase	4672,4674,5524,6468	515
CDS	sce3985	5545936	5544626	Positive regulator of sigma-B activity	4871,7165	2202
CDS	sce3988	5550275	5551282	Two-component response regulator		745
CDS	sce3989	5551347	5557358	Protein kinase	4672,4674,5524,6468	515
CDS	sce3997	5565649	5564186	Protein kinase	4672,4674,5524,6468	515
CDS	sce3998	5567211	5568965	Response regulator containing a guanylate cyclase domain	4383,7242	2114

CDS	sce4010	5582403	5583818	Protein kinase		4672,4674,5524,6468	515
CDS	sce4022	5601958	5600726	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce4025	5604688	5606043	Two-component sensor histidine kinase		7165,16301	642
CDS	sce4026	5606040	5607230	Sensor histidine kinase/response regulator hybrid		7165,16301	642
CDS	sce4030	5614201	5613179	Ribose transporter, periplasmic binding protein	rbsB1		1879
CDS	sce4031	5619462	5614381	Protein kinase		4672,4674,5524,6468	515
CDS	sce4041	5631325	5632266	Hypothetical protein		5554	0
CDS	sce4054	5646417	5648240	Protein kinase		4674,5524,6468,4672	515
CDS	sce4074	5683600	5681915	Protein kinase		4672,4674,5524,6468	515
CDS	sce4174	5899317	5897938	Protein kinase		4672,4674,5524,6468	515
CDS	sce4176	5905114	5901008	Protein kinase		4672,4674,5524,6468	515
CDS	sce4183	5916934	5915351	Protein kinase		4672,4674,5524,6468	515
CDS	sce4190	5929315	5925233	Sensor kinase/response regulator hybrid		6935,8757	1352
CDS	sce4192	5930964	5932271	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce4202	5945451	5948183	Protein kinase		4672,4674,5524,6468	515
CDS	sce4228	5982593	5981715	Protein kinase		4672,4674,5524,6468	515
CDS	sce4263	6031539	6030037	Protein kinase		4672,4674,5524,6468	515
CDS	sce4309	6093723	6091864	Hybrid sensory histidine kinase		7165,16301	642
CDS	sce4331	6116073	6117500	Protein kinase		4672,4674,5524,6468	515
CDS	sce4338	6123063	6124331	Protein kinase		4672,4674,5524,6468	515
CDS	sce4358	6157894	6161700	Protein kinase	,	4672,4674,5524,6468	515
CDS	sce4365	6170646	6173531	Hybrid histidine kinase		7165,16301	642
CDS	sce4368	6176665	6174344	Protein kinase		4672,4674,5524,6468	515
CDS	sce4426	6251127	6252863	Protein kinase		4672,4674,5524,6468	515
CDS	sce4487	6330077	6328521	Protein kinase		4672,4674,5524,6468	515
CDS	sce4512	6365558	6367048	Protein kinase		4672,4674,5524,6468	515
CDS	sce4534	6391177	6392883	Protein kinase		4672,4674,5524,6468	515
CDS	sce4539	6402665	6400752	Protein kinase		4672,4674,5524,6468	515
CDS	sce4543	6407740	6409392	Protein kinase		4672,4674,5524,6468	515
CDS	sce4548	6415986	6413767	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce4551	6424544	6419955	Protein kinase		4672,4674,5524,6468	515
CDS	sce4552	6429605	6425007	Protein kinase		4672,4674,5524,6468	515
CDS	sce4557	6437993	6439243	Protein kinase		4672,4674,5524,6468	515
CDS	sce4586	6479736	6478222	Protein kinase		4674,5524,6468,4672	515
CDS	sce4587	6479765	6483778	Protein kinase		4672,4674,5525,6468	515
CDS	sce4609	6515378	6516847	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce4613	6522256	6521159	Protein kinase		4674,5524,6468,4672	515
CDS	sce4614	6525063	6522301	Protein kinase		4674,5524,6468,4672	515
CDS	sce4615	6525243	6526769	Protein kinase		4674,5524,6468,4672	515
CDS	sce4634	6549492	6550682	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce4674	6602523	6598636	Protein kinase		4674,5524,6468,4672	515
CDS	sce4677	6604625	6608137	Protein kinase		4674,5524,6468,4672	515
CDS	sce4690	6627956	6625530	Putative sugar regulator			1879
CDS	sce4722	6665413	6664454	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce4767	6714171	6712945	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce4827	6781407	6782762	Signal transduction histidine kinase		7165,16301	642
CDS	sce4831	6789279	6785422	Protein kinase		4674,5524,6468,4672	515
CDS	sce4833	6789990	6790889	Protein kinase		4674,5524,6468,4672	515
CDS	sce4877	6847918	6846368	Two-component histidine kinase		7165,16301	642
CDS	sce4891	6869119	6870711	Protein kinase		4674,5524,6468,4672	515
CDS	sce4899	6879296	6881089	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce4929	6927798	6925879	Hypothetical protein			0
CDS	sce4952	6970249	6968522	Protein kinase		4674,5524,6468,4672	515
CDS	sce4956	6972114	6973244	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce4957	6973234	6975243	Two-component hybrid histidine kinase	torS	7165,16301	642
CDS	sce5013	7039662	7038103	Protein kinase		4674,5524,6468,4672	515
CDS	sce5052	7091205	7089565	Protein kinase		4674,5524,6468,4672	515
CDS	sce5082	7133838	7132294	Protein kinase		4674,5524,6468,4672	515
CDS	sce5100	7159051	7161702	Two-component hybrid histidine kinase		7165,16301	642
CDS	sce5107	7168401	7173431	Two-component hybrid sensor and regulator		7165,16301	2770
CDS	sce5109	7174406	7176310	Protein kinase		4674,5524,6468,4672	515
CDS	sce5120	7190060	7188576	Protein kinase		4674,5524,6468,4672	515
CDS	sce5129	7206180	7202284	Protein kinase		4674,5524,6468,4672	515
CDS	sce5130	7209840	7206412	WD-repeat protein			2319

CDS	sce5133	7214439	7210570	Protein kinase	4674,5524,6468,4672	515
CDS	sce5138	7222088	7223557	Protein kinase	4674,5524,6468,4672	515
CDS	sce5139	7223666	7224910	Protein kinase	4674,5524,6468,4672	515
CDS	sce5140	7226698	7224923	Protein kinase	4674,5524,6468,4672	515
CDS	sce5160	7246714	7247574	Anti-anti sigma factor protein	4871,7165	1366
CDS	sce5165	7250584	7254528	Protein kinase	4674,5524,6468,4672	515
CDS	sce5167	7256846	7255311	Sensor histidine kinase	7165,16301	642
CDS	sce5173	7265094	7269323	Protein kinase	4674,5524,6468,4672	515
CDS	sce5180	7279899	7279102	Two-component sensor histidine kinase	7165,16301	642
CDS	sce5207	7317164	7312581	Protein kinase	4672,5524,6468,4674	515
CDS	sce5209	7318206	7323341	Protein kinase	4674,5524,6468,4672	515
CDS	sce5225	7350490	7346996	Protein kinase	4672,5524,6468,4674	515
CDS	sce5237	7368927	7367455	Protein kinase	4674,5524,6468,4672	515
CDS	sce5294	7448136	7447210	Anti-anti sigma factor protein		1366
CDS	sce5311	7466589	7467821	Anti-anti sigma factor protein	4871,7165	1366
CDS	sce5315	7470508	7472400	Protein kinase	4674,5524,6468,4672	515
CDS	sce5317	7477477	7473584	Protein kinase	4674,5524,6468,4672	515
CDS	sce5318	7477684	7479243	Protein kinase	4674,4672,5524,6468	515
CDS	sce5338	7511730	7507723	Protein kinase	4674,5524,6468,4672	515
CDS	sce5340	7512811	7514217	Protein kinase	4674,4672,5524,6468	515
CDS	sce5356	7534221	7536299	Two-componenthybrid sensor histidine kinase	7165,16301	642
CDS	sce5427	7623015	7620592	Putative sugar regulator		1879
CDS	sce5443	7642092	7648151	Protein kinase	4674,5524,6468,4672	515
CDS	sce5444	7648278	7654319	Protein kinase	6468,16301,4674,5524,46	515
CDS	sce5445	7654534	7660566	Protein kinase	4674,5524,6468,4672	515
CDS	sce5446	7660714	7666752	Protein kinase	4674,5524,6468,4672	515
CDS	sce5457	7677969	7684025	Protein kinase	4674,5524,6468,4672	515
CDS	sce5462	7692926	7691820	Protein kinase	4674,5524,6468,4672	515
CDS	sce5470	7709478	7707916	Protein kinase	4672,4674,5524,6468	515
CDS	sce5487	7729580	7731364	Protein kinase	4674,5524,6468,4672	515
CDS	sce5502	7754967	7752883	Protein kinase	4674,5524,6468,4672	515
CDS	sce5516	7771736	7773076	Anti-anti sigma factor protein	4871,7165	1366
CDS	sce5533	7795568	7791537	Protein kinase	4674,5524,6468,4672	515
CDS	sce5534	7795660	7797174	Protein kinase	4674,4672,5524,6468	515
CDS	sce5570	7844757	7843690	Response regulator with anti-sigma factor antagonist output domain		784
CDS	sce5571	7847715	7844848	Two-component hybrid sensor and regulator	7165,16301	642
CDS	sce5574	7850271	7851920	Protein kinase	4674,5524,6468,4672	515
CDS	sce5588	7867496	7869109	Protein kinase	4672,5524,6468,4674	515
CDS	sce5592	7873738	7875360	Protein kinase	4674,5524,6468,4672	515
CDS	sce5598	7884559	7882343	Protein kinase	4674,5524,6468,4672	515
CDS	sce5636	7932376	7933980	Protein kinase	4674,5524,6468,4672	515
CDS	sce5691	8006652	8009249	Protein kinase	4674,5524,6468,4672	515
CDS	sce5749	8082723	8084696	Protein kinase	4674,5524,6468,4672	515
CDS	sce5772	8110510	8109452	Protein kinase	4674,5524,6468,4672	515
CDS	sce5774	8113535	8111775	Two-component sensor histidine kinase	7165,16301	642
CDS	sce5780	8121222	8118352	Hypothetical protein		457
CDS	sce5807	8155126	8156928	Protein kinase	4674,5524,6468,4672	515
CDS	sce5822	8177638	8176415	Methylamine utilization protein	6118	1858
CDS	sce5827	8184648	8182846	Protein kinase	4674,5524,6468,4672	515
CDS	sce5834	8192454	8194406	Protein kinase	4672,5524,6468,4674	515
CDS	sce5838	8198231	8203681	Protein kinase	4674,5524,6468,4672	515
CDS	sce5842	8208568	8206493	Protein kinase	4674,5524,6468,4672	515
CDS	sce5958	8366032	8364728	Protein kinase	4672,5524,6468,4674	515
CDS	sce5965	8372963	8374171	Protein kinase	4674,5524,6468,4672	515
CDS	sce5976	8385224	8382648	Putative sugar regulator		1879
CDS	sce5991	8398933	8403480	Protein kinase	4674,5524,6468,4672	515
CDS	sce6003	8415725	8419675	Protein kinase	4674,4672,6468,5524	515
CDS	sce6012	8430037	8431656	Two-component sensor histidine kinase	7165,16301	642
CDS	sce6018	8438161	8439249	Protein kinase	4674,5524,6468,4672	515
CDS	sce6025	8447271	8448788	Protein kinase	4674,5524,6468,4672	515
CDS	sce6037	8464867	8466477	Protein kinase	4674,5524,6468,4672	515
CDS	sce6042	8470844	8473396	Two-component sensor histidine kinase	7165,16301	642
CDS	sce6047	8483402	8481855	Protein kinase	4674,5524,6468,4672	515
CDS	sce6068	8500158	8502359	Protein kinase	4674,5524,6468,4672	515
CDS	sce6210	8683476	8685983	Protein kinase	4674,5524,6468,4672	515
CDS	sce6213	8687772	8688797	DUF323 hypothetical protein	5554	1262
CDS	sce6217	8697867	8698787	Hypothetical protein		0

CDS	sce6249	8734420	8732936	Sensor histidine kinase		7165,16301	642
CDS	sce6257	8745743	8743173	Protein kinase		4674,5524,6468,4672	515
CDS	sce6316	8807119	8806634	Putative exported alanine-rich protein			0
CDS	sce6317	8809065	8807083	Protein kinase		4672,5524,6468,4674	515
CDS	sce6336	8831215	8832675	Protein kinase		4674,5524,6468,4672	515
CDS	sce6351	8855806	8850779	Protein kinase		4674,5524,6468,4672	515
CDS	sce6354	8858779	8860290	Two-component system histidine kinase		7165,16301	642
CDS	sce6392	8916532	8920455	Protein kinase		4672,5524,6468,4674	515
CDS	sce6414	8950103	8951689	Protein kinase		4674,5524,6468,4672	515
CDS	sce6427	8963577	8966129	Protein kinase		4674,5524,6468,4672	515
CDS	sce6492	9047713	9049470	Protein kinase		4674,4672,5524,6468	515
CDS	sce6500	9057358	9058767	Protein kinase		4674,5524,6468,4672	515
CDS	sce6655	9258270	9256357	Protein kinase		4674,5524,6468,4672	515
CDS	sce6666	9276505	9273671	Protein kinase		4674,5524,6468,4672	515
CDS	sce6675	9287686	9284900	Protein kinase		4674,5524,6468,4672	515
CDS	sce6738	9392078	9393541	Protein kinase		4674,5524,6468,4672	515
CDS	sce6743	9397945	9401508	Protein kinase		4674,5528,6468,4672	515
CDS	sce6764	9432885	9434294	Anti-anti sigma factor protein			1366
CDS	sce6825	9523190	9518094	Protein kinase		4674,5524,6468,4672	515
CDS	sce6826	9525495	9523351	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce6827	9531713	9525492	Protein kinase		4674,5524,6468,4672	515
CDS	sce6840	9548992	9545117	Protein kinase		4674,5528,6468,4672	515
CDS	sce6844	9556972	9551822	Protein kinase		4674,5528,6468,4672	515
CDS	sce6858	9584425	9581711	Transcriptional regulator (LuxR/UhpA family)			5340
CDS	sce6896	9625919	9624174	Protein kinase		4672,5524,6468,4674	515
CDS	sce6904	9636779	9633549	Hypothetical protein			0
CDS	sce6924	9662943	9661330	Protein kinase		4674,5524,6468,4672	515
CDS	sce6952	9699266	9696867	Protein kinase		4674,5524,6468,4672	515
CDS	sce6956	9702159	9704066	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce6964	9711282	9712757	Sensor histidine kinase		7165,16301	642
CDS	sce6986	9756070	9757815	Hypothetical protein predicted by Glimmer/Critica		4383,7242	840
CDS	sce6991	9762975	9765809	Protein kinase		4674,5524,6468,4672	515
CDS	sce7016	9797669	9798952	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce7050	9843983	9842562	Protein kinase		4674,5524,6468,4672	515
CDS	sce7107	9907853	9906333	Sensor histidine kinase		7165,16301	642
CDS	sce7114	9917644	9913643	Protein kinase		4674,5524,6468,4672	515
CDS	sce7120	9927190	9923459	WD-repeat protein			2319
CDS	sce7126	9938513	9935040	Protein kinase		4674,4672,5524,6468	515
CDS	sce7129	9942335	9941460	Protein kinase		4674,4672,5524,6468	515
CDS	sce7136	9950842	9949697	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce7147	9964358	9962589	Protein kinase		4674,5524,6468,4672	515
CDS	sce7159	9984567	9981799	Two-component hybrid sensor and regulator		7165,16301	642
CDS	sce7194	10051793	10052761	Protein kinase		4672,5524,6468,4674	515
CDS	sce7195	10052847	10054538	Protein kinase		4672,5524,6468,4674	515
CDS	sce7209	10069615	10068356	Protein kinase		4674,4672,5524,6468	515
CDS	sce7212	10072468	10075197	Protein kinase		4674,4672,5524,6468	515
CDS	sce7214	10075871	10077433	Two-component sensor kinase		7165,16301	642
CDS	sce7218	10082578	10083777	Sensor histidine kinase		7165,16301	642
CDS	sce7262	10137232	10134485	Protein kinase		4672,5524,6468,4674	515
CDS	sce7295	10181967	10179691	Protein kinase		4674,5524,6468,4672	515
CDS	sce7356	10248264	10247029	Anti-anti sigma factor protein		4871,7165	1366
CDS	sce7369	10264145	10262895	Protein kinase		4674,5524,6468,4672	515
CDS	sce7396	10296089	10294743	Protein kinase		4674,5524,6468,4672	515
CDS	sce7406	10310462	10308702	Putative histidine kinase		7165,16301	5000
CDS	sce7428	10346995	10349160	Protein kinase		4674,5524,6468,4672	515
CDS	sce7433	10358566	10355738	Protein kinase		4674,5524,6468,4672	515
CDS	sce7451	10384204	10380050	Protein kinase		4674,5524,6468,4672	515
CDS	sce7468	10410010	10411449	Anti-anti simga factor protein		4871,7165	1366
CDS	sce7602	10581029	10579623	Protein kinase		4674,5524,6468,4672	515
CDS	sce7603	10582018	10581026	Protein kinase		4674,5524,6468,4672	515
CDS	sce7616	10601614	10599635	Adenylate cyclase		4383,7242	2114
CDS	sce7627	10616181	10617422	Protein kinase		4674,5524,6468,4672	515
CDS	sce7661	10660599	10662704	Protein kinase		4674,5524,6468,4672	515
CDS	sce7688	10712147	10706727	Protein kinase		4674,5524,6468,4672	515
CDS	sce7701	10725910	10731426	Protein kinase		4674,5524,6468,4672	515
CDS	sce7721	10752157	10753896	Protein kinase		4674,5524,6468,4672	515
CDS	sce7776	10829269	10826510	Two-component hybrid histidine kinase		7165,16301	642
CDS	sce7781	10836586	10840119	WD-40 repeat protein	hat		2319

CDS	sce7782	10840418	10844116	Protein kinase	4674,5524,6468,4672	515
CDS	sce7800	10866526	10868055	Sensor histidine kinase	7165,16301	642
CDS	sce7806	10875915	10873726	Two-component hybrid sensor histidine kinase	7165,16301	784
CDS	sce7807	10880266	10875932	Two-component hybrid sensor and regulator	7165,16301	2770
CDS	sce7809	10882435	10880816	Sensor histidine kinase	7165,16301	642
CDS	sce7821	10892735	10894339	Positive regulator of sigma-B	4871,7165	1366
CDS	sce7854	10950033	10953866	Protein kinase	4674,5524,6468,4672	515
CDS	sce7890	10996669	10998216	Protein kinase	4674,5524,6468,4672	515
CDS	sce7903	11017714	11020218	Hypothetical protein		0
CDS	sce7914	11033432	11034760	Protein kinase	4674,5524,6468,4672	515
CDS	sce7925	11046630	11048303	Protein kinase	4674,5524,6468,4672	515
CDS	sce7928	11052049	11053614	Protein kinase	4672,4674,5524,6468	515
CDS	sce7929	11055360	11053684	Sensor histidine kinase	7165,16301	642
CDS	sce8008	11138584	11140650	Protein kinase	4672,5524,6468,4674	515
CDS	sce8018	11156147	11158936	Protein kinase	4674,5524,6468,4672	515
CDS	sce8069	11223311	11221389	Putative membrane protein		0
CDS	sce8080	11243413	11241809	Protein kinase	4672,5524,6468,4674	515
CDS	sce8086	11250649	11253189	Two-component sensor kinase	7165,16301	2202
CDS	sce8108	11280529	11279033	Sensor histidine kinase	7165,16301	642
CDS	sce8125	11301954	11304101	Two-component hybrid histidine kinase	7165,16301	642
CDS	sce8135	11317911	11315683	Two-component hybrid sensor kinase/response regulator	7165,16301	642
CDS	sce8163	11354922	11353624	Protein kinase	4674,5524,6468,4672	515
CDS	sce8282	11556265	11555030	Protein kinase	4674,5524,6468,4672	515
CDS	sce8391	11680540	11685819	WD-repeat protein		2319
CDS	sce8402	11699583	11701118	Sensor histidine kinase	7165,16301	642
CDS	sce8428	11735295	11738954	Conserved hypothetical protein		3287
CDS	sce8429	11739022	11742387	Protein kinase	4674,5524,6468,4672	515
CDS	sce8430	11742603	11744588	Protein kinase	4674,5524,6468,4672	515
CDS	sce8433	11747973	11746804	Two-component response regulator	4383,7242	784
CDS	sce8434	11749631	11747970	Two-component hybrid sensor and regulator	7165,16301	642
CDS	sce8463	11790599	11791981	Protein kinase	4674,5524,6468,4672	515
CDS	sce8495	11836199	11833440	Two-component hybrid sensor and regulator	7165,16301	2203
CDS	sce8510	11860584	11861792	Putative positive regulator of sigma-B		2202
CDS	sce8523	11877945	11881604	protein kinase	4674,5528,6468,4672	515
CDS	sce8553	11923060	11918096	Protein kinase	4674,5524,6468,4672	515
CDS	sce8555	11925831	11928371	Protein kinase	4674,5524,6468,4672	515
CDS	sce8644	12056537	12058180	Sensor histidine kinase	7165,16301	642
CDS	sce8649	12070451	12067398	Protein kinase	4674,5524,6468,4672	515
CDS	sce8650	12074760	12070888	Protein kinase	4672,5524,6468,4674	515
CDS	sce8695	12132343	12130373	Protein kinase	4674,5524,6468,4672	515
CDS	sce8713	12164435	12162798	Two-component hybrid sensor histidine kinase/response regulator	7165,16301	642
CDS	sce8715	12167766	12164923	Two-component hybrid sensor and regulator	7165,16301	642
CDS	sce8728	12180340	12184287	Protein kinase	4674,5524,6468,4672	515
CDS	sce8729	12188590	12184316	Protein kinase	4674,5524,6468,4672	515
CDS	sce8731	12189621	12191105	Protein kinase	4672,5524,6468,4674	515
CDS	sce8738	12204444	12200401	Protein kinase	4674,5524,6468,4672	515
CDS	sce8741	12208045	12209451	Putative membrane protein	3677,5677,6342	0
CDS	sce8784	12274577	12276142	Protein kinase	4674,5524,6468,4672	515
CDS	sce8787	12279689	12278346	Anti-anti sigma factor protein	4871,7165	1366
CDS	sce8798	12288167	12289747	Sensor histidine kinase	7165,16301	642
CDS	sce8828	12324899	12322980	Two-component hybrid sensor and regulator	7165,16301	642
CDS	sce8866	12358896	12364649	Conserved hypothetical protein		0
CDS	sce8885	12389729	12391681	Protein kinase	4674,5524,6468,4672	515
CDS	sce8887	12394572	12399920	Protein kinase	4674,5524,6468,4672	515
CDS	sce8908	12425154	12426491	Anti-anti sigma factor protein	4871,7165	1366
CDS	sce8916	12434644	12438603	Protein kinase	4674,5524,6468,4672	515
CDS	sce8979	12512966	12511965	Anti-anti sigma factor protein	4871,7165	1366
CDS	sce8990	12528999	12527044	Putative two-component sensor kinase	7165,16301	5000
CDS	sce9017	12558096	12562463	Protein kinase	4674,5524,6468,4672	515
CDS	sce9135	12725063	12719937	Protein kinase	4674,5524,6468,4672	515
CDS	sce9149	12741309	12740110	Protein kinase	4674,5524,6468,4672	515
CDS	sce9150	12741805	12743481	Protein kinase	4674,5524,6468,4672	515
CDS	sce9151	12743936	12747022	Guanylate cyclase	4383	2114

CDS	sce9161	12762753	12766583	Protein kinase		4674,5524,6468,4672	515
CDS	sce9168	12774628	12776034	Protein kinase		4674,5524,6468,4672	515
CDS	sce9197	12814240	12810353	Protein kinase		4674,5524,6468,4672	515
CDS	sce9205	12823539	12824624	Protein kinase		4674,5524,6468,4672	515
CDS	sce9207	12827887	12826046	Response regulator containing PAS and STAS domains			2203
CDS	sce9290	12926451	12927107	Conserved hypothetical protein		5554	1262
CDS	sce9291	12927295	12929082	Two-component sensor histidine kinase		7165,16301	642
CDS	sce9326	12972645	12971542	Protein kinase		4672,5524,6468,4674	515
CDS	sce9327	12974826	12972742	Protein kinase		4674,5524,6468,4672	515
CDS	sce9354	13011977	13010490	Protein kinase		4674,5524,6468,4672	515

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Fam: 2 No. of CDS: 5 Dom. COG: 443 counter: 5 / 5 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0003	7350	5488	DnaK protein	dnaK1		443
CDS	sce2420	3259504	3261333	Hsp70 heat shock protein			443
CDS	sce7333	10225620	10227626	Putative Heat shock protein Hsp70			443
CDS	sce7648	10643478	10646057	Hsp70 heat shock protein			443
CDS	sce9025	12571969	12570050	Chaperone protein dnaK	dnaK2		443

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Fam: 3 No. of CDS: 9 Dom. COG: 160 counter: 5 / 9 percentage: 55.56%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0005	8397	9659	Acetylornithine aminotransferase	argD	8483	4992
CDS	sce0693	988297	987014	Adenosylmethionine--8-amino-7-oxononanoate transaminase	bioA	4015,9102	161
CDS	sce3889	5414427	5415749	Glutamate-1-semialdehyde 2,1-aminomutase	mxcL	8483	1
CDS	sce6419	8957095	8955764	4-aminobutyrate transaminase	gabT1	8483	160
CDS	sce8254	11486098	11484644	Diaminobutyrate--2-oxoglutarate transaminase		8483,9058	160
CDS	sce8625	12028271	12026913	4-aminobutyrate transaminase	gabT2	8483	160
CDS	sce9167	12774260	12772947	Glutamate-1-semialdehyde 2,1-aminomutase	hemL	5737,6779	1
CDS	sce9190	12800357	12801817	Putative 4-aminobutyrate transaminase.			160
CDS	sce9194	12806218	12807624	4-aminobutyrate transaminase		8483	160

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Fam: 4 No. of CDS: 9 Dom. COG: 2217 counter: 4 / 9 percentage: 44.44%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0006	9661	12108	cation-translocating P-type ATPase		5524,1602	2217
CDS	sce1254	1734530	1736683	Cation-transporting ATPase		16021,30001	2217
CDS	sce1353	1865962	1868154	Potassium-transporting ATPase B chain	kdpB	3824,8152	2216
CDS	sce2395	3227592	3231143	Putative cation-transporting ATPase		3824,8152	474
CDS	sce2485	3348862	3351699	cation-transporting P-type ATPase	ctpF	3824,8152	474
CDS	sce4013	5585999	5588461	Probable cation-transporting ATPase		4008,5524,16020,30001,4	2217
CDS	sce4567	6455693	6458407	Cation-transporting ATPase, E1-E2 family	pacL1	3824,8152	474
CDS	sce5473	7711166	7713988	Cation-transporting ATPase, E1-E2 family	pacL2	3824,8152	474
CDS	sce8106	11277417	11274940	Cation-transporting ATPase	copF	4008,5524,16020,30001,4	2217

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Fam: 5 No. of CDS: 2 Dom. COG: 0 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0008	13841	12768	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7274	10152874	10153947	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 6	No. of CDS: 2	Dom. COG: 564	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0011	17148	16078	Ribosomal large subunit pseudouridine synthase D	rluD1	4730	564
CDS	sce5931	8329156	8330193	Ribosomal large subunit pseudouridine synthase D	rluD3	4730	564

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Fam: 7	No. of CDS: 12	Dom. COG: 113	counter: 9 / 12	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0018	27211	25409	ABC transporter family carbohydrate exporter	msbA1	4009,5524,6810,16021	1132
CDS	sce0019	29157	27361	ABC transporter family carbohydrate exporter	msbA2	4009,5524,6810,16021	1132
CDS	sce0179	239412	241349	ABC transporter family carbohydrate exporter	msbA3	4009,5524,6810,16021	1132
CDS	sce0180	241346	243268	ABC transporter family carbohydrate exporter	msbA4	4009,5524,6810,16021	1132
CDS	sce1176	1631200	1629158	ABC transporter family carbohydrate exporter	msbA5		4591
CDS	sce2651	3586518	3584545	ABC transporter family carbohydrate exporter	msbA6	4009,5524,6810,16021	1132
CDS	sce5195	7299049	7297133	Putative ABC-transport protein		4009,5524,6810,16020	2274
CDS	sce5644	7943098	7944831	ABC transporter family carbohydrate exporter	msbA7	4009,5524,6810,16021	1132
CDS	sce5645	7944828	7946819	ABC transporter family carbohydrate exporter	msbA8	4009,5524,6810,16021	1132
CDS	sce6999	9775487	9773496	ABC transporter family carbohydrate exporter	msbA9	4009,5524,6810,16021	1132
CDS	sce7172	10023855	10020823	ABC transporter, nucleotide binding/ATPase protein		4009,5524,6810,16021	5265
CDS	sce7656	10655637	10653826	ABC transporter family carbohydrate exporter	msbA10	4009,5524,6810,16021	1132

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Fam: 8	No. of CDS: 3	Dom. COG: 0	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0024	35823	34663	Conserved hypothetical protein		8757	1092
CDS	sce0347	502725	501460	Conserved hypothetical protein			0
CDS	sce6541	9107227	9105227	Conserved hypothetical protein		3723,6396,9982	0

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Fam: 9	No. of CDS: 2	Dom. COG: 815	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0026	37138	38883	Apolipoprotein N-acyltransferase	lnt	16021,16410,42158	815
CDS	sce3705	5176968	5178683	Apolipoprotein N-acyltransferase	cutE	16021,16410,42158	815

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Fam: 10	No. of CDS: 3	Dom. COG: 664	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0032	45940	45194	CRP family of transcriptional regulators			664
CDS	sce3757	5239911	5239150	Global nitrogen regulatory protein, CRP family of transcriptional regulators	ntcA		664
CDS	sce7185	10038524	10037742	cAMP-binding protein, CRP family of transcriptional regulators			664

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Fam: 11	No. of CDS: 3	Dom. COG: 500	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0039	53766	56312	Penicillin-binding protein	pbp1	8658,9273	5009

CDS	sce0331	463371	465716	Conserved hypothetical protein		8658,9273	5009
CDS	sce4408	6225631	6223034	Penicillin-binding protein	pbp2	8658,9273	4953
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Fam: 12	No. of CDS: 2	Dom. COG: 10	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0044	62090	61113	Agmatinase	speB1	6596,8783	10
CDS	sce9154	12751595	12752563	Agmatinase	speB2	6596,8783	10
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[							
Fam: 13	No. of CDS: 8	Dom. COG: 1028	counter: 7 / 8	percentage: 87.50%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0047	64595	63615	Putative 3-oxoacyl-[acyl-carrier-protein] reductase		8152,16491	1028
CDS	sce0668	953322	952480	Putative Oxidoreductase		8152,16491	1028
CDS	sce1333	1837717	1838502	3-Oxoacyl-[acyl-carrier-protein] reductase	fabG1	8152,16491	1028
CDS	sce1411	1938136	1938879	Putative Dehydrogenase		8152,16491	1028
CDS	sce1683	2300073	2299195	Oxidoreductase, short-chain dehydrogenase/reductase family		8152,16491	4221
CDS	sce2121	2875117	2874074	Putative 3-oxoacyl-[acyl-carrier-protein] reductase	fabG4	8152,16491	1028
CDS	sce2602	3516781	3517641	3-Oxoacyl-[acyl-carrier-protein] reductase	fabG5	8152,16491	1028
CDS	sce3225	4511241	4510393	Putative Dehydrogenase		8152,16491	1028
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Fam: 14	No. of CDS: 3	Dom. COG: 1250	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0048	67065	64837	Enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3-hydroxybutyryl-CoA epimerase		6631,16491	1250
CDS	sce0251	351157	350267	3-Hydroxyacyl-CoA dehydrogenase		6631,16491	1250
CDS	sce7905	11020850	11021761	3-Hydroxyacyl-CoA dehydrogenase		6631,16491	1250
]							
[							
Fam: 15	No. of CDS: 5	Dom. COG: 0	counter: 4 / 5	percentage: 80.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0049	68372	67062	Thiolase			0
CDS	sce0373	541717	542928	Putative beta-ketoadipyl CoA thiolase			0
CDS	sce7105	9904196	9905380	Putative beta-ketoadipyl CoA thiolase	pcaF		0
CDS	sce7554	10526907	10525726	Thiolase			0
CDS	sce7652	10650501	10649269	Acetyl-CoA acyltransferase			183
]							
[							
Fam: 16	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0051	71187	69241	Hypothetical protein			0
CDS	sce2255	3040661	3039156	Hypothetical protein		4357,675	0
]							
[							
Fam: 17	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0052	72230	71337	Putative secreted protein			0
CDS	sce0355	514124	515074	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6838	9543473	9542538	Hypothetical protein			0
]							

[

Fam: 18	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0054	74886	73189	Putative membrane protein			0
CDS	sce2971	4071110	4069500	Hypothetical protein			0

]

[

Fam: 19	No. of CDS: 124	Dom. COG: 0	counter: 84 / 124	percentage: 67.74%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0058	82277	80931	Conserved hypothetical protein			3291
CDS	sce0069	99995	95736	Cell surface SD repeat protein precursor	sdr		0
CDS	sce0119	166753	162446	Putative cell surface protein			729
CDS	sce0136	190948	189962	Conserved hypothetical protein			0
CDS	sce0391	567137	566187	Hypothetical protein			1572
CDS	sce0519	736702	739611	Putative secreted protein			0
CDS	sce0520	739849	742377	Unknown protein			0
CDS	sce0688	983165	979641	Endonuclease/exonuclease/phosphatase family			2374
CDS	sce0785	1100139	1100957	PE-PGRS family protein			0
CDS	sce0895	1273224	1274477	Putative exported sugar-binding protein with thrombospondin-like C-terminal domain			2931
CDS	sce0987	1393204	1395465	Hypothetical protein			0
CDS	sce1024	1446649	1448685	Exported nucleotide-binding protein			2319
CDS	sce1039	1468042	1470138	Hypothetical protein		4289,6508	4935
CDS	sce1104	1549160	1548009	PE-PGRS family protein			0
CDS	sce1184	1644046	1640618	Conserved hypothetical protein			0
CDS	sce1187	1646900	1646073	Conserved hypothetical protein			0
CDS	sce1236	1708572	1711061	Putative secreted protein			0
CDS	sce1247	1727751	1726195	Hypothetical protein, conserved		4872	1537
CDS	sce1265	1753361	1754845	Conserved hypothetical protein			0
CDS	sce1368	1887387	1888589	PE-PGRS family protein			
CDS	sce1369	1889148	1890437	PE-PGRS family protein		5737,6817	0
CDS	sce1371	1891503	1892636	PE-PGRS family protein		5737,6817	0
CDS	sce1412	1939759	1938926	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1516	2079200	2077725	Conserved hypothetical protein			3291
CDS	sce1618	2220296	2221096	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1847	2507530	2503142	BNR repeat domain protein			0
CDS	sce2011	2731157	2724384	Hypothetical protein predicted by Glimmer/Critica			3209
CDS	sce2055	2787809	2785191	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce2216	2988431	2985663	Unknown protein			0
CDS	sce2494	3363451	3361652	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2626	3551406	3550222	Putative secreted protein			3391
CDS	sce2639	3566086	3570282	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2642	3574846	3573248	Hypothetical protein predicted by Glimmer/Critica		5509,7155	0
CDS	sce2643	3576309	3574870	Unknown protein			
CDS	sce2648	3580071	3581939	PE-PGRS family protein			3291
CDS	sce2674	3623116	3621482	Conserved hypothetical protein			0
CDS	sce2682	3639873	3637723	cell surface glycoprotein (s-layer protein) related protein			3291
CDS	sce2739	3728162	3726594	PE_PGRS family protein			0
CDS	sce2833	3865541	3863427	Hypothetical protein		5509,7155	0
CDS	sce3285	4602901	4602005	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3298	4619570	4617915	PE-PGRS family protein			0
CDS	sce3416	4768967	4767330	Conserved hypothetical protein			3291
CDS	sce3452	4818845	4819783	Hypothetical protein			0
CDS	sce3454	4822682	4821162	Unknown protein			3291
CDS	sce3465	4833299	4835482	Putative secreted protein			0
CDS	sce3468	4839420	4840280	Putative secreted protein			0
CDS	sce3551	4962467	4963735	Cartilage oligomeric matrix protein		5509,7155	0

CDS	sce3564	4985951	4982265	Putative secreted protein			0
CDS	sce3565	4986251	4989730	Conserved hypothetical protein		16337,716	
CDS	sce3663	5128040	5129137	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3664	5129270	5131195	Conserved hypothetical protein			0
CDS	sce3669	5138702	5136756	Regulatory protein FlaEY			0
CDS	sce4033	5622803	5621079	PE-PGRS family protein			0
CDS	sce4050	5639427	5640986	Putative secreted protein			0
CDS	sce4070	5672872	5674470	Putative endo alpha-1,4 polygalactosaminidase		5554	3868
CDS	sce4185	5921393	5918850	Putative RTX family exoprotein			0
CDS	sce4342	6131694	6134789	Keratin associated protein 5-1			0
CDS	sce4343	6134771	6136501	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4558	6439813	6442926	Hypothetical protein			0
CDS	sce4559	6443486	6445420	Conserved hypothetical protein			0
CDS	sce4688	6623228	6624376	Conserved hypothetical protein			1572
CDS	sce4940	6945503	6942660	Hypothetical protein		16787	1409
CDS	sce4949	6957940	6964326	Hypothetical protein			0
CDS	sce4975	6990774	6992450	Putative secreted protein			0
CDS	sce5233	7361324	7363015	PE_PGRS			2823
CDS	sce5241	7377322	7374386	Hypothetical protein			0
CDS	sce5353	7529832	7531742	Putative secreted protein			0
CDS	sce5367	7553030	7556434	BNR repeat domain protein			0
CDS	sce5513	7765848	7767392	Conserved hypothetical protein			0
CDS	sce5536	7798754	7800172	Conserved hypothetical protein			0
CDS	sce5576	7853214	7855025	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce5595	7878240	7879832	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce5638	7935013	7936626	Putative secreted protein			4246
CDS	sce5639	7936875	7938557	Putative secreted protein			0
CDS	sce5641	7939527	7941200	Conserved hypothetical protein			0
CDS	sce5655	7955682	7956992	Conserved hypothetical protein			0
CDS	sce5739	8069035	8069892	Putative secreted protein			0
CDS	sce6017	8437320	8436031	Hypothetical protein			0
CDS	sce6043	8476323	8473693	Hypothetical protein			0
CDS	sce6044	8478551	8476359	Putative transposase			2801
CDS	sce6359	8866458	8865007	Putative secreted protein			0
CDS	sce6360	8869023	8866885	Conserved hypothetical protein			
CDS	sce6370	8883140	8884471	Conserved hypothetical protein with Kelch motif			0
CDS	sce6375	8890091	8891410	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce6396	8924520	8928170	Hypothetical protein predicted by Glimmer/Critica		7155,7160,8305	0
CDS	sce6498	9056088	9054394	Conserved hypothetical protein			3291
CDS	sce6584	9156644	9158386	Putative secreted protein			0
CDS	sce6598	9186191	9188383	Conserved hypothetical protein		4872	3291
CDS	sce6661	9264113	9266257	Putative thrombospondin family protein		5509,7155	0
CDS	sce6691	9307650	9304165	Hypothetical protein			0
CDS	sce6692	9310944	9307825	Hypothetical exported glycine-rich protein			3291
CDS	sce6849	9562588	9566637	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6854	9573027	9577094	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6895	9624172	9623207	Conserved hypothetical protein			0
CDS	sce6995	9770213	9768606	Conserved hypothetical protein			3291
CDS	sce7066	9860639	9859881	Conserved hypothetical protein			0
CDS	sce7180	10035235	10034093	Conserved hypothetical protein			1572
CDS	sce7429	10349195	10351060	Putative secreted protein			3291
CDS	sce7489	10435577	10434612	Hypothetical protein			3868
CDS	sce7552	10524551	10525318	Conserved hypothetical protein			0
CDS	sce7658	10656674	10657186	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7692	10717258	10718151	Putative secreted protein			0
CDS	sce7731	10766929	10764788	Arylsulfatase (aryl-sulfate sulphohydrolase)	atsA	8152,8484	3119
CDS	sce7737	10779789	10776514	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7892	10999462	11002311	Conserved hypothetical protein			0
CDS	sce7893	11004152	11002716	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce8067	11217920	11219650	Conserved repeat domain protein			0

CDS	sce8071	11225787	11228108	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8339	11622781	11623635	Conserved hypothetical protein with Kelch motif			0
CDS	sce8480	11813728	11812211	Conserved hypothetical protein			0
CDS	sce8497	11838697	11837423	Putative PE-PGRS family protein			0
CDS	sce8575	11967204	11969816	PE-PGRS family protein			0
CDS	sce8637	12045543	12042952	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8648	12067156	12064169	Conserved hypothetical protein			0
CDS	sce8727	12179492	12180328	Putative secreted protein			0
CDS	sce8733	12193650	12192565	Putative secreted protein			0
CDS	sce8826	12321261	12319951	Conserved hypothetical protein			0
CDS	sce8929	12452737	12454155	Conserved hypothetical protein			3291
CDS	sce8971	12504380	12503940	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8989	12522828	12526760	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9106	12674267	12675139	Putative secreted protein with fibro-slime domain			3979
CDS	sce9256	12881529	12884966	Putative secreted protein			0
CDS	sce9259	12889592	12888150	Putative secreted protein			0
CDS	sce9349	13000657	13005933	Conserved hypothetical protein			0

]

[

Fam: 20 No. of CDS: 38 Dom. COG: 0 counter: 34 / 38 percentage: 89.47%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0059	83593	82601	Putative membrane protein			0
CDS	sce0283	403370	402294	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1407	1935457	1934411	Putative membrane protein			0
CDS	sce1606	2198522	2197482	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1608	2201510	2200440	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1611	2206450	2205416	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1850	2512696	2511629	Putative membrane protein			0
CDS	sce2644	3577376	3576309	Putative membrane protein			0
CDS	sce2814	3843551	3842547	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2926	4004419	4006134	Conserved hypothetical protein			0
CDS	sce3828	5326745	5325783	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce3943	5484934	5483855	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4011	5583824	5584897	Putative secreted protein			0
CDS	sce4182	5915361	5914369	Conserved hypothetical protein			0
CDS	sce4332	6117497	6118528	Putative membrane protein			0
CDS	sce4513	6367059	6368183	Putative membrane protein			0
CDS	sce5081	7132264	7131104	Hypothetical protein containing TPR like repeat			0
CDS	sce5236	7367413	7366367	TPR repeat hypothetical protein			0
CDS	sce5480	7721813	7720863	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5575	7851926	7853212	TPR domain hypothetical protein			0
CDS	sce5589	7869318	7870373	Hypothetical protein			0
CDS	sce5591	7872479	7873567	Putative membrane protein			0
CDS	sce5637	7933991	7934974	TPR repeat hypothetical protein			0
CDS	sce6026	8448766	8449800	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce6038	8466535	8467656	Putative membrane/secreted protein			0
CDS	sce6090	8528116	8529396	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6132	8596614	8595511	Conserved hypothetical protein			0
CDS	sce6343	8840108	8841196	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6415	8951680	8952687	Hypothetical protein			1404
CDS	sce6710	9340190	9341302	Putative exported protein			0
CDS	sce7531	10487210	10485897	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8423	11728301	11729395	Conserved hypothetical protein			0
CDS	sce8488	11821341	11822417	Putative membrane protein			0

CDS	sce8765	12250611	12249436	Putative membrane protein			
CDS	sce8785	12276147	12277307	Conserved hypothetical protein			0
CDS	sce8870	12368031	12369032	Conserved hypothetical protein			0
CDS	sce9273	12905783	12904671	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9348	12999728	13000663	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 21	No. of CDS: 2	Dom. COG: 412	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0062	88373	86883	Putative carboxymethylenebutenolidase	dlhH1	16787	412
CDS	sce7034	9825014	9824115	Carboxymethylenebutenolidase	dlhH2	16787	412

]

[

Fam: 22	No. of CDS: 6	Dom. COG: 1167	counter: 6 / 6	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0063	89980	88685	Putative transcriptional regulator			1167
CDS	sce0434	629775	631313	Transcriptional regulator, GntR family		3824,9058	1167
CDS	sce1140	1590300	1591841	Transcriptional regulator, GntR family			1167
CDS	sce1268	1759375	1757918	Transcriptional regulator, GntR family			1167
CDS	sce3223	4509578	4508139	GntR-family transcriptional regulator		8483,9058	1167
CDS	sce5745	8077836	8079290	Transcriptional regulator		8483,9058	1167

]

[

Fam: 23	No. of CDS: 8	Dom. COG: 654	counter: 8 / 8	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0066	92301	93923	Pentachlorophenol monooxygenase	yhjG1	4497,6725	654
CDS	sce1232	1703041	1704477	Pentachlorophenol 4-monooxygenase	pcpB1	4497,6725	654
CDS	sce2246	3021952	3023430	Putative monooxygenase	yhjG2	4497,6725	654
CDS	sce4973	6989669	6988131	Putative monooxygenase	yhjG3	4497,6725	654
CDS	sce6389	8914753	8913239	Pentachlorophenol monooxygenase	pcpB2	4497,6725	654
CDS	sce6695	9313154	9314962	FAD-binding monooxygenase, PheA/TfdB family	cadA	4497,6725	654
CDS	sce7022	9806608	9804998	2,4-Dichlorophenol 6-monooxygenase	tfdB	4497,6725	654
CDS	sce7879	10980068	10978560	Putative FAD-binding monooxygenase	yhjG4	4497,6725	654

]

[

Fam: 24	No. of CDS: 15	Dom. COG: 2885	counter: 14 / 15	percentage: 93.33%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0070	101835	100009	Outer membrane porin precursor		9279	2885
CDS	sce0120	168603	166750	Putative ompA family protein			2885
CDS	sce1502	2061569	2059764	Outer membrane protein	mopB1	9279	2885
CDS	sce2441	3287242	3288978	OmpA family outer membrane protein		9279	2885
CDS	sce2524	3403582	3405267	Putative membrane protein		9279	2885
CDS	sce2834	3867516	3865612	Putative membrane protein	mopB2	9279	2885
CDS	sce3419	4772483	4774381	Outer membrane protein		9279	2885
CDS	sce3444	4802936	4804009	Putative membrane protein		9279	2885
CDS	sce3567	4990841	4992727	Outer membrane protein	mopB3	9279	2885
CDS	sce4471	6307410	6308570	Outer membrane protein	oprF	9279	2885
CDS	sce5935	8332914	8334938	Thrombospondin-like alanine-rich exported protein		5509,7155	2885
CDS	sce6027	8451374	8449908	Putative OmpA family outer membrane protein		9279	2885
CDS	sce7551	10524108	10522039	OmpA-like outer membrane domain protein		9279	2885
CDS	sce8066	11216091	11217923	Exported OmpA domain protein		9279	2885

CDS	sce9146	12737376	12738560	Putative membrane protein			729
]							
[							
Fam: 25	No. of CDS: 2	Dom. COG: 5049	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0078	111771	108007	ATP-dependent deoxyribonuclease subunit A		3677,4003,5524,6281	5049
CDS	sce2839	3878033	3873990	Exodeoxyribonuclease V beta chain		3677,4003,5524,6281	1074
]							
[							
Fam: 26	No. of CDS: 2	Dom. COG: 382	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0079	112023	112982	Putative Octaprenyltransferase	chlG	16020	382
CDS	sce0081	113710	114627	Putative membrane protein		16020	0
]							
[							
Fam: 27	No. of CDS: 2	Dom. COG: 65	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0086	122201	120792	Isopropylmalate isomerase, large subunit	leuC1	8152,16829,3861,9098,93	65
CDS	sce8685	12121347	12123335	3-Isopropylmalate dehydratase	leuC2	8152,16829	65
]							
[							
Fam: 28	No. of CDS: 2	Dom. COG: 516	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0088	125002	123458	IMP dehydrogenase	guaB1	3824	516
CDS	sce1032	1460586	1462034	IMP dehydrogenase	guaB2		516
]							
[							
Fam: 29	No. of CDS: 8	Dom. COG: 1943	counter: 7 / 8	percentage: 87.50%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0090	126521	127459	Transposase			1943
CDS	sce0187	253911	254879	Transposase			1943
CDS	sce2634	3562846	3561815	Transposase			1943
CDS	sce4805	6758764	6757883	Hypothetical protein			
CDS	sce4926	6922240	6921320	Transposase			1943
CDS	sce5184	7284615	7285535	Transposase			1943
CDS	sce7144	9960181	9959213	Transposase			1943
CDS	sce7364	10256696	10255776	Transposase			1943
]							
[							
Fam: 30	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0091	129066	127945	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1384	1907195	1908313	Putative secreted protein			0
]							
[							
Fam: 31	No. of CDS: 2	Dom. COG: 1145	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0092	129715	129269	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8094	11260360	11260755	Conserved hypothetical protein			1145
]							
[							
Fam: 32	No. of CDS: 2	Dom. COG: 596	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce0097	134099	133239	Predicted proline iminopeptidase			596
CDS	sce6663	9269201	9268359	Putative hydrolase			596

]

[

Fam: 33	No. of CDS: 3	Dom. COG: 217	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0101	137234	136251	Putative Taurine dioxygenase	tauD1	6118,16491	2175
CDS	sce3045	4172032	4172991	Probable taurine catabolism dioxygenase	tauD2	6118,16491	2175
CDS	sce7513	10463029	10463979	Taurine dioxygenase	tauD3	6118,16491	2175

]

[

Fam: 34	No. of CDS: 41	Dom. COG: 535	counter: 20 / 41	percentage: 48.78%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0105	142281	140188	Hypothetical protein			1357
CDS	sce0106	144533	142197	Hypothetical protein			1357
CDS	sce0109	150511	148916	Hypothetical protein			5351
CDS	sce0908	1290548	1289436	Conserved hypothetical protein			5351
CDS	sce1202	1663572	1662550	Conserved hypothetical protein			5351
CDS	sce1205	1667283	1668641	Hypothetical protein			5351
CDS	sce1980	2689364	2687625	Hypothetical protein predicted by Glimmer/Critica			1357
CDS	sce1981	2691787	2689361	Hypothetical protein			
CDS	sce2704	3673171	3670820	Conserved hypothetical protein			5351
CDS	sce2719	3688740	3691142	Hypothetical protein			1357
CDS	sce2720	3691139	3692878	Hypothetical protein			1357
CDS	sce2865	3907564	3909678	Hypothetical protein			5351
CDS	sce3105	4249314	4250345	Conserved hypothetical protein			5351
CDS	sce4088	5710123	5708285	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4107	5731087	5730089	Conserved hypothetical protein			
CDS	sce4662	6582188	6581391	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4663	6584572	6582212	Hypothetical protein			5351
CDS	sce4932	6930229	6929156	Hypothetical protein			1357
CDS	sce4933	6932898	6930226	Hypothetical protein			5351
CDS	sce5664	7966748	7965699	Pentapeptide repeat hypothetical protein			1357
CDS	sce5665	7969387	7966745	Hypothetical protein			1357
CDS	sce5668	7974684	7972477	Hypothetical protein			5351
CDS	sce6785	9457068	9459989	Hypothetical protein			1357
CDS	sce6786	9459997	9461088	Conserved hypothetical protein			1357
CDS	sce7464	10405329	10404340	Hypothetical protein			5351
CDS	sce8032	11176236	11177456	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8144	11332088	11330931	Conserved hypothetical protein			5351
CDS	sce8146	11334091	11333108	Conserved hypothetical protein			5351
CDS	sce8148	11336488	11334722	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8323	11603592	11605829	Hypothetical protein			1357
CDS	sce8324	11605826	11607565	Hypothetical protein			1357
CDS	sce8328	11611974	11610247	Conserved hypothetical protein			5351
CDS	sce8356	11642062	11644095	Conserved hypothetical protein			5351
CDS	sce8357	11644098	11645117	Hypothetical protein			0
CDS	sce8420	11723498	11722290	Hypothetical protein			5351
CDS	sce8422	11725686	11727908	Hypothetical protein			5351
CDS	sce8470	11799470	11801965	Pentapeptide repeats hypothetical protein			5351
CDS	sce8473	11804300	11803230	Pentapeptide repeats hypothetical protein			1357
CDS	sce8474	11806984	11804297	Pentapeptide repeats hypothetical protein			1357
CDS	sce8512	11866231	11864366	Conserved hypothetical protein			5351
CDS	sce9336	12985049	12984018	Conserved hypothetical protein			5351

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Fam: 35	No. of CDS: 29	Dom. COG: 350	counter: 29 / 29	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0107	147296	144591	Conserved hypothetical protein			3501

CDS	sce0108	148753	147293	Conserved hypothetical protein			3501
CDS	sce0276	391229	393886	Conserved hypothetical protein			3501
CDS	sce1203	1663712	1665874	Conserved hypothetical protein			3501
CDS	sce2701	3667580	3669586	Rhs element Vgr protein			3501
CDS	sce3112	4264463	4266697	Conserved hypothetical protein			3501
CDS	sce3113	4266777	4269011	Conserved hypothetical protein			3501
CDS	sce3114	4269025	4271790	Conserved hypothetical protein			3501
CDS	sce4084	5699125	5701611	Conserved hypothetical protein			3501
CDS	sce4108	5731165	5733360	Conserved hypothetical protein			3501
CDS	sce4109	5733373	5735541	Conserved hypothetical protein			3501
CDS	sce4113	5742169	5744706	Conserved hypothetical protein			3501
CDS	sce4665	6588630	6585604	Rhs element Vgr protein			3501
CDS	sce4671	6594530	6592320	Rhs element Vgr protein			3501
CDS	sce4934	6935340	6932905	Conserved hypothetical protein			3501
CDS	sce5667	7972369	7969976	Conserved hypothetical protein			3501
CDS	sce6784	9454569	9456986	Conserved hypothetical protein			3501
CDS	sce7455	10386665	10388989	Conserved hypothetical protein			3501
CDS	sce7456	10388986	10391169	Rhs element Vgr protein			3501
CDS	sce7458	10391662	10394202	Conserved hypothetical protein			3501
CDS	sce8036	11180605	11182764	Conserved hypothetical protein			3501
CDS	sce8141	11326741	11328909	Conserved hypothetical protein, Rhs element family			3501
CDS	sce8196	11408143	11410785	Putative Rhs element Vgr protein			3501
CDS	sce8321	11601769	11600324	VrgS conserved hypothetical protein			3501
CDS	sce8353	11638614	11640791	Conserved hypothetical protein			3501
CDS	sce8421	11725498	11723588	Conserved hypothetical protein			3501
CDS	sce8477	11810180	11807787	Rhs family protein			3501
CDS	sce8511	11864268	11861812	Conserved hypothetical protein Vgr			3501
CDS	sce9329	12976178	12978136	Conserved hypothetical protein			3501

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Fam: 36	No. of CDS: 9	Dom. COG: 463(	counter: 7 / 9	percentage: 77.78%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0110	150812	151387	Conserved hypothetical protein			0
CDS	sce0505	715388	714783	Hypothetical protein			4636
CDS	sce2143	2909716	2910276	Hypothetical protein			4636
CDS	sce3871	5385102	5384509	Hypothetical protein			0
CDS	sce5025	7053773	7054372	DUF829 domain hypothetical protein			4636
CDS	sce5208	7317198	7317872	Conserved hypothetical protein DUF820 domain			4636
CDS	sce7056	9850297	9849704	Protein of unknown function DUF820			4636
CDS	sce7446	10371156	10370569	Hypothetical protein			4636
CDS	sce9308	12947650	12948234	Conserved hypothetical protein			4636

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Fam: 37	No. of CDS: 12	Dom. COG: 320(	counter: 11 / 12	percentage: 91.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0111	151480	153801	Conserved exported carbohydrate-binding protein, Rhs family			3209
CDS	sce3116	4272433	4276722	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce3197	4462937	4464595	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce3545	4955775	4954102	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce4086	5703079	5707182	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce4111	5736047	5739979	Conserved exported carbohydrate-binding protein, Rhs family			3209
CDS	sce4213	5960722	5964873	Hypothetical carbohydrate-binding protein, Rhs family			3209
CDS	sce4743	6685536	6686528	Hypothetical glycine-rich protein			0
CDS	sce4744	6686571	6689756	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce7460	10396721	10400779	Conserved carbohydrate-binding protein, Rhs family			3209

CDS	sce7882	10986886	10982984	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce9127	12708231	12704176	Conserved carbohydrate-binding protein, Rhs family			3209

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Fam: 38	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0112	153798	155090	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce0115	158075	159370	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 39	No. of CDS: 8	Dom. COG: 154	counter: 8 / 8	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0116	159493	161238	Putative amidase		4040	154
CDS	sce1497	2050819	2052360	Putative amidase	gatA1	4040	154
CDS	sce1749	2381867	2383471	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	gatA2	4040	154
CDS	sce2263	3051814	3050372	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases		4040	154
CDS	sce3176	4362961	4361570	Putative amidase	gatA3	4040	154
CDS	sce3727	5205247	5203787	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases		4040	154
CDS	sce4281	6052543	6054096	Glutamyl-tRNA(Gln) amidotransferase subunit A	gatA4	6412,17068	154
CDS	sce6000	8414201	8412690	Amidase family protein	gatA5	4040	154

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Fam: 40	No. of CDS: 12	Dom. COG: 212	counter: 12 / 12	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0122	169545	170762	Cytochrome P450 CYP109C1	cypA1	6118	2124
CDS	sce0675	959757	961046	Cytochrome P450 CYP267A1		6118	2124
CDS	sce1588	2168625	2169809	Cytochrome P450 CYP260A1		6118	2124
CDS	sce4633	6548984	6547758	Cytochrome P450 CYP109D1	cypA2	6118	2124
CDS	sce4806	6760376	6759198	Cytochrome P450 CYP260B1	cypA3	6118	2124
CDS	sce5624	7916995	7918224	Cytochrome P450 CYP266A1	cypA4	6118	2124
CDS	sce6323	8817601	8816429	Cytochrome P450 CYP264A1	cypA5	6118	2124
CDS	sce7167	10012191	10013408	Cytochrome P450	cypA6	6118	2124
CDS	sce7867	10967154	10965946	Cytochrome P450 CYP124E1		6118	2124
CDS	sce8224	11447261	11446065	Cytochrome P450 CYP265A1	cypA7	6118	2124
CDS	sce8551	11915725	11916963	Cytochrome P450 CYP264B1	cypA8	6118	2124
CDS	sce8913	12431202	12432395	Cytochrome P450 CYP109C2	cypA9	6118	2124

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Fam: 41	No. of CDS: 2	Dom. COG: 589	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0123	171490	172491	Hypothetical protein		6950	589
CDS	sce8583	11977589	11976624	Conserved hypothetical protein		6950	589

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Fam: 42	No. of CDS: 2	Dom. COG: 3507	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0125	174594	176240	Beta-xylosidase (14-beta-D-xylan xylohydrolase) (Xylan 14-beta-xylosidase)	yagH	5975	3507
CDS	sce4884	6854841	6856412	Xylan 1,4-beta-xylosidase	xynB4	5975	3507

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Fam: 43	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce0126	177702	176296	Conserved hypothetical protein			0
CDS	sce0484	687581	686502	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 44	No. of CDS: 4	Dom. COG: 143	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0127	180162	178072	Methionyl-tRNA synthetase	metG1	4825,5524,6431	143
CDS	sce7883	10989092	10987020	Methionyl-tRNA synthetase	metG2	4825,5524,6431	143
CDS	sce8081	11243771	11245693	Methionyl-tRNA synthetase	metG3	4812,5524,6418	143
CDS	sce8230	11452782	11454707	Methionyl-tRNA synthetase	metS	4812,5524,6418	143

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Fam: 45	No. of CDS: 27	Dom. COG: 0	counter: 17 / 27	percentage: 62.96%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0129	182949	181318	Hypothetical protein			0
CDS	sce0554	796175	794784	Putative secreted protein			599
CDS	sce0736	1039192	1040556	Hypothetical protein-signal peptide prediction			0
CDS	sce0795	1119932	1118460	Conserved hypothetical protein			1071
CDS	sce0994	1401391	1402782	Conserved hypothetical protein		9306	
CDS	sce1021	1443719	1442340	Conserved exported protein			3206
CDS	sce1499	2055699	2054323	Putative secreted protein			0
CDS	sce2268	3056989	3055685	Hypothetical protein			0
CDS	sce2931	4013333	4014697	Hypothetical protein			0
CDS	sce3315	4641955	4640519	Hypothetical conserved secreted protein			1411
CDS	sce3370	4711363	4712997	Putative membrane protein			0
CDS	sce4016	5594466	5593084	Hypothetical protein-signal peptide prediction			0
CDS	sce4155	5877375	5875999	Putative secreted protein			0
CDS	sce4381	6190418	6189033	Conserved hypothetical protein			0
CDS	sce4594	6494980	6493604	Putative secreted protein			0
CDS	sce4602	6505220	6503844	Hypothetical protein-signal peptide prediction			3443
CDS	sce4608	6513624	6515069	Hypothetical protein-signal peptide prediction			0
CDS	sce4611	6518786	6517407	Hypothetical protein			0
CDS	sce5210	7325055	7323442	Hypothetical protein			0
CDS	sce5651	7952508	7952744	Conserved hypothetical protein			0
CDS	sce6539	9102918	9104291	Hypothetical protein			246
CDS	sce6914	9647792	9646197	Tat pathway signal sequence			1122
CDS	sce6919	9655739	9654108	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7738	10781369	10779963	Conserved hypothetical protein with TAT signal sequence			0
CDS	sce8663	12092333	12093679	Hypothetical protein			0
CDS	sce9046	12600828	12602156	Putative secreted protein			431
CDS	sce9047	12602257	12603546	Putative secreted protein			1345

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Fam: 46	No. of CDS: 63	Dom. COG: 332	counter: 16 / 63	percentage: 25.40%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0134	187007	188023	Alcohol dehydrogenase, zinc-containing			604
CDS	sce0345	499710	488146	NRPS/PKS hybrid		3824,8152	3321
CDS	sce0436	633858	632350	AMP-dependent synthetase and ligase		3824,8152	1020
CDS	sce0818	1150403	1152052	Putative dioxygenase			2070
CDS	sce0819	1152079	1159791	Polyketide synthase			3321
CDS	sce0820	1159803	1167578	Polyketide synthase		3824,6633	3321
CDS	sce0903	1282632	1284428	Long-chain fatty-acid-CoA ligase		3824,8152	1022
CDS	sce1467	2012305	2013978	Putative Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II		3824,8152	318
CDS	sce1995	2710118	2708415	Acyl-CoA synthetase		3824,8152	365
CDS	sce2275	3064995	3065930	NADPH:quinone reductase	qor1	8270	604
CDS	sce2387	3216562	3206225	Non-ribosomal peptide synthetase		3824,8152	1020

CDS	sce2526	3409092	3407764	3-Oxoacyl-[acyl-carrier-protein] synthase		3824,6633	304
CDS	sce2530	3412950	3411127	Acyl-CoA synthetase		3824,8152	318
CDS	sce3015	4134492	4136051	*O* -Succinylbenzoate-CoA ligase	menE		318
CDS	sce3182	4370774	4369542	Putative beta-ketoacyl synthase		3824,6633	304
CDS	sce3184	4372382	4371003	Hypothetical protein			2070
CDS	sce3188	4376667	4392107	Polyketide synthase			3321
CDS	sce3189	4392104	4403590	Polyketide synthase			3321
CDS	sce3190	4403593	4414479	Polyketide synthase			3321
CDS	sce3191	4414476	4429688	Polyketide synthase			3321
CDS	sce3192	4429685	4440421	Polyketide synthase			3321
CDS	sce3193	4440441	4458362	Polyketide synthase			3321
CDS	sce3195	4459749	4461851	malonyl CoA-acyl carrier protein transacylase		8152,1674	331
CDS	sce3250	4555105	4554050	Alcohol dehydrogenase	adh3		604
CDS	sce3351	4688186	4690249	Putative beta-ketoacyl synthase		3824,6633	304
CDS	sce3355	4692332	4693261	[Acyl-carrier-protein] S-malonyltransferase	fabD2	8152,1674	331
CDS	sce3456	4824501	4825469	NADPH:quinone reductase	qor2		604
CDS	sce3813	5311523	5310279	Beta-ketoacyl-ACP synthase		3824,6633	304
CDS	sce3816	5313746	5312805	Malonyl CoA-acyl carrier protein transacylase	fabD3	8152,1674	331
CDS	sce3825	5320910	5322499	Putative Long-chain-fatty-acid-CoA ligase	fadD1	3824,8152	318
CDS	sce3880	5399428	5401086	(2,3-Dihydroxybenzoyl)adenylate synthase	mxcE	3824,8152	1021
CDS	sce3888	5409948	5414381	Nonribosomal peptide synthetase	mxcG	3824,8152	1020
CDS	sce4133	5779943	5762337	Polyketide synthase	chiF		3321
CDS	sce4134	5794474	5779934	Polyketide synthase	chiE	3824,6633	3321
CDS	sce4135	5808406	5794481	Hybrid polyketide synthase/nonribosomal peptide synthetase	chiD	16874	1020
CDS	sce4136	5833675	5808422	Polyketide synthase	chiC	3824,6633	3321
CDS	sce4137	5851209	5833675	Polyketide synthase	chiB		3321
CDS	sce4138	5853706	5851286	Putative acyltransferase/oxidoreductase	chiA	8152,1674	3321
CDS	sce4293	6070531	6069518	Alcohol dehydrogenase	adh4		604
CDS	sce4888	6867494	6860778	Probable glycolipid synthase		8152,1674	3321
CDS	sce5022	7050688	7049657	Conserved hypothetical protein			604
CDS	sce5271	7415510	7417354	Long-chain fatty-acid-CoA ligase	fadD2	3824,8152	1022
CDS	sce5642	7941386	7942351	Putative zinc-binding oxidoreductase		8270	604
CDS	sce5736	8065356	8067002	AMP-dependent synthetase and ligase		3824,8152	318
CDS	sce5853	8226418	8224670	AMP-dependent synthetase and ligase	fadD3	3824,8152	318
CDS	sce5920	8317020	8315110	3-Oxoacyl-(acyl-carrier-protein)-synthase II		3824,6633	304
CDS	sce5922	8320240	8317928	Oxoacyl-(acyl-carrier-protein) synthase II		3824,6633	304
CDS	sce6823	9502480	9513516	NRPS/PKS hybrid			1020
CDS	sce7053	9845552	9847357	Acyl-CoA synthetase		3824,8152	318
CDS	sce7641	10633302	10634930	Putative long-chain-fatty-acid--CoA ligase	fadD4	3824,8152	318
CDS	sce7927	11049814	11051781	Acetyl-coenzyme A synthetase	acs	3824,8152	365
CDS	sce8012	11144127	11148719	AMP-binding enzyme family protein		3824,8152	1022
CDS	sce8219	11441016	11439499	AMP-dependent synthetase and ligase		3824,8152	1020
CDS	sce8226	11449817	11448207	Acyl-CoA-ligase/synthetase		3824,8152	318
CDS	sce8255	11490092	11486109	Non-ribosomal peptide synthetase		16874	1020
CDS	sce8256	11499136	11490089	Non-ribosomal peptide synthetase			1020
CDS	sce8257	11513309	11499141	Non-ribosomal peptide synthetase			1020
CDS	sce8258	11514500	11513319	Putative syrP protein			0
CDS	sce8261	11523730	11518781	Polyketide synthase type I		8152,1674	3321
CDS	sce8262	11529102	11523727	Non-ribosomal peptide synthetase		3824,8152	1020
CDS	sce8562	11954863	11953886	Putative NADPH quinone oxidoreductase			604

CDS	sce8696	12132523	12134328	Putative long-chain fatty-acid--CoA ligase		3824,8152	1022
CDS	sce9148	12740086	12739100	Putative NADPH:quinone reductase.			604

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Fam: 47	No. of CDS: 8	Dom. COG: 0	counter: 7 / 8	percentage: 87.50%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0144	200717	199500	Conserved hypothetical protein			0
CDS	sce0148	204527	205540	Hypothetical protein			
CDS	sce1833	2480170	2481219	Hypothetical protein			0
CDS	sce2831	3860957	3859809	Conserved hypothetical protein			0
CDS	sce6525	9088405	9087461	Hypothetical protein			0
CDS	sce7724	10756524	10757567	Hypothetical protein			0
CDS	sce8570	11961892	11962542	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8572	11963376	11963840	Hypothetical protein			0

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Fam: 48	No. of CDS: 5	Dom. COG: 0	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0146	202451	201891	Conserved hypothetical protein			0
CDS	sce1835	2483984	2483490	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2829	3858063	3858623	Conserved hypothetical protein			0
CDS	sce6277	8767575	8767015	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7727	10760285	10759725	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 49	No. of CDS: 18	Dom. COG: 583	counter: 18 / 18	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0164	222568	223536	Transcriptional regulator, LysR family			583
CDS	sce0769	1077092	1078030	Transcriptional regulator, LysR family			583
CDS	sce1558	2125909	2126847	Transcriptional regulator, LysR family			583
CDS	sce3226	4511366	4512325	Transcriptional regulator, LysR family			583
CDS	sce3251	4555177	4556112	Transcriptional regulator, LysR family			583
CDS	sce3450	4817773	4816874	LysR-family transcriptional regulator			583
CDS	sce4163	5888539	5887586	LysR-family transcriptional regulator			583
CDS	sce4766	6711957	6712868	LysR-family transcriptional regulator			583
CDS	sce5425	7619937	7618999	LysR-family transcriptional regulator			583
CDS	sce5647	7947462	7948403	LysR-family transcriptional regulator			583
CDS	sce6116	8567053	8566136	LysR-family transcriptional regulator			583
CDS	sce6961	9709415	9708477	Transcriptional regulator, LysR family			583
CDS	sce7137	9952000	9951017	Transcriptional regulator, LysR family	ptxR		583
CDS	sce7764	10812126	10811089	Transcriptional regulator, LysR family			583
CDS	sce8348	11632284	11631253	Transcriptional regulator, LysR family			583
CDS	sce8573	11966151	11965249	Transcriptional regulator, LysR family			583
CDS	sce8585	11981075	11980491	Transcriptional regulator, LysR family			583
CDS	sce8950	12480154	12479102	Transcriptional regulator, LysR family			583

]

[

Fam: 50	No. of CDS: 8	Dom. COG: 600	counter: 8 / 8	percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0166	225004	225912	ABC transporter permease protein		5215,6810,16020	600
CDS	sce1322	1824451	1825311	ABC transporter permease protein		5215,6810,16020	600
CDS	sce1323	1825359	1826141	ABC transporter permease protein		5215,6810,16020	600
CDS	sce1863	2532378	2531563	Putative ABC-type permease protein		5215,6810,16020	600
CDS	sce2758	3760837	3761760	Putative ABC transporter permease protein		5215,6810,16020	600
CDS	sce4769	6715305	6716138	ABC-type transporter, permease protein		5215,6810,16020	600
CDS	sce4920	6913169	6913981	aliphatic sulfonate ABC transporter, membrane protein	ssuC	5215,6810,16020	600
CDS	sce5511	7763851	7764633	ABC transport system permease protein		5215,6810,16020	600

]

[

Fam: 51	No. of CDS: 10	Dom. COG: 1116	counter: 10 / 10	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0167	225888	226676	ABC transporter ATP-binding protein		4009,5524,6810,16020	1116
CDS	sce1324	1826211	1826966	ABC transporter ATP-binding protein		4009,5524,6810,16020	1116
CDS	sce1865	2534086	2534940	ABC transporter ATP-binding protein		4009,5524,6810,16020	1116
CDS	sce2759	3761757	3762605	ABC transporter ATP-binding protein		4009,5524,6810,16020	1116
CDS	sce3377	4720956	4720114	ABC transport system ATP-binding protein		4009,5524,6810,16020	1116
CDS	sce4034	5624069	5623188	nitrate/nitrite ABC transporter ATP-binding protein	nrtD	4009,5524,6810,16020	1116
CDS	sce4035	5624896	5624066	nitrate/nitrite ABC transporter ATP-binding protein	nrtC1	4009,5524,6810,16020	1116
CDS	sce4768	6714443	6715312	ABC-type transporter, ATP-binding protein		4009,5524,6810,16020	1116
CDS	sce4921	6913986	6914825	aliphatic sulfonate ABC transporter, nucleotide binding/ATPase protein	ssuB	4009,5524,6810,16020	1116
CDS	sce5488	7731502	7732344	Putative sulfonate transport system ATP-binding protein	nrtC2	4009,5524,6810,16020	1116

]

[

Fam: 52	No. of CDS: 5	Dom. COG: 2141	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0168	226673	228025	monooxygenase			2141
CDS	sce1311	1812775	1811405	monooxygenase			2141
CDS	sce5568	7840403	7839045	nitrilotriacetate monooxygenase component A	nrd		2141
CDS	sce6361	8869612	8870952	Putative monooxygenase			2141
CDS	sce8959	12491208	12492566	Putative monooxygenase			2141

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 115	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0176	235128	236018	Branched-chain-amino-acid transaminase	ilvE1	4084,9081	115
CDS	sce0253	362650	363624	Branched-chain-amino-acid transaminase	ilvE2	3824,8152	115

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[

Fam: 54	No. of CDS: 12	Dom. COG: 583	counter: 12 / 12	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0177	237044	236097	Transcriptional regulator, LysR family			583
CDS	sce1117	1570725	1569766	Transcriptional regulator, LysR family			583
CDS	sce1194	1654034	1654945	Transcriptional regulator, LysR family			583

CDS	sce1843	2494019	2493099	Transcriptional regulator, LysR family			583
CDS	sce2176	2939644	2938643	Transcriptional regulator, LysR family			583
CDS	sce2368	3180929	3181384	Transcriptional regulator, LysR family	leuO		583
CDS	sce5183	7283495	7284418	LysR-family transcriptional regulator			583
CDS	sce6183	8652435	8653373	LysR-family transcriptional regulator			583
CDS	sce6290	8781631	8781161	Nodulation protein D 1	nodD		583
CDS	sce6383	8900616	8901764	Transcriptional regulator, LysR family			583
CDS	sce7797	10865136	10864087	Transcriptional regulator, LysR family			583
CDS	sce8852	12345224	12346324	Nodulation protein D			583

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Fam: 55	No. of CDS: 4	Dom. COG: 568	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0190	258479	257139	RNA polymerase sigma factor		3677,3700,6352,16987	568
CDS	sce2611	3529195	3527804	RNA polymerase sigma factor		3677,3700,6352,16987	568
CDS	sce4447	6273654	6275573	RNA polymerase sigma factor RpoD	rpoD	3677,3700,6352,16987	568
CDS	sce7244	10113480	10111333	RNA polymerase sigma factor		3677,3700,6352,16987	568

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[

Fam: 56	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0198	271035	270205	Conserved hypothetical protein			0
CDS	sce0271	385372	384197	Hypothetical protein			0
CDS	sce7720	10751402	10750617	Conserved hypothetical protein			0

]

[

Fam: 57	No. of CDS: 9	Dom. COG: 212	counter: 9 / 9	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0200	273312	271864	Putative cytochrome P450 CYP261A1		6118	2124
CDS	sce1860	2527971	2526559	Cytochrome P450	cyc1	6118	2124
CDS	sce2191	2955837	2957144	Cytochrome P450 CYP262A1	cyc2	6118	2124
CDS	sce3065	4200711	4199377	Cytochrome P450 CYP110H1		6118	2124
CDS	sce4635	6550714	6552042	Cytochrome P450 CYP259A1		6118	2124
CDS	sce4885	6858368	6856887	Cytochrome P450 CYP263A1	cyc3	6118	2124
CDS	sce5528	7785007	7786386	Cytochrome P450 CYP117B1		6118	2124
CDS	sce5725	8054042	8052561	Cytochrome P450		6118	2124
CDS	sce6424	8961238	8959805	Cytochrome P450 CYP110J1		6118	2124

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[

Fam: 58	No. of CDS: 5	Dom. COG: 339	counter: 4 / 5	percentage: 80.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0202	277723	274886	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1942	2633997	2636801	Hypothetical protein predicted by Glimmer/Critica			3391
CDS	sce4720	6662299	6659483	Hypothetical protein			3391
CDS	sce5569	7843457	7840707	Hypothetical protein			3391
CDS	sce7469	10414316	10411542	Hypothetical protein			3391

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Fam: 59	No. of CDS: 80	Dom. COG: 220	counter: 52 / 80	percentage: 65.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0223	305062	306819	Transcriptional regulator containing AAA-type ATPase and DNA-binding domains		3677	2204
CDS	sce0307	434325	429595	Protein kinase		4674,5524,6468,4672	515
CDS	sce0439	635942	637309	Transcriptional regulator		160,3677	2204

CDS	sce0543	774966	776735	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce0666	950232	948286	Sigma-54 dependent transcriptional regulator.		160,3677	2204
CDS	sce0686	974888	973410	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce1325	1827113	1828282	Sigma-54 dependent transcriptional regulator		160,3677	1221
CDS	sce1432	1971692	1966671	Protein kinase		4672,4674,5524,6468	515
CDS	sce1472	2021824	2020370	Sigma-54 dependent transcription factor		160,3677	2204
CDS	sce1649	2259884	2261239	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce1691	2312621	2311239	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce1845	2497409	2499166	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce1948	2643146	2644540	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce2247	3025025	3023745	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce2459	3312115	3315867	Sigma-54 dependent activator			2204
CDS	sce2560	3454233	3455678	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528	2204
CDS	sce2668	3613040	3607821	Protein kinase		4674,5524,6468,4672	515
CDS	sce2692	3657658	3659055	Sigma-54 dependent transcriptional regulator/response regulator		160,3677	2204
CDS	sce2792	3809276	3810886	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce2848	3890339	3891802	Response regulator		160,3677	2204
CDS	sce2881	3928688	3930049	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce2900	3954799	3950294	Protein kinase		4674,5524,6468,4672	515
CDS	sce2974	4073778	4075592	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce3208	4479739	4481226	Sigma-54 dependent DNA-binding response regulator		160,3677	2204
CDS	sce3217	4494358	4497690	Serine/threonine-protein kinase		4672,4674,5524,6468	515
CDS	sce3218	4497600	4499189	Nitrogen regulation protein NR(I).	pilR1	160,3677,6355	3604
CDS	sce3228	4514373	4515938	Sigma-54 dependent transcriptional regulator		160,3677,6355	3604
CDS	sce3264	4573438	4572065	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce3280	4595025	4593430	Sigma-54 dependent transcriptional regulator			3604
CDS	sce3411	4759219	4757864	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce3597	5033014	5034525	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce3672	5141710	5142939	Sigma-54 dependent transcriptional regulator		160,3677	3283
CDS	sce3771	5255382	5253682	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce3793	5285665	5284214	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce4007	5578006	5579415	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce4069	5672606	5671116	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce4161	5884790	5886160	Transcriptional regulator		160,3677	2204
CDS	sce4272	6040798	6042279	Nitrogen regulation protein NR(I).	pilR2	160,3677,6355	2204
CDS	sce4306	6090253	6088265	Sigma-54 dependent transcriptional activator		160,3677	2204
CDS	sce4405	6218875	6217574	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce4588	6487040	6485607	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce4751	6696523	6695210	Sigma-54 dependent transcriptional regulator		160,3677	3829
CDS	sce4793	6744403	6743411	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce5065	7110925	7109537	Sigma-54 dependent transcriptional regulator		160,3677	3829
CDS	sce5086	7135958	7137514	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce5096	7154295	7152802	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce5177	7273384	7275582	Sigma-54 dependent transcriptional regulator		160,3677	2204

CDS	sce5469	7707914	7706523	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce5550	7815019	7816497	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce5791	8133927	8132500	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce5833	8192343	8190601	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce5993	8406881	8405319	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce6014	8432341	8433735	Response regulator		3677,5524,9605,30528,45	2204
CDS	sce6174	8640088	8641572	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce6324	8817753	8819399	Sigma-54 dependent transcriptional regulator		160,3677	1221
CDS	sce6472	9020629	9021876	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce6642	9238858	9240528	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce6656	9259888	9258251	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce6746	9406461	9405070	Sigma-54 dependent transcriptional regulator.		160,3677	2204
CDS	sce6842	9549988	9551082	Sigma-54 dependent transcriptional regulator.		160,3677	2204
CDS	sce6864	9589654	9590643	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce6966	9712882	9714264	Response regulator		3677,5524,9605,30528,45	2204
CDS	sce7009	9789752	9791323	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce7127	9940789	9938957	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce7155	9978233	9976539	Sigma-54 dependent transcriptional regulator	rtcR	160,3677	4650
CDS	sce7271	10150546	10148600	Transcriptional regulator		160,3677,6355	3604
CDS	sce7801	10868052	10869437	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce7808	10880819	10880379	Response regulator			2204
CDS	sce7862	10962406	10961021	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce8107	11279036	11277621	Response regulator containing CheY-like receiver AAA-type ATPase and DNA-binding domains		3677,5524,9605,30528,45	2204
CDS	sce8207	11426837	11425371	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce8647	12062235	12063890	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce8721	12171235	12172662	Response regulator containing CheY-like receiver AAA-type ATPase and DNA-binding domains		3677,5524,9605,30528,45	2204
CDS	sce8739	12206362	12204518	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce8837	12333813	12332404	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204
CDS	sce8884	12387774	12389651	Sigma-54 dependent transcriptional regulator		160,3677	2204
CDS	sce9016	12557795	12556290	Nif-specific regulatory protein		160,3677,6355	2204
CDS	sce9035	12582798	12584327	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce9198	12816072	12814240	Sigma-54 dependent transcriptional regulator		160,3677	3604
CDS	sce9222	12844441	12843035	Sigma-54 dependent DNA-binding response regulator		3677,5524,9605,30528,45	2204

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Fam: 60	No. of CDS: 2	Dom. COG: 215	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0226	312130	313284	Hypothetical protein		1760,8152	2159
CDS	sce5175	7271098	7269926	Amidohydrolase		1760,8152	2159

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Fam: 61	No. of CDS: 7	Dom. COG: 194	counter: 7 / 7	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0227	313425	315650	Conserved domain protein			1944
CDS	sce0540	770586	771860	Conserved hypothetical protein			1944

CDS	sce0791	1112575	1111337	Conserved hypothetical protein			1944
CDS	sce5176	7272737	7271307	Conserved hypothetical protein DUF181			1944
CDS	sce7124	9934258	9932984	Conserved hypothetical protein			1944
CDS	sce8753	12227252	12226038	Conserved hypothetical protein			1944
CDS	sce9072	12634130	12635413	Conserved hypothetical protein (YcaO-like family)			1944

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[

Fam: 62	No. of CDS: 5	Dom. COG: 102	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0250	349703	348876	3-Hydroxybutyryl-CoA dehydratase		3824,8152	1024
CDS	sce1998	2713739	2712858	Enoyl-CoA hydratase		3824,8152	1024
CDS	sce5924	8320617	8321408	3-Hydroxybutyryl-CoA dehydratase		3824,8152	1024
CDS	sce6905	9637547	9636792	Enoyl-CoA hydratase	fadB	3824,8152	1024
CDS	sce8632	12036706	12035918	Enoyl-CoA hydratase/isomerase family protein		3824,8152	1024

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[

Fam: 63	No. of CDS: 12	Dom. COG: 457	counter: 6 / 12	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0252	351395	362635	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce0608	865838	870739	Hypothetical protein			457
CDS	sce0609	870736	876738	Hypothetical protein			457
CDS	sce2920	3984212	3989536	Tetratricopeptide repeat protein			457
CDS	sce2921	3989487	3995732	Tetratricopeptide repeat protein			457
CDS	sce3913	5442824	5448121	Protein kinase		4672,4674,5524,6468	515
CDS	sce4262	6029872	6024533	Hypothetical protein			0
CDS	sce4463	6300094	6296612	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6592	9178554	9166393	Hypothetical protein predicted by Glimmer/Critica			457
CDS	sce7985	11111967	11114330	Hypothetical protein			0
CDS	sce8705	12142995	12151055	Hypothetical protein predicted by Glimmer/Critica			542
CDS	sce9355	13019337	13012618	Cellulose synthase 1 operon protein C precursor.			457

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[

Fam: 64	No. of CDS: 3	Dom. COG: 463	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0260	372019	371411	Conserved hypothetical protein			4636
CDS	sce2003	2717589	2716945	Hypothetical protein			4636
CDS	sce7168	10013535	10014155	Hypothetical protein			0

]

[

Fam: 65	No. of CDS: 2	Dom. COG: 151	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0269	382720	383652	Conserved hypothetical protein			1518
CDS	sce9176	12785697	12786794	Conserved hypothetical protein			1518

]

[

Fam: 66	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0277	393927	396044	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8197	11410797	11413181	Hypothetical protein			0

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[

Fam: 67	No. of CDS: 11	Dom. COG: 463	counter: 6 / 11	percentage: 54.55%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce0280	398934	398260	Hypothetical protein			4636
CDS	sce0306	428799	429503	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce0470	667985	668617	Hypothetical protein			0
CDS	sce0956	1354395	1354952	Conserved hypothetical protein			0
CDS	sce1045	1475895	1476461	Hypothetical protein			4636
CDS	sce1097	1539110	1539703	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2144	2911169	2910555	Hypothetical protein			4636
CDS	sce3636	5095307	5094717	Hypothetical protein			4636
CDS	sce4237	5996933	5997526	Hypothetical protein			4636
CDS	sce6161	8629716	8629048	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8403	11701818	11701234	Hypothetical protein			4636

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[

Fam: 68	No. of CDS: 21	Dom. COG: 1028	counter: 21 / 21	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0289	412398	413288	Putative Oxidoreductase		8152,16491	1028
CDS	sce0978	1384989	1384150	Putative Oxidoreductase		8152,16491	1028
CDS	sce1141	1592609	1591863	Short chain dehydrogenase		8152,16491	1028
CDS	sce2001	2715544	2714783	Putative 3-oxoacyl-[acyl-carrier-protein] reductase		8152,16491	1028
CDS	sce2893	3942391	3943236	Putative short-chain dehydrogenases		8152,16491	1028
CDS	sce3273	4584323	4585174	Putative short chain dehydrogenase		8152,16491	1028
CDS	sce3354	4691595	4692335	3-Oxoacyl-[acyl-carrier protein] reductase	fabG7	8152,16491	1028
CDS	sce3815	5312798	5312052	Short-chain dehydrogenase/reductase		8152,16491	1028
CDS	sce3883	5403079	5403855	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase	mxcC	8152,16491	1028
CDS	sce4661	6580931	6580143	Probable short chain dehydrogenase/reductase SDR family		8152,16491	1028
CDS	sce4886	6860016	6858469	3-Oxoacyl-[acyl-carrier-protein] reductase	fabG9	8152,16491	1028
CDS	sce5157	7243670	7242897	Gluconate dehydrogenase	kduD	8152,16491	1028
CDS	sce5302	7455502	7456263	3-Oxoacyl-[acyl-carrier-protein] reductase	fabG10	8152,16491	1028
CDS	sce6208	8682356	8681553	Putative 3-oxoacyl-[acyl-carrier-protein] reductase	fabG11	8152,16491	1028
CDS	sce6363	8872092	8872859	Short-chain dehydrogenase/reductase SDR		8152,16491	1028
CDS	sce7442	10367470	10368237	Dehydrogenase of unknown specificity			1028
CDS	sce7498	10443488	10444291	Putative 3-oxoacyl-[acyl-carrier-protein] reductase	fabG12	8152,16491	1028
CDS	sce7765	10812142	10812912	Probable dehydrogenase/reductase oxidoreductase protein		8152,16491	1028
CDS	sce8549	11913667	11912903	Putative short-chain dehydrogenase		8152,16491	1028
CDS	sce8810	12303835	12304560	Oxidoreductase, short-chain dehydrogenase/reductase family		8152,16491	1028
CDS	sce8812	12305309	12306049	Probable short-chain dehydrogenase		8152,16491	1028

]

[

Fam: 69	No. of CDS: 2	Dom. COG: 1716	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0296	419100	417997	FHA domain protein			1716
CDS	sce8329	11613063	11612005	FHA domain protein			1716

]

[

Fam: 70	No. of CDS: 2	Dom. COG: 457	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0300	422722	424362	Hypothetical protein			457

CDS	sce5337	7505489	7507588	TPR repeat hypothetical protein			457
]							
[							
Fam: 71	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0302	425401	426627	Hypothetical protein predicted by Glimmer/Critica		6508,8237	0
CDS	sce4774	6721386	6720337	Peptidase M10A		6508,4222	612
]							
[							
Fam: 72	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0303	427017	427466	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3070	4206339	4206788	Hypothetical protein predicted by Glimmer/Critica			0
]							
[							
Fam: 73	No. of CDS: 2	Dom. COG: 159	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0322	454350	455024	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce7566	10539493	10540179	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
]							
[							
Fam: 74	No. of CDS: 2	Dom. COG: 125	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0323	455129	456472	NADH dehydrogenase	ndh1	6118,15036	1252
CDS	sce3024	4146839	4145502	NADH dehydrogenase	ndh2	6118,15036	1252
]							
[							
Fam: 75	No. of CDS: 3	Dom. COG: 139	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0324	456514	457206	Transcriptional regulator			1396
CDS	sce6511	9069845	9070918	Putative transcriptional regulator			1396
CDS	sce7193	10051352	10050642	Putative DNA-binding protein			1396
]							
[							
Fam: 76	No. of CDS: 2	Dom. COG: 420	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0327	458751	459656	Sulfate transport system permease protein	cysT	5215,6810,16020	555
CDS	sce0328	459656	460561	Sulfate transport system permease protein	cysW	5215,6810,16020	4208
]							
[							
Fam: 77	No. of CDS: 8	Dom. COG: 542	counter: 8 / 8	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0334	470395	466742	ATP-dependent Clp protease, ATP-binding subunit , two ATP-binding domains		166	542
CDS	sce0335	474021	470422	ATPase with chaperone activity, two ATP-bindingdomains		166	542
CDS	sce4390	6199500	6201815	ATPase with chaperone activity, two ATP-bindingdomains		5524	542
CDS	sce4989	7011781	7009076	Endopeptidase Clp	clpA	5524	542
CDS	sce7162	9987367	9989739	ATP-dependent Clp protease, ATP-binding subunit, two ATP-binding domains		166	542

CDS	sce7923	11046065	11043450	ATPase with chaperone activity, two ATP-binding domains		5524	542
CDS	sce8167	11361098	11363707	ATPase with chaperone activity, two ATP-bindingdomains	clpB2	5524	542
CDS	sce8441	11759314	11756477	Endopeptidase ATPase with chaperone activity, two ATP-bindingdomains		166	542

]

[

Fam: 78	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0339	479804	477588	Hypothetical protein			0
CDS	sce8413	11710880	11712928	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8414	11712938	11715181	Putative membrane protein			0

]

[

Fam: 79	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0352	511053	509557	Conserved hypothetical protein/putative secreted protein			0
CDS	sce5067	7113335	7111908	Hypothetical protein			0

]

[

Fam: 80	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0360	522103	521525	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7047	9838371	9838952	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 81	No. of CDS: 3	Dom. COG: 0	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0362	525927	526529	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2978	4083043	4082360	Putative secreted protein			5263
CDS	sce6588	9164128	9163307	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 82	No. of CDS: 4	Dom. COG: 303	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0364	529275	528316	Putative general secretion pathway protein C		5515	3031
CDS	sce3266	4575276	4576163	General secretion pathway protein C	gspC1	5515	3031
CDS	sce9221	12842829	12841846	General secretion pathway protein C fragment	gspC2	5515	3031
CDS	sce9314	12956376	12957347	Putative general secretion pathway protein C		5515	3031

]

[

Fam: 83	No. of CDS: 2	Dom. COG: 652	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0374	543089	543658	Putative peptidyl-prolyl cis-trans isomerase		6457	652
CDS	sce4325	6110237	6109437	Putative peptidyl-prolyl cis-trans isomerase		6457	652

]

[

Fam: 84 No. of CDS: 2 Dom. COG: 595 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0377	547885	546044	Hypothetical metallo-beta-lactamase family protein			595
CDS	sce2612	3531058	3529460	Conserved hypothetical protein			595

]

[

Fam: 85 No. of CDS: 3 Dom. COG: 616 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0378	548077	549885	Protease IV	sppA1	9003,16021	616
CDS	sce8336	11621474	11618784	Protease IV	sppA2	9003,16021	616
CDS	sce8704	12141046	12142905	Signal peptide peptidase	sppA3	9003,16021	616

]

[

Fam: 86 No. of CDS: 2 Dom. COG: 0 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0381	554823	555611	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8508	11858302	11857508	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 87 No. of CDS: 4 Dom. COG: 110(counter: 4 / 4 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0386	559898	559170	Conserved hypothetical protein			1100
CDS	sce1492	2039066	2038476	Gliding motility protein			1100
CDS	sce2413	3253040	3251739	Gliding motility protein		5525,7264	1100
CDS	sce7249	10120073	10120663	Putative MglA1 protein			1100

]

[

Fam: 88 No. of CDS: 3 Dom. COG: 226(counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0390	564273	566141	Putative GTP-binding protein	hflX1	5525	2262
CDS	sce2147	2914087	2912747	GTP-binding protein HflX	hflX2	5525	2262
CDS	sce3166	4351283	4352713	GTP-binding protein HflX		5525	2262

]

[

Fam: 89 No. of CDS: 2 Dom. COG: 50 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0402	581602	582792	Elongation factor (EF)	tufA1	3746,5525,6414	50
CDS	sce0841	1193098	1194288	Elongation factor (EF)	tufA2	3746,5525,6414	50

]

[

Fam: 90 No. of CDS: 5 Dom. COG: 465 counter: 4 / 5 percentage: 80.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0417	603652	605511	Putative membrane bound zinc metallopeptidase		4222,16020,30163	465
CDS	sce1641	2255241	2253418	Putative membrane bound zinc metallopeptidase		4222,16020,30163	465
CDS	sce2762	3766104	3767912	Putative membrane bound zinc metallopeptidase		4222,16020,30163	465
CDS	sce5713	8040810	8042156	Cell division cycle protein 48-related protein			464
CDS	sce7292	10176756	10174810	Putative membrane bound zinc metallopeptidase		4222,16020,30163	465

]

[

Fam: 91 No. of CDS: 9 Dom. COG: 0 counter: 8 / 9 percentage: 88.89%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0422	611525	610515	Hypothetical protein			0

CDS	sce1326	1829374	1828370	Conserved hypothetical protein			0
CDS	sce2172	2934165	2933176	Conserved hypothetical protein			
CDS	sce5585	7864874	7863909	Hypothetical protein			0
CDS	sce8253	11483987	11484598	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8416	11718356	11717460	Hypothetical protein			0
CDS	sce8417	11719167	11718907	Hypothetical protein			0
CDS	sce8841	12336146	12337084	Hypothetical protein			0
CDS	sce8974	12507927	12508355	Hypothetical protein			0

]

[

Fam: 92	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0423	614126	612591	Putative membrane protein			0
CDS	sce5933	8332072	8330624	Putative membrane protein			0

]

[

Fam: 93	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0432	627663	628187	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6607	9198060	9198590	Putative secreted protein			0

]

[

Fam: 94	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0433	628421	629695	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1818	2463834	2464817	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9137	12727777	12726710	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 95	No. of CDS: 8	Dom. COG: 31	counter: 8 / 8	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0438	635558	634173	Cystathionine beta-synthase		6520,16829	31
CDS	sce3525	4928632	4929624	Cysteine synthase A	cysK2	4124,6535	31
CDS	sce4641	6558584	6557595	Cysteine synthase	cysK3	4124,6535	31
CDS	sce4786	6733132	6734022	Cysteine synthase	cysK4	4124,6535	31
CDS	sce5753	8089508	8088558	Cysteine synthase	cysK5	6520,16829	31
CDS	sce5757	8092190	8091129	Cysteine synthase	cysK6	6520,16829	31
CDS	sce7375	10272246	10271290	Cysteine synthase	cysK7	4124,6535	31
CDS	sce8782	12271989	12273389	Cystathionine beta-synthase	cysB	3824,8152	31

]

[

Fam: 96	No. of CDS: 2	Dom. COG: 38	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0443	641875	640043	Chloride channel	eriC	5247,6821,16020	38
CDS	sce7098	9893423	9895258	Chloride channel	eriL	5247,6821,16020	38

]

[

Fam: 97	No. of CDS: 3	Dom. COG: 2003	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0453	650047	649421	DNA repair protein		6281	2003
CDS	sce7501	10446717	10446247	DNA repair protein		6281	2003
CDS	sce7502	10447967	10447332	DNA repair protein RadC		6281	2003

]

[

Fam: 98	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce0454	650697	650044	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7503	10448311	10447964	Bipartite response regulator related protein			0

]

[

Fam: 99	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0460	655505	656617	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4094	5715562	5715879	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5698	8020422	8019352	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 10	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0463	659538	658672	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4497	6342949	6342059	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 10	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0468	666374	663249	Conserved hypothetical protein			0
CDS	sce5902	8297022	8294200	Hypothetical protein			0

]

[

Fam: 10	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0471	670547	668709	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9166	12771058	12772797	Hypothetical protein			0

]

[

Fam: 10	No. of CDS: 2	Dom. COG: 172	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0474	674317	673430	Conserved hypothetical protein			1721
CDS	sce5904	8299882	8298929	Conserved hypothetical protein			1721

]

[

Fam: 10	No. of CDS: 5	Dom. COG: 106	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0475	674649	675806	Alcohol dehydrogenase	adh1	8270	1063
CDS	sce4199	5940371	5941621	Alcohol dehydrogenase	fdh1	8270	1063
CDS	sce5374	7568073	7567039	Threonine dehydrogenase and related Zn-dependent dehydrogenases	gutB	8270	1063
CDS	sce5495	7743113	7744282	Alcohol dehydrogenase	fdh2	8270	1063
CDS	sce7010	9791540	9792691	Threonine dehydrogenase and related Zn-dependent dehydrogenases			1063

]

[

Fam: 10	No. of CDS: 12	Dom. COG: 230	counter: 7 / 12	percentage: 58.33%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0478	677728	679293	Hypothetical protein	yfbK		2304
CDS	sce1015	1435398	1433824	Conserved hypothetical protein yfbK-containing vWFA domain			2304
CDS	sce2918	3980675	3982720	FHA domain protein			1716

CDS	sce3505	4895239	4893986	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4345	6139023	6140588	Hypothetical protein			2304
CDS	sce5360	7540849	7544391	Hypothetical protein			2304
CDS	sce5811	8165499	8168222	Hypothetical protein predicted by Glimmer/Critica			2304
CDS	sce7031	9817412	9821785	Conserved hypothetical protein			0
CDS	sce7902	11012757	11017517	Hypothetical protein			0
CDS	sce7911	11030598	11028979	Hypothetical protein			0
CDS	sce8131	11313076	11311553	Hypothetical protein			2304
CDS	sce9315	12957648	12959501	Conserved hypothetical protein with a vWF type A domain			2304

]

[

Fam: 10	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0479	679557	680414	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8285	11559136	11559948	Putative secreted protein			0

]

[

Fam: 10	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0480	680425	681330	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6930	9669701	9670708	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 10	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0481	682826	681396	Hypothetical protein			0
CDS	sce3164	4347386	4348894	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6727	9380716	9382101	Hypothetical protein			0

]

[

Fam: 10	No. of CDS: 4	Dom. COG: 0	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0485	687866	689257	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2058	2791442	2790642	Hypothetical protein			
CDS	sce3524	4927972	4926839	Putative membrane protein			0
CDS	sce3767	5248257	5249330	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 11	No. of CDS: 2	Dom. COG: 380	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0488	692536	694725	Alpha,alpha-trehalose-phosphate synthase (UDP-forming)	otsA	5992	380
CDS	sce3268	4576971	4579211	Alpha,alpha-trehalose-phosphate synthase (UDP-forming)		5992	380

]

[

Fam: 11	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0489	696583	694742	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6974	9725499	9723589	Hypothetical protein			0

]

[

Fam: 11	No. of CDS: 2	Dom. COG: 223	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0491	697601	698935	Mg2+ transporter	mgtE1	6812,8324,15095,15693	2239
CDS	sce8613	12015324	12013939	Mg2+ transporter	mgtE2	6812,8324,15095,15693	2239

]

[

Fam: 11	No. of CDS: 2	Dom. COG: 625	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0496	704126	703434	Putative glutathione transferase			625
CDS	sce2195	2963048	2962428	Putative glutathione transferase	gst7		625

]

[

Fam: 11	No. of CDS: 2	Dom. COG: 493	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0499	706252	707856	Probable protease		4289,6508	4934
CDS	sce7535	10497935	10495971	kumamolisin		4289,6508	4934

]

[

Fam: 11	No. of CDS: 11	Dom. COG: 137	counter: 10 / 11	percentage: 90.91%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0501	708948	710522	Hypothetical protein			1376
CDS	sce1272	1762702	1764324	Putative secreted protein			1376
CDS	sce1992	2704953	2702884	Similar to glycine-rich protein			1376
CDS	sce2354	3167984	3166494	Hypothetical protein			1376
CDS	sce2592	3505544	3503868	Piccolo protein			1376
CDS	sce2794	3814147	3812435	Putative secreted protein			1376
CDS	sce2932	4015113	4016765	Hypothetical protein			1376
CDS	sce3172	4357652	4356054	Hypothetical protein			0
CDS	sce3607	5049457	5051217	Hypothetical protein			1376
CDS	sce3776	5261288	5262835	Hypothetical protein			1376
CDS	sce7981	11102766	11101408	Hypothetical protein			1376

]

[

Fam: 11	No. of CDS: 5	Dom. COG: 213	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0503	712552	713886	Multicopper oxidase	copA		2132
CDS	sce0798	1123984	1125456	Multicopper oxidase			2132
CDS	sce1180	1634621	1636042	Oxidoreductase	cumA		2132
CDS	sce8100	11269913	11268510	Multicopper oxidase			2132
CDS	sce8102	11270808	11272316	Multicopper oxidase			2132

]

[

Fam: 11	No. of CDS: 3	Dom. COG: 140	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0506	716808	715471	Putative integral membrane protein		16787	1408
CDS	sce7577	10550030	10548765	Putative integral membrane protein		16787	1408
CDS	sce8078	11237842	11239137	Putative integral membrane protein		16787	1408

]

[

Fam: 11	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0512	726736	724325	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce0783	1098544	1096322	Hypothetical protein predicted by Glimmer/Critica			0

CDS	sce2006	2719779	2721887	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 11	No. of CDS: 3	Dom. COG: 165	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0513	727173	729734	Possible Disulfide bond formation protein D precursor		15035,30288	1651
CDS	sce2958	4052082	4050055	Putative secreted protein		15035,30288	1651
CDS	sce9040	12591120	12593117	Conserved hypothetical protein		15035,30288	1651

]

[

Fam: 12	No. of CDS: 2	Dom. COG: 377	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0523	744475	745059	NADH dehydrogenase (ubiquinone)	nuoB1	8137	377
CDS	sce9059	12616538	12617086	NADH dehydrogenase (ubiquinone)	nuoB2	8137	377

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Fam: 12	No. of CDS: 2	Dom. COG: 649	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0525	745713	746927	NADH dehydrogenase (ubiquinone)	nuoD1	5489,6118	649
CDS	sce9061	12617664	12618830	NADH dehydrogenase (ubiquinone).	nuoD2	5489,6118	649

]

[

Fam: 12	No. of CDS: 2	Dom. COG: 100	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0527	748695	750461	NADH dehydrogenase (ubiquinone)	nuoH	6118,1602	1005
CDS	sce7563	10537691	10535754	NADH dehydrogenase subunit 1	ndhA	6118,1602	1005

]

[

Fam: 12	No. of CDS: 5	Dom. COG: 348	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0541	771857	772954	Conserved hypothetical protein			3482
CDS	sce0790	1111253	1109916	Conserved hypothetical protein			3482
CDS	sce7123	9932987	9931779	Conserved hypothetical protein			3482
CDS	sce8752	12226041	12224935	Uncharaterized conserved protein			3482
CDS	sce9073	12635410	12636816	Conserved hypothetical protein			3482

]

[

Fam: 12	No. of CDS: 5	Dom. COG: 438	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0549	782780	781428	Glycogen synthase	glgA1	9058	438
CDS	sce1300	1795773	1796852	Glycosyltransferase		9058	438
CDS	sce4241	6001453	6000188	Glycosyltransferase		9058	438
CDS	sce5461	7690278	7691696	Glycogen synthase	glgA3	9058	438
CDS	sce8918	12440289	12441464	Glycosyltransferase		9058	438

]

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Fam: 12	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0550	785801	783249	Hypothetical protein/Zn-dependent dipeptidase (fragment)			0
CDS	sce1419	1946298	1948337	Putative membrane protein			0

]

[

Fam: 12	No. of CDS: 7	Dom. COG: 2207	counter: 7 / 7	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0553	794642	793644	Transcriptional regulator, AraC family		3700,5622	2207
CDS	sce1946	2641291	2640260	Transcriptional regulator, AraC family		3700,5622	2207
CDS	sce3082	4223462	4222452	Transcriptional regulator, AraC family		3700,5622	2207
CDS	sce3332	4664656	4663616	Transcriptional regulator, AraC family		3700,5622	2207
CDS	sce6357	8863757	8862708	Transcriptional regulator, AraC family		3700,5622,6355	2207
CDS	sce6969	9716458	9717501	Ornithine utilization regulator.	oruR1	3700,5622,6355	2207
CDS	sce8943	12474107	12473049	Transcriptional regulator, AraC family	oruR2	3700,5622	2207

]

[

Fam: 12	No. of CDS: 27	Dom. COG: 0	counter: 18 / 27	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0555	797917	796172	Hypothetical protein-signal peptide and transmembrane prediction			2082
CDS	sce0735	1037450	1039195	Conserved hypothetical protein			0
CDS	sce0796	1121685	1119937	Hypothetical protein-transmembrane prediction			1882
CDS	sce0993	1399667	1401385	Hypothetical protein-transmembrane prediction			0
CDS	sce1022	1445443	1443719	Conserved hypothetical protein			5267
CDS	sce1336	1844277	1842655	Hypothetical protein			0
CDS	sce1500	2057435	2055714	Hypothetical protein-signal peptide			0
CDS	sce2269	3058699	3056999	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2930	4011633	4013336	Hypothetical transmembrane protein			344
CDS	sce3316	4643553	4641952	Hypothetical conserved protein			0
CDS	sce4017	5596189	5594468	Hypothetical protein-transmembrane prediction			1131
CDS	sce4156	5879072	5877372	Putative secreted protein			0
CDS	sce4382	6192123	6190441	Conserved hypothetical protein			0
CDS	sce4595	6496737	6494995	Conserved hypothetical protein			
CDS	sce4603	6506911	6505217	Putative secreted protein			0
CDS	sce4607	6511954	6513627	Hypothetical protein			0
CDS	sce4612	6520696	6518786	Hypothetical protein			0
CDS	sce4902	6883746	6885371	Conserved hypothetical protein			249
CDS	sce5211	7326821	7325052	Hypothetical protein predicted by Glimmer/Critica			1960
CDS	sce5420	7615203	7613386	Putative glycine-rich protein			0
CDS	sce5421	7616997	7615303	Hypothetical protein-signal peptide and transmembrane prediction			0
CDS	sce6915	9649264	9647807	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6920	9657480	9655759	Putative exported protein			0
CDS	sce7739	10783069	10781366	Conserved hypothetical protein with a signal sequence			3028
CDS	sce8662	12090559	12092289	Hypothetical protein-transmembrane prediction			0
CDS	sce8920	12443084	12444718	Hypothetical protein-signal peptide and transmembrane prediction			0
CDS	sce9045	12598959	12600776	Conserved hypothetical protein			0

]

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Fam: 12	No. of CDS: 7	Dom. COG: 1595	counter: 7 / 7	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0558	800074	799529	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce1340	1847917	1847291	RNA polymerase ECF-type sigma factor		3677,3700,6352,16987	1595
CDS	sce2365	3177327	3176719	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595

CDS	sce4901	6882810	6883469	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce5034	7067821	7067102	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce6659	9262378	9261839	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce7743	10786647	10786024	Putative RNA polymerase sigma factor			1595

]

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Fam: 12	No. of CDS: 2	Dom. COG: 118	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0564	807371	808513	D-Alanine-D-alanine ligase	ddlA1	5737,8716,9252	1181
CDS	sce6856	9579067	9578030	D-Alanine-D-alanine ligase B	ddlB	5737,8716,9252	1181

]

[

Fam: 13	No. of CDS: 2	Dom. COG: 397	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0567	810774	813125	Probable uvrD/Rep helicase family protein			3973
CDS	sce5957	8362567	8364711	Putative ATP/GTP binding protein			0

]

[

Fam: 13	No. of CDS: 3	Dom. COG: 477	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0571	820683	819277	Permease of the major facilitator superfamily		5215,6810,16021	477
CDS	sce1009	1428380	1427094	Permease of the major facilitator superfamily		5215,6810,16021	477
CDS	sce4660	6580009	6578627	Permease of the major facilitator superfamily		5215,6810,16021	477

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[

Fam: 13	No. of CDS: 2	Dom. COG: 123	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0580	830367	831902	Phytoene dehydrogenase	crtI1	6118,16491	1233
CDS	sce0585	837322	835769	Putative methoxyneurosporene dehydrogenase	crtD	6118,16491	1233

]

[

Fam: 13	No. of CDS: 10	Dom. COG: 196	counter: 10 / 10	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0587	838800	840566	Probable acyl-CoA dehydrogenase			1960
CDS	sce1166	1619637	1618471	Acyl-Coenzyme A dehydrogenase, short/branched chain			1960
CDS	sce1991	2702749	2701637	Glutaryl-CoA dehydrogenase			1960
CDS	sce1997	2712861	2711608	Putative Acyl-CoA dehydrogenase			1960
CDS	sce2853	3894728	3895867	Acyl-CoA dehydrogenase			1960
CDS	sce6907	9638913	9640082	Acyl-CoA dehydrogenase			1960
CDS	sce6972	9719803	9720942	Acyl-CoA dehydrogenase			1960
CDS	sce7626	10614193	10615920	Acyl-CoA dehydrogenase			1960
CDS	sce8921	12446125	12444851	Acyl-CoA dehydrogenase			1960
CDS	sce9239	12865006	12863843	Isovaleryl-CoA dehydrogenase			1960

]

[

Fam: 13	No. of CDS: 2	Dom. COG: 230	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0595	852007	850037	Conserved hypothetical protein			2304
CDS	sce8375	11660478	11662085	Conserved hypothetical protein with a vWF type A domain			2304

]

[

Fam: 13	No. of CDS: 2	Dom. COG: 846	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0596	852265	853074	Transcriptional regulatory protein, Sir2 family		3677,5677,6342	846
CDS	sce3874	5390035	5389169	Conserved hypothetical protein		3677,5677,6342	846

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[

Fam: 13	No. of CDS: 4	Dom. COG: 196(	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0600	855406	856587	Putative hydroxylase			1960
CDS	sce2876	3922957	3921761	Putative hydroxylase			1960
CDS	sce4164	5888883	5890136	Hypothetical protein			1960
CDS	sce4852	6814522	6815724	Hypothetical protein			1960

]

[

Fam: 13	No. of CDS: 2	Dom. COG: 123(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0611	878851	877214	Putative Phytoene dehydrogenase	crtI2	16117,5066	1233
CDS	sce3350	4687042	4685528	Putative phytoene dehydrogenase	crtI3		1233

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Fam: 13	No. of CDS: 4	Dom. COG: 767	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0613	880331	879468	Putative ABC transporter permease protein			767
CDS	sce3695	5166759	5167649	Putative ABC transport system permease protein			767
CDS	sce3696	5167665	5168522	Putative ABC transport system permease protein			767
CDS	sce8301	11577855	11577055	Putative ABC transport system permease protein			767

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Fam: 13	No. of CDS: 2	Dom. COG: 215	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0616	881981	883570	Cysteinyl-tRNA synthetase	cysS1	4817,5524,6423	215
CDS	sce5320	7480537	7482075	Cysteinyl-tRNA synthetase	cysS2	4817,5524,6423	215

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Fam: 14	No. of CDS: 3	Dom. COG: 484	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0617	883729	884685	Probable DnaJ molecular chaperone		3754,6457	2214
CDS	sce1669	2285650	2286735	Putative dnaJ protein			484
CDS	sce5852	8224617	8223517	Putative dnaJ protein			484

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[

Fam: 14	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0627	897273	896458	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6873	9599282	9600103	Hypothetical protein predicted by Glimmer/Critica			0

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[

Fam: 14	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce0634	903842	904954	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce0636	906905	908065	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7367	10260591	10259731	Hypothetical protein predicted by Glimmer/Critica			0

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[

Fam: 14	No. of CDS: 19	Dom. COG: 0	counter: 16 / 19	percentage: 84.21%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0635	904975	906546	Putative secreted protein			0
CDS	sce0637	908086	909645	Putative secreted protein			0
CDS	sce1605	2197448	2195745	PE_PGRS family protein			0
CDS	sce1607	2200428	2198701	PE_PGRS family protein			0
CDS	sce1610	2205383	2203728	PE_PGRS family protein			1511
CDS	sce3573	5000355	4998814	PGRS family protein			0
CDS	sce3603	5044215	5045930	PE_PGRS family protein			0
CDS	sce5244	7385429	7386955	PE_PGRS family protein			0
CDS	sce6091	8529417	8531063	PE_PGRS family protein			0
CDS	sce6131	8595490	8593850	Conserved hypothetical protein			
CDS	sce6344	8841214	8842806	Conserved hypothetical protein			0
CDS	sce6711	9341318	9342964	Putative exported protein with glycine-rich central und C-terminal region			0
CDS	sce7191	10048032	10049867	PE-PGRS family protein			0
CDS	sce7381	10277966	10277601	Putative PE-PGRS family protein			1429
CDS	sce8489	11822438	11824090	Conserved hypothetical protein			0
CDS	sce8490	11824111	11825682	Putative dehydrogenase/GMP reductase			0
CDS	sce8764	12249343	12247787	Partially conserved glycine-rich hypothetical protein			0
CDS	sce8871	12369128	12370681	Partially conserved glycine-rich hypothetical protein			0
CDS	sce9272	12904655	12903015	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 14	No. of CDS: 3	Dom. COG: 1053	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0639	913756	915432	L-Aspartate oxidase	nadB		29
CDS	sce6554	9122202	9124115	Succinate dehydrogenase	sdhA1		1053
CDS	sce8308	11585222	11587237	Succinate dehydrogenase	sdhA2		1053

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Fam: 14	No. of CDS: 4	Dom. COG: 480	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0644	919034	921142	Elongation factor (EF)	fusA1	3746,5525,6414	480
CDS	sce0840	1190974	1193088	Elongation factor (EF)	fusA2	5525	480
CDS	sce1273	1766452	1764341	Elongation factor (EF	fusA3	5525,6412	480
CDS	sce6179	8647824	8646232	Peptide chain release factor 3	prfC	5525,5737,6415	4108

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[

Fam: 14	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0653	929114	929686	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce0654	930102	930680	Hypothetical protein predicted by Glimmer/Critica			0

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[

Fam: 14	No. of CDS: 2	Dom. COG: 515	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0655	932561	930870	Protein kinase		4672,4674,5524,6468	515
CDS	sce5806	8154287	8152602	Protein kinase		4674,4672,5524,6468	515

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Fam: 14	No. of CDS: 12	Dom. COG: 1131	counter: 8 / 12	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0659	935664	936449	Sodium ABC transporter ATP-binding protein	natA	4009,5524,6810,16020	4555
CDS	sce0754	1060040	1061119	ABC transporter, ATP-binding protein		4009,5524,6810,16020	1131
CDS	sce2431	3274970	3273894	Sulfate/thiosulfate import ATP-binding protein cysA		5524,16887	3842
CDS	sce2534	3418405	3417233	Putative ABC-2 type transport system ATP-binding protein		4009,5524,6810,16020	1131
CDS	sce4421	6245501	6246583	Putative ABC-2 type transport system ATP-binding protein		4009,5524,6810,16020	1131
CDS	sce5573	7849941	7848997	Putative ABC transporter ATP-binding protein		4009,5524,6810,16020	1131
CDS	sce5790	8132503	8131496	Putative ABC transporter, ATP-binding protein		4009,5524,6810,16020	1131
CDS	sce6750	9410376	9409378	ABC transporter, ATP-binding protein		4009,5524,6810,16020	4586
CDS	sce6953	9699382	9700449	Putative ABC-2 type transport system ATP-binding protein		4009,5524,6810,16020	4586
CDS	sce7371	10267372	10266128	ABC-2 type transport system ATP-binding protein		4009,5524,6810,16020	1131
CDS	sce8809	12303492	12302662	ABC transporter ATP-binding protein		4009,5524,6810,16020	1131
CDS	sce9074	12636813	12637775	ABC transporter, ATP-binding protein		4009,5524,6810,16020	1131

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Fam: 14	No. of CDS: 16	Dom. COG: 667	counter: 15 / 16	percentage: 93.75%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0671	956425	955448	Probable oxidoreductase/voltage-gated potassium channel beta-1 subunit (K+ channel beta-1 subunit) (Kv-beta-1)			667
CDS	sce0715	1017555	1018592	Probable oxidoreductase			667
CDS	sce1193	1653976	1652969	Probable oxidoreductase			656
CDS	sce1524	2087531	2086521	Probable oxidoreductase			667
CDS	sce1969	2672677	2673660	Putative oxidoreductase			667
CDS	sce2134	2896644	2897606	Put. oxidoreductase; aldo-keto family			667
CDS	sce2610	3526772	3527767	Putative oxidoreductase			667
CDS	sce2819	3848349	3849446	Putative Oxidoreductase			667
CDS	sce4235	5991780	5992865	oxidoreductase	mocA		667
CDS	sce4728	6671280	6670297	Probable oxidoreductase			667
CDS	sce5048	7085025	7084042	Probable oxidoreductase			667
CDS	sce5264	7407947	7408918	Putative sugar-phosphate dehydrogenase			667
CDS	sce7582	10555833	10556843	Aldo-keto reductase family 1			667
CDS	sce8574	11966228	11967088	Putative oxidoreductase			667
CDS	sce8849	12342312	12343394	Probable oxidoreductase			667
CDS	sce8981	12516140	12515055	Oxidoreductase			667

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[

Fam: 15	No. of CDS: 11	Dom. COG: 1012	counter: 11 / 11	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0676	962756	961287	Succinylglutamic semialdehyde dehydrogenase	astD	8152,16491	1012
CDS	sce2164	2928034	2926451	Dehydrogenase		8152,16491	1012
CDS	sce2550	3444566	3443127	Aldehyde dehydrogenase		8152,16491	1012
CDS	sce2985	4090439	4088826	Putative succinate-semialdehyde dehydrogenase (NAD(P)(+))		8152,16491	1012
CDS	sce3095	4238399	4237014	Putative aldehyde dehydrogenase		8152,16491	1012
CDS	sce4459	6290919	6292559	1-pyrroline-5-carboxylate dehydrogenase	rocA	3842,5759,6561	1012
CDS	sce4495	6339871	6341451	Putative aldehyde dehydrogenase		8152,16491	1012
CDS	sce5007	7033767	7032373	Putative aldehyde dehydrogenase (NAD(+))		8152,16491	1012

CDS	sce5973	8379800	8381206	Succinate-semialdehyde dehydrogenase (NAD(P)(+))		8152,16491	1012
CDS	sce6401	8934870	8933422	Methylmalonate-semialdehyde dehydrogenase	mmsA		1012
CDS	sce9189	12800314	12798872	Aldehyde dehydrogenase (NAD(+)).		8152,16491	1012

]

[

Fam: 15	No. of CDS: 2	Dom. COG: 622	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0677	963273	964838	Hypothetical protein		16787	622
CDS	sce3568	4993031	4994482	Hypothetical protein		16787	0

]

[

Fam: 15	No. of CDS: 2	Dom. COG: 159	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0681	968241	967684	ECF-family RNA polymerase sigma factor			1595
CDS	sce4890	6868518	6869135	Hypothetical protein			1595

]

[

Fam: 15	No. of CDS: 4	Dom. COG: 103	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0689	983613	985106	Conserved hypothetical protein			1032
CDS	sce5304	7458415	7457027	Conserved hypothetical protein			1032
CDS	sce5467	7704645	7703242	Conserved hypothetical protein			1032
CDS	sce5522	7778300	7779730	Hypothetical protein predicted by Glimmer/Critica			1032

]

[

Fam: 15	No. of CDS: 2	Dom. COG: 139	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0690	985125	985961	Fatty acid desaturase		16491	1398
CDS	sce7238	10104029	10105030	Fatty acid desaturase		16491	1398

]

[

Fam: 15	No. of CDS: 5	Dom. COG: 0	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0691	985963	986397	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6571	9142202	9141726	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6572	9142693	9142148	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6573	9143162	9142728	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6574	9143664	9143239	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 15	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0697	991218	990766	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce0983	1389887	1388931	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1229	1700107	1699235	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 15	No. of CDS: 4	Dom. COG: 513	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce0700	999287	997413	ATP-independent RNA helicase	deaD1	5524,8026	513
CDS	sce3532	4938708	4940144	Superfamily II DNA and RNA helicases	deaD2	5524,8026	513
CDS	sce3615	5060165	5057727	Superfamily II DNA and RNA helicases		5524,8026	513
CDS	sce5308	7462942	7461044	Cold-shock DEAD-box protein A homolog	deaD3	5524,8026	513

]

[

Fam: 15	No. of CDS: 2	Dom. COG: 3812	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0725	1027441	1027947	Conserved hypothetical protein			3812
CDS	sce0957	1355505	1354993	Conserved hypothetical protein			3812

]

[

Fam: 15	No. of CDS: 6	Dom. COG: 3344	counter: 6 / 6	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0729	1030462	1031781	Probable reverse transcriptase/maturase family protein		3723,3964,6278	3344
CDS	sce5539	7805195	7803876	Integron/retron-type RNA-directed DNA polymerase (Reverse transcriptase)		3723,3964,6278	3344
CDS	sce6319	8812184	8810865	Integron/retron-type RNA-directed DNA polymerase (Reverse transcriptase)		3723,3964,6278	3344
CDS	sce6615	9206786	9205479	Group II intron, maturase		3723,3964,6278	3344
CDS	sce6637	9233168	9232476	Reverse transcriptase			3344
CDS	sce9281	12915914	12917068	Reverse transcriptase/maturase		3723,3964,6278	3344

]

[

Fam: 16	No. of CDS: 5	Dom. COG: 0	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0730	1031887	1033032	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4009	5582147	5581332	Putative secreted protein			0
CDS	sce4181	5914369	5913560	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4942	6948670	6949650	Putative membrane protein			0
CDS	sce5493	7742040	7741177	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 16	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0731	1033933	1033082	Conserved hypothetical protein			0
CDS	sce8968	12500898	12500050	Predicted nucleotide-diphosphate-sugar epimerase			702

]

[

Fam: 16	No. of CDS: 3	Dom. COG: 2207	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0732	1033984	1034898	Transcriptional regulator, AraC family		3700,5622	2207
CDS	sce4234	5991722	5990799	Arabinose operon regulatory protein.		3700,5622,6355	4753
CDS	sce8850	12343452	12344246	Transcriptional regulator, AraC family		3700,5622	2207

]

[

Fam: 16	No. of CDS: 2	Dom. COG: 2046	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0740	1043552	1045288	Sulfate adenylyltransferase		103,4781	2046
CDS	sce5751	8087862	8086117	Sulfate adenylyltransferase		103,4781	2046

]

[

Fam: 16	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0745	1050328	1049246	Putative secreted protein			0
CDS	sce5538	7802101	7803378	Conserved hypothetical protein			0
CDS	sce7836	10925989	10927110	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 16	No. of CDS: 11	Dom. COG: 0	counter: 11 / 11	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0746	1050789	1052111	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3049	4178169	4179341	Putative secreted protein			0
CDS	sce3976	5535242	5536510	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4171	5896584	5895280	Conserved hypothetical protein			0
CDS	sce4375	6184330	6185652	Conserved hypothetical protein			0
CDS	sce4808	6762620	6764242	Hypothetical protein			0
CDS	sce5735	8064801	8063017	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6599	9189589	9188513	Conserved hypothetical protein			0
CDS	sce7437	10362690	10361623	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7449	10378661	10377480	Putative secreted protein			0
CDS	sce9187	12796340	12797830	Tenascin precursor			0

]

[

Fam: 16	No. of CDS: 17	Dom. COG: 350	counter: 8 / 17	percentage: 47.06%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0748	1053436	1054851	Ricin precursor and Poly(3-hydroxybutyrate) depolymerase fusion			3509
CDS	sce1896	2572370	2571156	Putative esterase			3509
CDS	sce2743	3733714	3736512	Putative secreted protein			0
CDS	sce3276	4588704	4589774	Esterase/lipase/thioesterase family protein		3824	400
CDS	sce3398	4748519	4749718	endo-1,4-beta-glucanase		3824	0
CDS	sce4100	5722762	5721587	Probable secreted esterase		3824	3509
CDS	sce4178	5908462	5909532	Hypothetical protein predicted by Glimmer/Critica			4188
CDS	sce4590	6489107	6489799	Conserved hypothetical protein			0
CDS	sce4592	6490804	6492426	Alpha-L-arabinofuranosidase precursor	abfB		0
CDS	sce4605	6509392	6510480	Conserved hypothetical protein			3509
CDS	sce4606	6510607	6511809	Putative PHB depolymerase		3824	3509
CDS	sce5021	7049165	7048185	Putative hydrolase		3824	3509
CDS	sce7481	10425702	10424530	Putative secreted esterase		3824	3509
CDS	sce7736	10775188	10776300	Putative secreted protein			0
CDS	sce7850	10945912	10947171	Alpha-L-arabinofuranosidase precursor			3534
CDS	sce7853	10948478	10949803	Exported O-glycosyl hydrolase			0
CDS	sce8927	12451624	12450554	Esterase			3509

]

[

Fam: 16	No. of CDS: 6	Dom. COG: 277	counter: 6 / 6	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0752	1057499	1058857	Putative glycolate oxidase			277
CDS	sce2118	2871000	2867686	Putative oxidoreductase			277
CDS	sce4149	5868338	5869744	Oxidoreductase			277
CDS	sce5078	7125885	7124368	D-lactate dehydrogenase	glcD		277
CDS	sce9031	12578273	12576219	Putative alkyl-dihydroxyacetonephosphate synthase			277
CDS	sce9321	12965723	12967609	Alkyldihydroxyacetonephosphate synthase, putative			277

]

[

Fam: 16	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0753	1059635	1058940	Hypothetical protein			0
CDS	sce4531	6386761	6387354	Hypothetical protein			0

]

[

Fam: 16	No. of CDS: 2	Dom. COG: 177(	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0762	1066453	1068705	Prolyl endopeptidase		4252,6508	1505
CDS	sce8590	11985629	11987767	Prolyl oligopeptidase		4252,6508	1770

]

[

Fam: 17	No. of CDS: 2	Dom. COG: 136(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0766	1074226	1073108	Anti-anti sigma factor protein			1366
CDS	sce6321	8814782	8813730	Anti-anti sigma factor protein			1366

]

[

Fam: 17	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0771	1080381	1078609	Hypothetical protein			0
CDS	sce8379	11669168	11667318	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 17	No. of CDS: 2	Dom. COG: 231(	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0773	1082196	1083929	Hypothetical protein			
CDS	sce1429	1962592	1964286	Hypothetical protein			2319

]

[

Fam: 17	No. of CDS: 5	Dom. COG: 643	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0777	1090059	1087867	CheA-like hybrid histidine kinase		4871,5622,6935,7165	643
CDS	sce1226	1694931	1696619	Chemotaxis protein CheA	cheA2	5524	643
CDS	sce1594	2177137	2179401	Chemotaxis sensor histidine kinase CheA	cheA3	7165,16301	643
CDS	sce2203	2971607	2969889	Putative chemotaxis protein CheA	cheA4	7165,16301	643
CDS	sce2657	3593960	3596026	Chemotaxis protein	cheA5	7165,16301	643

]

[

Fam: 17	No. of CDS: 2	Dom. COG: 454	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0789	1109144	1109944	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3978	5537773	5538594	Conserved hypothetical protein		8080	454

]

[

Fam: 17	No. of CDS: 3	Dom. COG: 354(	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0799	1127692	1125482	Putative alkaline phosphatase		8152	3540
CDS	sce1179	1632909	1634534	Putative alkaline phosphatase	phoD	8152	3540
CDS	sce5883	8262981	8265233	phosphodiesterase/alkaline phosphatase D		8152	3540

]

[

Fam: 17	No. of CDS: 2	Dom. COG: 139	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0812	1141965	1141192	Fatty acid desaturase		16491	1398
CDS	sce6078	8513876	8513103	Fatty acid desaturase		16491	1398

]

[

Fam: 17	No. of CDS: 3	Dom. COG: 491	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0814	1143535	1144974	Hypothetical protein			0
CDS	sce5875	8254499	8255359	Hypothetical protein			491
CDS	sce6832	9536553	9537863	Beta-lactamase-like protein			491

]

[

Fam: 17	No. of CDS: 2	Dom. COG: 119	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0822	1169724	1168354	Chromosome partition protein fragment		4009,5524,6810,16020	1196
CDS	sce7532	10487563	10488933	Conserved hypothetical protein			4637

]

[

Fam: 17	No. of CDS: 2	Dom. COG: 126	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0825	1172032	1173498	Conserved hypothetical protein			1262
CDS	sce0826	1173498	1174880	Conserved hypothetical protein			1262

]

[

Fam: 18	No. of CDS: 7	Dom. COG: 0	counter: 5 / 7	percentage: 71.43%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0831	1181353	1180220	Hypothetical protein predicted by Glimmer/Critica			2304
CDS	sce2874	3919356	3920555	Conserved hypothetical protein			0
CDS	sce3319	4648558	4647305	Putative secreted protein			0
CDS	sce3392	4742512	4743690	Putative secreted protein			0
CDS	sce3556	4970203	4968983	LPXTG-motif cell wall anchor domain protein			0
CDS	sce5231	7357638	7359110	Hypothetical protein			0
CDS	sce7190	10047766	10046630	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain			2304

]

[

Fam: 18	No. of CDS: 2	Dom. COG: 441	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0833	1181803	1183359	Hypothetical protein predicted by Glimmer/Critica		16020	4412
CDS	sce4527	6382818	6383525	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 18	No. of CDS: 2	Dom. COG: 275	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0851	1205971	1204874	Putative periplasmic protein			0
CDS	sce6262	8749975	8751429	Probable lysophospholipase L1 and related esterases			2755

]

[

Fam: 18	No. of CDS: 3	Dom. COG: 0	counter: 1 / 3	percentage: 33.33%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0856	1213477	1217679	Tetratricopeptide repeat protein			2206

CDS	sce1692	2312792	2313937	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7783	10844113	10847256	Hypothetical protein			3468

]

[

Fam: 18	No. of CDS: 3	Dom. COG: 568	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0858	1219950	1220777	RNA polymerase sigma factor		3677,3700,6352,16987	568
CDS	sce5869	8246527	8245676	RNA polymerase sigma factor		3677,3700,6352,16987	568
CDS	sce9054	12611581	12612912	RNA polymerase sigma factor rpoD			1191

]

[

Fam: 18	No. of CDS: 2	Dom. COG: 123	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0859	1221845	1221012	Conserved hypothetical protein			1235
CDS	sce9034	12581944	12582789	Hypothetical protein			1235

]

[

Fam: 18	No. of CDS: 7	Dom. COG: 0	counter: 4 / 7	percentage: 57.14%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0865	1230755	1229289	Conserved hypothetical protein			0
CDS	sce1805	2447949	2446774	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1806	2448121	2449416	Hypothetical protein			0
CDS	sce2323	3129040	3131478	Conserved hypothetical protein			2133
CDS	sce3043	4170616	4169348	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4514	6370001	6368262	Hypothetical protein			2133
CDS	sce5080	7129893	7128697	Conserved hypothetical protein			2133

]

[

Fam: 18	No. of CDS: 2	Dom. COG: 337	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0872	1239393	1238083	3-Dehydroquinate synthase	aroB1	3856,9073	337
CDS	sce4842	6803159	6801549	3-Dehydroquinate synthase	aroB2	3856,9073	337

]

[

Fam: 18	No. of CDS: 2	Dom. COG: 100	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0875	1242033	1243367	UDP-glucose/GDP-mannose dehydrogenase		6118	677
CDS	sce2793	3812249	3810948	Conserved hypothetical protein	rkpK		1004

]

[

Fam: 18	No. of CDS: 2	Dom. COG: 214	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0882	1251808	1252539	Glycosyltransferase			2148
CDS	sce3584	5013040	5014437	Glycosyltransferase			2148

]

[

Fam: 19	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0883	1253990	1252614	Polysaccharide polymerase	wzy1		0
CDS	sce3085	4225962	4227491	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 19	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce0885	1257690	1255225	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3580	5008191	5005843	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 19	No. of CDS: 3	Dom. COG: 438	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0888	1260058	1261203	Glycosyltransferase		9058	438
CDS	sce1036	1464364	1465593	Glycosyltransferase		9058	438
CDS	sce7321	10213439	10214704	Glycosyltransferase		9058	438

]

[

Fam: 19	No. of CDS: 3	Dom. COG: 1181	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0890	1265440	1261883	D-Alanine-D-alanine ligase / aminopeptidase	ddlA2		1181
CDS	sce2763	3768415	3769551	Putative D-alanine--D-alanine ligase A			1181
CDS	sce5442	7640871	7641956	Aminopeptidase	dmpA		3191

]

[

Fam: 19	No. of CDS: 3	Dom. COG: 210	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0891	1265620	1268082	ATP-dependend DNA helicase	pcrA	3677,4003,5524,6281	210
CDS	sce3530	4936739	4933470	ATP-dependent DNA helicase	uvrD	3677,4003,5524,6281	210
CDS	sce7600	10578432	10576375	ATP-dependent DNA helicase.		3677,4003,5524,6281	210

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[

Fam: 19	No. of CDS: 2	Dom. COG: 477	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0894	1271338	1272561	Permease of the major facilitator superfamily		5215,6810,16021	477
CDS	sce2060	2793642	2794976	Putative membrane protein			477

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[

Fam: 19	No. of CDS: 5	Dom. COG: 466	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0897	1278006	1275571	ATP-dependent protease La	lon1	4176,5524,6510	466
CDS	sce2838	3871505	3873919	ATP-dependent protease La	lon2	4176,5524,6510	466
CDS	sce3149	4326749	4329241	Endopeptidase LA	lon3	4176,5524,6510	466
CDS	sce4504	6358246	6355847	ATP-dependent protease La	lon4	4176,5524,6510	466
CDS	sce5003	7029043	7026590	ATP-dependent protease La	lon5	4176,5524,6510	466

]

[

Fam: 19	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0920	1305035	1305925	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3870	5384194	5383307	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 19	No. of CDS: 2	Dom. COG: 583	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0924	1310389	1311327	Transcriptional regulator, LysR family			583
CDS	sce6754	9417353	9418291	Transcriptional regulator, LysR family			583

]

[

Fam: 19	No. of CDS: 2	Dom. COG: 1217	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0926	1313773	1311887	GTP-binding protein		5525,6412	1217
CDS	sce3836	5337347	5335545	GTP-binding protein LepA	lepA	5525	481

]

[

Fam: 20	No. of CDS: 3	Dom. COG: 1629	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0927	1314370	1316571	TonB-dependent receptor, putative		4872,5215,6810,16020	1629
CDS	sce5824	8179065	8181053	TonB-dependent receptor, putative			1629
CDS	sce7062	9854974	9857583	TonB-dependent receptor		8565,15031,16020,30288	1629

]

[

Fam: 20	No. of CDS: 3	Dom. COG: 3808	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0934	1325337	1327826	Inorganic pyrophosphatase		9678,15992,16020	3808
CDS	sce2989	4096983	4099199	Inorganic diphosphatase	rrpP	9678,15992,16020	3808
CDS	sce5649	7951837	7949783	Vacuolar-type H+-pyrophosphatase	ppa	4427,9678,15992,16020	0

]

[

Fam: 20	No. of CDS: 2	Dom. COG: 2355	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0943	1337660	1336581	Putative dipeptidase		4237,6508,8239	2355
CDS	sce5830	8187897	8186872	Putative peptidase		4237,6508,8239	0

]

[

Fam: 20	No. of CDS: 2	Dom. COG: 741	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0945	1341683	1339086	Soluble lytic murein transglycosylase	mltE		741
CDS	sce6155	8622874	8620553	Exported transglycosylase			741

]

[

Fam: 20	No. of CDS: 2	Dom. COG: 3083	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0950	1346209	1348398	Putative membrane protein		8152,8484	3119
CDS	sce0951	1348395	1350422	Conserved hypothetical protein		8152,8484	3083

]

[

Fam: 20	No. of CDS: 2	Dom. COG: 4637	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0953	1352305	1351019	Putative ATPase			4637
CDS	sce7545	10514591	10515820	Conserved hypothetical protein			4637

]

[

Fam: 20	No. of CDS: 4	Dom. COG: 0	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0958	1358860	1355720	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1237	1711365	1713527	Hypothetical protein			574
CDS	sce5363	7549758	7546687	Conserved hypothetical protein			0
CDS	sce7837	10927200	10929272	Putative secreted protein			0

]

[

Fam: 20	No. of CDS: 12	Dom. COG: 0	counter: 8 / 12	percentage: 66.67%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0965	1367982	1366981	Glycosyl hydrolase family 11 member			0
CDS	sce0998	1410899	1412701	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2175	2938256	2936739	PE_PGRS family protein			0
CDS	sce2212	2981575	2983041	Putative topoisomerase			446
CDS	sce2729	3705521	3707065	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2869	3914994	3915962	Putative secreted protein			0
CDS	sce4005	5575883	5574648	Glycosyl hydrolases family 11 member			0
CDS	sce5260	7403011	7404327	Conserved hypothetical protein			0
CDS	sce5436	7634069	7632945	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce5551	7817355	7818560	Endoglucanase			2730
CDS	sce7001	9781115	9779823	Put. Polysaccharide deacetylase		5975	726
CDS	sce7672	10674437	10673397	Conserved hypothetical protein			0

]

[

Fam: 20	No. of CDS: 2	Dom. COG: 2017	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0968	1372774	1371527	Aldose 1-epimerase	galM2	4034	2017
CDS	sce8213	11434728	11435717	Aldose 1-epimerase	galM1	4034	2017

]

[

Fam: 20	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0973	1379420	1379749	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce0974	1380014	1380343	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 21	No. of CDS: 2	Dom. COG: 346	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0979	1385371	1385736	Metallothiol transferase fosB			346
CDS	sce3980	5540727	5541113	Lactoylglutathione lyase and related lyases			346

]

[

Fam: 21	No. of CDS: 3	Dom. COG: 1309	counter: 1 / 3	percentage: 33.33%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0980	1386721	1385762	Putative transcriptional regulator			1609
CDS	sce6697	9316587	9317582	Putative transcriptional regulator		16481,16566	0
CDS	sce7023	9806682	9807476	Transcriptional regulator, TetR family			1309

]

[

Fam: 21	No. of CDS: 2	Dom. COG: 3573	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0981	1386927	1388108	Putative oxidoreductase		4497,6725	3573
CDS	sce8961	12494609	12493413	Putative oxidoreductase		4497,6725	4989

]

[

Fam: 21	No. of CDS: 3	Dom. COG: 5018	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0985	1391022	1391597	Predicted exonuclease		4527,5622	5018
CDS	sce4229	5983091	5983645	Putative exonuclease		4527,5622	5018
CDS	sce8842	12337242	12337886	Hypothetical protein T07A9.5a		4527,5622	5018

]

[

Fam: 21	No. of CDS: 2	Dom. COG: 583	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce0992	1398110	1399045	Transcriptional regulator, LysR family			583
CDS	sce8076	11235346	11234417	Transcriptional regulator, LysR family			583

]

[

Fam: 21	No. of CDS: 9	Dom. COG: 113(	counter: 7 / 9	percentage: 77.78%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1003	1420049	1420993	ABC transporter, ATP-binding protein		5524,16887	1123
CDS	sce1112	1564586	1565272	ABC transporter, ATP-binding protein	lolD	4009,5524,6810,16020	1136
CDS	sce1636	2247553	2248287	ABC transporter, ATP-binding protein		4009,5524,6810,16020	1136
CDS	sce4823	6777728	6776997	ABC transporter, ATP-binding protein		4009,5524,6810,16020	1136
CDS	sce6717	9351877	9351179	ABC transporter, ATP-binding protein		4009,5524,6810,16020	1136
CDS	sce7227	10089815	10090615	ABC transporter, ATP-binding protein		4009,5524,6810,16020	1136
CDS	sce7972	11094525	11095343	Conserved hypothetical protein		4009,5524,6810,16020	2884
CDS	sce8643	12055842	12055078	Putative ABC transporter ATP-binding protein		4009,5524,6810,16020	1136
CDS	sce8833	12327888	12328607	ABC transporter, ATP-binding protein		4009,5524,6810,16020	1136

]

[

Fam: 21	No. of CDS: 3	Dom. COG: 845	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1004	1420990	1422111	Putative membrane protein		16020	845
CDS	sce4824	6778980	6777730	Putative HlyD family secretion protein	macA		845
CDS	sce7226	10088357	10089811	Conserved hypothetical protein		8565,9306,16020	845

]

[

Fam: 21	No. of CDS: 5	Dom. COG: 577	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1005	1422108	1423334	Macrolide-specific ABC-type efflux carrier.		16020	577
CDS	sce1006	1423277	1424578	Hypothetical protein		16020	577
CDS	sce4822	6777003	6775792	Hypothetical protein	macB	16020	577
CDS	sce7228	10090612	10091832	Hypothetical protein		16020	577
CDS	sce7229	10091829	10093061	Conserved hypothetical protein	salY	16020	577

]

[

Fam: 21	No. of CDS: 4	Dom. COG: 0	counter: 2 / 4	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1020	1440856	1442082	Putative nucleotide-binding protein			5263
CDS	sce2826	3855247	3856362	Putative membrane protein			0
CDS	sce2835	3867548	3868558	Hypothetical protein			0
CDS	sce6046	8481821	8480802	Putative S-layer protein fragment			457

]

[

Fam: 21	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1023	1445811	1446659	Putative exported protein			0
CDS	sce2271	3061223	3062605	Hypothetical protein predicted by Glimmer/Critica			0

CDS	sce2929	4011598	4009943	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 22	No. of CDS: 4	Dom. COG: 438	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1025	1448968	1450284	Glycosyltransferase		9058	438
CDS	sce1301	1796849	1798060	Glycosyltransferase		9058	438
CDS	sce3582	5011056	5009533	Glycosyltransferase		9058	438
CDS	sce4240	5999987	5998635	Glycosyltransferase		9058	438

]

[

Fam: 22	No. of CDS: 3	Dom. COG: 1033	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1029	1455297	1457930	Exporter of the RND superfamily			1033
CDS	sce3440	4798895	4796406	Membrane protein, putative			1033
CDS	sce7413	10321522	10319063	Putative membrane protein			0

]

[

Fam: 22	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1035	1463378	1464097	Putative exported protein			0
CDS	sce6292	8783022	8783471	Putative secreted protein			0
CDS	sce8092	11258404	11257955	Conserved hypothetical protein			0

]

[

Fam: 22	No. of CDS: 11	Dom. COG: 451	counter: 6 / 11	percentage: 54.55%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1037	1465712	1466707	NDP-sugar oxidoreductase		3824,9225	451
CDS	sce3447	4811102	4812118	UDP-glucose 4-epimerase	galE1	3978,6012	1087
CDS	sce3760	5241186	5242232	UDP-glucose 4-epimerase	galE3	3824,9225	1087
CDS	sce4784	6731372	6730374	UDP-glucose 4-epimerase	galE5	3824,9225	1087
CDS	sce6687	9298621	9299559	dTDP-glucose 4,6-dehydratase	rmlB1	3824,9225,8460	451
CDS	sce6771	9441058	9442176	NDP-sugar oxidoreductase similar to UDP-glucose 4-epimerase		3824,9225	1087
CDS	sce6772	9442173	9443309	Sugar nucleotide epimerase		3824,9225	451
CDS	sce6778	9449213	9450220	dTDP-glucose 4,6-dehydratase	rmlB2	3824,9225,3824	451
CDS	sce7377	10274009	10274968	NDP-sugar oxidoreductase		3824,9225	451
CDS	sce8935	12463791	12465065	Probable UDP-glucose 4-epimerase	galE6	3824,9225	1087
CDS	sce8939	12468799	12469809	dTDP-glucose 4,6-dehydratase	rmlB3	3824,9225,8460	451

]

[

Fam: 22	No. of CDS: 2	Dom. COG: 696	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1044	1475792	1474161	Phosphoglycerate mutase	pgm1	4619,6007	696
CDS	sce4502	6355180	6353522	Phosphoglycerate mutase	pgm2	4619,6007	696

]

[

Fam: 22	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1046	1477266	1477814	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8449	11770317	11770871	Hypothetical protein			0

]

[

Fam: 22	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1047	1477811	1478773	Hypothetical protein			0

CDS	sce8450	11770868	11771848	Hypothetical protein			0
]							
[							
Fam: 22	No. of CDS: 2	Dom. COG: 39	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1050	1481897	1480956	Malate dehydrogenase	mdh		39
CDS	sce5245	7387992	7387030	L-lactate dehydrogenase	ldh		39
]							
[							
Fam: 22	No. of CDS: 2	Dom. COG: 297	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1063	1497178	1498626	Put. Glycogen synthase			297
CDS	sce3161	4344381	4345835	Glycogen synthase	glgA2	9058	297
]							
[							
Fam: 22	No. of CDS: 2	Dom. COG: 24	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1069	1508095	1507277	Methionyl aminopeptidase	map1	4239,6508	24
CDS	sce3541	4948766	4948017	Methionine aminopeptidase	map2	4239,6508	24
]							
[							
Fam: 23	No. of CDS: 2	Dom. COG: 459	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1088	1527623	1525986	ABC transporter, permease protein		16020	4591
CDS	sce1635	2245383	2247545	Integral membrane protein		16020	4591
]							
[							
Fam: 23	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1091	1531525	1532916	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6393	8922038	8920731	Conserved hypothetical protein			0
]							
[							
Fam: 23	No. of CDS: 8	Dom. COG: 126	counter: 7 / 8	percentage: 87.50%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1095	1536351	1535260	Putative secreted protein			1262
CDS	sce3783	5271926	5270943	cell wall surface anchor family protein			1262
CDS	sce3784	5272533	5271928	Conserved hypothetical protein			1262
CDS	sce4329	6113804	6114742	Hypothetical protein			1262
CDS	sce4694	6630989	6632008	Hypothetical protein			1262
CDS	sce5004	7029474	7030298	Conserved hypothetical protein			1262
CDS	sce5259	7401880	7402623	Hypothetical protein predicted by Glimmer/Critica			1262
CDS	sce9090	12654413	12655501	Putative secreted protein			0
]							
[							
Fam: 23	No. of CDS: 4	Dom. COG: 311	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1096	1538616	1536370	Cell wall surface anchor family protein		8152,8484	3119
CDS	sce3594	5031116	5027631	Conserved hypothetical protein		8152,8484	3119
CDS	sce3929	5467627	5469039	Choline sulfatase	betC	8152,8484	3119
CDS	sce7789	10852148	10854460	Sulfatase family protein		8152,8484	3119
]							
[							
Fam: 23	No. of CDS: 7	Dom. COG: 488	counter: 7 / 7	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1108	1559977	1558346	ABC transporter, ATP-binding protein		166	488
CDS	sce5490	7736118	7738049	Putative ATP-binding component of a transport system	ybiT	4009,5524,6810,16020	488
CDS	sce5634	7931338	7929719	ABC transporter, ATP-binding protein		4009,5524,6810,16020	488
CDS	sce6041	8469085	8470707	ABC transporter, ATP-binding protein		4009,5524,6810,16020	488
CDS	sce6528	9092926	9095022	ABC transporter, ATP-binding protein		4009,5524,6810,16020	488
CDS	sce8545	11905905	11907881	ABC transporter, ATP-binding protein	uup	4009,5524,6810,16020	488
CDS	sce8548	11912583	11911057	ABC transporter, ATP-binding protein		4009,5524,6810,16020	488

]

[

Fam: 23	No. of CDS: 3	Dom. COG: 583	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1114	1566751	1567707	Transcriptional regulator, LysR family			583
CDS	sce1423	1954077	1955060	Transcriptional regulator, LysR family			583
CDS	sce8586	11982206	11981118	Transcriptional regulator, LysR family			583

]

[

Fam: 23	No. of CDS: 3	Dom. COG: 477	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1119	1571483	1572838	Permeases of the major facilitator superfamily			477
CDS	sce1483	2030515	2032005	Permease of the major facilitator superfamily		5215,6810,16021	477
CDS	sce7848	10943330	10944712	Permease of the major facilitator superfamily		5215,6810,16021	477

]

[

Fam: 23	No. of CDS: 2	Dom. COG: 189	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1124	1577565	1578410	2-Dehydropantoate 2-reductase	panE1		1893
CDS	sce9123	12697271	12696420	Putative oxidoreductase			1893

]

[

Fam: 23	No. of CDS: 2	Dom. COG: 240	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1131	1581296	1581790	Conserved hypothetical protein			2405
CDS	sce5012	7037588	7038088	Hypothetical protein			0

]

[

Fam: 23	No. of CDS: 18	Dom. COG: 112	counter: 4 / 18	percentage: 22.22%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1133	1583873	1583097	ABC-type molybdate transporter, ATP-binding protein	modC	4009,5524,6810,16020	3842
CDS	sce3056	4188186	4189262	Put. Multiple sugar ABC transporter ATP-binding protein		4009,5524,6810,16020	3839
CDS	sce3139	4314493	4313639	Putative ABC transporter, ATP-binding protein		4009,5524,6810,16020	1127
CDS	sce3460	4828317	4829330	Oligopeptide ABC transporter ATP-binding protein	oppD	4009,5524,6810,16020	444
CDS	sce3461	4829327	4830343	Oligopeptide ABC transporter ATP-binding protein	oppF	4009,5524,6810,16020	4608
CDS	sce3697	5169294	5168554	ABC transporter ATP-binding protein		4009,5524,6810,16020	1127
CDS	sce3963	5506200	5506937	Putative ABC transport system ATP-binding protein		4009,5524,6810,16020	1127

CDS	sce4298	6076683	6075625	ABC-type oligopeptide transport system, ATPase component		4009,5524,6810,16020	4608
CDS	sce4299	6077645	6076686	Peptide ABC transporter, ATP-binding protein		4009,5524,6810,16020	444
CDS	sce4479	6319261	6318482	Putative ABC transport system ATP-binding protein		4009,5524,6810,16020	1127
CDS	sce7072	9869515	9868721	Putative Sulfate-transporting ATPase		5524,16887	3839
CDS	sce7376	10273368	10272298	Sulfate-transporting ATPase	cysA	4009,5524,6810,16020	1118
CDS	sce7779	10833950	10832871	ABC-type sugar transport systems ATPase component		4009,5524,6810,16020	3839
CDS	sce8565	11957911	11956823	Peptide ABC transporter ATP-binding protein		4009,5524,6810,16020	4608
CDS	sce8566	11958921	11957908	ABC transporter ATP-binding protein		4009,5524,6810,16020	444
CDS	sce9160	12762316	12761201	Spermidine/putrescine transport system ATP-binding protein	potA1	4009,5524,6810,16020	3842
CDS	sce9263	12893862	12894971	Sugar ABC transporter, ATP-binding protein		4009,5524,6810,16020	3839
CDS	sce9306	12944481	12945566	Spermidine/putrescine transport system ATP-binding protein	potA2	15417,15846,16020	3842

]

[

Fam: 24	No. of CDS: 5	Dom. COG: 243	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1149	1600794	1602926	Ferredoxin-nitrate reductase	narB1	16491	243
CDS	sce3157	4340625	4338640	Molybdopterin-containing oxidoreductase catalytic subunit		16491	243
CDS	sce4702	6639684	6637297	Nitrate reductase	napA	16491	243
CDS	sce8491	11828229	11825956	Nitrate reductase	narB2	16491	243
CDS	sce9118	12689892	12692822	Nitrate reductase	narB3	16491	243

]

[

Fam: 24	No. of CDS: 3	Dom. COG: 125	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1150	1602926	1604377	Nitrite reductase (NAD(P)H)	nasD	6118,15036	1251
CDS	sce3488	4866474	4868918	Nitrite reductase	nirB1	6118,15036	1251
CDS	sce8494	11833067	11830527	Nitrite reductase	nirB2	6118,15036	1251

]

[

Fam: 24	No. of CDS: 4	Dom. COG: 534	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1157	1609046	1610434	Conserved hypothetical protein		6855,15238,15297,16020	0
CDS	sce2961	4056180	4057685	Probable Na+-driven multidrug efflux pump		6855,15238,15297,16020	534
CDS	sce3194	4458359	4459735	MATE efflux family protein		6855,15238,15297,16020	534
CDS	sce4373	6182907	6181447	Conserved hypothetical protein		6855,15238,15297,16020	534

]

[

Fam: 24	No. of CDS: 2	Dom. COG: 145	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1169	1622473	1621295	Alcohol dehydrogenase		5506,8152,16491	1454
CDS	sce3952	5495816	5494662	Alcohol dehydrogenase	gbd	5506,8152,16491	1454

]

[

Fam: 24	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1186	1644516	1646048	Conserved hypothetical protein			0
CDS	sce7537	10502247	10500718	Conserved hypothetical protein			4625

]

[

Fam: 24	No. of CDS: 2	Dom. COG: 625	counter: 2 / 2	percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1188	1647745	1647074	Glutathione transferase			625
CDS	sce1191	1651157	1650621	Glutathione transferase			625

]

[

Fam: 24	No. of CDS: 2	Dom. COG: 340	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1198	1659368	1658643	Hypothetical protein predicted by Glimmer/Critica			3409
CDS	sce4082	5695955	5697256	Hypothetical protein predicted by Glimmer/Critica			3409

]

[

Fam: 24	No. of CDS: 5	Dom. COG: 0	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1204	1665966	1667222	Hypothetical protein			0
CDS	sce4147	5867586	5866609	Conserved hypothetical protein			0
CDS	sce8354	11640823	11641620	Conserved hypothetical protein			0
CDS	sce8355	11641565	11642065	Conserved hypothetical protein			0
CDS	sce9330	12978180	12979421	Hypothetical protein			0

]

[

Fam: 24	No. of CDS: 3	Dom. COG: 520	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1210	1674796	1673468	Putative aminotransferase		8152,8483	520
CDS	sce4643	6560015	6562003	Probable cysteine desulfurase			520
CDS	sce8911	12430312	12429140	Probable class-V aminotransferase		8152,8483	0

]

[

Fam: 24	No. of CDS: 3	Dom. COG: 405	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1211	1675382	1677214	Gamma-glutamyltransferase	ggt1	3840	405
CDS	sce8286	11560104	11562002	Gamma-glutamyltransferase	ggt2	3840	405
CDS	sce8554	11925550	11923721	Gamma-glutamyltranferase	ggt3	3840	405

]

[

Fam: 25	No. of CDS: 5	Dom. COG: 28	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1214	1679310	1681067	Acetolactate synthase large subunit	ilvB1		28
CDS	sce2120	2873906	2872119	Pyruvate oxidase			28
CDS	sce3730	5207763	5209472	Acetolactate synthase	ilvB2	3984,9082	28
CDS	sce8127	11306309	11304669	Putative acetolactate synthase	ilvG1		28
CDS	sce8755	12228278	12229993	Acetolactate synthase	ilvG2		28

]

[

Fam: 25	No. of CDS: 2	Dom. COG: 288	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1217	1682957	1686046	Oar protein	oar1		2885
CDS	sce4255	6014919	6018194	Oar protein	oar2		2885

]

[

Fam: 25	No. of CDS: 3	Dom. COG: 220	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1222	1691151	1692272	Putative araC-like transcription regulator			4977
CDS	sce1410	1938062	1937163	Putative araC-like transcription regulator		3700,5622,6355	2207

CDS	sce6362	8871953	8870970	Transcriptional regulator, AraC family		3700,5622	2207

]

[

Fam: 25	No. of CDS: 2	Dom. COG: 477	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1223	1692411	1693652	Permease of the major facilitator superfamily		5215,6810,16021	477
CDS	sce1439	1979642	1980886	Permease of the major facilitator superfamily		5215,6810,16021	477

]

[

Fam: 25	No. of CDS: 2	Dom. COG: 835	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1227	1696675	1697229	Purine-binding chemotaxis protein CheW	cheW2	4871,5622,6935,7165	835
CDS	sce2201	2968129	2967575	Chemotaxis protein	cheW5		835

]

[

Fam: 25	No. of CDS: 2	Dom. COG: 840	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1228	1697396	1699075	Probable chemotaxis transducer		4871,6935,7165,16020	840
CDS	sce2202	2969892	2968126	Putative methyl-accepting chemotaxis protein	mcp	4871,6935,7165,16020	840

]

[

Fam: 25	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1234	1706575	1707618	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2843	3883517	3884935	Putative secreted protein			0

]

[

Fam: 25	No. of CDS: 2	Dom. COG: 800	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1239	1715330	1714659	4-Hydroxy-2-oxoglutarate aldolase	kdgA1	3824,8152	800
CDS	sce5154	7240031	7239390	KDPG and KHG aldolase	kdgA2	3824,8152	800

]

[

Fam: 25	No. of CDS: 2	Dom. COG: 524	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1240	1716427	1715339	Carbohydrate kinase, pfkB family			524
CDS	sce5155	7241125	7240028	Put. 2-Dehydro-3-deoxygluconokinase			524

]

[

Fam: 25	No. of CDS: 2	Dom. COG: 1063	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1242	1718559	1719572	Putative alcohol dehydrogenase	yjjN	8270	1063
CDS	sce9297	12937402	12936392	Putative zinc-binding dehydrogenase			1063

]

[

Fam: 26	No. of CDS: 2	Dom. COG: 477	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1244	1720942	1722255	Permease of the major facilitator superfamily, putative D-galactonate transporter	dgoT	5215,6810,16021	477
CDS	sce5156	7242900	7241236	Permease of the major facilitator superfamily, probably glucarate/galactonate transport	exuT	5215,6810,16021	477

]

[

Fam: 26	No. of CDS: 3	Dom. COG: 3517	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1251	1733118	1731553	Conserved hypothetical protein			3517
CDS	sce4981	6998110	6996626	Conserved hypothetical protein			3517
CDS	sce9341	12990595	12989108	Conserved hypothetical protein			3517

]

[

Fam: 26	No. of CDS: 7	Dom. COG: 4826	counter: 7 / 7	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1266	1755513	1756829	Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member		4867	4826
CDS	sce1563	2134017	2135354	Alpha-1-antitrypsin-like protein CM55-MS precursor.		4867	4826
CDS	sce2877	3924523	3923075	Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member		4867	4826
CDS	sce4096	5718822	5717377	Probable secreted serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member		4867	4826
CDS	sce5376	7571459	7569873	Similar to serine protease inhibitor		4867	4826
CDS	sce5377	7572892	7571525	Serine protease inhibitor		4867	4826
CDS	sce8453	11780681	11779152	Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member		4867	4826

]

[

Fam: 26	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1277	1770701	1771501	Conserved hypothetical protein			0
CDS	sce7384	10279694	10280518	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 26	No. of CDS: 2	Dom. COG: 582	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1283	1779394	1780293	Integrase-like protein			582
CDS	sce1284	1780523	1781320	Integrase-like protein		3677,6310,15074	582

]

[

Fam: 26	No. of CDS: 7	Dom. COG: 0	counter: 6 / 7	percentage: 85.71%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1285	1781418	1782389	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6088	8526743	8525946	Hypothetical protein predicted by Glimmer/Critica			2959
CDS	sce6134	8598395	8598913	Leucine-rich repeat family protein / extensin family protein			0
CDS	sce6708	9338757	9337861	Putative exported protein			0
CDS	sce8767	12252067	12252963	No similarity			0
CDS	sce8868	12366511	12365537	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9275	12907216	12908112	Putative membrane protein			0

]

[

Fam: 26	No. of CDS: 18	Dom. COG: 1595	counter: 17 / 18	percentage: 94.44%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1286	1782404	1782976	RNA polymerase ECF-type sigma factor		3677,3700,6352,16987	1595
CDS	sce2497	3367696	3366902	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce2498	3369214	3367877	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce5229	7356448	7355054	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce5481	7721812	7723365	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce6087	8525890	8525330	sigma24 homolog	rpoE	3677,3700,6352,6355,169	1595
CDS	sce6089	8528056	8526977	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce6133	8596835	8597887	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce6138	8601738	8602307	Hypothetical protein predicted by Glimmer/Critica		3677,3700,6352,6355,169	0
CDS	sce6704	9334908	9334438	Hypothetical protein			1595
CDS	sce6709	9339959	9338874	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce7045	9836929	9837570	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce8487	11821111	11820017	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce8766	12250826	12251947	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce8867	12365349	12364786	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce8869	12367696	12366554	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce9274	12906014	12907099	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce9276	12908105	12908695	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog			1595

]

[

Fam: 26	No. of CDS: 3	Dom. COG: 0	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1288	1785205	1784342	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce1290	1786871	1785999	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7751	10796876	10797766	Putative secreted protein			0

]

[

Fam: 26	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1291	1788374	1786896	Conserved hypothetical protein			
CDS	sce6871	9597774	9596410	Conserved hypothetical protein			0

]

[

Fam: 26	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1292	1789471	1788368	Putative secreted protein			0
CDS	sce4687	6622010	6623035				0
CDS	sce6872	9598784	9597828	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7750	10795561	10796808	Putative membrane protein			0

]

[

Fam: 27	No. of CDS: 9	Dom. COG: 0	counter: 7 / 9	percentage: 77.78%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1293	1789831	1790364	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2867	3911390	3912745	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6123	8586341	8585856	Hypothetical protein predicted by Glimmer/Critica			0

CDS	sce6125	8588183	8588512	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6139	8603291	8602335	Probable ATPase with chaperone activity			542
CDS	sce6330	8824315	8824848	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7179	10033924	10033382	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8415	11715970	11716929	Conserved hypothetical protein			542
CDS	sce9268	12899065	12899604	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 27	No. of CDS: 2	Dom. COG: 152	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1303	1800273	1802402	Glycogen operon protein		4556,5975	1523
CDS	sce2378	3193056	3195401	Glycogen debranching enzyme		4556,5975	1523

]

[

Fam: 27	No. of CDS: 5	Dom. COG: 169(	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1307	1807815	1806649	Conserved hypothetical protein		5554	1690
CDS	sce1954	2656912	2658474	Conserved hypothetical protein		5554	1690
CDS	sce3688	5157078	5158205	Conserved hypothetical protein		5554	1690
CDS	sce7008	9789554	9788319	Conserved hypothetical protein		5554	1690
CDS	sce7156	9978398	9979624	Rtcb protein	rtcB	5554	1690

]

[

Fam: 27	No. of CDS: 2	Dom. COG: 187	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1310	1811291	1810455	Putative secreted protein			1878
CDS	sce8783	12273598	12274263	Conserved hypothetical protein			1878

]

[

Fam: 27	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1312	1813137	1814162	Conserved hypothetical protein			0
CDS	sce2807	3833284	3834252	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4193	5933311	5932325	Hypothetical protein			0
CDS	sce8813	12306167	12307129	Hypothetical protein			0

]

[

Fam: 27	No. of CDS: 2	Dom. COG: 215	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1319	1819957	1821486	Hypothetical protein			0
CDS	sce3373	4716762	4715065	Hypothetical protein			2159

]

[

Fam: 27	No. of CDS: 2	Dom. COG: 715	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1321	1823304	1824386	ABC transporter substrate-binding protein			715
CDS	sce2287	3082986	3084053	Sulfate ester binding protein (ABC superfamily, peri_bind)	astR		715

]

[

Fam: 27	No. of CDS: 4	Dom. COG: 612	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1330	1833211	1831568	Putative secreted zinc protease			612
CDS	sce2070	2808270	2809823	Putative zinc protease			612

CDS	sce3833	5333354	5331990	Hypothetical protein predicted by Glimmer/Critica			612
CDS	sce8461	11787575	11789224	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 27	No. of CDS: 4	Dom. COG: 612	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1331	1834976	1833216	Putative zinc protease			612
CDS	sce2069	2806681	2808273	Conserved hypothetical protein			612
CDS	sce3834	5334793	5333351	Hypothetical protein predicted by Glimmer/Critica			612
CDS	sce8460	11785464	11787539	Predicted Zn-dependent peptidases			612

]

[

Fam: 27	No. of CDS: 2	Dom. COG: 348	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1334	1840954	1838615	Conserved hypothetical protein			3488
CDS	sce3571	4997804	4996572	Predicted thiol oxidoreductase			3488

]

[

Fam: 28	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1335	1842584	1841007	Hypothetical protein			1801
CDS	sce4903	6885424	6886998	Hypothetical protein			0

]

[

Fam: 28	No. of CDS: 11	Dom. COG: 745	counter: 11 / 11	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1356	1871509	1872213	Two-component system transcriptional regulatory protein	kdpE		745
CDS	sce2049	2779476	2780162	Two-component system response regulator			745
CDS	sce2434	3277098	3276373	Two-component response regulator			745
CDS	sce2555	3449670	3448969	Two-component response regulator			745
CDS	sce2948	4038380	4037685	Phosphate regulon transcriptional regulatory protein phoB.	phoB		745
CDS	sce3288	4606053	4605283	Two-component response regulator			745
CDS	sce4826	6780608	6781381	Response regulator			745
CDS	sce4878	6848633	6847929	Two-component response regulator			745
CDS	sce5073	7119820	7119113	DNA-binding response regulator			745
CDS	sce6353	8857992	8858789	Response regulator			745
CDS	sce8615	12018412	12019224	response regulator			745

]

[

Fam: 28	No. of CDS: 4	Dom. COG: 0	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1358	1873574	1872714	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3515	4909803	4910315	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce3578	5005309	5004392	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6339	8835612	8834425	Hypothetical protein			0

]

[

Fam: 28	No. of CDS: 6	Dom. COG: 159	counter: 5 / 6	percentage: 83.33%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1359	1874341	1875582	Putative membrane protein		3677,3700,6352,16987	1595
CDS	sce3500	4889885	4889259	Hypothetical protein		3677,3700,6352,16987	0
CDS	sce3681	5149870	5150613	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce5218	7338843	7340411	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce5925	8321583	8322431	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce8640	12049929	12050603	ECF-family RNA polymerase sigma factor			1595

]

[

Fam: 28	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1360	1875783	1876787	Conserved hypothetical protein			0
CDS	sce3499	4889262	4888135	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5219	7340408	7341544	Hypothetical protein			0

]

[

Fam: 28	No. of CDS: 8	Dom. COG: 0	counter: 6 / 8	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1361	1876853	1878073	Conserved hypothetical protein			0
CDS	sce2501	3372680	3371520	Putative secreted protein			0
CDS	sce3498	4887933	4887361	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4714	6652604	6653659	Hypothetical protein			0
CDS	sce5220	7341724	7342842	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5478	7719591	7718476	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce5479	7720831	7719707	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce9248	12874857	12873613	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 28	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1363	1881620	1882690	Conserved hypothetical protein			0
CDS	sce5435	7631479	7632534	Putative secreted protein			0
CDS	sce7824	10901526	10899763	Hypothetical protein		4295,6508	0
CDS	sce8400	11698225	11697143	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 28	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1372	1892914	1893777	Conserved hypothetical protein			0
CDS	sce3175	4361407	4360619	Conserved hypothetical protein			0

]

[

Fam: 28	No. of CDS: 2	Dom. COG: 188	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1373	1893755	1894201	Hypothetical protein predicted by Glimmer/Critica			1884
CDS	sce3174	4360575	4360219	Conserved hypothetical protein			0

]

[

Fam: 28	No. of CDS: 7	Dom. COG: 714	counter: 7 / 7	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1389	1914537	1913572	Putative regulatory protein		166	714
CDS	sce4441	6265670	6266647	Putative regulatory protein			714

CDS	sce5905	8300905	8299901	Methanol dehydrogenase regulator (moxR) homolog	moxR1	166	714
CDS	sce5927	8324167	8325201	Methanol dehydrogenase regulator (moxR) homolog	moxR2		714
CDS	sce6501	9058859	9059845	MoxR-like ATPases		160,3677	714
CDS	sce7373	10270568	10269504	Methanol dehydrogenase regulator (moxR) homolog	moxR3	166	714
CDS	sce8273	11546635	11545709	Putative methanol dehydrogenase regulatory protein		166	714

]

[

Fam: 29	No. of CDS: 2	Dom. COG: 477	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1415	1941833	1943017	Permease of the major facilitator superfamily		5215,6810,16021	477
CDS	sce7494	10440523	10439300	Permease of the major facilitator superfamily			477

]

[

Fam: 29	No. of CDS: 2	Dom. COG: 715	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1416	1943040	1944098	ABC transport system substrate-binding protein			715
CDS	sce4103	5727699	5726587	ABC transporter, periplasmic substrate-binding protein			715

]

[

Fam: 29	No. of CDS: 9	Dom. COG: 841	counter: 5 / 9	percentage: 55.56%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1422	1954016	1950783	Probable multidrug efflux membrane protein			841
CDS	sce1628	2234639	2237866	RND family efflux transporter			841
CDS	sce2737	3722868	3725999	Cobalt/zinc/cadmium efflux RND transporter, permease protein, CzcA family	czcA1	6812,8324,16021	3696
CDS	sce2805	3829434	3832751	Probable membrane protein	acrB		841
CDS	sce5284	7436153	7432971	Acriflavin resistance protein			841
CDS	sce8095	11264280	11260813	Probable cation efflux system transmembrane protein		6812,8324,16021	3696
CDS	sce8113	11284842	11288030	Cation efflux system protein		6812,8324,16021	3696
CDS	sce8249	11477723	11480926	AcrB/AcrD/AcrF family protein	nolG		841
CDS	sce8711	12158867	12162061	RND divalent metal cation efflux transporter CzcA	czcA2	6812,8324,16021	3696

]

[

Fam: 29	No. of CDS: 16	Dom. COG: 160	counter: 10 / 16	percentage: 62.50%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1424	1957251	1955086	HTH-type transcriptional repressor purR	purR		1609
CDS	sce1435	1973425	1975539	Transcriptional regulator, LacI family			1609
CDS	sce1777	2413825	2416212	Phosphoserine phosphatase		3824	0
CDS	sce2321	3127699	3125240	Phosphoserine phosphatase			1609
CDS	sce2367	3178645	3180834	Transcriptional regulator, LacI family			1609
CDS	sce2617	3535661	3538144	Putative LacI-family transcriptional regulator			2208
CDS	sce3081	4221172	4222332	Lactose operon repressor	lacI1		1609
CDS	sce3317	4644230	4645537	HTH-type transcriptional repressor purR	lacI2		1609
CDS	sce4152	5873237	5872212	Transcriptional regulator lacI family			1609
CDS	sce5198	7304391	7301899	Conserved hypothetical protein			2208
CDS	sce5201	7308056	7305444	Hypothetical protein			2208
CDS	sce5204	7311449	7308942	Phosphoserine phosphatase			2208
CDS	sce7773	10824715	10822394	Ribose operon repressor.			1609
CDS	sce8931	12456004	12458238	Glucose-resistance amylase regulator			1609

CDS	sce8932	12458363	12460684	Glucose-resistance amylase regulator			1609
CDS	sce9114	12683814	12683305	Hypothetical protein			2208

]

[

Fam: 29	No. of CDS: 3	Dom. COG: 537	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1441	1983752	1985158	Putative nucleotide-binding protein			5378
CDS	sce1442	1985255	1986655	Putative nucleotide-binding protein			5378
CDS	sce4642	6559123	6560028	Putative nucleotide-binding protein			0

]

[

Fam: 29	No. of CDS: 2	Dom. COG: 308	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1444	1988511	1991072	Aminopeptidase	pepN1	4179,6508	308
CDS	sce6029	8453171	8455672	Putative aminopeptidase		4179,6508	308

]

[

Fam: 29	No. of CDS: 2	Dom. COG: 273	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1468	2015765	2014536	Endoglucanase	celA	5975	2730
CDS	sce4910	6896157	6897056	Cellulase	celB	5975	2730

]

[

Fam: 29	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1469	2017735	2016260	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1768	2402240	2403706	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 29	No. of CDS: 2	Dom. COG: 119	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1479	2027161	2026358	Chromosome partitioning protein	parA1		1192
CDS	sce7060	9854254	9853445	Chromosome partitioning protein ParA	parA4		1192

]

[

Fam: 29	No. of CDS: 2	Dom. COG: 275	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1489	2036046	2036828	Probable lysophospholipase L1 and related esterases/Probable similar to rhamnogalacturonan acetylesterase		3824	2755
CDS	sce5169	7258385	7259464	Hypothetical protein		3824	0

]

[

Fam: 30	No. of CDS: 2	Dom. COG: 168	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1495	2047517	2048794	Putative beta-lactamase			1680
CDS	sce6641	9238510	9237215	Putative beta-lactamase precursor	yfeW		1680

]

[

Fam: 30	No. of CDS: 2	Dom. COG: 324	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1521	2083330	2083923	Hypothetical protein			3247
CDS	sce7014	9796128	9795529	Conserved hypothetical protein			3247
]							
[							
Fam: 30	No. of CDS: 2	Dom. COG: 340	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1523	2084402	2086456	Glycogen debranching enzyme (Glycogen debrancher)			3408
CDS	sce2115	2866661	2864367	Glycogen debranching enzyme (Glycogen debrancher)			3408
]							
[							
Fam: 30	No. of CDS: 3	Dom. COG: 129	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1527	2091075	2089300	Dihydroxy-acid dehydratase	ilvD1	3824,8152	129
CDS	sce5328	7492310	7494226	Dihydroxy-acid dehydratase	ilvD2	4160,9082	129
CDS	sce8241	11470236	11468287	Dihydroxy-acid dehydratase	ilvD3	3824,8152	129
]							
[							
Fam: 30	No. of CDS: 3	Dom. COG: 488	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1531	2093472	2094677	Conserved hypothetical protein			4886
CDS	sce6593	9181234	9179231	Putative adenylate cyclase regulatory protein			
CDS	sce6600	9191565	9189988	Leucine-rich protein			4886
]							
[							
Fam: 30	No. of CDS: 3	Dom. COG: 604	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1535	2097343	2096357	Alcohol dehydrogenase			604
CDS	sce6223	8703519	8704487	Putative alcohol dehydrogenase			604
CDS	sce9319	12963063	12964028	Alcohol dehydrogenase.			604
]							
[							
Fam: 30	No. of CDS: 2	Dom. COG: 379	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1539	2101314	2101760	Hypothetical protein			3795
CDS	sce2158	2921928	2921482	Conserved hypothetical protein			3795
]							
[							
Fam: 30	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1540	2102001	2102450	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3977	5536833	5537486	Hypothetical protein predicted by Glimmer/Critica			0
]							
[							
Fam: 30	No. of CDS: 5	Dom. COG: 0	counter: 4 / 5	percentage: 80.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1542	2104173	2105558	Putative protease inhibitor			4826
CDS	sce2670	3614033	3615154	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4098	5719820	5719413	Probable serine protease precursor			0
CDS	sce6861	9588008	9586911	Hypothetical protein similar to eukaryotic regulators / effectors			0
CDS	sce7668	10668699	10669394	Putative secreted protease inhibitor			0

]

[

Fam: 30	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1557	2125735	2124875	Conserved hypothetical protein			0
CDS	sce7138	9952028	9952921	Predicted nucleoside-diphosphate-sugar epimerases			702

]

[

Fam: 31	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1559	2126959	2128896	Putative secreted protein			0
CDS	sce6365	8876868	8879081	Conserved hypothetical protein			0

]

[

Fam: 31	No. of CDS: 3	Dom. COG: 3387	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1562	2131877	2133970	Glycosyl hydrolase			3387
CDS	sce6733	9386253	9388109	Glycosyl hydrolase			3387
CDS	sce8050	11202399	11200501	Glycosyl hydrolase			3387

]

[

Fam: 31	No. of CDS: 3	Dom. COG: 508	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1569	2142341	2140905	Dihydrolipoyllysine-residue acetyltransferase	pdhC	8152,8415	508
CDS	sce3802	5295261	5296577	Dihydrolipoyllysine-residue acetyltransferase	aceF1	8152,8415	508
CDS	sce6586	9160574	9161899	Dihydrolipoyllysine-residue acetyltransferase	aceF2	8152,8415	508

]

[

Fam: 31	No. of CDS: 2	Dom. COG: 22	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1570	2143319	2142345	Pyruvate dehydrogenase (acetyl-transferring)	pdhB1		22
CDS	sce3801	5294238	5295221	Pyruvate dehydrogenase (acetyl-transferring)	pdhB2		22

]

[

Fam: 31	No. of CDS: 3	Dom. COG: 1071	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1571	2144663	2143473	Pyruvate dehydrogenase (acetyl-transferring)	pdhA	8152	1071
CDS	sce3800	5293264	5294241	Pyruvate dehydrogenase (acetyl-transferring)	aceE	8152	1071
CDS	sce8001	11133033	11131978	3-Methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)		8152	1071

]

[

Fam: 31	No. of CDS: 3	Dom. COG: 820	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1580	2153825	2155021	Conserved hypothetical protein		5554	820
CDS	sce3898	5424141	5425322	Conserved hypothetical protein			820
CDS	sce4835	6792968	6794137	Radical SAM superfamily protein		5554	820

]

[

Fam: 31	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1581	2155787	2154999	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6556	9126058	9126840	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 31	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1585	2163240	2162323	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5584	7863419	7863069	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7454	10386185	10385790	Conserved hypothetical protein			0
CDS	sce7785	10848042	10848947	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 31	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1590	2173833	2171302	Hypothetical protein			0
CDS	sce6745	9405070	9401912	Conserved hypothetical protein			457

]

[

Fam: 31	No. of CDS: 2	Dom. COG: 220	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1599	2183609	2184691	Putative chemotaxis response regulator CheB type	cheB	5737,6935,8984	2201
CDS	sce2662	3602197	3603231	Chemotaxis response regulator	cheR4	5737,6935,8984	2201

]

[

Fam: 32	No. of CDS: 3	Dom. COG: 741	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1600	2184763	2187450	Murein transglycosylase	mltD1		741
CDS	sce3852	5361767	5358897	Membrane-bound lytic murein transglycosylase D	mltD2		741
CDS	sce4990	7013689	7011818	Transglycosylase, Slt family	mltD3		791

]

[

Fam: 32	No. of CDS: 2	Dom. COG: 118	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1621	2226189	2227007	Phosphatidylserine synthase	pssA1	3882,6656	1183
CDS	sce6767	9437699	9436776	Phosphatidylserine synthase	pssA3	3882,6656	1183

]

[

Fam: 32	No. of CDS: 4	Dom. COG: 845	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1627	2233294	2234595	RND family efflux transporter		8565,9306,16020	845
CDS	sce2804	3828164	3829432	Efflux transporter, RND family, MFP subunit	arcA	8565,9306,16020	845
CDS	sce5285	7437439	7436150	Putative multidrug resistance protein precursor			845
CDS	sce8248	11476789	11477715	Multidrug resistance protein	mdtA2	8565,9306,16020	845

]

[

Fam: 32	No. of CDS: 2	Dom. COG: 216	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1633	2242616	2243668	Peptide chain release factor 2	prfB1	5737,6415	1186
CDS	sce9028	12574140	12575234	Peptide chain release factor RF-1	prfA	5737,6415	216

]

[

Fam: 32	No. of CDS: 2	Dom. COG: 119(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1634	2243665	2245386	Lysine--tRNA ligase	lysS	4824,5524,6430	1190
CDS	sce2808	3836192	3834873	Lysine--tRNA ligase	yieA	4812,5524,5737,6418	1190

]

[

Fam: 32	No. of CDS: 3	Dom. COG: 230(	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1637	2250357	2248276	GMC oxidoreductase			2303
CDS	sce2045	2775986	2774412	Hypothetical protein			0
CDS	sce2973	4071922	4073559	Putative choline dehydrogenase		6118,16491	2303

]

[

Fam: 32	No. of CDS: 3	Dom. COG: 768	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1659	2271387	2273474	Peptidoglycan glycosyltransferase	ftsI1	8658,9273	768
CDS	sce2411	3248614	3250569	Peptidoglycan glycosyltransferase	ftsI2	8658,9273	768
CDS	sce7487	10430674	10432854	Pencillin-binding transpeptidase with putative regulatory N-terminal domain	ftsI3	8658,9273	768

]

[

Fam: 32	No. of CDS: 2	Dom. COG: 772	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1663	2277574	2278899	Cell division protein	ftsW	7049,16021	772
CDS	sce2412	3250566	3251702	Rod shape-determining protein RodA	rodA	7049,16021	772

]

[

Fam: 32	No. of CDS: 2	Dom. COG: 773	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1665	2280110	2281519	UDP-N-acetylmuramate-alanine ligase	murC1	5737,8763,9273	773
CDS	sce7631	10620645	10622132	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	murC2		773

]

[

Fam: 32	No. of CDS: 4	Dom. COG: 265	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1673	2290528	2289287	Probable serine protease			265
CDS	sce4154	5874794	5875960	Probable serine protease			265
CDS	sce5867	8243781	8242297	Probable serine protease			265
CDS	sce7222	10087102	10085954	Serine protease, HtrA/DegQ/DegS family			265

]

[

Fam: 33	No. of CDS: 2	Dom. COG: 493(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1686	2305768	2304485	Conserved hypothetical protein			4938
CDS	sce8542	11902559	11903875	Hypothetical protein			4938

]

[

Fam: 33	No. of CDS: 3	Dom. COG: 136(	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1706	2326032	2325208	Outer membrane protein		9279	1360

CDS	sce5128	7201431	7202222	Putative outer membrane protein		9279	1360
CDS	sce6431	8970952	8970071	Putative outer membrane protein		9279	1360

]

[

Fam: 33	No. of CDS: 2	Dom. COG: 745	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1728	2352002	2352373	Response regulator			745
CDS	sce2654	3590089	3590469	Two-component response regulator			745

]

[

Fam: 33	No. of CDS: 2	Dom. COG: 157	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1734	2358444	2359106	Putative DNA polymerase related protein			1573
CDS	sce7637	10629424	10630071	DNA-directed DNA polymerase			1573

]

[

Fam: 33	No. of CDS: 3	Dom. COG: 372	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1736	2362415	2361126	Citrate synthase (EC 2.3.3.1).		6092,46912	372
CDS	sce1738	2362585	2363805	Citrate synthase	cis1	4108,6099	372
CDS	sce8281	11553634	11554935	Citrate synthase	cis2	4108,6099	372

]

[

Fam: 33	No. of CDS: 2	Dom. COG: 587	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1741	2366757	2370083	DNA polymerase III, alpha subunit	dnaE1	3889,5737,6260,8408	587
CDS	sce3750	5233573	5229935	DNA polymerase III, alpha subunit	dnaE2	3889,5737,6260,8408	587

]

[

Fam: 33	No. of CDS: 3	Dom. COG: 77	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1746	2376921	2378015	Chorismate mutase/Prephenate dehydratase	pheA1	4106,9073	77
CDS	sce7043	9836373	9835456	P-protein (prephenate dehydratase / chorismate mutase)	pheA2	4664,9094	77
CDS	sce7831	10920107	10921186	Chorismate mutase	pheA3	4664,9094	77

]

[

Fam: 33	No. of CDS: 2	Dom. COG: 164	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1748	2381777	2379054	ATP-dependent RNA helicase	hrpB		1643
CDS	sce6384	8901802	8905593	ATP-dependent helicase HrpA	hrpA		1643

]

[

Fam: 33	No. of CDS: 3	Dom. COG: 219	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1764	2397019	2396087	FHA and GGDEF domain protein		5554	2199
CDS	sce2902	3955692	3956588	GGDEF domain protein		5554	2199
CDS	sce8626	12029214	12028315	FHA domain protein		5554	1716

]

[

Fam: 33	No. of CDS: 2	Dom. COG: 324	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1784	2421312	2422250	Hypothetical protein			3246
CDS	sce6192	8665502	8664120	Conserved hypothetical protein			3246

]

[

Fam: 34	No. of CDS: 3	Dom. COG: 479	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1787	2423070	2424632	Acyl-CoA carboxylase subunit		4075,9343	4799
CDS	sce2589	3498428	3499960	Probable Acetyl-CoA carboxylase		4075,9343	4799
CDS	sce3292	4611973	4610240	Probable Acyl-CoA carboxylase		4075,9343	4799

]

[

Fam: 34	No. of CDS: 5	Dom. COG: 463	counter: 3 / 5	percentage: 60.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1796	2434654	2434136	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4127	5757376	5757876	Hypothetical protein			4636
CDS	sce4139	5855453	5856277	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6780	9451998	9451357	Conserved hypothetical protein			4636
CDS	sce7445	10370446	10369841	Conserved hypothetical protein			4636

]

[

Fam: 34	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1798	2438763	2437012	Putative secreted protein			0
CDS	sce7161	9987018	9985228	Hypothetical protein			0

]

[

Fam: 34	No. of CDS: 2	Dom. COG: 140	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1810	2453127	2455781	Putative phosphohydrolase			1409
CDS	sce2660	3598996	3601359	Unknown protein			0

]

[

Fam: 34	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1811	2455812	2457569	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3631	5086392	5084638	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 34	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1815	2460322	2461806	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5656	7958560	7957058	Putative secreted protein			0

]

[

Fam: 34	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1821	2466491	2466895	Conserved hypothetical protein		8152,16846	3791
CDS	sce5222	7345109	7344654	Conserved hypothetical protein			0

]

[

Fam: 34	No. of CDS: 2	Dom. COG: 189	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1825	2471099	2470119	2-Dehydropantoate 2-reductase	panE2	6206,8677	1893
CDS	sce8496	11836286	11837215	Putative 2-dehydropantoate 2-reductase	panE3	6206,8677	1893

]

[

Fam: 34	No. of CDS: 2	Dom. COG: 338(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1826	2471475	2472527	Gluconolactonase	gnl1		3386
CDS	sce8236	11461812	11462732	Gluconolactonase	gnl2		3386

]

[

Fam: 34	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1836	2484379	2484047	Putative transcriptional regulator			0
CDS	sce7728	10760617	10760282	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 35	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1837	2484882	2488241	Hypothetical protein			0
CDS	sce1840	2490380	2490883	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 35	No. of CDS: 2	Dom. COG: 300(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1841	2491817	2490918	Hypothetical protein		3824,8152	3000
CDS	sce2370	3182024	3182932	Hypothetical protein		3824,8152	3000

]

[

Fam: 35	No. of CDS: 2	Dom. COG: 338(	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1842	2492944	2491850	Oxidoreductase		6118,16491	3380
CDS	sce2369	3181683	3182042	Putative oxidoreductase		5489,6118	2414

]

[

Fam: 35	No. of CDS: 2	Dom. COG: 181(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1866	2536267	2534993	Put. Glucosyltransferase		5975,30259	1819
CDS	sce8970	12502702	12503898	Glycosyl transferase	gtfE	5975,30259	1819

]

[

Fam: 35	No. of CDS: 2	Dom. COG: 220(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1871	2540528	2541436	Transcriptional regulator, AraC family		3700,5622,6355	2207
CDS	sce5997	8410278	8409325	Transcriptional regulator, ArsR family		3700,5622	2207

]

[

Fam: 35	No. of CDS: 5	Dom. COG: 724	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1876	2547969	2547682	RNA-binding protein			724
CDS	sce5988	8396897	8396481	RNA-binding protein	grp		724

CDS	sce7410	10315964	10315545	RNA-binding region RNP-1 (RNA recognition motif)			724
CDS	sce7495	10441816	10441493	RNA-binding protein	rbpF		724
CDS	sce7697	10722000	10722371	Putative RNA-binding protein			724

]

[

Fam: 35	No. of CDS: 4	Dom. COG: 322(	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1885	2558055	2559542	Conserved hypothetical protein			3220
CDS	sce3435	4792417	4791578	Conserved hypothetical protein			3220
CDS	sce6052	8486664	8487545	Conserved hypothetical protein			
CDS	sce7706	10735172	10736032	Conserved hypothetical protein			3220

]

[

Fam: 35	No. of CDS: 9	Dom. COG: 0	counter: 9 / 9	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1891	2564919	2566304	Transposase, IS4 family			0
CDS	sce1984	2695778	2694393	Transposase, IS4 family			0
CDS	sce2845	3887747	3886362	Transposase, IS4 family			0
CDS	sce4158	5883109	5881769	Transposase			0
CDS	sce4287	6061634	6060249	Transposase, IS4 family			0
CDS	sce4473	6310709	6312049	Transposase, IS4 family			0
CDS	sce5051	7088103	7089488	Transposase, IS4 family			0
CDS	sce6808	9482438	9481053	Transposase, IS4 family			0
CDS	sce9162	12768042	12766657	Transposase, IS4 family			0

]

[

Fam: 35	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1897	2573541	2573155	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6332	8827345	8826746	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 35	No. of CDS: 10	Dom. COG: 280:	counter: 7 / 10	percentage: 70.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1898	2574822	2573581	Transposase			2801
CDS	sce1899	2576050	2575028	Hypothetical transposase		3677,631	2801
CDS	sce4652	6570352	6570044	Putative transposase			2801
CDS	sce5537	7800245	7801426	Transposase-like protein			0
CDS	sce6110	8559460	8560482	Transposase		3677,631	2801
CDS	sce6284	8773904	8774926	Transposase		3677,631	2801
CDS	sce6291	8782247	8781783	Probable transposase protein			
CDS	sce6293	8785807	8784470	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce6613	9204719	9203697	Transposase		3677,631	2801
CDS	sce6860	9585218	9586453	Transposase		3677,631	2801

]

[

Fam: 36	No. of CDS: 4	Dom. COG: 280:	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1900	2576508	2576047	Transposase			2801
CDS	sce6109	8559002	8559463	Transposase			2801
CDS	sce6283	8773446	8773907	Transposase			2801
CDS	sce6614	9205177	9204716	Transposase			2801

]

[

Fam: 36	No. of CDS: 2	Dom. COG: 334	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1914	2592336	2590834	RNA-directed DNA polymerase		3723,3964,6278	3344
CDS	sce2673	3619572	3621197	RNA-directed DNA polymerase		3723,3964,6278	3344

]

[

Fam: 36	No. of CDS: 2	Dom. COG: 2319	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1915	2594612	2592723	Hypothetical protein			2319
CDS	sce2672	3616981	3619131	Hypothetical protein			0

]

[

Fam: 36	No. of CDS: 5	Dom. COG: 1629	counter: 3 / 5	percentage: 60.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1920	2610259	2607560	TonB family protein			1629
CDS	sce2511	3389163	3386350	Conserved hypothetical protein			0
CDS	sce3259	4565858	4563081	Conserved hypothetical protein			810
CDS	sce4711	6650380	6648308	TonB family protein			1629
CDS	sce9312	12953769	12951445	TonB family protein		8565,15031,16020,30288	1629

]

[

Fam: 36	No. of CDS: 15	Dom. COG: 1009	counter: 6 / 15	percentage: 40.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1933	2622887	2621376	Putative Na(+)/H(+) antiporter subunit D	mnhD	8137,42773	651
CDS	sce1936	2625939	2623651	Putative NADH dehydrogenase		8137,42773	1009
CDS	sce4218	5970966	5969440	NADH dehydrogenase (ubiquinone)	nuoN1	8137,42773	1007
CDS	sce4219	5972978	5970963	NADH dehydrogenase (ubiquinone)	nuoM1	8137,42773	1008
CDS	sce4220	5975539	5972975	NADH dehydrogenase (ubiquinone)	nuoL1	8137,42773	1009
CDS	sce4787	6735622	6734075	Probable NADH dehydrogenase subunit	ndhM1	8137,42773	1008
CDS	sce4788	6737052	6735619	Probable NADH dehydrogenase subunit	ndhF1	8137,42773	1009
CDS	sce4801	6754411	6752435	hydrogenase-4 component B	hyfB	8137,42773	651
CDS	sce7609	10590670	10589150	NADH dehydrogenase I chain N	nuoN2	8137,42773	1007
CDS	sce7610	10592938	10590674	NADH dehydrogenase I chain M	nuoM2	8137,42773	1008
CDS	sce7611	10595561	10592946	NADH dehydrogenase I chain L	nuoL2	8137,42773	1009
CDS	sce8577	11970570	11973485	pH adaptation potassium efflux protein PhaA	phaA	8137,42773	1009
CDS	sce8579	11973827	11975485	pH adaption potassium efflux protein PhaD	phaD	8137,42773	651
CDS	sce8743	12211731	12210211	Probable NADH dehydrogenase subunit	ndhM2	8137,42773	1008
CDS	sce8744	12213170	12211728	Probable NADH dehydrogenase subunit	ndhF2	8137,42773	1009

]

[

Fam: 36	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1951	2649835	2651922	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5321	7482791	7485424	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 36	No. of CDS: 4	Dom. COG: 3693	counter: 2 / 4	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1955	2660253	2658553	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce3118	4281496	4279751	Conserved hypothetical protein		5975	3693
CDS	sce4598	6502067	6500322	Endo-1,4-beta-xylanase	xynD	5975	3693
CDS	sce8904	12418747	12417443	Hypothetical protein predicted by Glimmer/Critica		5975	0

]

[

Fam: 36 No. of CDS: 4 Dom. COG: 0 counter: 4 / 4 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1956	2660802	2661221	Putative secreted protein			0
CDS	sce2270	3060205	3059798	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2446	3298433	3299089	Hypothetical protein			0
CDS	sce7116	9918488	9918895	Putative membrane protein			0

]

[

Fam: 36 No. of CDS: 2 Dom. COG: 392 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1959	2663332	2662304	Hypothetical protein			392
CDS	sce7386	10282167	10283150	Predicted integral membrane protein			392

]

[

Fam: 36 No. of CDS: 2 Dom. COG: 0 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1962	2665493	2665852	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6728	9383404	9382145	Putative exported protein			0

]

[

Fam: 37 No. of CDS: 2 Dom. COG: 583 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1964	2666718	2667656	Transcriptional regulator, LysR family			583
CDS	sce4120	5750786	5751682	LysR-family transcriptional regulator			583

]

[

Fam: 37 No. of CDS: 3 Dom. COG: 222(counter: 2 / 3 percentage: 66.67%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1968	2671592	2672392	Methyltransferase		8757	500
CDS	sce3044	4171133	4171948	Trans-aconitate 2-methyltransferase	tam1	8757	2226
CDS	sce5625	7919242	7918439	Ubiquinone/menaquinone biosynthesis methyltransferase	ubiE4	8757	2226

]

[

Fam: 37 No. of CDS: 3 Dom. COG: 793 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1978	2686894	2685827	Putative peptidase		6508,8236	793
CDS	sce2722	3693477	3694478	Carboxyl-terminal protease	ctpA1	6508,8236	793
CDS	sce8325	11607586	11608569	C-terminal processing peptidase	prc2	6508,8236	793

]

[

Fam: 37 No. of CDS: 3 Dom. COG: 0 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1979	2687614	2686907	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2721	3692904	3693446	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8327	11610216	11609665	Hypothetical protein			0

]

[

Fam: 37 No. of CDS: 4 Dom. COG: 0 counter: 2 / 4 percentage: 50.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce1982	2692931	2691813	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce1983	2694230	2692977	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2718	3687514	3688695	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce8322	11602393	11603592	Conserved hypothetical protein			3501

]

[

Fam: 37	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1985	2697089	2695968	no hits			0
CDS	sce2265	3054223	3053132	Hypothetical protein			0
CDS	sce7163	9990910	9989789	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7816	10889812	10890981	Hypothetical protein			0

]

[

Fam: 37	No. of CDS: 12	Dom. COG: 1262	counter: 6 / 12	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce1993	2707075	2705180	Hypothetical protein predicted by Glimmer/Critica		5554	0
CDS	sce2816	3846377	3845385	Hypothetical protein			1262
CDS	sce3992	5559226	5560572	Conserved hypothetical protein		5554	1262
CDS	sce5329	7494779	7495861	Hypothetical protein		5554	0
CDS	sce5586	7865237	7866550	Putative membrane protein		5554	0
CDS	sce5590	7870743	7872278	Conserved hypothetical protein			
CDS	sce5593	7876307	7877497	DUF323 domain conserved hypothetical protein		5554	1262
CDS	sce5880	8260808	8259477	Conserved hypothetical protein		5554	1262
CDS	sce7485	10429054	10430067	Conserved hypothetical protein			1262
CDS	sce7530	10485897	10484950	Conserved hypothetical protein		5554	1262
CDS	sce7790	10855717	10854554	Putative membrane protein		5554	0
CDS	sce8780	12268720	12269802	Putative secreted protein			0

]

[

Fam: 37	No. of CDS: 4	Dom. COG: 1249	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2004	2719138	2717741	Dihydrolipoyl dehydrogenase		6118,15036	1249
CDS	sce2324	3132897	3131497	Dihydrolipoyl dehydrogenase		6118,15036	1249
CDS	sce6561	9132548	9131121	Glutathione-disulfide reductase	gor	4362,6749	1249
CDS	sce8000	11131816	11130410	Pyruvate dehydrogenase E3 (dihydrolipoamide dehydrogenase)	pdhD	4148,6096	1249

]

[

Fam: 37	No. of CDS: 3	Dom. COG: 1173	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2036	2762490	2761498	Oligopeptide ABC transporter, permease component	appC	5215,6810,16020	1173
CDS	sce3459	4827213	4828265	Oligopeptide transport permease protein	oppC	5215,6810,16020	1173
CDS	sce3647	5107057	5109747	Putative oligopeptide ABC transporter integral membrane protein		5215,681	747

]

[

Fam: 37	No. of CDS: 2	Dom. COG: 265	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2038	2765616	2764033	Putative protease			265
CDS	sce2039	2766689	2765616	Glutamyl endopeptidase			3591

]

[

Fam: 38	No. of CDS: 13	Dom. COG: 631	counter: 13 / 13	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce2040	2768532	2766721	Phosphoprotein phosphatase	pp2c2	3824	631
CDS	sce2784	3797792	3796974	Phosphoprotein phosphatase	pp2c4	3824	631
CDS	sce2855	3897592	3898800	Phosphoprotein phosphatase	pp2c5	3824	631
CDS	sce3096	4238457	4239248	Phosphoprotein phosphatase	pp2c6	3824	631
CDS	sce3126	4293726	4292773	Phosphoprotein phosphatase	pp2c7	3824	631
CDS	sce3569	4994603	4995376	Phosphoprotein phosphatase	pp2c8	3824	631
CDS	sce3795	5286650	5287885	Phosphoprotein phosphatase	pp2c9	3824	631
CDS	sce4754	6699537	6700442	Phosphoprotein phosphatase	pp2c10		631
CDS	sce6171	8638619	8637735	Phosphoprotein phosphatase	pp2c11	3824	631
CDS	sce6484	9038854	9037517	Phosphoprotein phosphatase	pp2c12	3824	631
CDS	sce6950	9695418	9694663	Phosphoprotein phosphatase	pp2c13	3824	631
CDS	sce7899	11010536	11009763	Phosphoprotein phosphatase	pp2c14	3824	631
CDS	sce8596	11994689	11995507	Phosphoprotein phosphatase	pp2c15	3824	631

]

[

Fam: 38	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2054	2785194	2784181	Putative membrane protein			0
CDS	sce6894	9623210	9622245	Hypothetical protein			0

]

[

Fam: 38	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2061	2795186	2795974	Putative membrane protein			0
CDS	sce5558	7827517	7826738	Putative membrane protein			0

]

[

Fam: 38	No. of CDS: 5	Dom. COG: 367	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2064	2800360	2798354	Asparagine synthetase		4066,6529	367
CDS	sce3187	4374706	4376670	Asparagine synthetase	asnB1	4066,6529	367
CDS	sce3826	5322501	5324513	Asparagine synthase (glutamine-hydrolyzing)	asnB2	4066,6529	367
CDS	sce4939	6942424	6940574	Asparagine synthase (glutamine-hydrolyzing)	asnH	4066,6529	367
CDS	sce8804	12296259	12294454	Asparagine synthase (glutamine-hydrolyzing)	asnB3	4066,6529	367

]

[

Fam: 38	No. of CDS: 2	Dom. COG: 320	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2073	2815989	2812378	Putative membrane protein			0
CDS	sce6976	9730047	9727465	Putative membrane protein			3202

]

[

Fam: 38	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2081	2822829	2823335	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6875	9601982	9601080	Conserved hypothetical protein			0

]

[

Fam: 38	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2107	2856168	2855695	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7907	11023764	11023057	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 38	No. of CDS: 2	Dom. COG: 222	counter: 2 / 2	percentage: 100.00%			

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2156	2919934	2920875	Conserved hypothetical protein			2220
CDS	sce9325	12970902	12969901	Conserved hypothetical protein			2220

]

[

Fam: 38	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2178	2942001	2940964	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9112	12681488	12680538	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 38	No. of CDS: 6	Dom. COG: 369	counter: 6 / 6	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2188	2953049	2951700	Endo-1,4-beta-xylanase	xysA	5975	3693
CDS	sce3318	4645977	4647068	Put. Endoglucanase		5975	3693
CDS	sce4591	6489800	6490621	Endo-1,4-beta-xylanase	xynB2	5975	3693
CDS	sce4601	6503736	6502528	Endo-1,4-beta-xylanase	xynB3	5975	3693
CDS	sce6693	9311465	9312526	O-Glycosyl hydrolase		5975	3693
CDS	sce7089	9884656	9885852		xynA2	5975	3693

]

[

Fam: 39	No. of CDS: 3	Dom. COG: 100	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2194	2962362	2959015	Conserved hypothetical protein		3677,6306,8170	1002
CDS	sce3242	4541811	4537606	Conserved hypothetical protein		3677,6306,8170	1002
CDS	sce8073	11232353	11229084	Unknown protein		3677,6306,8170	1002

]

[

Fam: 39	No. of CDS: 2	Dom. COG: 745	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2206	2973271	2972897	Two-component response regulator			745
CDS	sce2424	3266255	3266740	Two-component response regulator			784

]

[

Fam: 39	No. of CDS: 2	Dom. COG: 187	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2220	2994153	2995151	LACI-type transcriptional regulator			1609
CDS	sce3308	4633776	4632805	Put.Periplasmic protein precursor			1879

]

[

Fam: 39	No. of CDS: 10	Dom. COG: 112	counter: 7 / 10	percentage: 70.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2221	2995161	2996681	ABC-type sugar transport system ATPase component		4009,5524,6810,16020	1129
CDS	sce3101	4244787	4243249	ABC transporter, nucleotide binding/ATPase protein		4009,5524,6810,16020	1129
CDS	sce3307	4632758	4631235	Put. ATP-binding component of a transport system		4009,5524,6810,16020	1129
CDS	sce3323	4654681	4656201	Sugar ABC transporter ATP-binding protein		4009,5524,6810,16020	1129
CDS	sce3554	4967573	4965906	Putative sugar ABC transporter ATP-binding protein		4009,5524,6810,16020	3845
CDS	sce4029	5613099	5611573	Ribose transport ATP-binding protein	rbsA1	4009,5524,6810,16020	1129
CDS	sce4415	6238440	6240035	Similar to sugar ABC transporter, ATP-binding protein		4009,5524,6810,16020	3845

CDS	sce5492	7740908	7739385	ABC transporter, nucleotide binding/ATPase protein	xylG	4009,5524,6810,16020	1129
CDS	sce7755	10802644	10801091	Sugar ABC transporter, ATP-binding protein		4009,5524,6810,16020	3845
CDS	sce8239	11466538	11464970	Ribose transport ATP-binding protein	rbsA2		1129

]

[

Fam: 39	No. of CDS: 8	Dom. COG: 117	counter: 7 / 8	percentage: 87.50%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2222	2996770	2997756	Sugar ABC transport system permease protein		5215,6810,16020	1172
CDS	sce2223	2997759	2998763	Put. Sugar transport system permease		5215,6810,16020	1172
CDS	sce3100	4243234	4242137	Sugar transport system permease		5215,6810,16020	1172
CDS	sce3305	4630165	4629134	Put. Sugar transport system permease		5215,6810,16020	1172
CDS	sce3306	4631238	4630180	Put.Ribose/xylose/arabinose/galactoside ABC-type transport system permease		5215,6810,16020	1172
CDS	sce3324	4656198	4657139	Transport system permease protein		5215,6810,16020	1172
CDS	sce4028	5611507	5610371	Ribose transport system permease protein	rbsC2	5215,6810,16020	1172
CDS	sce5491	7739388	7738288	D-xylose ABC transporter, permease protein	xylH	5215,6810,16020	4214

]

[

Fam: 39	No. of CDS: 4	Dom. COG: 367	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2231	3006249	3007409	Probable Lipase		4806,6629	3675
CDS	sce4046	5636644	5635460	Probable Lipase		4806,6629	3675
CDS	sce7028	9815005	9813827	Probable Lipase		4806,6629	3675
CDS	sce7029	9816361	9815183	Probable Lipase		4806,6629	3675

]

[

Fam: 39	No. of CDS: 2	Dom. COG: 136	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2234	3008406	3010724	Cellulase	yhjM		1363
CDS	sce5309	7465242	7463206	Putative glycosyl hydrolase			

]

[

Fam: 39	No. of CDS: 2	Dom. COG: 740	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2239	3016483	3015866	Endopeptidase Clp	clpP1	6508,8462	740
CDS	sce3147	4324154	4324798	Endopeptidase Clp	clpP2	6508,8462	740

]

[

Fam: 39	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2242	3018294	3019469	Putative hydrolase			0
CDS	sce4006	5578193	5575962	Bacterial type 3a, cellulose-binding domain			0

]

[

Fam: 39	No. of CDS: 2	Dom. COG: 451	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2249	3032225	3033262	dTDP-glucose 4,6-dehydratase			1088
CDS	sce7003	9783477	9782434	NDP-sugar oxidoreductase		3824,9225	451

]

[

Fam: 40	No. of CDS: 2	Dom. COG: 121	counter: 2 / 2	percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2253	3037737	3036880	Putative amidotransferase	yafJ	8152	121
CDS	sce8627	12031061	12030276	Putative amidotransferase		8152	121

]

[

Fam: 40	No. of CDS: 2	Dom. COG: 222(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2266	3054447	3055400	Conserved hypothetical protein			2220
CDS	sce2742	3732710	3731667	Conserved hypothetical protein			2220

]

[

Fam: 40	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2272	3062629	3063111	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2928	4009922	4009326	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 40	No. of CDS: 2	Dom. COG: 583	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2273	3064543	3063545	Transcriptional regulator, LysR family			583
CDS	sce4966	6983174	6984142	LysR-family transcriptional regulator			583

]

[

Fam: 40	No. of CDS: 3	Dom. COG: 714	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2278	3068987	3069970	Hypothetical protein		166	714
CDS	sce6215	8692236	8691319	Conserved hypothetical protein		166	714
CDS	sce6513	9072281	9073120	Hypothetical ATPase-like protein		5524	714

]

[

Fam: 40	No. of CDS: 12	Dom. COG: 343(	counter: 12 / 12	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2281	3077918	3076254	Transposase			3436
CDS	sce5563	7833553	7831889	Transposase			3436
CDS	sce6099	8543043	8544707	Transposase			3436
CDS	sce6102	8552546	8550882	Transposase			3436
CDS	sce6105	8555138	8553474	Transposase			3436
CDS	sce6137	8599876	8601540	Transposase			3436
CDS	sce6285	8774948	8776441	Transposase			3436
CDS	sce6616	9207181	9208650	Transposase			3436
CDS	sce6617	9211312	9209648	Transposase			3436
CDS	sce6621	9216447	9215452	Transposase (possibly truncated)			3436
CDS	sce6707	9335713	9337377	Transposase			3436
CDS	sce9101	12670632	12668968	Transposase			3436

]

[

Fam: 40	No. of CDS: 11	Dom. COG: 343(	counter: 11 / 11	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2282	3078337	3077915	Transposase			3436
CDS	sce5564	7833972	7833550	Transposase			3436
CDS	sce6098	8542624	8543046	Transposase			3436
CDS	sce6103	8552965	8552543	Transposase			3436
CDS	sce6106	8555557	8555135	Transposase			3436
CDS	sce6136	8599457	8599879	Transposase			3436
CDS	sce6281	8772679	8773101	Transposase			3436
CDS	sce6618	9211731	9211309	Transposase			3436

CDS	sce6622	9216866	9216444	Transposase			3436
CDS	sce6706	9335294	9335716	Transposase			3436
CDS	sce9102	12671051	12670629	Transposase			3436

]

[

Fam: 40	No. of CDS: 12	Dom. COG: 343(	counter: 9 / 12	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2283	3078669	3078331	Transposase			3436
CDS	sce5565	7834304	7833966	Transposase			3436
CDS	sce6097	8542292	8542630	Transposase			3436
CDS	sce6104	8553297	8552959	Transposase			3436
CDS	sce6107	8555889	8555551	Transposase			3436
CDS	sce6108	8558125	8557787	Putative transposase			0
CDS	sce6135	8599125	8599463	Transposase			3436
CDS	sce6280	8772347	8772685	Putative transposase			0
CDS	sce6619	9212063	9211725	Transposase			3436
CDS	sce6623	9217198	9216860	Transposase			2963
CDS	sce6705	9334962	9335300	Transposase			3436
CDS	sce9103	12671383	12671045	Transposase			3436

]

[

Fam: 40	No. of CDS: 2	Dom. COG: 108	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2288	3084238	3085332	GTP cyclohydrolase II	ribA1	9231	108
CDS	sce7267	10143889	10145058	Riboflavin biosynthesis protein	ribA4	9231	108

]

[

Fam: 40	No. of CDS: 2	Dom. COG: 162(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2290	3091187	3088278	Hypothetical protein predicted by Glimmer/Critica		4872,5215,6810,16020	1629
CDS	sce9157	12758987	12755874	Probable tonb-dependent receptor signal peptide protein		4872,5215,6810,16020	1629

]

[

Fam: 41	No. of CDS: 3	Dom. COG: 340(	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2296	3097269	3099275	4-Alpha-glucanotransferase	malQ1		3408
CDS	sce2477	3339698	3341887	4-Alpha-glucanotransferase	malQ3		3408
CDS	sce7169	10016259	10014187	4-Alpha-glucanotransferase	malQ4		3408

]

[

Fam: 41	No. of CDS: 2	Dom. COG: 76	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2299	3101776	3100325	Putative decarboxylase		6520,16831	76
CDS	sce6892	9621175	9619757	Glutamate decarboxylase and related PLP-dependent proteins		6520,16831	76

]

[

Fam: 41	No. of CDS: 2	Dom. COG: 691	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2300	3102498	3102010	SmpB-like protein		3723,6412	691
CDS	sce2569	3463382	3462963	SmpB-like protein		3723,6412	691

]

[

Fam: 41	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2306	3106944	3105988	Hypothetical protein predicted by Glimmer/Critica		4867	0
CDS	sce7740	10784180	10783392	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 41	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2308	3107707	3108609	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5365	7551118	7551591	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 41	No. of CDS: 3	Dom. COG: 488(	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2311	3114289	3110927	Hypothetical protein			4880
CDS	sce6466	9014144	9017164	Hypothetical protein			4880
CDS	sce8447	11769193	11766032	Hypothetical protein			4880

]

[

Fam: 41	No. of CDS: 5	Dom. COG: 0	counter: 2 / 5	percentage: 40.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2322	3128094	3127717	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2616	3535291	3535668	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5199	7304765	7304388	Hypothetical protein			
CDS	sce5202	7308328	7307951	Hypothetical protein			
CDS	sce5205	7311823	7311446	Hypothetical protein			

]

[

Fam: 41	No. of CDS: 2	Dom. COG: 561	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2325	3133771	3132920	Hypothetical protein		8152,16787	561
CDS	sce7013	9794674	9795489	Conserved hypothetical protein			561

]

[

Fam: 41	No. of CDS: 4	Dom. COG: 0	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2332	3144509	3145516	Hypothetical protein			0
CDS	sce3086	4227577	4228518	Hypothetical protein			0
CDS	sce3540	4947939	4947034	Conserved hypothetical protein			4636
CDS	sce7033	9823160	9824056	Conserved hypothetical protein			0

]

[

Fam: 41	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2347	3158524	3159492	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7792	10856636	10857619	Hypothetical protein			0

]

[

Fam: 42	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2363	3175480	3173453	Hypothetical protein			0
CDS	sce4917	6910035	6908023	Hypothetical protein			0

]

[

Fam: 42	No. of CDS: 2	Dom. COG: 4	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2376	3190892	3189588	Ammonium transporter	amt1	6810,8519,16020	4
CDS	sce7390	10286840	10288054	Ammonium transporter	amt2	6810,8519,16020	4

]

[

Fam: 42	No. of CDS: 2	Dom. COG: 147	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2384	3202370	3201186	Putative hydrolase		6508,8237	1473
CDS	sce4971	6986447	6987610	putatuve Metallocarboxypeptidase	ama	6508,8237	1473

]

[

Fam: 42	No. of CDS: 3	Dom. COG: 296	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2392	3223715	3225559	Malto-oligosyltrehalose trehalohydrolase	treZ	5975	296
CDS	sce4494	6339534	6337288	1,4-Alpha-glucan branching enzyme	glgB	5978	296
CDS	sce7170	10018195	10016249	Alpha-amylase-family protein		4556,5975	296

]

[

Fam: 42	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2398	3232970	3234277	Conserved hypothetical protein		5737,6817	0
CDS	sce2570	3464090	3465760	Conserved hypothetical protein			0
CDS	sce3832	5331655	5330660	Procollagen, type XI, alpha		5737,6817	0
CDS	sce5460	7686963	7689632	Collagen alpha 2(I) chain precursor		5737,6817	0

]

[

Fam: 42	No. of CDS: 2	Dom. COG: 303	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2402	3242407	3241190	Probable molybdopterin biosynthesis protein	moeA1	6777	303
CDS	sce9309	12948260	12949504	Molybdenum cofactor biosynthesis protein	moeA2	6777	303

]

[

Fam: 42	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2442	3292784	3289140	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9134	12716330	12719857	Putative secreted protein			0

]

[

Fam: 42	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2443	3294139	3292796	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9133	12714614	12716173	Putative secreted protein			0

]

[

Fam: 42	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2445	3296250	3298310	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce2774	3783652	3782411	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7313	10198437	10199738	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7659	10658610	10657267	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 42 No. of CDS: 2 Dom. COG: 150 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2448	3302280	3300895	Lysine 2,3-aminomutase	kamA1		1509
CDS	sce7261	10133240	10134475	Lysine 2,3-aminomutase	kamA2		1509

]

[

Fam: 43 No. of CDS: 2 Dom. COG: 126 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2451	3304990	3303959	Conserved hypothetical protein			1266
CDS	sce5305	7459361	7458519	Conserved hypothetical protein			1266

]

[

Fam: 43 No. of CDS: 3 Dom. COG: 171 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2478	3342850	3341921	FHA domain protein			1716
CDS	sce2703	3669959	3670801	FHA domain protein			1716
CDS	sce4669	6591918	6591022	FHA domain protein			1716

]

[

Fam: 43 No. of CDS: 3 Dom. COG: 216 counter: 2 / 3 percentage: 66.67%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2487	3353217	3353837	Type II secretory pathway pseudopilin			2165
CDS	sce4274	6043181	6043792	Fimbiral protein pilA	pilA2	7155,9289	4969
CDS	sce4275	6043872	6044483	pilin	pilA3		2165

]

[

Fam: 43 No. of CDS: 7 Dom. COG: 574 counter: 5 / 7 percentage: 71.43%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2489	3358078	3355556	Fructose-specific MTP	fruB		1080
CDS	sce4177	5905323	5907935	Phosphoenolpyruvate synthase	ppsA1	5524,16301,16310	574
CDS	sce4570	6461808	6459481	Phosphoenolpyruvate synthase	ppsA2	6094	574
CDS	sce5764	8103562	8101592	Phosphoenolpyruvate--protein phosphotransferase.	ptsI	16772	1080
CDS	sce7543	10513396	10510634	Pyruvate, phosphate dikinase	ppdK		574
CDS	sce7847	10940806	10943337	Pyruvate, water dikinase	ppsA3	5524,16301,16310	574
CDS	sce7909	11027878	11024810	Probable phosphoenolpyruvate synthase		16310,16772	574

]

[

Fam: 43 No. of CDS: 2 Dom. COG: 429 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2493	3361604	3360648	Conserved hypothetical protein	yheT	3824	429
CDS	sce3475	4851167	4850109	Conserved hypothetical protein		3824	429

]

[

Fam: 43 No. of CDS: 3 Dom. COG: 125 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2495	3365334	3363958	Probable hemolysin			1253
CDS	sce4286	6058754	6060046	Conserved hypothetical membrane protein			1253
CDS	sce5899	8291564	8290251	CBS domain protein			1253

]

[

Fam: 43 No. of CDS: 5 Dom. COG: 553 counter: 5 / 5 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2503	3374319	3377414	Helicase, SNF2/RAD54 family		3677,5524	553
CDS	sce2990	4099199	4102624	Conserved hypothetical protein		3677,5524	553

CDS	sce3369	4710462	4707427	SWF/SNF family helicase	helZ	3677,5524	553
CDS	sce4555	6436450	6432638	Conserved hypothetical protein		3677,5524	553
CDS	sce7539	10506710	10503876	Helicase, Snf2 family		3677,5524	553

]

[

Fam: 43	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2510	3386348	3385209	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3258	4563081	4561663	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 43	No. of CDS: 2	Dom. COG: 1716	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2516	3398513	3397344	FHA domain protein			1716
CDS	sce5002	7026306	7025152	FHA domain protein			1716

]

[

Fam: 43	No. of CDS: 3	Dom. COG: 527	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2535	3418798	3420045	Aspartate kinase	lysC1		527
CDS	sce6246	8729242	8727962	Aspartate kinase	lysC2	4072,8652	527
CDS	sce9261	12891463	12892794	Aspartate kinase		4072,8652	527

]

[

Fam: 44	No. of CDS: 2	Dom. COG: 1506	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2540	3428433	3426637	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases			1506
CDS	sce6409	8944988	8942850	Putative peptidase			1506

]

[

Fam: 44	No. of CDS: 2	Dom. COG: 20	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2553	3447278	3446538	Undecaprenyl pyrophosphate synthetase	uppS1	8152,1674	20
CDS	sce6193	8665561	8666421	Undecaprenyl diphosphate synthase	uppS2	8152,1674	20

]

[

Fam: 44	No. of CDS: 4	Dom. COG: 178	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2571	3466011	3471356	Excinuclease ABC subunit A	uvrA1	6289,9380,9381	178
CDS	sce3785	5273262	5276255	Excinuclease ABC subunit A	uvrA2	6289,9380,9381	178
CDS	sce6315	8804129	8806558	Similar to excinuclease ABC (subunit A)	uvrA3	4009,5524,6810,16020	178
CDS	sce8597	11995645	11998689	Excinuclease ABC subunit A	uvrA4	6289,9380,9381	178

]

[

Fam: 44	No. of CDS: 5	Dom. COG: 0	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2595	3509222	3507054	Autotransporter			0
CDS	sce2732	3716407	3713858	Putative cell surface protein			0
CDS	sce4303	6084520	6082118	Probable extracellular nuclease			0
CDS	sce7118	9920277	9922322	Conserved hypothetical protein			0
CDS	sce9064	12623508	12621376	Hypothetical protein			0

]

[

Fam: 44 No. of CDS: 3 Dom. COG: 332 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2600	3513247	3514251	3-Oxoacyl-(acyl-carrier-protein) synthase III	fabH2		332
CDS	sce3817	5314901	5313906	3-Oxoacyl-(acyl-carrier-protein) synthase III	fabH3	4315,6633	332
CDS	sce5053	7092894	7091833	3-Oxoacyl-[acyl-carrier-protein] synthase	fabH4	4315,6633	332

]

[

Fam: 44 No. of CDS: 3 Dom. COG: 1472 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2601	3514431	3516617	Beta-glucosidase	bglX	5975	1472
CDS	sce6897	9628660	9626162	Beta-glucosidase-related glycosidases		5975	1472
CDS	sce8559	11932877	11935096	Beta-glucosidase	bglA4	5975	1472

]

[

Fam: 44 No. of CDS: 5 Dom. COG: 1858 counter: 3 / 5 percentage: 60.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2614	3532150	3534270	Hypothetical protein			1858
CDS	sce2987	4094662	4092842	Conserved hypothetical protein			
CDS	sce4039	5628455	5630647	Hypothetical protein			3391
CDS	sce8814	12309488	12307218	Putative cytochrome c peroxidase			1858
CDS	sce9284	12919982	12921793	Putative cytochrome c peroxidase			1858

]

[

Fam: 44 No. of CDS: 3 Dom. COG: 145 counter: 2 / 3 percentage: 66.67%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2621	3543921	3542200	N-methylhydantoinase B, alpha subunit	huyB	3824	146
CDS	sce2622	3546015	3543955	N-methylhydantoinase A, beta subunit	huyA1	16787	145
CDS	sce4077	5686243	5689908	5-Oxoprolinase (ATP-hydrolyzing)	oplaH	3824	145

]

[

Fam: 44 No. of CDS: 2 Dom. COG: 468 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2624	3548126	3549154	RecA protein	recA1	3684,5524,6281,6310,809	468
CDS	sce5959	8366333	8367514	RecA protein	recA2	3684,5524,6281,6310,809	468

]

[

Fam: 44 No. of CDS: 3 Dom. COG: 629 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2625	3549384	3549860	ssDNA-binding protein	ssb		629
CDS	sce2627	3551806	3552117	Single-strand binding protein		3676	629
CDS	sce8612	12013684	12013073	Single-stranded DNA binding protein			629

]

[

Fam: 45 No. of CDS: 2 Dom. COG: 0 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2628	3552644	3553399	Putative secreted protein			0
CDS	sce4340	6128560	6127739	Putative secreted protein			0

]

[

Fam: 45 No. of CDS: 2 Dom. COG: 2911 counter: 1 / 2 percentage: 50.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce2640	3571668	3570307	Hypothetical protein			2911
CDS	sce4707	6643332	6645146	Conserved hypothetical protein			0

]

[

Fam: 45	No. of CDS: 2	Dom. COG: 372	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2649	3582392	3582006	Conserved hypothetical protein			3729
CDS	sce4398	6209759	6210217	Hypothetical protein			0

]

[

Fam: 45	No. of CDS: 4	Dom. COG: 840	counter: 2 / 4	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2659	3596450	3598999	Probable chemotaxis sensory transducer		4871,6935,7165,16020	840
CDS	sce5864	8239350	8236051	Response regulator		156,160,3677	784
CDS	sce8592	11988699	11992055	Putative membrane protein			0
CDS	sce8991	12529264	12531252	Methyl-accepting chemotaxis protein		4871,6935,7165,16020	840

]

[

Fam: 45	No. of CDS: 2	Dom. COG: 275	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2691	3656019	3657419	Putative secreted protein		3824	0
CDS	sce5221	7343079	7344440	Lysophospholipase L1 and related esterases		3824	2755

]

[

Fam: 45	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2694	3663066	3661492	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3041	4167224	4168813	Putative secreted protein			0

]

[

Fam: 45	No. of CDS: 12	Dom. COG: 320	counter: 9 / 12	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2713	3680739	3682238	Conserved hypothetical protein		4182,6508	0
CDS	sce3516	4910724	4917440	Rhs family protein			3209
CDS	sce3518	4918098	4921211	Conserved hypothetical protein		4182,6508	0
CDS	sce6722	9367135	9374415	insecticidal toxin complex-like protein		5737	0
CDS	sce6980	9736861	9733955	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce6981	9740298	9737770	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce6982	9741952	9740750	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce6984	9754509	9744238	RhsA protein precursor.			3209
CDS	sce7678	10692402	10685749	Hypothetical carbohydrate-binding protein, Rhs family			3209
CDS	sce7825	10905853	10902962	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce7826	10916081	10906632	Conserved carbohydrate-binding protein, Rhs family			3209
CDS	sce8560	11944349	11937126	Rhs family protein		5737	3209

]

[

Fam: 45	No. of CDS: 2	Dom. COG: 188	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2716	3683778	3686426	Methylmalonyl-CoA mutase	mcm	4494,8152	1884
CDS	sce7549	10521377	10519563	Isobutyryl-CoA mutase		4494,8152	1884

]

[

Fam: 45 No. of CDS: 2 Dom. COG: 170 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2717	3686428	3687420	Methylmalonyl-CoA mutase component	meaB		1703
CDS	sce3917	5452792	5451716	Putative transport system kinase			1703

]

[

Fam: 45 No. of CDS: 2 Dom. COG: 342 counter: 1 / 2 percentage: 50.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2731	3712236	3713708	Conserved hypothetical protein			3420
CDS	sce9018	12562519	12563988	Conserved hypothetical protein			0

]

[

Fam: 46 No. of CDS: 2 Dom. COG: 845 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2736	3721493	3722857	Heavy metal efflux pump, CzcB family	czcB1		845
CDS	sce8710	12157450	12158850	Heavy metal efflux pump, CzcB family	czcB2	8565,9306,16020	845

]

[

Fam: 46 No. of CDS: 7 Dom. COG: 0 counter: 5 / 7 percentage: 71.43%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2744	3738198	3736825	Mucin			3712
CDS	sce3657	5121201	5122472	Conserved hypothetical protein			3712
CDS	sce4863	6827014	6825794	Putative membrane protein			0
CDS	sce4906	6890961	6889684	Hypothetical protein			0
CDS	sce5454	7674426	7676003	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6997	9772735	9771440	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7068	9863567	9861984	Conserved hypothetical protein			0

]

[

Fam: 46 No. of CDS: 7 Dom. COG: 159 counter: 7 / 7 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2745	3738928	3738191	RNA polymerase sigma factor		3677,3700,6352,6355,169	1595
CDS	sce3656	5120581	5121204	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce4864	6827676	6827002	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce4907	6891593	6890958	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce5453	7673803	7674450	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce6998	9773358	9772726	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce7069	9864204	9863560	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595

]

[

Fam: 46 No. of CDS: 4 Dom. COG: 175 counter: 4 / 4 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2752	3751341	3750055	Conserved hypothetical protein		3824,45735	1752
CDS	sce4655	6574028	6575272	Conserved hypothetical protein		3824,45735	1752
CDS	sce5503	7756474	7755110	patatin like phospholipase		3824	1752
CDS	sce5630	7922010	7923395	Conserved hypothetical protein		3824,45735	1752

]

[

Fam: 46 No. of CDS: 2 Dom. COG: 0 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2768	3775463	3774249	Putative secreted protein			0

CDS	sce5720	8047111	8048196	Hypothetical endo-1,4-beta-glucanase			0

]

[

Fam: 46	No. of CDS: 2	Dom. COG: 234	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2780	3793044	3793340	GroES-like protein			234
CDS	sce5910	8306020	8306310	GroES-like protein			234

]

[

Fam: 46	No. of CDS: 2	Dom. COG: 459	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2781	3793409	3795097	GroEL like chaperone, HSP60 family			459
CDS	sce5911	8306344	8307972	Heat shock protein groEL			459

]

[

Fam: 46	No. of CDS: 2	Dom. COG: 642	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2791	3806916	3809279	Sensor histidine kinase		7165,16301	642
CDS	sce3207	4477298	4479742	Two-component sensor kinase		7165,16301	2205

]

[

Fam: 46	No. of CDS: 3	Dom. COG: 0	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2800	3819490	3820530	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5293	7446149	7444767	Hypothetical protein			0
CDS	sce8655	12081810	12083039	Hypothetical protein		166	3950

]

[

Fam: 46	No. of CDS: 4	Dom. COG: 1201	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2802	3822283	3826776	Putative ATP-dependent helicase, N-terminal fragment	lhr1	5524,8026	1201
CDS	sce3906	5431280	5433682	Nucleotidyltransferase	yprA	5524,8026	1205
CDS	sce3970	5518905	5514001	Putative ATP-dependent helicase	lhr2	166	1201
CDS	sce7687	10704573	10706714	ATP-dependent helicase		5524,8026	1201

]

[

Fam: 47	No. of CDS: 3	Dom. COG: 0	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2827	3856359	3857267	Putative secreted protein			0
CDS	sce2836	3868558	3870522	Putative membrane protein			0
CDS	sce6045	8480805	8478934	Hypothetical protein predicted by Glimmer/Critica			

]

[

Fam: 47	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2830	3858620	3858868	Conserved hypothetical protein			0
CDS	sce6524	9086442	9086687	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 47	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2832	3862560	3863408	Conserved hypothetical protein			0

CDS	sce4829	6784232	6785116	Hypothetical protein			0
CDS	sce6944	9686589	9685750	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 47	No. of CDS: 2	Dom. COG: 282	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2860	3902354	3901758	Outer membrane protein, putative			2825
CDS	sce3122	4286946	4286227	Putative membrane protein	ompH		2825

]

[

Fam: 47	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2863	3904910	3906526	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6670	9281726	9279675	Conserved hypothetical protein			0

]

[

Fam: 47	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2864	3906536	3907396	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6669	9279831	9278860	Hypothetical protein			0

]

[

Fam: 47	No. of CDS: 2	Dom. COG: 508	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2875	3921706	3920648	Phosphatidylinositol transfer protein, membrane-associated			5083
CDS	sce3019	4140019	4138832	Putative membrane protein			5083

]

[

Fam: 47	No. of CDS: 3	Dom. COG: 156	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2880	3927841	3926609	8-Amino-7-oxononanoate synthase	bioF1	8483,9058	156
CDS	sce7278	10158247	10157093	Glycine C-acetyltransferase	kbl		156
CDS	sce8160	11350833	11351945	Putative 8-amino-7-oxononanoate synthase	bioF2	8483,9058	156

]

[

Fam: 47	No. of CDS: 2	Dom. COG: 550	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2885	3935372	3933198	ATP-dependent DNA helicase RecQ	recQ	6259,8026	514
CDS	sce3415	4762538	4766968	DNA topoisomerase III	topB	3677,3916,5694,6265,626	550

]

[

Fam: 47	No. of CDS: 2	Dom. COG: 541	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2908	3966236	3964875	Cell division membrane protein	ftsY	5525	552
CDS	sce8540	11899814	11901454	Signal recognition particle protein	ffh	3723,5786,6614	541

]

[

Fam: 48	No. of CDS: 2	Dom. COG: 642	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2911	3969508	3970377	Hypothetical protein predicted by Glimmer/Critica		4871,7165,16020	642

CDS	sce5254	7396886	7397665	Hypothetical protein			0
]							
[							
Fam: 48	No. of CDS: 2	Dom. COG: 624	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2952	4040955	4042058	Succinyl-diaminopimelate desuccinylase	dapE2	6508,8237	624
CDS	sce6318	8809621	8810673	Succinyl-diaminopimelate desuccinylase	dapE3	6508,8237	624
]							
[							
Fam: 48	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2982	4086114	4087376	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8816	12310535	12311635	Hypothetical protein			0
]							
[							
Fam: 48	No. of CDS: 2	Dom. COG: 811	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2993	4104639	4103962	Adventurous gliding motility protein R	aglR1	6810,8565,16020	811
CDS	sce2994	4105598	4106260	Adventurous gliding motility protein R	aglR2	6810,8565,16020	811
]							
[							
Fam: 48	No. of CDS: 2	Dom. COG: 848	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce2995	4106487	4107056	Putative biopolymer transport protein			848
CDS	sce6510	9069364	9068801	Putative ExbD/TolR-like translocation protein			848
]							
[							
Fam: 48	No. of CDS: 3	Dom. COG: 127	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3007	4124650	4126398	Phosphoenolpyruvate carboxykinase (GTP)	pckA1	4611,5525,6094	1274
CDS	sce4201	5945025	5943073	Phosphoenolpyruvate carboxykinase (GTP)	pckG	4611,5525,6094	1274
CDS	sce4794	6744652	6746442	Phosphoenolpyruvate carboxykinase (GTP)	pckA2	4611,5525,6094	1274
]							
[							
Fam: 48	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3023	4145415	4144624	Putative membrane protein		45735	0
CDS	sce5657	7959245	7960123	Putative membrane protein			0
CDS	sce5658	7960170	7960883	Putative membrane protein		45735	0
]							
[							
Fam: 48	No. of CDS: 2	Dom. COG: 144	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3033	4156484	4157398	Asparaginase		4067,6516	1446
CDS	sce3769	5251107	5252141	Putative L-asparaginase		4067,6516	1446
]							
[							
Fam: 48	No. of CDS: 3	Dom. COG: 340	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3034	4157646	4159049	Endo-1,4-beta-xylanase	xynA1		3405

CDS	sce3220	4502363	4500870	Endo-1,4-beta-glucanase	xynB1		3405
CDS	sce5506	7759862	7758711	Cellulase	celY	5975	3405

]

[

Fam: 48	No. of CDS: 2	Dom. COG: 128	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3035	4159157	4160443	3-Phosphoshikimate 1-carboxyvinyltransferase	aroA1		128
CDS	sce6876	9602123	9603508	3-Phosphoshikimate 1-carboxyvinyltransferase	aroA2	3866	128

]

[

Fam: 49	No. of CDS: 2	Dom. COG: 1175	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3058	4190583	4191473	Sugar ABC transporter, permease protein		5215,6810,16020	1175
CDS	sce9265	12896293	12897174	Probable ABC transporter permease protein y4oQ.		5215,6810,16020	1175

]

[

Fam: 49	No. of CDS: 4	Dom. COG: 395	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3059	4191466	4192311	Sugar ABC transporter, permease protein		5215,6810,16020	395
CDS	sce5039	7071827	7070949	Trehalose/maltose transport system, permease protein	thuG	5215,6810,16020	395
CDS	sce7777	10830563	10829703	Put. Maltose permease		5215,6810,16020	395
CDS	sce9266	12897171	12898037	Put. ABC transporter sugar permease		5215,6810,16020	395

]

[

Fam: 49	No. of CDS: 2	Dom. COG: 4312	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3066	4201127	4201996	Conserved hypothetical protein			4312
CDS	sce4386	6194819	6195601	Conserved hypothetical protein			4312

]

[

Fam: 49	No. of CDS: 2	Dom. COG: 522	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3091	4232601	4233212	30S ribosomal protein S4	rpsD1	3735,6412,15935	522
CDS	sce7937	11065438	11064809	30S ribosomal protein S4	rpsD2	3735,6412,15935	522

]

[

Fam: 49	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3103	4246412	4247680	Putative secreted protein			0
CDS	sce3909	5437923	5436697	Hypothetical protein			0

]

[

Fam: 49	No. of CDS: 6	Dom. COG: 0	counter: 6 / 6	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3107	4252528	4253412	Hypothetical protein			0
CDS	sce5339	7512623	7511739	Hypothetical protein			0
CDS	sce5362	7545810	7546670	Hypothetical protein			0
CDS	sce7113	9913370	9912528	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7855	10954007	10954852	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8730	12189449	12188598	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 49	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3130	4304148	4302091	Putative secreted protein			0
CDS	sce8599	11999230	12000939	Conserved hypothetical protein			0

]

[

Fam: 49	No. of CDS: 5	Dom. COG: 0	counter: 5 / 5	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3137	4311913	4313487	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5676	7985640	7987250	Conserved hypothetical protein		166	0
CDS	sce6578	9148162	9150090	Conserved hypothetical protein			0
CDS	sce7473	10416997	10418550	Conserved hypothetical protein			0
CDS	sce9331	12979540	12981120	Hypothetical protein		166	0

]

[

Fam: 49	No. of CDS: 2	Dom. COG: 119	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3144	4321601	4320669	Partition protein, ParA homolog	parA2		1192
CDS	sce3151	4331623	4332480	ATPase	parA3		1192

]

[

Fam: 49	No. of CDS: 2	Dom. COG: 342	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3181	4369525	4368263	Probable hydroxymethylglutaryl-CoA synthase		4421,6084	3425
CDS	sce6394	8922434	8923657	Putative Hydroxymethylglutaryl-CoA synthase		4421,6084	3425

]

[

Fam: 50	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3199	4465312	4468080	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9125	12701568	12699130	Unknown protein			0
CDS	sce9126	12704167	12701732	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 50	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3200	4468402	4469286	Conserved hypothetical protein			0
CDS	sce3232	4521801	4522685	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4562	6448991	6449860	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 50	No. of CDS: 3	Dom. COG: 106	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3234	4523959	4527051	Putative helicase		5524,8026	1061
CDS	sce8195	11405317	11407743	Helicase-related protein		5524,8026	1061
CDS	sce8964	12498245	12496572	Hypothetical protein predicted by Glimmer/Critica		5524,8026	0

]

[

Fam: 50	No. of CDS: 3	Dom. COG: 395	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3241	4537519	4536248	Conserved hypothetical protein		166	3950

CDS	sce7683	10698343	10699629	Conserved hypothetical protein	pgaA	166	3950
CDS	sce8302	11578279	11579610	Conserved hypothetical protein		166	3950

]

[

Fam: 50	No. of CDS: 5	Dom. COG: 0	counter: 4 / 5	percentage: 80.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3263	4570678	4571961	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5240	7374273	7372882	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6696	9316491	9315097	Hypothetical secreted protein			0
CDS	sce7465	10406737	10405412	Putative monooxygenase			4989
CDS	sce8827	12322648	12321272	Putative secreted protein			0

]

[

Fam: 50	No. of CDS: 2	Dom. COG: 300	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3269	4580684	4579275	Na+/H antiporter	nhaA1	6814,6885,16021	3004
CDS	sce7409	10314024	10315430	Na+/H+ antiporter	nhaA2	6814,6885,16021	3004

]

[

Fam: 50	No. of CDS: 3	Dom. COG: 220	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3272	4584170	4583238	Transcriptional regulator, AraC family			2207
CDS	sce8589	11984173	11985081	Transcriptional regulator, AraC family			2207
CDS	sce8847	12341482	12340616	Transcriptional regulator, AraC family			2207

]

[

Fam: 50	No. of CDS: 3	Dom. COG: 350	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3277	4590003	4591373	Putative ssterase		3824	3509
CDS	sce4184	5917410	5918693	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce6739	9395069	9393681	Putative lipase			3509

]

[

Fam: 50	No. of CDS: 2	Dom. COG: 325	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3281	4595196	4597514	Nitric oxide reductase	norB		3256
CDS	sce8584	11980472	11977968	Nitric oxide reductase		4129,6118,16020	3256

]

[

Fam: 50	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3302	4623957	4624901	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3344	4676634	4677539	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 51	No. of CDS: 2	Dom. COG: 306	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3330	4662712	4661702	Probable low-affinity inorganic phosphate permease	pit1	5315,6817,16020	306
CDS	sce3425	4779195	4780202	Probable low-affinity inorganic phosphate transporter	pit2	5315,6817,16020	306

]

[

Fam: 51 No. of CDS: 2 Dom. COG: 3258 counter: 1 / 2 percentage: 50.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3335	4667559	4666966	Conserved hypothetical protein			0
CDS	sce6335	8830752	8830102	Cytochrome c-type protein			3258

]

[

Fam: 51 No. of CDS: 3 Dom. COG: 1529 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3336	4669326	4667569	Putative Isoquinoline 1-oxidoreductase		6118,16491	1529
CDS	sce6329	8823982	8823290	Putative aldehyde dehydrogenase		6118,16491	1529
CDS	sce6333	8829644	8827374	Putative aldehyde dehydrogenase		6118,16491	1529

]

[

Fam: 51 No. of CDS: 3 Dom. COG: 2080 counter: 2 / 3 percentage: 66.67%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3337	4670162	4669701	[2Fe-2S]-binding protein			
CDS	sce5894	8282489	8282007	Hypothetical protein			2080
CDS	sce6334	8830105	8829647	Hypothetical protein predicted by Glimmer/Critica			2080

]

[

Fam: 51 No. of CDS: 4 Dom. COG: 0 counter: 3 / 4 percentage: 75.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3348	4684482	4683637	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3910	5439728	5438172	Hypothetical protein predicted by Glimmer/Critica		6508,8237	0
CDS	sce3967	5511262	5509676	Hypothetical protein/extracellular protease		6508,8237	3227
CDS	sce5343	7517156	7516326	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 51 No. of CDS: 4 Dom. COG: 747 counter: 4 / 4 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3360	4698921	4697179	ABC-type dipeptide transport system, periplasmic component		5215,681	747
CDS	sce4302	6081360	6079639	ABC-type dipeptide transport system, periplasmic component		5215,681	747
CDS	sce7548	10519241	10517508	ABC-type dipeptide transport system, periplasmic component		5215,681	747
CDS	sce8424	11731192	11729468	ABC-type dipeptide transport system, periplasmic component		5215,681	747

]

[

Fam: 51 No. of CDS: 2 Dom. COG: 0 counter: 1 / 2 percentage: 50.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3361	4700173	4699208	Transcriptional regulator			0
CDS	sce7857	10955595	10956572	Protein with nucleic acid binding motif		3677	5378

]

[

Fam: 51 No. of CDS: 2 Dom. COG: 1741 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3383	4727550	4726423	Conserved hypothetical protein			1741
CDS	sce8347	11631154	11630228	Conserved hypothetical protein			1741

]

[

Fam: 51 No. of CDS: 2 Dom. COG: 2375 counter: 1 / 2 percentage: 50.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3384	4727712	4728983	Probable multidrug resistance protein			0
CDS	sce3890	5415760	5417013	Efflux pump	mxcK	5215,6810,16021	2375

]

[

Fam: 51	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3394	4745615	4746439	Putative membrane protein			0
CDS	sce4055	5648245	5649123	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 52	No. of CDS: 4	Dom. COG: 280	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3395	4746614	4747435	Putative transposase			2801
CDS	sce4052	5645252	5644089	Transposase		3677,631	2801
CDS	sce6140	8604674	8604234	Transposase fragment			2801
CDS	sce6651	9253395	9252232	Transposase		3677,631	2801

]

[

Fam: 52	No. of CDS: 2	Dom. COG: 148	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3396	4747734	4747366	IstB-like ATP-binding protein			1484
CDS	sce3400	4750487	4750119	IstB-like ATP-binding protein			1484

]

[

Fam: 52	No. of CDS: 2	Dom. COG: 148	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3397	4748127	4747780	IstB-like ATP-binding protein			1484
CDS	sce3401	4750871	4750533	IstB-like ATP-binding protein			1484

]

[

Fam: 52	No. of CDS: 2	Dom. COG: 458	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3403	4752370	4751267	Transposase			4584
CDS	sce8451	11772339	11771929	Transposase			4584

]

[

Fam: 52	No. of CDS: 5	Dom. COG: 0	counter: 3 / 5	percentage: 60.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3438	4794267	4795343	Conserved hypothetical protein			0
CDS	sce4313	6098066	6097212	Conserved hypothetical protein			0
CDS	sce7960	11076933	11077826	Hypothetical protein predicted by Glimmer/Critica			1262
CDS	sce7993	11122039	11123019	Putative secreted protein			1262
CDS	sce9241	12868677	12865249	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 52	No. of CDS: 2	Dom. COG: 416	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3446	4808524	4810983	Periplasmic oligopeptide-binding protein precursor	oppA1	5215,681	4166
CDS	sce3448	4812129	4814441	Periplasmic oligopeptide-binding protein precursor	oppA2	5215,681	4166

]

[

Fam: 52	No. of CDS: 4	Dom. COG: 272	counter: 3 / 4	percentage: 75.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3455	4824380	4822869	Beta-glucosidase	bglA1	5975	2723
CDS	sce4196	5937457	5936174	beta-glucosidase			366
CDS	sce4297	6075443	6074052	Beta-glucosidase	bglA2	5975	2723
CDS	sce7663	10665032	10663653	Beta-glucosidase	bglA3	5975	2723

]

[

Fam: 52	No. of CDS: 2	Dom. COG: 601	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3458	4826290	4827210	Oligopeptide transport permease protein	oppB2	5215,6810,16020	601
CDS	sce3648	5109744	5110856	ABC transporter permease protein	dppB	5215,6810,16020	601

]

[

Fam: 52	No. of CDS: 2	Dom. COG: 159	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3482	4858263	4857640	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce6054	8488504	8489187	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595

]

[

Fam: 52	No. of CDS: 2	Dom. COG: 596	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3492	4872702	4873553	Epoxide hydrolase			596
CDS	sce4150	5869875	5870747	Putative hydrolase of unknown specificity			596

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 104	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3526	4929632	4930624	Serine acetyltransferase	srpH1		1045
CDS	sce4640	6557598	6556624	Serine acetyltransferase	srpH2		1045

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3531	4938176	4937013	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3939	5476078	5477271	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 53	No. of CDS: 3	Dom. COG: 107	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3552	4964763	4963720	Putative simple sugar transport system permease protein		5215,6810,16020	1079
CDS	sce4413	6236682	6237611	ABC transporter, permease protein		5215,6810,16020	1079
CDS	sce7756	10803723	10802641	Uncharacterized ABC-type transport system, permease component		5215,6810,16020	1079

]

[

Fam: 53	No. of CDS: 3	Dom. COG: 460	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3553	4965909	4964824	Putative simple sugar transport system permease protein		5215,6810,16020	4603
CDS	sce4412	6235582	6236682	Putative simple sugar transport system permease protein		5215,6810,16020	4603

CDS	sce7757	10804904	10803786	Similar to ABC transporter (permease proteins)		5215,6810,16020	4603

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 140	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3560	4975097	4976377	Conserved hypothetical protein			1404
CDS	sce9085	12647579	12646677	Hypothetical protein			1262

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3563	4980293	4982188	Conserved hypothetical protein			0
CDS	sce7432	10355732	10353876	Putative S-layer-like protein			457

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 196(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3575	5003045	5001186	Butyryl-CoA dehydrogenase			1960
CDS	sce5282	7431160	7429358	Butyryl-CoA dehydrogenase			1960

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3585	5014555	5016093	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce3971	5526374	5527933	Putative secreted protein			0

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3629	5079561	5080625	Conserved hypothetical protein			0
CDS	sce7829	10917367	10918461	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 53	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3658	5122473	5123603	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5455	7676000	7677076	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 54	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3684	5153091	5154074	Hypothetical protein			0
CDS	sce4476	6314402	6315367	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 54	No. of CDS: 2	Dom. COG: 475	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3693	5163726	5165471	Putative transport protein		6813	4651
CDS	sce5468	7704690	7706492	Glutathione-regulated potassium-efflux system protein KefC	kefC	6812,8324,16021	475

]

[

Fam: 54	No. of CDS: 2	Dom. COG: 1104	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3703	5175352	5174180	Cysteine desulfurase	nifS	8152,8483	1104
CDS	sce7329	10222745	10223968	Cysteine desulfurase	yfhO	8152,8483	1104

]

[

Fam: 54	No. of CDS: 2	Dom. COG: 188	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3724	5199284	5201905	DNA gyrase subunit A	gyrA	3677,3918,5694,6265,626	188
CDS	sce4451	6280005	6282407	DNA gyrase subunit A		3677,3918,5524,6259,626	188

]

[

Fam: 54	No. of CDS: 2	Dom. COG: 119	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3733	5211300	5212994	2-Isopropylmalate synthase	leuA1	9098,16833	119
CDS	sce3734	5213078	5214724	2-Isopropylmalate synthase		8152,16829	119

]

[

Fam: 54	No. of CDS: 4	Dom. COG: 473	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3735	5214721	5215785	3-Isopropylmalate dehydrogenase	leuB1	8152,16491	473
CDS	sce5773	8110677	8111708	Isocitrate dehydrogenase	icd1	8152,16491	538
CDS	sce6432	8971256	8972272	3-Isopropylmalate dehydrogenase	leuB2	8152,16491	473
CDS	sce8151	11342556	11341465	3-Isopropylmalate dehydrogenase	leuB3	8152,16491	473

]

[

Fam: 54	No. of CDS: 2	Dom. COG: 3491	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3739	5222328	5220823	5'-Nucleotidase, cytosolic II	surE2		3491
CDS	sce4311	6094951	6096807	5'-Nucleotidase			419

]

[

Fam: 54	No. of CDS: 3	Dom. COG: 3511	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3773	5257135	5258667	Phosphoesterase			3511
CDS	sce6979	9732808	9731579	Phosphoesterase precursor	phlC2		3511
CDS	sce7154	9976287	9974533	Phospholipase C	phlC1		3511

]

[

Fam: 54	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3779	5267782	5265380	Protein kinase	prkA1	4672	0
CDS	sce6948	9692187	9694244	Protein kinase	prkA2	4672	2766

]

[

Fam: 54	No. of CDS: 2	Dom. COG: 476	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3858	5367693	5368856	Molybdopterin synthase sulfurylase	moeB1		476
CDS	sce5756	8091132	8090128	Putative adenylyltransferase			476

]

[

Fam: 55	No. of CDS: 3	Dom. COG: 1680	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce3868	5381289	5379841	Alkaline D-peptidase			1680
CDS	sce3869	5382905	5381517	Hypothetical protein predicted by Glimmer/Critica			1680
CDS	sce6437	8976947	8975724	Hypothetical protein predicted by Glimmer/Critica			1680

]

[

Fam: 55	No. of CDS: 2	Dom. COG: 116	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3879	5398169	5399431	Isochorismate synthase	mxcD	8909,9058	1169
CDS	sce5042	7075006	7076286	Isochorismate synthase	dhbC	8909,9058	1169

]

[

Fam: 55	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3885	5406296	5405004	Hypothetical protein	mxcI		0
CDS	sce8264	11532390	11533673	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 55	No. of CDS: 2	Dom. COG: 162	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3886	5408973	5406346	Probable TonB-dependent receptor	mxcH	4872,5215,6810,16020	1629
CDS	sce8263	11529757	11532336	TonB family protein		4872,5215,6810,16020	1629

]

[

Fam: 55	No. of CDS: 2	Dom. COG: 597	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3902	5428559	5427969	Signal peptidase II	lspA1	4190,6508,16020	597
CDS	sce3903	5429597	5428914	Signal peptidase II	lspA2	4190,6508,16020	597

]

[

Fam: 55	No. of CDS: 2	Dom. COG: 177	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3915	5450466	5451227	Endonuclease III	nth1		177
CDS	sce4746	6691580	6692221	Putative endonuclease III	nth2		177

]

[

Fam: 55	No. of CDS: 4	Dom. COG: 0	counter: 2 / 4	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3922	5460217	5458871	Biotin carboxylase	accC1	16874	439
CDS	sce4836	6794230	6795630	Biotin carboxylase subunit of acetyl-CoA carboxylase	accC2	5524	4770
CDS	sce4915	6902701	6906357	Urea amidolyase-related protein			0
CDS	sce8736	12196664	12198892	Biotin carboxylase related protein		5524	0

]

[

Fam: 55	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3927	5466335	5464260	Hypothetical protein			
CDS	sce4619	6529601	6531610	Hypothetical protein			0

]

[

Fam: 55	No. of CDS: 2	Dom. COG: 156	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce3964	5507924	5507100	Hypothetical protein predicted by Glimmer/Critica			1560
CDS	sce4433	6259561	6258614	Conserved hypothetical protein			0

]

[

Fam: 55	No. of CDS: 2	Dom. COG: 219	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3965	5508386	5509024	Putative two-component system response regulator			2197
CDS	sce8119	11293377	11292676	DNA-binding response regulator			2197

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 150	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3979	5540443	5538611	Dipeptidyl carboxypeptidase		4246,6508,16020	1506
CDS	sce5088	7140194	7138197	Peptidyl-dipeptidase Dcp		4246,6508,16020	339

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 21	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3987	5549247	5547250	Transketolase	tkt1	4802	21
CDS	sce8467	11795685	11797397	Transketolase	tkt2		21

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 625	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3993	5560711	5561898	Glutathione S-transferase	gst9		625
CDS	sce4965	6983097	6982429	Glutathione transferase	gst11		625

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce3994	5561965	5562672	Hypothetical protein			0
CDS	sce8844	12338379	12339056	Hypothetical protein			0

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4014	5588726	5590678	Putative secreted protein			0
CDS	sce6662	9266359	9268197	Putative secreted protein			0

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 338	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4027	5609892	5607265	Glucan 1,4-alpha-glucosidase	cga1		3387
CDS	sce4102	5726321	5723943	Glucan 1,4-alpha-glucosidase	cga2		3387

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 230	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4032	5621024	5619798	Glycine-rich protein			2304
CDS	sce7252	10123078	10124286	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 196	counter: 2 / 2	percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4051	5643417	5641297	Recombinase			1961
CDS	sce6650	9251560	9249440	Recombinase			1961

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4057	5651134	5651553	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6649	9248451	9248032	Hypothetical protein			

]

[

Fam: 56	No. of CDS: 2	Dom. COG: 337	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4063	5663639	5665015	Phage-related protein			3378
CDS	sce7874	10974385	10975011	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 57	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4076	5685768	5684758	Similar to putative transposase			0
CDS	sce8068	11220664	11219666	Similar to putative transposase			0

]

[

Fam: 57	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4114	5744703	5745761	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4115	5745758	5747596	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7459	10394199	10396688	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 57	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4116	5747703	5749313	Hypothetical protein			0
CDS	sce8201	11415899	11417698	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 57	No. of CDS: 2	Dom. COG: 111	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4153	5874564	5873305	Phosphoglycerate dehydrogenase	serA1	6564	111
CDS	sce5802	8149059	8147851	D-3-Phosphoglycerate dehydrogenase	serA2	6564	111

]

[

Fam: 57	No. of CDS: 2	Dom. COG: 379	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4173	5897499	5897933	Conserved hypothetical protein			0
CDS	sce6416	8952888	8953313	Conserved hypothetical protein			3795

]

[

Fam: 57	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce4198	5938382	5940079	Conserved hypothetical protein			0
CDS	sce5557	7826581	7824878	Conserved hypothetical protein			0

]

[

Fam: 57	No. of CDS: 2	Dom. COG: 360	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4211	5958541	5959308	Phosphoenolpyruvate--protein phosphotransferase			3605
CDS	sce9246	12871395	12872135	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 57	No. of CDS: 3	Dom. COG: 79	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4215	5965919	5967010	Histidinol-phosphate aminotransferase	hisC2	105,44	79
CDS	sce8855	12350086	12348989	Histidinol-phosphate transaminase	hisC3	105,44	79
CDS	sce8915	12434531	12433449	Histidinol-phosphate transaminase	hisC4	105,44	79

]

[

Fam: 57	No. of CDS: 2	Dom. COG: 231	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4225	5978995	5980383	Putative membrane protein			2319
CDS	sce8934	12462118	12463440	Protein of unknown function (DUF975)			0

]

[

Fam: 57	No. of CDS: 2	Dom. COG: 463	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4233	5990103	5988874	Hypothetical protein			0
CDS	sce8290	11566396	11567523	predicted ATPase		5524	4637

]

[

Fam: 58	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4244	6003462	6004337	Hypothetical protein	,	4222,5578,6508	
CDS	sce6730	9385009	9384041	Putative exported protease precursor			0

]

[

Fam: 58	No. of CDS: 3	Dom. COG: 668	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4246	6005736	6007493	Conserved hypothetical protein		16020	3264
CDS	sce5105	7166807	7165626	Conserved hypothetical protein		16020	668
CDS	sce6347	8846371	8848287	Putative mechanosensitive channel protein		16020	668

]

[

Fam: 58	No. of CDS: 7	Dom. COG: 280	counter: 4 / 7	percentage: 57.14%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4248	6009718	6008666	Putative twitching motility protein PilT	pilT1	5524,681	2805
CDS	sce4296	6072813	6073997	General secretion pathway protein E	gspE1	5524,5622,6810	2804
CDS	sce4467	6303250	6304950	Type IV pilus biogenesis protein PilB	pilB	5524,5622,6810	2804
CDS	sce4468	6304955	6306094	Twitching motility protein	pilT2	5524,681	2805
CDS	sce5323	7487509	7486439	Twitching motility protein PilT	pilT3	5524,681	2805
CDS	sce5324	7488704	7487511	PilT-like protein	pilT4	5524,681	2805

CDS	sce9218	12838862	12837084	General secretion pathway protein E	gspE2	5524,5622,6810	2804

]

[

Fam: 58	No. of CDS: 2	Dom. COG: 811	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4253	6013755	6013039	TolQ protein	tolQ2	6810,8565,16020	811
CDS	sce5071	7118107	7117397	TolQ protein	tolQ3	6810,8565,16020	811

]

[

Fam: 58	No. of CDS: 3	Dom. COG: 1087	counter: 1 / 3	percentage: 33.33%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4259	6022502	6021537	Conserved hypothetical protein			0
CDS	sce4283	6054788	6055960	UDP-glucose 4-epimerase	galE4		1087
CDS	sce6496	9051841	9052776	UDP-glucose 4-epimerase			1086

]

[

Fam: 58	No. of CDS: 3	Dom. COG: 204	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4260	6022602	6023528	Glycerol-3-phosphate acyltransferase			204
CDS	sce4284	6055981	6057246	Putative 1-acyl-sn-glycerol-3-phosphate acyltransferase		8152,8415	204
CDS	sce6495	9050981	9051844	1-Acylglycerol-3-phosphate O-acyltransferase		8152,8415	204

]

[

Fam: 58	No. of CDS: 3	Dom. COG: 44	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4269	6037375	6038706	Dihydroorotase	pyrC		44
CDS	sce5876	8255462	8256817	Allantoinase	allB		44
CDS	sce6399	8932471	8931068	Dihydropyrimidinase	dht		44

]

[

Fam: 58	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4270	6038703	6040169	Conserved hypothetical protein		5554	0
CDS	sce5270	7415261	7413765	Conserved hypothetical protein			0

]

[

Fam: 58	No. of CDS: 3	Dom. COG: 334	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4305	6086647	6088188	Glutamate dehydrogenase	gdhA1	6520,16491	334
CDS	sce6195	8667492	8668817	Glutamate dehydrogenase	gdhA2	6520,16491	334
CDS	sce9109	12679058	12677709	Glutamate dehydrogenase (NADP(+))	gdhA3	6520,16491	334

]

[

Fam: 58	No. of CDS: 2	Dom. COG: 1028	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4308	6091018	6091845	Dehydrogenase		8152,16491	1028
CDS	sce5369	7558633	7557806	Putative retinol dehydrogenase		8152,16491	1028

]

[

Fam: 59	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4334	6120423	6119626	Hypothetical protein predicted by Glimmer/Critica			0

CDS	sce8665	12095312	12094527	Hypothetical protein predicted by Glimmer/Critica			0
]							
[							
Fam: 59	No. of CDS: 2	Dom. COG: 364	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4355	6155286	6153697	Glucose-6-phosphate 1-dehydrogenase	zwf1	4345,6006	364
CDS	sce7012	9793283	9794677	Glucose-6-phosphate 1-dehydrogenase	zwf2	4345,6006	364
]							
[							
Fam: 59	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4357	6156232	6157566	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6970	9718771	9717581	Hypothetical protein			0
]							
[							
Fam: 59	No. of CDS: 2	Dom. COG: 433	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4369	6176805	6179747	Hypothetical protein			433
CDS	sce5407	7601686	7604235	Conserved hypothetical protein			433
]							
[							
Fam: 59	No. of CDS: 2	Dom. COG: 2515	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4395	6207025	6205850	Putative 1-aminocyclopropane-1-carboxylate deaminase		6520,16829	2515
CDS	sce5738	8067690	8068754	1-Aminocyclopropane-1-carboxylate deaminase			2515
]							
[							
Fam: 59	No. of CDS: 2	Dom. COG: 1335	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4414	6237748	6238443	Hypothetical isochorismatase family protein		3824,8152	1535
CDS	sce4416	6240032	6240706	Putative isochorismatase		3824,8152	1335
]							
[							
Fam: 59	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4417	6241117	6242295	Lectin-like glycine/serine-rich protein			0
CDS	sce5553	7820232	7821248	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6640	9236212	9237201	Putative secreted protein			0
]							
[							
Fam: 59	No. of CDS: 2	Dom. COG: 4974	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4427	6253850	6252879	Site-specific recombinase	xerD		4974
CDS	sce7788	10851075	10852151	Integrase/recombinase	xerC		4973
]							
[							
Fam: 59	No. of CDS: 2	Dom. COG: 3741	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4428	6253919	6254791	N-formylglutamate amidohydrolase			3741

CDS	sce4935	6936477	6935683	Predicted N-formylglutamate amidohydrolase			3741

]

[

Fam: 59	No. of CDS: 2	Dom. COG: 187	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4452	6282410	6284347	DNA gyrase subunit B	gyrB	3677,3918,5524,6259,626	187
CDS	sce8166	11358284	11360782	DNA gyrase subunit B			187

]

[

Fam: 60	No. of CDS: 2	Dom. COG: 339	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4462	6295028	6297175	Oligopeptidase A	prlC1	4222,6508	339
CDS	sce6973	9721168	9723222	Oligopeptidase A	prlC2	4222,6508	339

]

[

Fam: 60	No. of CDS: 3	Dom. COG: 436	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4477	6317250	6316051	Aspartate transaminase	aspB1	8483,9058	436
CDS	sce5648	7949606	7948437	Aspartate transaminase	aspB2	8483,9058	436
CDS	sce8802	12293381	12292230	Probable transaminase protein		8483,9058	436

]

[

Fam: 60	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4515	6369901	6370602	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7584	10557969	10558664	Cytochrome c family protein			0

]

[

Fam: 60	No. of CDS: 3	Dom. COG: 437	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4516	6370758	6373793	Putative oxidoreductase, iron-sulfur binding			437
CDS	sce4705	6640852	6641754	Molybdopterin oxidoreductase, iron-sulfur binding subunit			437
CDS	sce7585	10558661	10561660	Molybdopterin oxidoreductase, iron-sulfur binding subunit	hmoA		437

]

[

Fam: 60	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4517	6373790	6375136	Conserved hypothetical protein			0
CDS	sce7586	10561657	10563090	Molybdopterin oxidoreductase, membrane subunit	moz		0

]

[

Fam: 60	No. of CDS: 2	Dom. COG: 3256	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4518	6375138	6375680	Conserved hypothetical protein			3256
CDS	sce7587	10563080	10563847	Hypothetical protein			1252

]

[

Fam: 60	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4520	6376306	6377493	Conserved hypothetical protein			0
CDS	sce7589	10564446	10565651	Conserved hypothetical membrane protein			0

]

[

Fam: 60	No. of CDS: 2	Dom. COG: 199	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4522	6377882	6378718	Conserved hypothetical protein			1999
CDS	sce7591	10566318	10567160	Conserved hypothetical protein			1999

]

[

Fam: 60	No. of CDS: 2	Dom. COG: 162	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4523	6378715	6379803	Cytochrome-c oxidase			1622
CDS	sce7592	10567185	10568135	Putative cytochrome-c oxidase			1622

]

[

Fam: 60	No. of CDS: 2	Dom. COG: 843	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4524	6379800	6381458	Cytochrome-c oxidase		4129,6118,16020	843
CDS	sce7593	10568155	10569792	Putative cytochrome-c oxidase		4129,6118,16020	843

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 184	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4525	6381433	6382095	Putative cytochrome-c oxidase		4129,6118,16020	1845
CDS	sce7594	10569840	10570475	Putative cytochrome-c oxidase		4129,6118,16020	1845

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 291	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4535	6393094	6398160	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5029	7057648	7062645	Conserved hypothetical protein			2911

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 213	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4565	6451789	6453822	Putative spore coat protein			2132
CDS	sce6009	8426255	8428150	Putative spore coat protein-like protein			2132

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 673	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4596	6497987	6499027	Glucose-fructose oxidoreductase precursor	gfo	6118,8152,16491	673
CDS	sce5361	7545451	7544411	Putative oxidoreductase		6118,8152,16491	673

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 122	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4618	6529003	6529485	Peroxiredoxin (AhpC/TSA family)			1225
CDS	sce7104	9903596	9903009	Bacterioferritin comigratory protein			1225

]

[

Fam: 61	No. of CDS: 3	Dom. COG: 480	counter: 2 / 3	percentage: 66.67%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4645	6562571	6564451	Conserved hypothetical secreted protein			4805
CDS	sce6178	8644192	8646090	Hypothetical protein			4805
CDS	sce8289	11564415	11566211	Putative secreted protein			0

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 627	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4649	6567682	6568632	Conserved hypothetical protein			
CDS	sce7910	11028823	11027900	Putative esterase			627

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4680	6610997	6610230	Hypothetical protein			0
CDS	sce4682	6614829	6614074	Hypothetical protein			0

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4681	6613122	6611179	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce4683	6616954	6615011	Hypothetical protein			0

]

[

Fam: 61	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4692	6629416	6630105	Hypothetical protein			0
CDS	sce7838	10929454	10930098	Putative membrane protein			0

]

[

Fam: 62	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4715	6653780	6654781	Hypothetical protein			0
CDS	sce6066	8497958	8496960	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 62	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4729	6672362	6671934	Putative membrane protein			0
CDS	sce7491	10436801	10436310	Unknown protein			0

]

[

Fam: 62	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4730	6672577	6675027	Hypothetical protein			0
CDS	sce5031	7065613	7063610	Putative secreted protein			0
CDS	sce5610	7899980	7902352	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8614	12015917	12018334	Putative secreted protein			0

]

[

Fam: 62	No. of CDS: 2	Dom. COG: 768	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4742	6684203	6685354	Penicillin-binding protein	pbp3	8658,9273	768

CDS	sce7967	11086112	11087395	Penicillin-binding protein	pbp4	8658,9273	768
]							
[							
Fam: 62	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4757	6702724	6703584	Hypothetical protein predicted			0
CDS	sce6734	9389089	9388259	Hypothetical protein predicted by Glimmer/Critica			0
]							
[							
Fam: 62	No. of CDS: 3	Dom. COG: 399	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4783	6730304	6729159	Putative enzyme	yfbE		399
CDS	sce6680	9292030	9290864	Nucleotide sugar aminotransferase			399
CDS	sce7344	10236125	10235007	NDP-sugar aminotransferase			399
]							
[							
Fam: 62	No. of CDS: 2	Dom. COG: 300	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4789	6740101	6737042	Conserved hypothetical protein			3002
CDS	sce8745	12216216	12213160	Conserved hypothetical protein			3002
]							
[							
Fam: 62	No. of CDS: 4	Dom. COG: 659	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4790	6741820	6740180	Putative sulfate transporter, SulP family			659
CDS	sce5150	7235403	7233721	Putative sulfate permease, SulP family	ychM		659
CDS	sce6889	9615398	9616957	Putative sulfate transporter, SulP family			659
CDS	sce8746	12217915	12216272	Probable sulfate transporter, SulP family			659
]							
[							
Fam: 62	No. of CDS: 3	Dom. COG: 654	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4807	6762518	6761220	Probable FAD-dependent monooxygenase		4497,6725	654
CDS	sce4897	6877420	6876194	Probable FAD-dependent monooxygenase		4497,6725	654
CDS	sce7525	10474301	10475530	Putative hydroxylase		4497,6725	654
]							
[							
Fam: 62	No. of CDS: 2	Dom. COG: 386	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4816	6770960	6769668	Pectate lyase	pelB		3866
CDS	sce6839	9544874	9543624	Pectate lyase	pelA		3866
]							
[							
Fam: 63	No. of CDS: 2	Dom. COG: 136	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4819	6774077	6772905	Anti-anti sigma factor protein			1366
CDS	sce6798	9470435	9471562	Anti-anti sigma factor protein			1366
]							
[							
Fam: 63	No. of CDS: 4	Dom. COG: 464	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce4834	6791753	6792904	Conserved hypothetical protein	cgeB		4641
CDS	sce6776	9446917	9448056	Conserved hypothetical protein			4641
CDS	sce6777	9448053	9449216	Conserved hypothetical protein			4641
CDS	sce6795	9468526	9467447	Glycosyltransferase-like conserved protein			4641

]

[

Fam: 63	No. of CDS: 2	Dom. COG: 807	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4848	6811104	6811784	GTP cyclohydrolase II	ribA2	3935,9231	807
CDS	sce5281	7428996	7428319	GTP cyclohydrolase II	ribA3	3935,9231	807

]

[

Fam: 63	No. of CDS: 2	Dom. COG: 3508	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4892	6871961	6870801	Homogentisate 1,2-dioxygenase	hgo		3508
CDS	sce5980	8388067	8389227	Homogentisate 1,2-dioxygenase			3508

]

[

Fam: 63	No. of CDS: 2	Dom. COG: 3185	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4893	6873112	6871961	4-Hydroxyphenylpyruvate dioxygenase	hppD1		3185
CDS	sce5979	8386919	8388067	4-Hydroxyphenylpyruvate dioxygenase	hppD2		3185

]

[

Fam: 63	No. of CDS: 2	Dom. COG: 179	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4894	6874086	6873109	2-Keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase	uptA	3824,8152	179
CDS	sce5977	8385242	8386219	Putative fumarylacetoacetate hydrolase family protein		3824,8152	179

]

[

Fam: 63	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4904	6887106	6888626	Conserved hypothetical protein			0
CDS	sce5832	8190302	8188518	Probable pectate lyase precursor			0

]

[

Fam: 63	No. of CDS: 2	Dom. COG: 2203	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4909	6893919	6894893	GAF domain protein			2203
CDS	sce9200	12818747	12819886	Conserved hypothetical protein			2203

]

[

Fam: 63	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4923	6915866	6917869	Hypothetical secreted protein			0
CDS	sce6289	8779103	8781016	Hypothetical protein predicted by Glimmer/Critica			

]

[

Fam: 63	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce4930	6928187	6927795	Hypothetical protein			0
CDS	sce5662	7965025	7964633	Hypothetical protein			0
CDS	sce8471	11802471	11802070	Hypothetical protein			0

]

[

Fam: 64	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4931	6928965	6928240	Hypothetical protein			0
CDS	sce5663	7965679	7965035	Hypothetical protein			0
CDS	sce6787	9461096	9461746	Hypothetical protein			0
CDS	sce8472	11803141	11802500	Hypothetical protein			0

]

[

Fam: 64	No. of CDS: 2	Dom. COG: 2038	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4943	6951449	6949602	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	cobT1		2038
CDS	sce6908	9640464	9641552	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	cobT2		2038

]

[

Fam: 64	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4964	6982294	6980624	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5929	8327793	8325844	Hypothetical protein			0
CDS	sce8903	12417162	12416062	Hypothetical protein			0

]

[

Fam: 64	No. of CDS: 2	Dom. COG: 3523	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4985	7005884	7002168	Hypothetical protein			3523
CDS	sce7254	10127735	10124823	Putative membrane protein			3523

]

[

Fam: 64	No. of CDS: 2	Dom. COG: 3157	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4994	7017795	7018307	Conserved hypothetical protein			3157
CDS	sce4995	7018446	7018931	Conserved hypothetical protein			3157

]

[

Fam: 64	No. of CDS: 2	Dom. COG: 3519	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce4997	7019471	7021240	Conserved hypothetical protein			3519
CDS	sce9338	12987985	12986183	Conserved hypothetical protein			3519

]

[

Fam: 64	No. of CDS: 2	Dom. COG: 4637	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5018	7045878	7044793	Conserved hypothetical protein		166	4637
CDS	sce6252	8738347	8737208	Hypothetical protein predicted by Glimmer/Critica			4637

]

[

Fam: 64	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5019	7047242	7046292	Hypothetical protein			0

CDS	sce8444	11762925	11763869	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 64	No. of CDS: 3	Dom. COG: 0	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5032	7067105	7066029	Translation initiation factor IF-2, chloroplast precursor	tif2		744
CDS	sce5033	7067105	7066736	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8902	12414885	12415925	Hypothetical protein			0

]

[

Fam: 64	No. of CDS: 2	Dom. COG: 249	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5049	7086946	7085075	Putative DNA mismatch repair protein		3684,5524,6298	249
CDS	sce5295	7448300	7450114	DNA mismatch repair protein	mutS2	3684,5524,6298	1193

]

[

Fam: 65	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5066	7110964	7111779	Hypothetical protein			0
CDS	sce5782	8123080	8122454	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9050	12606953	12607693	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 65	No. of CDS: 2	Dom. COG: 283	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5076	7123530	7122832	Putative exported protein	lolA1	15031,30288	2834
CDS	sce6542	9108252	9107227	outer-membrane lipoprotein carrier protein precursor	lolA2	15031,30288	2834

]

[

Fam: 65	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5094	7149397	7146056	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5095	7152743	7149549	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5097	7157646	7154407	Putative secreted protein			0

]

[

Fam: 65	No. of CDS: 2	Dom. COG: 150	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5110	7177575	7176466	Cardiolipin synthetase			1502
CDS	sce6512	9071130	9072233	CDP-diacylglycerol--serine O-phosphatidyltransferase		3824,8152	1502

]

[

Fam: 65	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5113	7180505	7179018	Hypothetical protein			4402
CDS	sce9307	12945680	12947572	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 65	No. of CDS: 2	Dom. COG: 393	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce5137	7222071	7220599	Conserved hypothetical protein			3930
CDS	sce5926	8324036	8322492	Conserved hypothetical protein			3930
]							
[							
Fam: 65	No. of CDS: 2	Dom. COG: 3607	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5142	7228126	7228542	Conserved hypothetical protein			3607
CDS	sce6311	8802358	8802783	Conserved hypothetical protein			3607
]							
[							
Fam: 65	No. of CDS: 2	Dom. COG: 4941	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5149	7232452	7233639	Probable sigma-70 factor, ECF subfamily			4941
CDS	sce6417	8953422	8954690	RNA polymerase sigma-70 factor, ECF subfamily		3677,3700,6352,6355,169	4941
]							
[							
Fam: 65	No. of CDS: 2	Dom. COG: 2204	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5166	7255314	7254544	Two-component response regulator		156,160,3677	2204
CDS	sce8799	12289770	12290504	Response regulator	dctD	156,160,3677	2204
]							
[							
Fam: 65	No. of CDS: 2	Dom. COG: 642	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5168	7257668	7256937	Sensor histidine kinase		7165,16301	642
CDS	sce8797	12287407	12288141	Sensor histidine kinase		7165,16301	642
]							
[							
Fam: 66	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5200	7305201	7304746	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5203	7308860	7308309	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5206	7312337	7311804	Hypothetical protein predicted by Glimmer/Critica			0
]							
[							
Fam: 66	No. of CDS: 2	Dom. COG: 3039	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5215	7334941	7334624	Putative transposase			3039
CDS	sce8571	11963062	11962514	Putative transposase			3039
]							
[							
Fam: 66	No. of CDS: 2	Dom. COG: 3501	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5257	7400951	7399968	Endo-1,4-beta-glucanase			3501
CDS	sce5258	7401491	7400973	Hypothetical protein predicted by Glimmer/Critica			0
]							
[							
Fam: 66	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5261	7405045	7404380	Putative secreted protein			0
CDS	sce7546	10516003	10516683	PE-PGRS family protein			0

]

[

Fam: 66	No. of CDS: 2	Dom. COG: 272(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5267	7412804	7411443	Vancomycin resistance gene	vanW		2720
CDS	sce7395	10294678	10292921	Putative secreted protein			2720

]

[

Fam: 66	No. of CDS: 2	Dom. COG: 2207	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5287	7439319	7438522	Transcriptional regulator, AraC family			2207
CDS	sce5415	7608931	7607852	Transcriptional regulator, AraC family			2207

]

[

Fam: 66	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5316	7473354	7472440	Hypothetical protein			0
CDS	sce5532	7791342	7790464	Hypothetical protein			0

]

[

Fam: 66	No. of CDS: 2	Dom. COG: 448	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5346	7520506	7521768	Glucose-1-phosphate adenylyltransferase	glgC1	9058,16779	448
CDS	sce7094	9890917	9889700	Glucose-1-phosphate adenylyltransferase	glgC2	9058,16779	448

]

[

Fam: 66	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5359	7539143	7540738	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9258	12886489	12888075	Conserved hypothetical protein			0

]

[

Fam: 66	No. of CDS: 3	Dom. COG: 554	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5375	7568210	7569727	Glycerol Kinase			554
CDS	sce7617	10601731	10603299	Glycerol kinase	glpK	4370,6072	554
CDS	sce9296	12936289	12934733	Xylulokinase	xylB	4856,5997	1070

]

[

Fam: 67	No. of CDS: 3	Dom. COG: 1902	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5402	7595477	7596565	Putative NADH-dependent flavin oxidoreductase		6118,16491	1902
CDS	sce7811	10883345	10884475	Similar to xenobiotic reductase		6118,16491	1902
CDS	sce8661	12089856	12087610	Probable oxidoreductase		6118,16491	654

]

[

Fam: 67	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5424	7618863	7618438	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7018	9800527	9800934	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 67	No. of CDS: 3	Dom. COG: 159	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5448	7667910	7668542	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce5508	7761389	7760766	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce8901	12414262	12414888	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595

]

[

Fam: 67	No. of CDS: 3	Dom. COG: 0	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5452	7673569	7671326	Conserved hypothetical protein with a signal peptide			0
CDS	sce6526	9091618	9089348	Conserved hypothetical protein			0
CDS	sce7079	9878411	9875664	Conserved hypothetical protein			

]

[

Fam: 67	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5463	7698262	7693349	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5843	8209079	8214061	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 67	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5465	7700849	7699287	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce5466	7703072	7701489	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7542	10510431	10508887	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 67	No. of CDS: 2	Dom. COG: 286	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5520	7775290	7776750	Probable type I restriction-modification system, M subunit		6304,9007	286
CDS	sce8509	11858581	11859663	Probable type I restriction-modification system, M subunit		3677,6306,8170	286

]

[

Fam: 67	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5577	7855713	7855192	Putative secreted protein			0
CDS	sce6391	8915943	8915392	Putative secreted protein			0

]

[

Fam: 67	No. of CDS: 2	Dom. COG: 112	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5583	7862063	7862764	Putative branched-chain amino acid transport system ATP-binding protein		4009,5524,6810,16020	410
CDS	sce8605	12006677	12007435	ABC transport protein, ATP-binding component		4009,5524,6810,16020	1126

]

[

Fam: 67	No. of CDS: 2	Dom. COG: 281	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce5603	7892686	7894509	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP(+))	maeB1	4470,6108	281
CDS	sce9116	12687785	12686145	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP(+)).	maeB2	4470,6108	281

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 504	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5618	7910387	7908738	CTP synthase	pyrG2	3883,6221	504
CDS	sce7239	10107007	10105322	CTP synthase	pyrG3	3883,6221	504

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 1716	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5690	8006527	8005649	FHA domain protein			1716
CDS	sce9289	12926036	12925353	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 377(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5783	8124550	8123231	Putative exported endopeptidase		6508,8931,30288	3770
CDS	sce8115	11289161	11290213	Exported murein endopeptidase		6508,8931,30288	3770

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 110	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5789	8129968	8131410	Phosphoglucosamine mutase	glmM	8966	1109
CDS	sce8057	11208492	11207065	Phosphomannomutase	algC	5975	1109

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 141(	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5871	8247749	8251528	Methionine synthase	metH1	8898	1410
CDS	sce7733	10768451	10772296	Methionine synthase	metH2	8898	1410

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 417	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5891	8276373	8277851	Gamma-glutamyl carboxylase			4177
CDS	sce9136	12726816	12725347	Vitamin K-dependent gamma-carboxylase			0

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce5939	8338479	8337904	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6620	9214759	9214046	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 784	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce5995	8407918	8408682	Response regulator			784
CDS	sce8796	12286749	12287360	Two-component response regulator			2204

]

[

Fam: 68	No. of CDS: 2	Dom. COG: 778	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6023	8445317	8446090	Conserved hypothetical protein		6118,16491	778
CDS	sce7139	9953749	9952922	Conserved hypothetical protein	noxC		778

]

[

Fam: 68	No. of CDS: 4	Dom. COG: 582	counter: 2 / 4	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6084	8521841	8520339	Probable integrase/recombinase			582
CDS	sce6111	8562364	8561825	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6112	8562875	8562381	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6713	9345618	9347564	DNA integration/recombination/invertion protein			582

]

[

Fam: 69	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6085	8522699	8521851	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8776	12263241	12263768	Putative secreted protein			0

]

[

Fam: 69	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6086	8523433	8522948	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8775	12262634	12263143	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 69	No. of CDS: 8	Dom. COG: 0	counter: 8 / 8	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6092	8531103	8532647	PE-PGRS family protein			0
CDS	sce6130	8593812	8592259	Putative secreted protein			0
CDS	sce6345	8842845	8844404	PE_PGRS family protein			0
CDS	sce6712	9343002	9344540	Putative exported protein with glycine-rich central and C-terminal region			0
CDS	sce7514	10465427	10464498	PE-PGRS family protein			0
CDS	sce8763	12247749	12246214	PE-PGRS family protein			0
CDS	sce8872	12370720	12372264	PE-PGRS family protein			0
CDS	sce9271	12902977	12901436	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 69	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6093	8533418	8532849	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6127	8589489	8590031	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6128	8590299	8590862	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 69 No. of CDS: 4 Dom. COG: 0 counter: 4 / 4 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6094	8534188	8533415	Putative secreted protein			0
CDS	sce6126	8588719	8589492	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8761	12244192	12245100	Putative membrane protein			0
CDS	sce9269	12899601	12900311	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 69 No. of CDS: 2 Dom. COG: 0 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6124	8587757	8586669	Conserved hypothetical protein			0
CDS	sce7178	10032260	10033348	Conserved hypothetical protein			0

]

[

Fam: 69 No. of CDS: 4 Dom. COG: 0 counter: 4 / 4 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6129	8590960	8592060	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6851	9569631	9570272	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8762	12245105	12246202	Conserved hypothetical protein			0
CDS	sce9270	12900308	12901429	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 69 No. of CDS: 2 Dom. COG: 626 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6169	8635830	8637020	Cystathionine gamma-synthase	metB1	6520	626
CDS	sce7598	10574406	10573210	Cystathionine gamma-synthase	metB2	6520	626

]

[

Fam: 69 No. of CDS: 2 Dom. COG: 1459 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6250	8735637	8734420	Type II secretory pathway component pulF	pulF	9306,1602	1459
CDS	sce9217	12837075	12835849	General secretion pathway protein F	gspF	9306,1602	1459

]

[

Fam: 69 No. of CDS: 3 Dom. COG: 661 counter: 3 / 3 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6255	8740626	8742632	Putative membrane protein			661
CDS	sce7427	10345495	10346886	ABC1 family protein		4672,5524,6468	661
CDS	sce8279	11551362	11552807	Putative membrane protein			661

]

[

Fam: 70 No. of CDS: 2 Dom. COG: 2013 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6258	8745903	8746598	Conserved hypothetical protein			2013
CDS	sce6259	8746619	8747287	Conserved hypothetical protein			2013

]

[

Fam: 70 No. of CDS: 2 Dom. COG: 0 counter: 2 / 2 percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6278	8769734	8769399	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6296	8788058	8787813	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 70	No. of CDS: 3	Dom. COG: 497	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6302	8797466	8796375	Putative AraC-family transcriptional regulator			4977
CDS	sce6372	8885884	8886900	Putative AraC-family transcriptional regulator			4977
CDS	sce8832	12327732	12326779	Putative AraC-family transcriptional regulator			4977

]

[

Fam: 70	No. of CDS: 2	Dom. COG: 566	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6303	8797669	8798037	Conserved hypothetical protein			0
CDS	sce8830	12325762	12325445	Conserved hypothetical protein			5663

]

[

Fam: 70	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6304	8798034	8798348	Putative membrane protein	ydzA1		0
CDS	sce8829	12325448	12325134	Putative membrane protein	ydzA2		0

]

[

Fam: 70	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6346	8845064	8846128	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9185	12794958	12795989	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 70	No. of CDS: 2	Dom. COG: 234	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6352	8856748	8856176	Pathogenesis-related protein, putative		5576	2340
CDS	sce6971	9719170	9719730	Cysteine-rich secretory protein precursor		5576	2340

]

[

Fam: 70	No. of CDS: 4	Dom. COG: 0	counter: 3 / 4	percentage: 75.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6366	8879871	8879143	Probable endo-1,4-beta-glucanase			4547
CDS	sce9062	12619466	12618849	Putative secreted protein			0
CDS	sce9080	12641629	12641114	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce9081	12642528	12642046	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 70	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6368	8880405	8881520	Hypothetical protein		3824	0
CDS	sce6378	8894096	8894725	Hypothetical protein			0

]

[

Fam: 70	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6369	8882134	8883081	Putative pentalenene synthase			
CDS	sce8552	11917026	11918015	Putative terpene cyclase	geoA		0

]

[

Fam: 71	No. of CDS: 2	Dom. COG: 793	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6451	8995868	8992722	C-terminal processing peptidase.	prc1	6508,8236	793
CDS	sce8681	12114327	12115877	C-terminal processing peptidase	ctpA2	6508,8236	793

]

[

Fam: 71	No. of CDS: 2	Dom. COG: 443	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6455	8997931	8999808	Hsp70 heat shock protein			443
CDS	sce6464	9009646	9012603	Hsp70 heat shock protein			443

]

[

Fam: 71	No. of CDS: 2	Dom. COG: 1305	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6456	8999826	9000704	Conserved hypothetical protein			1305
CDS	sce7102	9898794	9900539	Conserved hypothetical protein		8152	1305

]

[

Fam: 71	No. of CDS: 2	Dom. COG: 667	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6461	9007405	9006434	Probable oxidoreductase			667
CDS	sce7729	10762063	10761155	Putative oxidoreductase			667

]

[

Fam: 71	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6462	9008400	9007624	Hypothetical protein predicted by Glimmer/Critica			
CDS	sce7363	10254809	10255591	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 71	No. of CDS: 2	Dom. COG: 1032	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6517	9079124	9076071	Hypothetical protein			1032
CDS	sce8317	11597010	11598500	Hypothetical protein			1032

]

[

Fam: 71	No. of CDS: 2	Dom. COG: 438	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6583	9156545	9155262	Glycogen synthase	glgA4	9058	438
CDS	sce6790	9463816	9462767	Putative glycosyltransferase		9058	438

]

[

Fam: 71	No. of CDS: 2	Dom. COG: 776	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6591	9166041	9165703	Histone-like protein		3677	776
CDS	sce8278	11550880	11551215	Histone-like protein		3677	776

]

[

Fam: 71	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce6597	9186087	9185533	Related S23 ribosomal protein			0
CDS	sce6843	9551617	9551258	23S rRNA-like protein			0
CDS	sce7858	10957171	10956485	Hypothetical protein			0

]

[

Fam: 71	No. of CDS: 3	Dom. COG: 457	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6700	9322622	9326398	Hypothetical protein			457
CDS	sce6702	9327016	9330429	Hypothetical protein			457
CDS	sce6703	9330538	9334077	Hypothetical protein			0

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6720	9355142	9365815	Hypothetical protein			0
CDS	sce8561	11953336	11944352	Putative toxin subunit	tcbA	3824,6725,8199	0

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 625	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6741	9396163	9396837	Glutathione S-transferase	gst15		625
CDS	sce7734	10772314	10772946	Glutathione S-transferase	gst18		625

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 103	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6773	9443306	9444607	Conserved hypothetical protein			1032
CDS	sce8936	12465062	12466354	Conserved hypothetical protein			1032

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 438	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6774	9444600	9445784	Glycosyltransferase		9058	438
CDS	sce8937	12466404	12467540	Putative glycosyltransferase			438

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 464	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6775	9445775	9446920	Conserved hypothetical protein			4641
CDS	sce8938	12467531	12468730	Conserved hypothetical protein			4641

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 265	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6822	9500685	9501680	Serine protease			265
CDS	sce7119	9923366	9922353	Probable serine protease			265

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 159	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6834	9538533	9539426	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595
CDS	sce8387	11674954	11675898	ECF-family RNA polymerase sigma factor		3677,3700,6352,16987	1595

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 693	counter: 2 / 2	percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6836	9540794	9540108	ThiJ/PfpI family protein	thiJ		693
CDS	sce8831	12326501	12325785	Putative ThiJ/PfpI family protein			693

]

[

Fam: 72	No. of CDS: 3	Dom. COG: 0	counter: 3 / 3	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6868	9593718	9592582	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6869	9594307	9595461	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8925	12448014	12449117	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 72	No. of CDS: 2	Dom. COG: 539	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6880	9606784	9608472	30S ribosomal protein S1	rpsA2	3723,3735,5840,6412	539
CDS	sce7230	10095198	10093147	Ribosomal protein S1	rpsA3	3676	539

]

[

Fam: 73	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6893	9622116	9621172	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7090	9886765	9886001	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 73	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6913	9645208	9646041	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce6917	9652479	9653051	Putative exported protein			0

]

[

Fam: 73	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6918	9653911	9653138	Putative secreted protein			0
CDS	sce6922	9658665	9659459	Putative exported protein			0

]

[

Fam: 73	No. of CDS: 2	Dom. COG: 524	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6940	9680372	9679410	Put. Sugar kinase			524
CDS	sce8825	12319020	12319922	Put.Carbohydrate kinase, PfkB family			524

]

[

Fam: 73	No. of CDS: 2	Dom. COG: 363	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce6960	9706873	9708435	Alkyl hydroperoxide reductase subunit F		6118,15036	3634
CDS	sce7636	10627998	10628957	Thioredoxin-disulfide reductase	trxB	4791,5737,19430	492

]

[

Fam: 73	No. of CDS: 2	Dom. COG: 236	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce7000	9778346	9775653	Probable beta-lactam antibiotic acylase family protein		16787,17	2366
CDS	sce8259	11516991	11514604	Penicillin amidase			2366
]							
[							
Fam: 73	No. of CDS: 2	Dom. COG: 185	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7006	9785804	9787393	Cytochrome C peroxidase			1858
CDS	sce7024	9808828	9807488	Cytochrome c peroxidase	mauG		1858
]							
[							
Fam: 73	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7021	9803904	9804908	Hypothetical protein/putative endoglucanase		3824	0
CDS	sce8862	12356468	12357499	BKRF1 encodes EBNA-1 protein, latent cycle gene		3824	0
]							
[							
Fam: 73	No. of CDS: 2	Dom. COG: 348	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7037	9826245	9827156	Protocatechuate 3,4-dioxygenase	pcaH	3824,6725,8199	3485
CDS	sce7041	9832652	9831534	Conserved hypothetical protein			0
]							
[							
Fam: 73	No. of CDS: 2	Dom. COG: 139	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7046	9838029	9837583	Putative HTH-type transcriptional regulator ydcN.			0
CDS	sce7655	10653804	10653262	Transcriptional regulator			1396
]							
[							
Fam: 74	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7140	9955268	9953877	Conserved domain protein			0
CDS	sce9066	12624304	12625620	Conserved domain protein			1944
]							
[							
Fam: 74	No. of CDS: 2	Dom. COG: 0	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7175	10026061	10027080	Glutathione synthase/Ribosomal protein S6 modification enzyme	rimK2		189
CDS	sce7176	10027077	10028102	Hypothetical protein			0
]							
[							
Fam: 74	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7247	10118829	10115026	Hypothetical protein			0
CDS	sce8015	11154801	11150878	Hypothetical protein			0
]							
[							
Fam: 74	No. of CDS: 2	Dom. COG: 739	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7403	10304571	10306694	Peptidase		4222,6508	739
CDS	sce8860	12353774	12354886	Conserved hypothetical protein		4222,6508	739
]							

[

Fam: 74	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7418	10328463	10329629	Possible peptidase		4295,6508	0
CDS	sce8315	11594099	11592918	Hypothetical secreted peptidase			0

]

[

Fam: 74	No. of CDS: 2	Dom. COG: 557	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7430	10353026	10351080	Ribonuclease R		3723,4540,16070	557
CDS	sce9004	12543816	12541444	Ribonuclease R	pacI	3723,4540,16070	557

]

[

Fam: 74	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7461	10402002	10400842	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7462	10403100	10402024	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 74	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7477	10421628	10422152	Hypothetical protein		5344,5506,6810	0
CDS	sce8139	11323812	11323048	Hypothetical protein		5344,5506,6810	0

]

[

Fam: 74	No. of CDS: 2	Dom. COG: 165	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7573	10545638	10544544	Hypothetical protein		15035,30288	1651
CDS	sce7704	10733877	10732885	Hypothetical protein		15035,30288	1651

]

[

Fam: 74	No. of CDS: 2	Dom. COG: 642	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7596	10571182	10572654	Putative two component system, histidine kinase		7165,16301	642
CDS	sce8052	11204242	11202941	Sensor histidine kinase		7165,16301	642

]

[

Fam: 75	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7618	10603576	10604361	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce7802	10869630	10870328	Hypothetical protein			0

]

[

Fam: 75	No. of CDS: 2	Dom. COG: 114	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7766	10813097	10814635	Hypothetical protein predicted by Glimmer/Critica			1145
CDS	sce7767	10814798	10816306	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 75	No. of CDS: 2	Dom. COG: 784	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers

CDS	sce7813	10888184	10887762	Response regulator			784
CDS	sce8714	12164848	12164432	Response regulator			784

]

[

Fam: 75	No. of CDS: 3	Dom. COG: 154	counter: 1 / 3	percentage: 33.33%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce7844	10936349	10938595	Putative capK; capsular polysaccharide biosynthesis protein			0
CDS	sce8601	12002233	12003630	CapK related-protein	capK1		1541
CDS	sce8917	12438922	12440292	Putative capK related-protein	capK2		3944

]

[

Fam: 75	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8033	11177453	11178613	Putative membrane protein			0
CDS	sce8034	11178978	11179943	Putative membrane protein			0

]

[

Fam: 75	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8142	11328919	11329848	Hypothetical protein			0
CDS	sce8143	11329994	11330926	Hypothetical protein predicted by Glimmer/Critica			0

]

[

Fam: 75	No. of CDS: 2	Dom. COG: 119	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8174	11371378	11372640	2-Isopropylmalate synthase	leuA3	3824	119
CDS	sce8481	11814021	11815229	Putative 2-isopropylmalate synthase		3824	119

]

[

Fam: 75	No. of CDS: 2	Dom. COG: 304	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8358	11645114	11646175	Putative 3-oxoacyl-[acyl-carrier-protein] synthase domain protein			304
CDS	sce9335	12984021	12982966	Hypothetical protein predicted by Glimmer/Critica			304

]

[

Fam: 75	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8479	11812137	11811703	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8673	12105139	12105993	Hypothetical protein predicted by Glimmer/Critica			0

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[

Fam: 75	No. of CDS: 7	Dom. COG: 0	counter: 7 / 7	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8501	11848303	11847233	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8502	11849440	11848334	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8503	11850580	11849765	Hypothetical protein			0
CDS	sce8505	11853419	11852379	Hypothetical protein			0
CDS	sce8875	12376329	12377396	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8876	12377410	12378471	Conserved hypothetical protein			0

CDS	sce9280	12914012	12915064	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 76	No. of CDS: 4	Dom. COG: 0	counter: 4 / 4	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8504	11852370	11850820	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8506	11855632	11853416	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8874	12374128	12376332	Putative secreted protein			0
CDS	sce9279	12911814	12914015	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 76	No. of CDS: 3	Dom. COG: 0	counter: 2 / 3	percentage: 66.67%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8507	11857083	11855629	Putative membrane protein			577
CDS	sce8873	12372734	12374131	Putative secreted protein			0
CDS	sce9278	12910363	12911817	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 76	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8515	11869105	11867741	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8674	12107415	12106012	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 76	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8563	11955580	11954954	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8564	11956537	11955779	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 76	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8652	12078197	12076383	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8653	12080149	12078200	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 76	No. of CDS: 2	Dom. COG: 749	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8671	12101976	12104678	DNA polymerase I	polA1	3677,3887,6260	749
CDS	sce8676	12109477	12111090	DNA polymerase I	polA2	3677,3887,6260	749

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Fam: 76	No. of CDS: 2	Dom. COG: 4636	counter: 1 / 2	percentage: 50.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8859	12352793	12353539	Hypothetical protein predicted by Glimmer/Critica			0
CDS	sce8882	12385665	12386507	Conserved hypothetical protein			4636

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Fam: 76	No. of CDS: 2	Dom. COG: 0	counter: 2 / 2	percentage: 100.00%

	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce8945	12475415	12474819	Conserved hypothetical protein			0
CDS	sce8987	12520350	12519667	Hypothetical protein predicted by Glimmer/Critica			0

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Fam: 76	No. of CDS: 2	Dom. COG: 1716	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce9011	12552605	12551757	FHA domain protein			1716
CDS	sce9012	12553487	12552609	FHA domain protein			1716

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Fam: 76	No. of CDS: 2	Dom. COG: 114	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce9115	12686123	12684672	Fumarate hydratase	fumC1	4333,6106,45239	114
CDS	sce9130	12710538	12711962	Fumarate hydratase	fumC2	4333,6106,45239	114

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Fam: 77	No. of CDS: 2	Dom. COG: 687	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce9153	12750124	12751239	Spermidine/putrescine transport system substrate-binding protein		5215,681	687
CDS	sce9304	12942394	12943488	Spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein	potD	5215,681	687

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Fam: 77	No. of CDS: 2	Dom. COG: 1177	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce9158	12760318	12759488	Spermidine/putrescine ABC transporter, permease protein	potC1	5215,6810,16020	1177
CDS	sce9303	12941483	12942328	Spermidine/putrescine ABC transporter, permease protein	potC2	5215,6810,16020	1177

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Fam: 77	No. of CDS: 2	Dom. COG: 1176	counter: 2 / 2	percentage: 100.00%			
	RegName	RegStart	RegStop	GeneProduct	GeneName	GoNumbers	CogNumbers
CDS	sce9159	12761208	12760315	Spermidine/putrescine transport system permease protein	potB1	5215,6810,16020	1176
CDS	sce9305	12943502	12944380	Spermidine/putrescine ABC transporter, permease protein	potB2	5215,6810,16020	1176

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Total number of families: 772

Total number of paralogs: 3402

Supplementary Table 2 Statistical enrichment of functional groups for each mountain on the *S. cellulosum* phylogenomic map. The GO::TermFinder[1] software was used in conjunction with a generated Gene Ontology[2] (GO) file for *S. cellulosum* to assign GO annotations for each mountain. A total of 36 of 39 mountains were found to be statistically significant for GO functional enrichment. The top 3 GO terms with a *P* value < 0.05 were retained for each mountain in this analysis. Also shown is the number of significant proteins among the total number of proteins with GO annotations, used to determine each GO functional enrichment. In addition, the total number of statistically significant GO functional enrichments for each mountain is shown.

Mountain	No. of proteins	No. of proteins with GO annotation	GO terms found	Number of sig. proteins	GOID	Term	*P* value
1	17	-	-	-	-	-	-
2	27	27	18	17	GO:0006935	chemotaxis	1.51E-35
				17	GO:0007626	locomotory behavior	1.51E-35
				17	GO:0042330	taxis	1.51E-35
3	36	31	10	20	GO:0005215	transporter activity	2.88E-15
				20	GO:0006810	transport	7.13E-15
				20	GO:0051234	establishment of localization	3.53E-14
4	37	9	11	6	GO:0015074	DNA integration	1.56E-11
				8	GO:0006259	DNA metabolic process	2.63E-10
				3	GO:0003677	DNA binding	5.88E-07
5	38	-	-	-	-	-	-
6	48	40	19	29	GO:0016651	oxidoreductase activity, acting on NADH or NADPH	7.61E-52
				28	GO:0009055	electron carrier activity	5.15E-49
				25	GO:0003954	NADH dehydrogenase activity	3.18E-47
7	49	49	35	48	GO:0006468	protein amino acid phosphorylation	3.87E-48
				48	GO:0006464	protein modification	1.38E-45
				48	GO:0016310	phosphorylation	8.40E-45
8	51	33	5	14	GO:0016887	ATPase activity	2.09E-10
				14	GO:0017111	nucleoside-triphosphatase activity	2.53E-10
				14	GO:0016462	pyrophosphatase activity	4.02E-10
9	51	13	14	3	GO:0050897	cobalt ion binding	3.09E-04
				4	GO:0005506	iron ion binding	3.74E-03
				4	GO:0046914	transition metal ion binding	2.78E-02
10	52	39	28	34	GO:0006468	protein amino acid phosphorylation	5.75E-29
				34	GO:0006464	protein modification	3.18E-27
				34	GO:0016310	phosphorylation	1.10E-26

11	58	8	11	5	GO:0006355	regulation of transcription, DNA-dependent	2.94E-02
				5	GO:0006351	transcription, DNA-dependent	3.01E-02
				5	GO:0032774	RNA biosynthetic process	3.01E-02
12	59	46	23	9	GO:0006396	RNA processing	2.56E-08
				10	GO:0003723	RNA binding	8.63E-08
				8	GO:0006399	tRNA metabolic process	6.32E-06
13	62	55	17	13	GO:0030529	ribonucleoprotein complex	5.74E-12
				14	GO:0044444	cytoplasmic part	1.75E-11
				14	GO:0043228	non-membrane-bound organelle	3.39E-11
14	69	37	9	12	GO:0016887	ATPase activity	6.30E-07
				12	GO:0017111	nucleoside-triphosphatase activity	7.37E-07
				12	GO:0016462	pyrophosphatase activity	1.08E-06
15	76	42	4	3	GO:0006814	sodium ion transport	2.48E-03
				2	GO:0030261	chromosome condensation	2.15E-02
				4	GO:0015672	monovalent inorganic cation transport	4.13E-02
16	78	52	23	11	GO:0009306	protein secretion	9.23E-14
				11	GO:0008565	protein transporter activity	2.29E-13
				11	GO:0046903	secretion	3.46E-13
17	78	66	19	14	GO:0003995	acyl-CoA dehydrogenase activity	7.60E-21
				14	GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	3.33E-18
				30	GO:0016491	oxidoreductase activity	6.45E-09
18	90	87	34	52	GO:0009058	biosynthetic process	3.15E-22
				21	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	7.56E-18
				16	GO:0006694	steroid biosynthetic process	5.29E-17
19	93	81	19	15	GO:0005623	cell	2.56E-04
				39	GO:0044464	cell part	2.56E-04
				27	GO:0016020	membrane	9.50E-04
20	94	74	30	22	GO:0020037	heme binding	3.81E-32
				22	GO:0046906	tetrapyrrole binding	3.81E-32
				23	GO:0004497	monooxygenase activity	2.33E-28

21	98	97	28	94	GO:0006468	protein amino acid phosphorylation	4.01E-96
				94	GO:0006464	protein modification	1.05E-90
				94	GO:0016310	phosphorylation	4.73E-89
22	119	119	33	118	GO:0006468	protein amino acid phosphorylation	2.21E-127
				118	GO:0006464	protein modification	3.10E-120
				118	GO:0016310	phosphorylation	4.63E-118
23	122	92	4	62	GO:0016491	oxidoreductase activity	2.97E-32
				83	GO:0003824	catalytic activity	2.15E-07
				85	GO:0048037	cofactor binding	4.46E-03
24	127	105	36	6	GO:0030288	outer membrane-bounded periplasmic space	6.76E-09
				6	GO:0015035	protein disulfide oxidoreductase activity	1.98E-08
				6	GO:0030313	cell envelope	4.43E-05
25	128	30	16	19	GO:0006412	translation	1.73E-08
				20	GO:0044249	cellular biosynthetic process	2.39E-08
				36	GO:0009058	biosynthetic process	3.76E-06
26	138	67	6	22	GO:0006118	electron transport	5.15E-09
				22	GO:0006091	generation of precursor metabolites and energy	1.60E-07
				26	GO:0016491	oxidoreductase activity	1.17E-05
27	144	119	22	14	GO:0016987	sigma factor activity	6.56E-09
				14	GO:0016986	transcription initiation factor activity	9.44E-09
				14	GO:0006352	transcription initiation	1.09E-08
28	146	40	13	9	GO:0016021	integral to membrane	1.71E-04
				9	GO:0031224	intrinsic to membrane	1.71E-04
				17	GO:0016020	membrane	3.71E-04
29	149	139	31	34	GO:0000155	two-component sensor activity	1.79E-22
				34	GO:0004673	protein histidine kinase activity	1.79E-22
				53	GO:0007154	cell communication	1.88E-22
30	150	84	6	6	GO:0016846	carbon-sulfur lyase activity	1.44E-07
				7	GO:0043565	sequence-specific DNA binding	2.17E-04
				3	GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	1.62E-03
31	162	148	46	79	GO:0008134	transcription factor binding	8.11E-114
				81	GO:0005515	protein binding	3.09E-91
				79	GO:0005622	intracellular	9.19E-43

32	175	153	41	99	GO:0007165	signal transduction	2.24E-75
				99	GO:0007154	cell communication	8.30E-75
				99	GO:0000156	two-component response regulator activity	1.36E-62
33	213	124	10	41	GO:0004553	hydrolase activity, hydrolyzing *O*-glycosyl compounds	4.39E-39
				41	GO:0016798	hydrolase activity, acting on glycosyl bonds	9.03E-39
				47	GO:0005975	carbohydrate metabolic process	9.85E-26
34	238	100	10	7	GO:0004867	serine-type endopeptidase inhibitor activity	6.05E-08
				7	GO:0004857	enzyme inhibitor activity	5.28E-07
				7	GO:0004866	endopeptidase inhibitor activity	5.28E-07
35	256	145	7	7	GO:0004289	subtilase activity	2.12E-05
				9	GO:0004386	helicase activity	5.68E-03
				14	GO:0050896	response to stimulus	8.55E-03
36	284	-	-	-	-	-	-
37	291	211	24	54	GO:0003700	transcription factor activity	7.21E-21
				56	GO:0003677	DNA binding	1.93E-11
				58	GO:0030528	transcription regulator activity	1.67E-10
38	343	193	37	7	GO:0016851	magnesium chelatase activity	2.26E-06
				8	GO:0051002	ligase activity, forming nitrogen-metal bonds	2.30E-06
				8	GO:0051003	ligase activity, forming nitrogen-metal bonds, forming coordination complexes	2.30E-06
39	1415	408	15	8	GO:0003964	RNA-directed DNA polymerase activity	9.81E-06
				8	GO:0006278	RNA-dependent DNA replication	1.41E-05
				35	GO:0006259	DNA metabolic process	8.67E-05

References

1. Boyle, E. I. *et al.* GO::TermFinder − open source software for accessing Gene Ontology information and finding significantly enriched Gene Ontology terms associated with a list of genes. *Bioinformatics* **20**, 3710–3715 (2004).
2. Harris, M. A. *et al*. The Gene Ontology (GO) database and informatics resource. *Nucleic Acids Res.* **32**, D258–261 (2004).

Supplementary Table 3 Putative assignment of roles to each hypothetical and conserved hypothetical protein on the *S. cellulosum* phylogenomic map. Roles assigned to each protein based on the Gene Ontology annotation of the mountain are shown. This method allowed the assignment of a total of 1,416 hypothetical and conserved hypothetical proteins.

ID	Product	Mountain	GO_Annotation
sce0013	conserved hypothetical protein	36	-
sce0023	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0024	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce0028	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce0037	conserved hypothetical protein YfiH	27	sigma factor activity; transcription initiation factor activity; transcription initiation
sce0051	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0054	Putative membrane protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce0056	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0058	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce0064	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing O-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce0065	hypothetical protein predicted by Glimmer/Critica	36	-
sce0091	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0092	hypothetical protein predicted by Glimmer/Critica	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0095	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce0102	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce0103	hypothetical protein	36	-
sce0104	hypothetical protein predicted by Glimmer/Critica	36	-
sce0105	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0106	hypothetical protein	5	-
sce0107	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce0108	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce0109	hypothetical protein	5	-
sce0110	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0136	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0141	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0143	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0144	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0154	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0162	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce0163	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce0173	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce0174	hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce0185	hypothetical protein Rv2300c/MT2357.	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0188	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0197	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0202	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0207	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0208	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0216	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0221	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0226	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0227	conserved domain protein	36	-
sce0229	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0243	hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce0252	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce0258	conserved hypothetical protein 103	25	translation; cellular biosynthetic process; biosynthetic process
sce0260	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0262	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0264	moaA2 hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0266	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0272	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0273	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0276	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce0278	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0280	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0285	hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce0300	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0302	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0306	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0318	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce0330	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0339	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce0346	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0347	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce0349	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0352	conserved hypothetical protein/putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0358	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0371	conserved secreted protein, lemA family	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0382	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce0386	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0387	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce0416	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0422	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0424	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0425	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0435	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce0468	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0470	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0474	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0478	yfbK hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0481	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0486	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0501	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0505	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0507	conserved hypothetical protein	36	-
sce0517	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce0519	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0520	unknown protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0537	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0540	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0541	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0546	conserved hypothetical protein	36	-
sce0548	yebN putative membrane protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce0551	hypothetical protein with NHL repeat	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0552	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce0554	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0560	ygcH hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0582	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0595	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0597	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce0605	hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce0607	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce0610	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0641	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0642	ychJ hypothetical UPF0225 protein ychJ.	28	integral to membrane; intrinsic to membrane; membrane
sce0646	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0665	conserved hypothetical protein	25	translation; cellular biosynthetic process; biosynthetic process
sce0692	hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce0703	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0707	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0717	hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce0725	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce0731	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0735	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0736	hypothetical protein-signal peptide prediction	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0738	cupin-like protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0739	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0741	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce0745	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0753	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce0770	putative membrane protein	36	-
sce0771	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0772		39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0773	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0787	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0789	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0790	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce0791	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0792	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0806	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0814	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0823	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0825	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0826	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0859	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce0863	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0864	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0865	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0866	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0867	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0868	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0869	hypothetical protein predicted by Glimmer/Critica	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce0871	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0876	hypothetical protein predicted by Glimmer/Critica	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0878	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0893	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0901	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0904	hypothetical protein predicted by Glimmer/Critica	35	subtilase activity; helicase activity; response to stimulus
sce0908	conserved hypothetical protein	5	-
sce0916	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce0936	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0937	putative exported protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0951	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce0955	conserved hypothetical protein	36	-
sce0956	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce0957	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce0964	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0966	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0972	conserved hypothetical protein	36	-

sce0987	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0988	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0993	hypothetical protein-transmembrane prediction	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0994	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce0998	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1000	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1011	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1022	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1031	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1045	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1047	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1049	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1064	hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce1068		38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1077	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1085	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1095	putative secreted protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce1097	hypothetical protein predicted by Glimmer/Critica	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1098	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1107	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1115	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce1121	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1126	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce1128	hypothetical protein predicted by Glimmer/Critica	36	-
sce1131	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1142	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1157	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1158	conserved hypothetical protein	36	-
sce1159	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1165	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1170	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce1182	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1184	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce1186	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1187	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1202	conserved hypothetical protein	5	-
sce1203	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce1212	conserved hypothetical protein	36	-
sce1216	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1224	conserved hypothetical protein	36	-
sce1236	putative secreted protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1238	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1241	hypothetical protein predicted by Glimmer/Critica	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce1251	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce1259	hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce1265	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce1270	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1271	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1272	putative secreted protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1276	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1279	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1282		39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1291	Protein kinase 2.7.1.37	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1307	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1309	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1314	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1319	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1328	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1335	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1336	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1337	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1363	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1372	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce1374	yedI putative membrane protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1379	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1384	putative secreted protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1388	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1392	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1393	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1394	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1395	hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce1399	conserved hypothetical protein	16	protein secretion; protein transporter activity; secretion
sce1405	conserved hypothetical protein	36	-
sce1419	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1429	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1430	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1431	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1436	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1445	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1450	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce1452	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1462	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1463	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1473	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1482	hypothetical protein	36	-
sce1490	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce1499	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1500	hypothetical protein-signal peptide	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1507	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1514	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce1516	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce1521	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1525	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce1529	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce1531	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce1537	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1539	hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce1544	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1557	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1559	putative secreted protein	36	-
sce1560	conserved hypothetical protein	36	-
sce1561	conserved hypothetical protein	36	-
sce1566	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1568	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1580	conserved hypothetical protein	27	sigma factor activity; transcription initiation factor activity; transcription initiation
sce1590	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1601	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1626	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1630	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1670	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1672	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1677	hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce1678	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1684	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1686	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1687	protein of unknown function DUF262	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1721	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1729	conserved hypothetical protein	36	-
sce1745	hypothetical protein	36	-
sce1755	hypothetical protein	36	-
sce1774	hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce1778	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce1784	hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce1792	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce1795	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1797	hypothetical protein predicted by Glimmer/Critica	35	subtilase activity; helicase activity; response to stimulus
sce1805	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1806	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1816	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity

sce1821	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce1830	hypothetical conserved protein	35	subtilase activity; helicase activity; response to stimulus
sce1833	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1834	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1839	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1844	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1853	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1855	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce1861	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1864	conserved hypothetical protein	36	-
sce1869	Predicted membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1870	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce1885	conserved hypothetical protein	36	-
sce1893	hypothetical protein predicted by Glimmer/Critica	36	-
sce1915	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1917	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce1918	hypothetical protein predicted by Glimmer/Critica	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce1942	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1953	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1954	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1955	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce1965	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1967	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1970	celD hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1974	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1977	hypothetical protein predicted by Glimmer/Critica	36	-
sce1980	hypothetical protein predicted by Glimmer/Critica	5	-
sce1981	hypothetical protein	5	-
sce1986	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce1987	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce1993	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce1994	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes

sce2003	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2005	hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce2027	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce2031	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2033	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2034	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2045	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce2055	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2065	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2069	conserved hypothetical protein	16	protein secretion; protein transporter activity; secretion
sce2072	putative secreted protein	36	-
sce2073	putative membrane protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce2081	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2082	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2085	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2086	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2087	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2092	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2095	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2097		39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2098	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2099	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2100	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2105	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2110	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2124	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2125	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2126	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2127	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2130	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2137	hypothetical protein	36	-
sce2139	hypothetical protein	36	-
sce2140	putative secreted protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen

sce2143	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2144	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2156	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce2158	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce2172	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2177	hypothetical protein predicted by Glimmer/Critica	35	subtilase activity; helicase activity; response to stimulus
sce2190	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce2198	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2205	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2216	unknown protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2218	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2227	putative membrane protein	36	-
sce2243	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce2254	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2255	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce2259	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2260	putative secreted protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2264	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2266	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce2268	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2269	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2276	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2278	hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce2293	conserved hypothetical protein	36	-
sce2303	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2307	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2309	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2311	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2315	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce2317	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2319	putative secreted protein	35	subtilase activity; helicase activity; response to stimulus
sce2325	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce2334	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2341	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce2347	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2350	hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce2354	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2358	hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce2371	putative secreted protein	35	subtilase activity; helicase activity; response to stimulus
sce2372	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2374	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce2382	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2386	hypothetical protein predicted by Glimmer/Critica	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2393	hypothetical protein predicted by Glimmer/Critica	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce2414	no similarity	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2415	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2429	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2439	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2440	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2451	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2458	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2468	hypothetical protein predicted by Glimmer/Critica	35	subtilase activity; helicase activity; response to stimulus
sce2471	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2473	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2488	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2493	yheT conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce2494	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2511	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce2512	hypothetical protein	20	heme binding; tetrapyrrole binding; monooxygenase activity
sce2515	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2521	conserved hypothetical protein	12	RNA processing; RNA binding; tRNA metabolic process
sce2537	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2561	hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce2567	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2588	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce2596	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2606	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce2612	conserved hypothetical protein	13	ribonucleoprotein complex; cytoplasmic part; non-membrane-bound organelle
sce2619	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2626	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2630	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2639	hypothetical protein predicted by Glimmer/Critica	36	-
sce2642	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2643	unknown protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce2649	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce2660	unknown protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2663	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2664	conserved hypothetical protein	20	heme binding; tetrapyrrole binding; monooxygenase activity
sce2667	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2670	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2672	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2674	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce2683	hypothetical protein	1	-
sce2684	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2686	hypothetical WD-repeat protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2691	putative secreted protein	36	-
sce2694	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2702		39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2704	conserved hypothetical protein	5	-
sce2713	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce2719	hypothetical protein	5	-
sce2720	hypothetical protein	5	-
sce2724	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2742	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce2743	putative secreted protein	36	-
sce2752	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce2760	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2765	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce2785	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce2787	putative secreted protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce2794	putative secreted protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity

sce2800	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2809	Putative membrane protein	35	subtilase activity; helicase activity; response to stimulus
sce2812	hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce2816	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2817	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2821	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2831	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2835	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2865	hypothetical protein	5	-
sce2869	putative secreted protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce2883	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2886	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce2897	conserved putative secreted protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce2916	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce2931	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2932	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce2957	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2965	hypothetical protein predicted by Glimmer/Critica	32	signal transduction; cell communication; two-component response regulator activity
sce2971	hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce2981	hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce2987	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce2998	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3005	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3016	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3022	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3040	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce3043	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3048	hypothetical protein predicted by Glimmer/Critica	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce3066	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce3073	putative membrane-associated protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3075	hypothetical transferase	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce3079	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3087	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce3088	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce3094	hypothetical protein predicted by Glimmer/Critica	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce3103	putative secreted protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce3105	conserved hypothetical protein	5	-
sce3106	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3112	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce3113	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce3114	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce3119	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3130	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3154	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3164	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3172	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3174	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3175	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3177	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce3210	hypothetical WD-repeat protein all2124.	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3213	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3215	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3227	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce3231	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3238	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3255	conserved hypothetical protein	20	heme binding; tetrapyrrole binding; monooxygenase activity
sce3263	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3275	hypothetical serine rich protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3295	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3303	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3316	hypothetical conserved protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3325	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3334	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce3335	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3341	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce3364	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3368	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3370	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3371	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3373	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3374	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3381	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3383	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce3413	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce3416	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce3430	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3433	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3434	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3435	conserved hypothetical protein	36	-
sce3439	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3442	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3467	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce3475	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce3477	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3485	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3487	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3511	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3512	ynil conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3514	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3518	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce3519	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3521	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3534	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3539	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3540	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3550	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity

sce3564	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3565	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3579	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce3587	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3607	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3622	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce3623	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3628	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3636	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3638	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3644	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3651	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce3653	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3661	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3663	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3674	conserved hypothetical protein TIGR00246	25	translation; cellular biosynthetic process; biosynthetic process
sce3675	hypothetical protein predicted by Glimmer/Critica	25	translation; cellular biosynthetic process; biosynthetic process
sce3688	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3690	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce3699	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3707	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3717	conserved hypothetical protein	36	-
sce3726	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce3759	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3761	yloC conserved hypothetical protein	31	transcription factor binding; protein binding; intracellular
sce3775	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3776	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3782	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3784	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce3805	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3806	conserved hypothetical protein	1	-
sce3819	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce3833	hypothetical protein predicted by Glimmer/Critica	32	signal transduction; cell communication; two-component response regulator activity
sce3834	hypothetical protein predicted by Glimmer/Critica	16	protein secretion; protein transporter activity; secretion
sce3843	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3856	conserved hypothetical protein	17	acyl-CoA dehydrogenase activity; oxidoreductase activity, acting on the CH-CH group of donors; oxidoreductase activity
sce3866	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3871	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3893	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3894	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce3895	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3898	conserved hypothetical protein	29	two-component sensor activity; protein histidine kinase activity; cell communication
sce3909	hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce3910	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce3914	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3921	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3925	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3927	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3938	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3941	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3945	putative membrane protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce3962	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3969	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce3974	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce3992	conserved hypothetical protein	1	-
sce3994	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4001	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4008	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce4015	conserved hypothetical protein	36	-
sce4016	hypothetical protein-signal peptide prediction	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4038	hypothetical protein predicted by Glimmer/Critica	25	translation; cellular biosynthetic process; biosynthetic process
sce4039	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4041	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4050	putative secreted protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity

sce4053		39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4059	putative membrane protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce4060	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4079	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4083	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4084	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4088	hypothetical protein predicted by Glimmer/Critica	36	-
sce4107	conserved hypothetical protein	5	-
sce4108	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4109	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4113	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4116	hypothetical protein	36	-
sce4122	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4139	hypothetical protein predicted by Glimmer/Critica	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce4143	conserved hypothetical protein	36	-
sce4146	conserved hypothetical protein	36	-
sce4147	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4155	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4156	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4168	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4169	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4173	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce4184	hypothetical protein predicted by Glimmer/Critica 3.1.-.-	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce4187	putative secreted protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4189	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4191	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4198	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4227	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4230	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4237	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce4258	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4259	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4261	hypothetical protein predicted by Glimmer/Critica	35	subtilase activity; helicase activity; response to stimulus
sce4270	conserved hypothetical protein	31	transcription factor binding; protein binding; intracellular

sce4282	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4295	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4307	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4314	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce4326	putative secreted protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce4329	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4339	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4345	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4346	conserved hypothetical protein	31	transcription factor binding; protein binding; intracellular
sce4350	hypothetical membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4360	Protein of unknown function	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce4361	Protein of unknown function	35	subtilase activity; helicase activity; response to stimulus
sce4363	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4369	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4371	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4374	conserved hypothetical protein TIGR00486	21	protein amino acid phosphorylation; protein modification; phosphorylation
sce4381	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4382	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4383	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce4384	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce4386	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce4389	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce4398	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4403	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce4407	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4409	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce4410	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce4433	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4435	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4438	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce4442	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4458	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4466		39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4490	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4492	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4499	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4500	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4505	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4515	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce4520	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce4522	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce4531	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce4535	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4558	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4559	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce4561	unknown protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce4563	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4569	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4583	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4584	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4590	conserved hypothetical protein	36	-
sce4594	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4595	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4602	hypothetical protein-signal peptide prediction	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4603	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4604	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4607	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4608	hypothetical protein-signal peptide prediction	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4611	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4612	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4619	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4621	conserved hypothetical protein	36	-

sce4625	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4629	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce4636	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4645	conserved hypothetical secreted protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce4647	hypothetical protein predicted by Glimmer/Critica	36	-
sce4648	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4650	yjdI EbsC protein	35	subtilase activity; helicase activity; response to stimulus
sce4655	conserved hypothetical protein	36	-
sce4657	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4663	hypothetical protein	5	-
sce4670	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4684	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4691	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4693	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4698	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4718	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4720	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4729	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4731	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4732	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4741	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4762	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4764	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4779	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4789	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce4803	mazG conserved hypothetical protein	32	signal transduction; cell communication; two-component response regulator activity
sce4809	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4813		39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4830	Protein of unknown function DUF1255	28	integral to membrane; intrinsic to membrane; membrane
sce4834	cgeB conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4840	conserved hypothetical protein	36	-
sce4846	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4847	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4850	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4853	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus

sce4856	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce4857	putative membrane protein	36	-
sce4858	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4861	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4871	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4874	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4895	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4896	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4903	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4904	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4913	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4914	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4930	hypothetical protein	36	-
sce4931	hypothetical protein	36	-
sce4932	hypothetical protein	5	-
sce4933	hypothetical protein	5	-
sce4934	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4940	hypothetical protein	36	-
sce4941	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4949	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce4950	putative membrane protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce4953	hypothetical protein	36	-
sce4958	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce4975	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4980	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce4981	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4982	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4983	hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4984	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4985	hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4986	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4987	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4988	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce4994	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4995	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4996	hypothetical protein DUF 1316 domain	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce4997	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce4998	hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane

sce5004	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce5011	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce5012	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce5023	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5025	DUF829 domain hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce5026	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5029	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5030	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5038	hypothetical protein	36	-
sce5045	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce5056	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5057	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5067	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce5075	hypothetical membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5084	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5087	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5101	hypothetical protein predicted by Glimmer/Critica	36	-
sce5104	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5112	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5113	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce5118	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5137	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce5142	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5143	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce5147	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce5148	hypothetical protein predicted by Glimmer/Critica	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce5169	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce5176	conserved hypothetical protein DUF181	36	-
sce5182	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce5191	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5193	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce5208	conserved hypothetical protein DUF820 domain	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity

sce5210	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5222	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce5230	hypothetical protein	36	-
sce5232	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5238	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5239	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce5240	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5241	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5242	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5243	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5247	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5259	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce5260	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce5269	hypothetical protein	32	signal transduction; cell communication; two-component response regulator activity
sce5270	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce5273	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce5279	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5283	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5293	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5305	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce5321	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5329	hypothetical protein	1	-
sce5333	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce5344	no similarity	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5348	hypothetical protein predicted by Glimmer/Critica	36	-
sce5357	conserved hypothetical protein containing the kelch-motif	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce5360	hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce5363	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5370	fibronectin type III domain protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5371	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce5382	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce5387	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce5407	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5414	hypothetical protein ybaA	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce5418	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5419	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce5421	hypothetical protein-signal peptide and transmembrane prediction	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5430	hypothetical protein predicted by Glimmer/Critica	35	subtilase activity; helicase activity; response to stimulus
sce5435	putative secreted protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce5438	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5452	conserved hypothetical protein with a signal peptide	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5486	hypothetical protein predicted by Glimmer/Critica	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce5489	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5496	hypothetical protein	36	-
sce5500	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5504	putative membrane protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce5513	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce5515	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5518	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5531	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5536	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce5538	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5541	putative membrane protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce5557	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5569	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5576	hypothetical protein predicted by Glimmer/Critica	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce5585	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5586	putative membrane protein	1	-
sce5590	conserved hypothetical protein	1	-
sce5593	DUF323 domain conserved hypothetical protein	1	-
sce5605	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce5613	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce5630	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce5632	hypothetical protein predicted by Glimmer/Critica	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce5633	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5650	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce5655	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce5660	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5662	hypothetical protein	36	-
sce5663	hypothetical protein	36	-
sce5665	hypothetical protein	5	-
sce5667	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce5668	hypothetical protein	5	-
sce5671	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5678	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5689	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5701	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5717	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce5733	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce5763	hypothetical protein predicted by Glimmer/Critica	35	subtilase activity; helicase activity; response to stimulus
sce5771	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5780	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce5788	hypothetical protein	20	heme binding; tetrapyrrole binding; monooxygenase activity
sce5792	hypothetical protein	31	transcription factor binding; protein binding; intracellular
sce5797	ylxP conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5801	conserved hypothetical protein	25	translation; cellular biosynthetic process; biosynthetic process
sce5811	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5817	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce5823	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce5837	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5851	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce5856	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5866	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5870	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce5874	hypothetical protein predicted by Glimmer/Critica	36	-
sce5875	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce5878	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce5880	conserved hypothetical protein	1	-
sce5882	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce5889	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5902	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5903	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5904	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce5909	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5916	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce5926	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce5932	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5936	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5961	hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce5970	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5971	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5972	conserved membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce5984	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce5996	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce6004	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce6043	hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce6052	conserved hypothetical protein	36	-
sce6056	conserved hypothetical protein	36	-
sce6058	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce6060	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6062	uncharacterized conserved protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6063	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6070	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6074	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce6077	hypothetical protein predicted by Glimmer/Critica	36	-
sce6096	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6113	hypothetical conserved protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce6114	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce6117	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce6120	hypothetical protein predicted by Glimmer/Critica	36	-
sce6122	hypothetical protein predicted by Glimmer/Critica	36	-
sce6124	conserved hypothetical protein	36	-
sce6146	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6154	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6161	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6165	putative membrane protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce6178	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce6189	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce6192	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce6209	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce6211	hypothetical protein	4	DNA integration; DNA metabolic process; DNA binding
sce6212	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce6213	DUF323 hypothetical protein	1	-
sce6215	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce6216	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6217	hypothetical protein	1	-
sce6220	hypothetical protein predicted by Glimmer/Critica	36	-
sce6226	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6234	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6239	conserved hypothetical protein / putative transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce6240	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6254	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6258	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce6259	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce6260	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce6268	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce6269	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6293	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6304	ydzA1 putative membrane protein	35	subtilase activity; helicase activity; response to stimulus

sce6306	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6309	hypothetical protein predicted by Glimmer/Critica	20	heme binding; tetrapyrrole binding; monooxygenase activity
sce6311	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6313	yndB hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce6314	conserved membrane hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce6325	conserved hypothetical protein	36	-
sce6327	putative membrane protein	36	-
sce6341	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6360	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6368	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6370	conserved hypothetical protein with Kelch motif	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6375	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6377	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce6382	conserved hypothetical protein	36	-
sce6387	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6396	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6413	putative membrane protein	28	integral to membrane; intrinsic to membrane; membrane
sce6416	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce6421	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce6439	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce6447	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce6454	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6466	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6481	hypothetical protein predicted by Glimmer/Critica	12	RNA processing; RNA binding; tRNA metabolic process
sce6497	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6498	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce6502	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce6504	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6505	putative membrane protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce6507	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6514	Uncharacterized protein conserved in bacteria	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce6526	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6541	conserved hypothetical protein	12	RNA processing; RNA binding; tRNA metabolic process

sce6558	putative membrane protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce6560	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce6563	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce6567	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce6579	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce6596	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce6598	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce6601	putative WD-40 repeat protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6611	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6612	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce6626	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6638	hypothetical protein yijF precursor	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce6645	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce6648	hypothetical protein	36	-
sce6664	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6679	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce6682	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6686	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce6689	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce6690	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6691	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6696	hypothetical secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6700	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce6702	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce6703	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6714	hypothetical protein	36	-
sce6720	hypothetical protein	36	-
sce6721	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce6727	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6731	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6745	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce6752	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce6757	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6761	conserved hypothetical protein	1	-
sce6768	putative membrane protein	36	-
sce6770	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus

sce6775	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6776	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6777	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6780	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce6782	putative membrane protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce6783	Putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6784	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce6785	hypothetical protein	5	-
sce6786	conserved hypothetical protein	5	-
sce6787	hypothetical protein	36	-
sce6788	conserved hypothetical protein	36	-
sce6791	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6795	glycosyltransferase-like conserved protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6799	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6800	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6812	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6816	hypothetical membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6817	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce6833	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce6849	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6854	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6863	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce6866	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6871	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6875	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6904	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6915	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6920	putative exported protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6923	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6925	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce6926	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce6951	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce6963	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce6974	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce6987	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce6995	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce7008	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7013	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce7014	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7017	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce7031	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7040	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce7041	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7049	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7056	Protein of unknown function DUF820	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce7073	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce7074	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce7077	conserved hypothetical protein	36	-
sce7079	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7082	hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce7091	conserved hypothetical protein	25	translation; cellular biosynthetic process; biosynthetic process
sce7100	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce7101	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce7109	conserved hypothetical protein	36	-
sce7111	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7117	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7121	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7123	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7124	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce7128	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7140	conserved domain protein	35	subtilase activity; helicase activity; response to stimulus
sce7146	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7148	conserved hypothetical protein	36	-
sce7161	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7164	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce7168	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce7176	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7178	conserved hypothetical protein	36	-

sce7181	hypothetical protein predicted by Glimmer/Critica	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce7182	conserved hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce7186	hypothetical protein predicted by Glimmer/Critica	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce7197	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7198	hypothetical protein predicted by Glimmer/Critica	32	signal transduction; cell communication; two-component response regulator activity
sce7208	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7223	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7247	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce7254	putative membrane protein	28	integral to membrane; intrinsic to membrane; membrane
sce7301	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7309	conserved membrane protein	36	-
sce7314	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7317	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7322	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7331	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce7336	hypothetical protein predicted by Glimmer/Critica	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce7337	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7341	hypothetical protein predicted by Glimmer/Critica	36	-
sce7360	Uncharacterized conserved protein	13	ribonucleoprotein complex; cytoplasmic part; non-membrane-bound organelle
sce7366	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7383	conserved hypothetical protein	22	protein amino acid phosphorylation; protein modification; phosphorylation
sce7386	Predicted integral membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7388	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce7391	conserved hypothetical protein	27	sigma factor activity; transcription initiation factor activity; transcription initiation
sce7401	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7402	hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce7419	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7422	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7429	putative secreted protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce7443	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce7446	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce7455	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce7458	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane

sce7464	hypothetical protein	5	-
sce7469	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7470	tolA hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7474	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce7477	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7480	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce7485	conserved hypothetical protein	1	-
sce7488	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7489	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7491	unknown protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7515	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7518	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce7526	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7530	conserved hypothetical protein	1	-
sce7537	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7565	hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce7580	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7589	conserved hypothetical membrane protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce7591	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce7601	hypothetical protein predicted by Glimmer/Critica	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce7605	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7606	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce7618	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7621	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce7622	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7623	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce7642	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7645	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7647	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7672	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce7690	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7699	putative membrane protein	5	-
sce7700	putative membrane protein	28	integral to membrane; intrinsic to membrane; membrane
sce7706	conserved hypothetical protein	36	-

sce7712	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7714	conserved secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7715	putative membrane protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce7724	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7725	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7726	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7730	putative membrane protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce7737	hypothetical protein predicted by Glimmer/Critica	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce7738	conserved hypothetical protein with TAT signal sequence	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7739	conserved hypothetical protein with a signal sequence	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7745	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7763	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce7768	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7770	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce7790	putative membrane protein	1	-
sce7792	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7795	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7798	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7805	conserved hypothetical protein containing a vWA domain	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7824	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7836	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7837	Putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7838	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7839	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7845	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7859	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7863	conserved hypothetical protein	36	-
sce7865	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7866	hypothetical protein predicted by Glimmer/Critica	35	subtilase activity; helicase activity; response to stimulus
sce7868	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7871	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7877	hypothetical integral membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7892	conserved hypothetical protein	36	-
sce7893	hypothetical protein predicted by Glimmer/Critica	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce7902	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce7903	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7916	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce7920	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce7960	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce7969	conserved hypothetical protein	19	cell; cell part; membrane
sce7981	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8015	hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8030	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8032	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8036	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce8048	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8063	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8067	conserved repeat domain protein	35	subtilase activity; helicase activity; response to stimulus
sce8071	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8098	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8114	hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce8118	hypothetical	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce8131	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8134	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce8138	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce8139	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce8141	conserved hypothetical protein, Rhs element family	28	integral to membrane; intrinsic to membrane; membrane
sce8144	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8146	conserved hypothetical protein	5	-
sce8148	hypothetical protein predicted by Glimmer/Critica	36	-
sce8156	hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce8161	bioD conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8169	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8175	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8181	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8184	conserved hypothetical protein UPF0001	25	translation; cellular biosynthetic process; biosynthetic process
sce8190	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce8191	conserved hypothetical protein	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce8192	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce8198	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8201	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8214	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce8233	hypothetical protein predicted by Glimmer/Critica	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce8234	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8253	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8272	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8274	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce8284	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8289	putative secreted protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8293	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8303	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8304	hypothetical UPF0079 protein yjeE	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8315	hypothetical secreted peptidase	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8323	hypothetical protein	5	-
sce8324	hypothetical protein	5	-
sce8339	conserved hypothetical protein with Kelch motif	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8347	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce8353	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce8354	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8355	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8356	conserved hypothetical protein	5	-
sce8357	hypothetical protein	5	-
sce8359	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8373	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce8379	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8384	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce8385	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce8400	hypothetical protein predicted by Glimmer/Critica	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce8403	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8404	conserved hypothetical protein	36	-
sce8414	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce8416	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8417	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8418	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8419	hypothetical protein	5	-
sce8420	hypothetical protein	5	-
sce8421	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce8422	hypothetical protein	5	-
sce8428	conserved hypothetical protein	36	-
sce8436	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8440	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8447	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8450	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8459	hypothetical protein predicted by Glimmer/Critica	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce8461	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8464	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8465	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8466	conserved hypothetical protein	36	-
sce8471	hypothetical protein	36	-
sce8472	hypothetical protein	36	-
sce8480	conserved hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce8498	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8500	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8511	conserved hypothetical protein Vgr	28	integral to membrane; intrinsic to membrane; membrane
sce8514	conserved hypothetical protein	30	carbon-sulfur lyase activity; sequence-specific DNA binding; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
sce8516	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8530	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8531	conserved hypothetical protein	36	-
sce8533	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8541	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8542	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8547	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8592	putative membrane protein	36	-
sce8599	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8637	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce8648	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8659	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce8662	hypothetical protein-transmembrane prediction	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8663	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8664	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8687	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce8720	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8732	hypothetical protein predicted by Glimmer/Critica	36	-
sce8741	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8745	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce8752	uncharaterized conserved protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8753	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8758	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8759	conserved hypothetical protein with Apaf-1 domain	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8780	putative secreted protein	1	-
sce8783	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8789	putative membrane protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8795	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8807	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8819	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8823	putative membrane protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce8827	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8829	ydzA2 putative membrane protein	35	subtilase activity; helicase activity; response to stimulus
sce8841	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8842	hypothetical protein T07A9.5a	35	subtilase activity; helicase activity; response to stimulus
sce8844	hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce8845	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8880	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8890	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8892	hypothetical protein	36	-
sce8893	conserved hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce8904	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8905	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce8906	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8920	hypothetical protein-signal peptide and transmembrane prediction	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8929	conserved hypothetical protein	9	ATPase activity; nucleoside-triphosphatase activity; pyrophosphatase activity
sce8934	Protein of unknown function (DUF975)	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce8938	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8944	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8946	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8953	hypothetical protein predicted by Glimmer/Critica	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce8964	hypothetical protein predicted by Glimmer/Critica	15	sodium ion transport; chromosome condensation; monovalent inorganic cation transport
sce8973	ycaQ hypothetical protein	26	electron transport; generation of precursor metabolites and energy; oxidoreductase activity
sce8974	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8975	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8978	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8988	hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce8989	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8994	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8995	conserved hypothetical protein	17	acyl-CoA dehydrogenase activity; oxidoreductase activity, acting on the CH-CH group of donors; oxidoreductase activity
sce8997	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce8998	putative secreted protein	18	biosynthetic process; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; steroid biosynthetic process
sce8999	hypothetical protein	36	-
sce9001	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9003	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9010	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9027	putative membrane protein	35	subtilase activity; helicase activity; response to stimulus
sce9034	hypothetical protein	24	periplasmic space (sensu the ProteoBacteria research community); protein disulfide oxidoreductase activity; cell envelope
sce9042	hypothetical protein	38	magnesium chelatase activity; ligase activity, forming nitrogen-metal bonds; ligase activity, forming nitrogen-metal bonds, forming coordination complexes
sce9045	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9049	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9066	conserved domain protein	35	subtilase activity; helicase activity; response to stimulus
sce9072	conserved hypothetical protein (YcaO-like family)	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9073	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9076	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

sce9089	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce9094	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9097	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9113	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9128	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9138	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9166	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9171	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9188	conserved hypothetical protein	36	-
sce9202	conserved hypothetical protein	37	transcription factor activity; DNA binding; transcription regulator activity
sce9236	putative secreted protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9253	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9258	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9285	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9289	hypothetical protein predicted by Glimmer/Critica	36	-
sce9290	conserved hypothetical protein	1	-
sce9302	conserved hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9308	conserved hypothetical protein	34	serine-type endopeptidase inhibitor activity; enzyme inhibitor activity; endopeptidase inhibitor activity
sce9310	conserved hypothetical protein	33	hydrolase activity, hydrolyzing *O*-glycosyl compounds; hydrolase activity, acting on glycosyl bonds; carbohydrate metabolic process
sce9311	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9317	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9318	no hits	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9325	conserved hypothetical protein	35	subtilase activity; helicase activity; response to stimulus
sce9329	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce9334	conserved hypothetical protein	5	-
sce9336	conserved hypothetical protein	5	-
sce9337	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce9338	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce9339	hypothetical protein predicted by Glimmer/Critica	36	-
sce9340	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce9341	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce9342	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce9343	conserved hypothetical protein	36	-
sce9344	hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce9345	hypothetical protein predicted by Glimmer/Critica	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process
sce9346	conserved hypothetical protein	28	integral to membrane; intrinsic to membrane; membrane
sce9347	hypothetical protein	39	RNA-directed DNA polymerase activity; RNA-dependent DNA replication; DNA metabolic process

Supplementary Table 4 a) Protein composition of mountain 23 on the *S. cellulosum* phylogenomic map. The majority of the proteins found in this mountain are associated with secondary metabolism. Gene IDs and their associated products are shown. b) Protein composition of mountain 27 of the S. cellulosum phylogenomic map. The majority of the proteins found in this mountain are associated with secondary metabolism and signal transduction. Gene IDs and their associated products are shown. Secondary metabolites biosynthetic genes are indicated in bold.

a) Mountain 23			
ID	**Product**	**ID**	**Product**
sce0047	Putative 3-oxoacyl-[acyl-carrier-protein] reductase	sce3542	Transcriptional regulator, LysR family
sce0063	Putative transcriptional regulator	sce3620	PaaZ aldehyde dehydrogenase
sce0097	Predicted proline iminopeptidase	sce3825	FadD1 putative long-chain-fatty-acid-CoA ligase
sce0134	Alcohol dehydrogenase, zinc-containing	**sce3888**	**MxcG Nonribosomal peptide synthetase**
sce0289	Putative oxidoreductase	sce4121	Cytosine/adenosine deaminase
sce0337	Oxidoreductase, short chain dehydrogenase/reductase	**sce4135**	**ChiD hybrid polyketide synthase/nonribosomal peptide synthetase**
sce0345	**NRPS/PKS hybrid**	sce4199	Fdh1 alcohol dehydrogenase
sce0434	Transcriptional regulator	sce4235	MocA oxidoreductase
sce0436	AMP-dependent synthetase and ligase	sce4293	Adh4 alcohol dehydrogenase
sce0475	Adh1 alcohol dehydrogenase	sce4459	RocA 1-pyrroline-5-carboxylate dehydrogenase
sce0668	Putative oxidoreductase	sce4495	Putative aldehyde dehydrogenase
sce0671	Oxidoreductase/voltage-gated potassium channel β-1 subunit (K+ channel β-1 subunit) (Kv-β-1)	sce4676	Probable short-chain dehydrogenase/reductase family protein
sce0676	AstD succinylglutamic semialdehyde dehydrogenase	sce4728	Probable oxidoreductase
sce0715	Probable oxidoreductase	sce4756	Aldo/keto reductase
sce0716	Selenocysteine lyase	sce4770	Putative aldo/keto reductase family protein
sce0805	Probable oxidoreductase	sce4818	FabG8 3-oxoacyl-[acyl-carrier-protein] reductase
sce0991	Dehydrogenase with different specifities	sce4882	Conserved hypothetical protein
sce1012	Putative hydrolase	sce4900	Adh5 alcohol dehydrogenase
sce1116	YahK alcohol dehydrogenase	sce5007	Putative aldehyde dehydrogenase (NAD(+))
sce1140	Probable transcriptional regulator	sce5022	Conserved hypothetical protein
sce1150	NasD nitrite reductase (NAD(P)H)	sce5048	Probable oxidoreductase

sce1175	GlpD glycerol-3-phosphate dehydrogenase	sce5062	Threonine dehydrogenase and related Zn-dependent dehydrogenases
sce1193	Probable oxidoreductase	sce5264	Putative sugar-phosphate dehydrogenase
sce1242	YjjN putative alcohol dehydrogenase	sce5374	GutB threonine dehydrogenase
sce1268	Transcriptional regulator	sce5402	Putative NADH-dependent flavin oxidoreductase
sce1333	FabG1 3-oxoacyl-[acyl-carrier-protein] reductase	sce5485	Putative dehydrogenase
sce1353	KdpB potassium-transporting ATPase B chain	sce5495	Fdh2 alcohol dehydrogenase
sce1411	Putative dehydrogenase	sce5642	Zinc-binding oxidoreductase
sce1483	Permease of the major facilitator superfamily	sce5973	Succinate-semialdehyde dehydrogenase (NAD(P)(+))
sce1524	Probable oxidoreductase	sce6223	Putative alcohol dehydrogenase
sce1535	Alcohol dehydrogenase	sce6685	SDR family short chain oxidoreductase
sce1569	PdhC dihydrolipoyllysine-residue acetyltransferase	**sce6823**	**NRPS/PKS hybrid**
sce1576	FabG2 3-oxoacyl-[acyl-carrier-protein] reductase	sce7010	Threonine dehydrogenase and related Zn-dependent dehydrogenases
sce1582	Nos nitric-oxide synthase, oxygenase subunit	sce7277	Tdh threonine 3-dehydrogenase
sce1683	Oxidoreductase, short-chain dehydrogenase/reductase family	sce7493	Putative hydrolase
sce1736	Citrate synthase	sce7528	Oxidoreductase
sce1809	Conserved hypothetical protein	sce7582	Aldo-keto reductase family
sce1814	PurK phosphoribosylaminoimidazole carboxylase	sce7729	Putative oxidoreductase
sce1969	Putative oxidoreductase	sce8093	Putative oxidoreductase
sce2120	Pyruvate oxidase	sce8137	AcnA aconitate hydratase
sce2121	FabG4 putative 3-oxoacyl-[acyl-carrier-protein] reductase	sce8219	AMP-dependent synthetase and ligase
sce2134	Putative oxidoreductase; aldo-keto family	sce8242	AldH aldehyde dehydrogenase (NAD(+)) 1.2.1.3
sce2164	Dehydrogenase	**sce8255**	**Non-ribosomal peptide synthetase**
sce2275	Qor1 NADPH:quinone reductase	**sce8256**	**Non-ribosomal peptide synthetase**
sce2387	**Non-ribosomal peptide synthetase**	**sce8257**	**Non-ribosomal peptide synthetase**
sce2550	Aldehyde dehydrogenase	**sce8262**	**Non-ribosomal peptide synthetase**
sce2602	FabG5 3-oxoacyl-[acyl-carrier-protein] reductase	sce8298	Putative NADP-dependent oxidoreductase
sce2610	Putative oxidoreductase	sce8343	DkgB putative 2,5-didehydrogluconate reductase

sce2819	Putative oxidoreductase	sce8562	Putative NADPH quinone oxidoreductase
sce2941	MoaE probably molybdopterin-converting factor chain 2	sce8574	Putative oxidoreductase
sce2962	Putative oxidoreductase	sce8586	Putative HTH-type transcriptional regulator
sce2985	Putative succinate-semialdehyde dehydrogenase	sce8660	Transcriptional regulator, MerR family
sce3064	Alpha amylase, catalytic region	sce8661	Probable oxidoreductase
sce3095	Putative aldehyde dehydrogenase	sce8666	Probable dehydrogenase
sce3223	GntR-family transcriptional regulator	sce8849	Probable oxidoreductase
sce3225	Putatvie dehydrogenase	sce8851	Putative NADPH:quinone reductase
sce3250	Adh3 alcohol dehydrogenase	sce8981	Oxidoreductase
sce3333	YqkF oxidoreductase, aldo/keto reductase family	sce9148	Putative NADPH:quinone reductase
sce3417	Putative short chain dehydrogenase	sce9189	Aldehyde dehydrogenase (NAD(+))
sce3456	NADPH:quinone reductase	sce9297	Putative zinc-binding dehydrogenase
sce3488	NirB1 nitrite reductase	sce9319	Alcohol dehydrogenase

b) Mpuntain 27			
ID	**Product**	**ID**	**Product**
sce0014	HemD uroporphyrinogen-III synthase	sce5060	GltB1 glutamate synthase (NADPH)
sce0037	Conserved hypothetical protein YfiH	sce5061	GltD glutamate synthase
sce0086	LeuC1 Isopropylmalate isomerase, large subunit	sce5141	ECF-family RNA polymerase sigma factor
sce0297	RuvA holliday junction DNA helicase	sce5271	FadD2 long-chain fatty-acid-CoA ligase
sce0323	Ndh1 NADH dehydrogenase	sce5399	XseA exodeoxyribonuclease VII, large subunit
sce0361	TreS trehalose synthase	sce5453	ECF-family RNA polymerase sigma factor
sce0558	ECF-family RNA polymerase sigma factor	sce5625	Ubiquinone/menaquinone biosynthesis methyltransferase
sce0639	NadB L-aspartate oxidase	sce5748	TrxC2 thioredoxin
sce0695	ECF-family RNA polymerase sigma factor	sce5756	Putative adenylyltransferase
sce0819	**Polyketide synthase**	sce5758	Conserved hypothetical protein
sce0820	**Polyketide synthase**	sce5860	ECF-family RNA polymerase sigma factor
sce0835	PanC putative pantoate-β-alanine ligase	sce5871	MetH1 methionine synthase
sce0844	RplW 50S ribosomal protein L23	sce5947	ECF-family RNA polymerase sigma factor
sce0872	AroB1 3-dehydroquinate synthase	sce6016	Metallo-β-lactamase family protein

sce0903	Long-chain fatty-acid-CoA ligase	sce6054	ECF-family RNA polymerase sigma factor
sce1303	Glycogen operon protein	sce6175	Antioxidant protein
sce1340	RNA polymerase ECF-type sigma factor	sce6204	*O*-6-alkylguanine-DNA/cysteine-protein methyltransferase
sce1467	Putative acyl-CoA synthetases (AMP-forming)/AMP-acid ligases	sce6480	Putative exported peptidase
sce1580	Conserved hypothetical protein	sce6889	Putative sulfate transporter, SulP family
sce1624	HemA Glutamyl-tRNA reductase	sce6933	Riboflavin biosynthesis protein
sce1660	MurE UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase	sce7012	Zwf2 glucose-6-phosphate 1-dehydrogenase
sce1662	MurD UDP-N-acetylmuramoylalanine-D-glutamate ligase	sce7043	PheA2 P-protein (prephenate dehydratase
sce1664	MurG UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol	sce7053	Acyl-CoA synthetase
sce1705	Ppx1 exopolyphosphatase	sce7106	Metallo-β-lactamase family protein
sce1717	PcnB poly(A) polymerase	sce7170	α-Amylase-family protein
sce1741	DnaE1 DNA polymerase III, alpha subunit	sce7171	ABC transporter ATP-binding protein
sce1746	PheA1 chorismate mutase/prephenate dehydratase	sce7185	cAMP-binding protein, CRP family of transcriptional regulators
sce2013	Glycine cleavage system protein H homologue	sce7210	GlnA2 Glutamate-ammonia ligase
sce2050	Sensor histidine kinase	sce7221	ECF-family RNA polymerase sigma factor
sce2378	Glycogen debranching enzyme	sce7243	DacB probable D-alanyl-D-alanine carboxypeptidase
sce2392	TreZ malto-oligosyltrehalose trehalohydrolase	sce7266	RibC riboflavin synthase 2.5.1.9
sce2530	Acyl-CoA synthetase	sce7267	RibA4 riboflavin biosynthesis protein
sce2545	LipB putative lipoate-protein ligase B	sce7348	Tpi triose-phosphate isomerase
sce2880	BioF1 8-amino-7-oxononanoate synthase	sce7350	Gap glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) 1.2.1.12
sce2970	YoaA ATP-dependent helicase	sce7391	Conserved hypothetical protein
sce3011	MenG ubiquinone/menaquinone biosynthesis methyltransferase	sce7407	GlmS glucosamine--fructose-6-phosphate aminotransferase
sce3024	Ndh2 NADH dehydrogenase	sce7414	Def2 polypeptide deformylase
sce3035	AroA1 3-phosphoshikimate 1-carboxyvinyltransferase	sce7483	Gph2 phosphoglycolate phosphatase 3.1.3.18
sce3166	GTP-binding protein HflX	sce7487	FtsI3 pencillin-binding transpeptidase with putative regulatory N-terminal domain
sce3182	Putative β-ketoacyl synthase	sce7566	ECF-family RNA polymerase sigma factor
sce3188	**Polyketide synthase**	sce7592	Putative cytochrome-c oxidase

sce3189	**Polyketide synthase**	sce7593	Putative cytochrome-c oxidase
sce3190	**Polyketide synthase**	sce7594	Putative cytochrome-c oxidase
sce3191	**Polyketide synthase**	sce7631	MurC2 UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase
sce3192	**Polyketide synthase**	sce7632	SuhB inositol-phosphate phosphatase
sce3193	**Polyketide synthase**	sce7636	TrxB thioredoxin-disulfide reductase
sce3288	Two-component response regulator	sce7733	MetH2 methionine synthase
sce3432	PlsC3 1-acylglycerol-3-phosphate *O*-acyltransferase	sce7788	XerC integrase/recombinase
sce3546	Gnd1 phosphogluconate dehydrogenase 1.1.1.44	sce7823	MurB UDP-N-acetylmuramate dehydrogenase
sce4133	**ChiF Polyketide synthase**	sce7897	ECF-family RNA polymerase sigma factor
sce4134	**ChiE Polyketide synthase**	sce7975	Rph ribonuclease PH
sce4136	**ChiC Polyketide synthase**	sce8012	AMP-binding enzyme family protein
sce4137	**ChiB Polyketide synthase**	sce8052	Sensor histidine kinase
sce4215	HisC2 histidinol-phosphate aminotransferase	sce8065	Putative metal-dependent phosphohydrolase
sce4242	ThiG thiamine biosynthesis protein	sce8127	IlvG1 putative acetolactate synthase
sce4250	ThiC thiamin biosynthesis protein	sce8155	DapF diaminopimelate epimerase
sce4286	Conserved hypothetical membrane protein	sce8160	BioF2 putative 8-amino-7-oxononanoate synthase
sce4352	ThrS threonyl-tRNA synthetase	sce8167	ClpB2 ATPase with chaperone activity, two ATP-bindingdomains
sce4355	Zwf1 glucose-6-phosphate 1-dehydrogenase	sce8182	ATPase
sce4359	PlsC4 1-acylglycerol-3-phosphate *O*-acyltransferase	**sce8261**	**Polyketide synthase**
sce4397	SerC phosphoserine aminotransferase	sce8534	GoxB glycine oxidase
sce4494	GlgB 1,4-alpha-glucan branching enzyme	sce8545	Uup ABC transporter, ATP-binding protein
sce4523	Cytochrome-c oxidase	sce8628	HemE putative uroporphyrinogen decarboxylase
sce4524	Cytochrome-c oxidase	sce8680	ECF-family RNA polymerase sigma factor
sce4525	Putative cytochrome-c oxidase	sce8696	Putative long-chain fatty-acid-CoA ligase
sce4790	Putative sulfate transporter, SulP family	sce8734	ECF-family RNA polymerase sigma factor
sce4791	ECF-family RNA polymerase sigma factor	sce8746	Probable sulfate transporter, SulP family
sce4827	Signal transduction histidine kinase	sce8897	ECF-family RNA polymerase sigma factor

sce4864	ECF-family RNA polymerase sigma factor	sce9022	Def3 peptide deformylase
sce4888	Probable glycolipid synthase	sce9228	Inositol monophosphatase family protein
sce4901	ECF-family RNA polymerase sigma factor	sce9261	Aspartate kinase
sce5034	ECF-family RNA polymerase sigma factor	sce9359	YrdC2 putative translation factor

Supplementary Table 5 a) List of genes known to encode developmental, motility and chemosensory proteins in *M. xanthus* and similar genes identified in the *S. cellulosum* genome based on bidirectional BLASTP analysis (see Methods section). Shading indicates that the genes are clustered. b) List of developmental genes in *M. xanthus* which are not found in *S. cellulosum* based on bidirectional BLASTP analysis.

a) Genes which are similar in *M. xanthus* and *S. cellulosum*			
***M. xanthus* locus**[1]	**Gene name**[2,3,4]	**E-value**	***S. cellulosum* locus**
Development and/or sporulation			
MXAN0581	*dsgA, infC*	1.4E-51	sce4486
MXAN0755	*pkn9*	1.7E-76	sce4952
MXAN0930	*pktA5, pknD1*	5.2E-90	sce8731
MXAN0933	*pktB8, pknD2*	0.0E+00	sce5317
		0.0E+00	sce5338
		0.0E+00	sce8729
MXAN1078	*nla19*	8.0E-139	sce1649
MXAN1925	*mglA*	2.1E-59	sce7249
MXAN1926	*mglB*	6.1E-92	sce7248
MXAN1929	*masK*	9.8E-75	sce6482
MXAN2044	*pph1*	4.8E-85	sce7899, *pp2c14*
MXAN2913	*asgB*	1.4E-36	sce3644
MXAN3122	*bcsA*	3.0E-103	sce1445
MXAN3214	*asgC, rpoD*	0.0E+00	sce4447
MXAN3215	*actC*	1.6E-50	sce1795
MXAN3555	*sasR*	1.0E-159	sce2560
MXAN3993	*bsgA*	0.0E+00	sce0897, *lon1*
		0.0E+00	sce2838, *lon2*
		0.0E+00	sce4504, *lon4*
		0.0E+00	sce5003, *lon5*
MXAN4017	*pkn4*	1.4E-74	sce4539
MXAN4151	*brgE*	3.6E-82	sce0293
MXAN4276	*spiR, Ω4521*	2.5E-81	sce4096
MXAN5116	*pkn14*	1.3E-81	sce8429
MXAN5125	*mrpC*	2.4E-15	sce7185
MXAN5592	*digR*	3.8E-60	sce0622
MXAN6890	*hthB*	1.5E-51	sce6724
MXAN7259	*cas2*	2.0E-16	sce9177
MXAN7260		9.4E-91	sce9176
MXAN7261	*devS*	1.0E-24	sce9175
MXAN7262	*devR*	2.8E-41	sce9174
MXAN7263	*devT*	7.6E-15	sce9173
MXAN7264	*orf2*	4.0E-112	sce9172
MXAN7265	*orf1*	2.5E-30	sce9171
A-motility			
MXAN2923	*agmQ*	3.9E-43	sce1929
MXAN3008	*aglS*	3.2E-16	sce2996

MXAN3060	*cglB*	3.4E-12	sce7252
MXAN3502	*agmI*	3.1E-16	sce3655
MXAN3886	*agmA*	7.4E-47	sce3789
MXAN4638	*agmH*	1.9E-18	sce0898
MXAN4862	*agmX*	3.6E-42	sce1654
MXAN4863	*agmK*	0.0E+00	sce2921
MXAN4869	*aglT*	6.1E-22	sce2916
MXAN6607	*agmT*	4.0E-19	sce4346
S-motility			
MXAN1106	*sgmC*	2.5E-37	sce0856
MXAN1795	*sgmE*	5.0E-111	sce1586
MXAN2128	*sgmF*	7.4E-36	sce4966
MXAN3084	*tgl*	4.3E-27	sce1677
MXAN3506	*sgmL*	1.9E-90	sce6778
MXAN3759	*sgmM*	0.0E+00	sce2589
MXAN3840	*scpB*	1.2E-48	sce2028
MXAN4150	*sgmO*	2.5E-46	sce3653
MXAN5134	*mutS*	9.0E-120	sce1459
MXAN5592	*sgmW*	3.8E-60	sce0622
MXAN5766	*sgmX*	2.9E-58	sce6446
MXAN5770	*sgmY*	1.0E-18	sce3925
MXAN5772	*pilQ*	2.0E-137	sce6184
MXAN5774	*pilO*	3.0E-15	sce6186
MXAN5776	*pilM*	6.7E-86	sce6188
MXAN5777	*nla23*	3.0E-123	sce2881
MXAN5780	*pilI*	7.5E-22	sce8041
MXAN5781	*pilH*	7.4E-71	sce5790
MXAN5783	*pilA*	4.2E-11	sce4274
MXAN5784	*pilR*	7.0E-119	sce4272
MXAN5786	*pilC*	2.0E-119	sce6250
MXAN5787	*pilT*	5.0E-144	sce4468
MXAN5788	*pilB*	0.0E+00	sce4467
MXAN5831	*sgmZ; glgP*	0.0E+00	sce4388
MXAN6671	*sglK, dnaK*	0.0E+00	sce0003
MXAN6705	*pilT*	8.0E-142	sce5324
MXAN6706	*pilT*	1.0E-144	sce5323
MXAN6908	*sgnD; pgi*	1.0E-178	sce5669
MXAN7448	*epsD*	6.5E-12	sce1548
MXAN7449	*epsC*	1.4E-23	sce5074
MXAN7451	*epsA*	2.0E-30	sce6681
Chemotaxis			
MXAN4140	*frzE*	1.4E-73	sce0777
MXAN4752	*cheB8*	1.3E-79	sce1599
MXAN4753	*cheR8*	3.4E-67	sce1598
MXAN4756	*cheW8b*	3.9E-16	sce1596
MXAN4757	*cheW8a*	2.3E-18	sce1595
MXAN4758	*cheA8*	2.0E-106	sce1594
MXAN4759	*cheY8a*	9.6E-27	sce1593

MXAN5149	*mcp3A*	5.2E-40	sce0778
MXAN5153	*crdA*	4.0E-115	sce3597
MXAN6695	*difB*	2.9E-45	sce4698
MXAN6959	*cheB7*	6.7E-99	sce2662
MXAN6960	*cheR7*	3.2E-90	sce2661
MXAN6961	*cpc7*	0.0E+00	sce2660
MXAN6962	*mcp7*	0.0E+00	sce2659
MXAN6963	*cheW7*	1.1E-45	sce2658
MXAN6964	*cheA7*	0.0E+00	sce2657
MXAN6965	*cheY7*	4.0E-40	sce2656
Stringent response			
MXAN3204	*relA*	0.0E+00	sce3845, *rel*

b) Genes in *M. xanthus* which are not present in *S. cellulosum*		
MXAN0931-0932	*espAB*	
MXAN1014	*sdeK*	
MXAN1146	*Ω4442*	
MXAN1467	*pkn1*	
MXAN1501	*Ω4403*	
MXAN1710	*pkn8*	
MXAN2269	*spore protein A gene*	
MXAN2391	*csgA*	
MXAN2432	*spore protein B gene*	
MXAN2549	*pkn5*	
MXAN2550	*pkn6*	
MXAN2670	*asgA*	
MXAN2681-2686	*che4 operon*	
MXAN2884	*Ω4400*	
MXAN2991	*aglZ*	
MXAN3008	*aglU*	
MXAN3117	*fruA*	
MXAN3214	*actB*	
MXAN4139-4138	*frzFG*	
MXAN4144-4141	*frzZABCD*	
MXAN4149	*frzS*	
MXAN4337	*actA*	
MXAN5144-4148	*cheR3-mcp3B*	
MXAN5150-5152	*crdC-cheW3*	
MXAN5260	*asgE*	
MXAN5430	*protein S gene*	
MXAN5432	*protein S1 gene*	
MXAN6106	*fibA*	
MXAN6420	*pkn2*	
MXAN6691-6694	*difGEDC*	
MXAN6696	*difA*	
MXAN6889	*hthA*	
MXAN6955	*todK*	
MXAN6969	*spore protein C gene*	
MXAN6996	*asgD*	

MXAN7061	*mbhA*	
MXAN7402	*nsd, Ω4469*	

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Supplementary Table 6 Proteins identified in phosphoproteome analysis, indicating presence and possible position of phosphorylation.

a) Examples of proteins determined to be phosphorylated, with potential phosphorylation sites shown in bold. The numbers indicate a selection of the protein spots used for identification and shown in Figure 5.

No.	Gene name	No. of phosphorylated peptides	Phosphorylation position (AA sequence)	Theoretical mass	Observed mass	Observed mass after neutral loss
1	sce5429	1	MKMDANFEFI**T**K	1570,6681	1570,7251	1489,8005
2	sce8895	1	E**T**GVPVDVV**S**VGADR	1579,7363	1579,7387	1499,7802
3	sce7349	1	LPLAR**T**IM**S**K	1225,6375	1225,6342	1145,8904
4	sce7698	1	**S**EIQ**S**VIAREVID**S**R	1781,8793	1781,9083	1701,9452
5	sce7698	1	LP**S**NRAALE**Y**VVR	1647,7655	1647,7812	1567,7378
6	sce7619	2	LGDAAALEGLA**T**FH**YT**K	1857,8783	1857,9771	1778,0797
			AAVRALGLL**S**V**S**ALCL**T**AAPR	2133,1614	2133,1399	2052,9394
7	sce0071	1	AHF**T**L**Y**QG**Y**VK	1406,6504	1406,7397	1326,8805
8	sce9025	1	QM**S**PPEV**S**AKVLQK	1621,8019	1621,7852	1541,9927
9	sce8808	1	GKELNHVP**S**F**S**AK	1493,7148	1493,76	1413,9098
10	sce6973	3	AR**T**EPVFAR	1126,5405	1126,5919	1046,6349
			A**T**EGDHDNRPLIRR	1729,813	1729,9058	1650,0317
			RL**S**EIDVELA**T**L**T**LR	1888,9181	1888,8978	1809,1978

b) Proteins identified in phosphoproteome analysis, indicating presence of phosphorylation. Phosphorylations: "–": no phosphoresidue detected; 1, 2: number of phosphoresidues detected

Protein ID			**Phosphorylation**	**Function**
	Name	**Score**	**(– / 1 / 2)**	
1	sce0001	79	–	dnaA chromosomal replication initiator protein DnaA
2	sce0012	123	1	response regulator
3	sce0071	111	1	sodA superoxide dismutase 1.15.1.1

4	sce0387	64	−	hypothetical protein
5	sce0425	95	−	conserved hypothetical protein
6	sce0573	109	−	gltX2 Glutamyl-tRNA synthetase 6.1.1.17
7	sce0625	107	−	electron transfer flavoprotein alpha-subunit
8	sce0626	63	−	putative electron transfer flavoprotein beta-subunit
9	sce0667	94	1	putative secreted protein
10	sce0936	85	−	hypothetical protein
11	sce1648	160	−	bacterioferritin
12	sce1688	96	4	hypothetical protein
13	sce1744	88	−	chromosome segregation ATPases
14	sce1774	73	−	hypothetical protein
15	sce2464	151	2	hisD Histidinol dehydrogenase 1.1.1.23
16	sce2534	98	−	putative ABC-2 type transport system ATP-binding protein
17	sce2770	94	−	pepA2 putative aminopeptidase 3.4.11.1
18	sce2781	94	1	GroEL like chaperone, HSP60 family
19	sce2819	66	−	putative Oxidoreductase
20	sce2988	101	−	outer membrane efflux protein
21	sce3147	90	−	clpP2 Endopeptidase Clp 3.4.21.92
22	sce3483	137	−	N-terminal domain intergin-like repeats and c-terminal- cell wall-associated hydrolase
23	sce3952	113	−	gbd alcohol dehydrogenase
24	sce4167	84	−	sodB superoxide dismutase 1.15.1.1
25	sce4421	109	−	putative ABC-2 type transport system ATP-binding protein
26	sce4540	142	1	pyk Pyruvate kinase 2.7.1.40
27	sce4819	103	1	anti-anti sigma factor protein
28	sce4981	97	2	conserved hypothetical protein
29	sce5046	98	−	argG Argininosuccinate synthase 6.3.4.5
30	sce5264	72	−	putative sugar-phosphate dehydrogenase
31	sce5429	100	1	xylA Xylose isomerase 5.3.1.5
32	sce5800	114	−	nusA N utilization substance protein A
33	sce5911	393	−	heat shock protein groEL
34	sce5936	99	1	conserved hypothetical protein
35	sce6446	102	-	tldD Peptidase U62
36	sce6973	223	3	prlC2 Oligopeptidase A 3.4.24.70

37	sce7003	90	−	NDP-sugar oxidoreductase
38	sce7105	68	1	pcaF Putative beta-ketoadipyl CoA thiolase 2.3.1
39	sce7210	219	1	glnA2 Glutamate--ammonia ligase 6.3.1.2
40	sce7349	99	1	pgk Phosphoglycerate kinase 2.7.2.3
41	sce7350	80	−	gap Glyceraldehyde-3-phosphate dehydrogenase
42	sce7427	67	−	ABC1 family protein
43	sce7541	72	−	similar to chloroplast membrane-associated 30 kD protein
44	sce7548	67	1	ABC-type dipeptide transport system, periplasmic component
45	sce7619	217	2	lamB maltoporin precursor
46	sce7698	235	2	eno Phosphopyruvate hydratase 4.2.1.11
47	sce7919	84	−	TPR-like protein
48	sce7936	68	−	rpoA DNA-directed RNA polymerase, alpha subunit 2.7.7.6
49	sce8164	80	−	dnaN DNA polymerase III beta subunit 2.7.7.7
50	sce8808	117	1	fecA probable TonB-dependent receptor
51	sce8895	95	1	purA Adenylosuccinate synthase 6.3.4.4
52	sce8973	71	−	ycaQ hypothetical protein
53	sce9025	230	1	dnaK2 chaperone protein dnaK

53 individual proteins in DHB
21 individual proteins carry 1 or more P (39,62%)

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Supplementary Table 7 Domain architectures of *Sorangium cellulosum* ELKs. Blue: modular organizations that have not been found in any other organism. White: modular organizations that have homologs in other bacterial species, albeit with some differences in the number and distribution of the various domains. [1]PKinase: Protein Kinase (PF00069); [2]GAF: cNMP-binding domain (PF01590); [3]STAS: Sulphate transporter and antisigma factor antagonist domain (PF01740): [4]TPR: Tetratricopeptide repeat (PF00515); [5]HTH: Helix-turn-helix motif, Fis family (PF02954); [6]Bacterial RNA polymerase, alpha chain C terminal domain (PF03118); [7]A1pp: ADP-ribose binding module (PF01661); [8]PAS: PAS domain (PF00989); [9]HWE: HWE family histidine kinase (PF07536); [10]DUF323: Domain of unknown function 323 (PF03781); [11]WD40: WD G-beta repeat (PF00400); [12]FHA: Fork head-associated domain (PF00498); [13]PDZ: Discs-large homologous region (DHR) or GLGF (PF00595).

Domain combinations	Number
PKinase[1]-GAF[2]-STAS[3]	8
PKinase-TPR[4]-GAF-Sigma 54 interaction domain-HTH[5]	4
PKinase-Response regulator-Adenylate/guanylate cyclase	3
Pkinase-Pkinase-RNA polymerase[6]	1
PKinase-A1pp[7]	1
Pkinase-Globin-Alpha/beta hydrolase fold	1
PKinase- Di-haem cytochrome c peroxidase	1
Pkinase-GAF-PAS[8]-HWE[9]	1
PKinase-GAF-Histidine kinase	6
PKinase-GAF-PAS-GAF-Histidine kinase	5
PKinase-GAF-Histidine kinase-Response regulator	2
PKinase-GAF-PAS-Histidine kinase	2
PKinase-GAF-GAF-Histidine kinase	1
PKinase-Response regulator	1
PKinase- DUF323[10]	11
PKinase-Adenylate/guanylate cyclase	6
PKinase-WD40[11]	3
PKinase-PKinase	3
PKinase-FHA[12]	2
Pkinase-PDZ[13]	1

Supplementary Table 8 Putative EBPs in *S. cellulosum*. The most common N-terminal signaling domain is the forkhead-associated (FHA) domain, which is found in 31 of the 76 proteins. A two-component receiver domain was identified in 22 of the 76 *S. cellulosum* EBPs. FHA domains are rare in EBPs, and have never been observed in such numbers (in *M. xanthus* 12 of the putative EBPs contain an FHA domain[1]). The FHA domain is a phosphothreonine-specific recognition domain involved in specific phosphorylation-dependent protein-protein interactions. The 31 FHA-EBPs are therefore likely to interact with protein partners in a process regulated by ELK-catalyzed phosphorylation.

ORF	COG	Signaling domain
sce0223	2204	None
sce0439	2204	FHA
sce0543	3604	None
sce0666	2204	FHA/GAF
sce0686	2204	FHA
sce1325	1221	None
sce1472	2204	FHA
sce1649	2204	Rec
sce1691	2204	Rec
sce1845	2204	None
sce1948	2204	FHA
sce2247	2204	FHA
sce2459	2204	TPR-like
sce2560	2204	Rec
sce2692	2204	Rec
sce2792	2204	Rec
sce2848	2204	Rec
sce2881	2204	Rec
sce2927	2204	None
sce2974	2204	Rec
sce3208	2204	Rec
sce3218	3604	None
sce3228	3604	FHA
sce3264	2204	Rec
sce3280	3604	GAF
sce3411	2204	FHA
sce3597	2204	Rec
sce3672	3283	FHA
sce3771	2204	FHA
sce3793	3604	None
sce3842	2204	FHA
sce4007	2204	FHA
sce4069	2204	FHA
sce4161	2204	FHA
sce4272	2204	Rec

sce4306	2204	FHA/GGDEF
sce4405	2204	FHA
sce4588	3604	FHA
sce4751	3829	FHA
sce4793	3604	None
sce5065	3829	FHA
sce5086	3604	GAF
sce5096	2204	FHA
sce5177	2204	FHA/GGDEF
sce5469	2204	FHA
sce5550	2204	None
sce5791	2204	Rec
sce5833	3604	None
sce5993	3604	None
sce6014	2204	Rec
sce6174	2204	Rec
sce6324	1221	XylR_N/v4r
sce6472	2204	FHA
sce6642	2204	None
sce6656	3604	FHA
sce6746	2204	FHA
sce6842	2204	None
sce6864	2204	None
sce6966	2204	Rec
sce7009	2204	RtcR
sce7127	3604	FHA
sce7155	4650	RtcR
sce7271	3604	FHA/GAF
sce7801	2204	Rec
sce7862	2204	Rec
sce8107	2204	Rec
sce8207	2204	None
sce8647	3604	GAF
sce8721	2204	Rec
sce8739	3604	FHA
sce8837	2204	Rec
sce8884	2204	FHA
sce9016	2204	FHA
sce9035	3604	GAF
sce9198	3604	FHA
sce9222	2204	Rec

Reference

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Supplementary Table 9 List of enzymes involved in cellulose and hemicellulose degradation in *S. cellulosum* So ce56.

EC number	Gene sce	Gene product	E-value	Related to
Cellulose degrading enzymes				
3.2.1.91	8077	1,4-β-Cellobiohydrolase	1.0E-159	
3.2.1.4	902	Endo-β-glucanase (Cellulase B)	2.0E-36	
	1468	Endo-β-glucanase (Cellulase B)	7.8E-67	*Clostridium acetobutylicum*
	1498	β-Mannase/endoglucanse (includes 3.2.1.4, 3.2.1.78)	5.3E-89	*Clostridium acetobutylicum*
	2234	Endo-1,5-β-glucanase (Cellulase 1, Avicelase)	0.0E+00	*Clostridium acetobutylicum*
	4910	Endoglucanse B	1.9E-66	*Bacillus subtilis*
	5506	Endo-1,4-β-glucanase (Cellulase 2)	2.0E-45	*Bacillus halodurans*
	5722	Endoglucanase E	3.7E-70	
	3220	Endoglucanase	1.7E-74	*Bacillus halodurans*
	5351	Endoglucanase	2.0E-147	
	6846	Endoglucanase	1.7E-87	
3.2.1.21	2601	Periplasmic β-glucosidase (Cellobiase)	0.0E+00	*Bifidobacterium*
	3455	β-Glucosidase	1.0E-109	*Streptomyces coelicolor*
	4297	β-Glucosidase	1.0E-125	*Thermoanaerobacter tengcongensis*
	6897	β-Glucosidase	0.0E+00	*Streptomyces coelicolor*
	7663	β-Glucosidase	5.0E-113	*Streptomyces coelicolor*
3.2.1.20	3449	α-Glucosidase	2.0E-136	*Gloeobacter violaceus*
2.4.1.20	6460	Cellobiose phosphorylase	0.0E+00	*Clostridium* spec.
Hemicellulose degrading enzymes				
Xylanases				
3.2.1.8	7089	Xylanase	1.7E-58	*Xanthomonas axonopodis*
	2188	Secreted xylanase	3.5E-63	*Streptomyces coelicolor*
3.2.1.1	965	Endo-1,4,-β-xylanase	2.0E-44	
	1866	Endo-1,4-β-xylanase D	1.8E-66	*Gloeobacter violaceus*
	3118	Endo-1,4-β-xylanase D	4.0E-88	
	3318	Endo-β-1,4-xylanase B	3.1E-94	*Clostridium acetobutylicum*
	4598	Endo-β-1,4-xylanase D	6.0E-52	
	5551	Endo-β-1,4-xylanase	1.0E-48	
	7089	Endo-β-1,4-xylanase A	1.5E-54	*Streptomyces coelicolor*
	1893	Endo-β-1,4-xylanse Z	9.0E-94	
	4591	Endo-β-1,4-xylanase	9.8E-72	*Clostridium acetobutylicum*
	2188	Endo-β-1,4-xylanase	3.5E-63	*Streptomyces coelicolor*
	3034	Endo-β-1,4-xylanase	1.0E-58	*Bacillus halodurans*

Xylosidases				
3.2.1.37	125	β-Xylosidase	0.0E+00	*Caulobacter crescentus*
	1485	β-Xylosidase	1.1E-66	*Bacillus licheniformis*
	2693	β-Xylosidase	9.1E-68	*Bacteroides fragilis*
	4884	β-Xylosidase	5.0E-174	*Bacillus halodurans*
α-Glucuronidase				
3.2.1.139	996	α-Glucuronidase	0.0E+00	*Caulobacter crescentus*
α-L-Arabino-furanosidase				
3.2.1.55	1246	α-N-Arabinofuranosidase II	8.0E-115	*Streptomyces avermitilis*
				Bacillus halodurans
	7850	α-L-Arabinofuranosidase	1.0E-159	
3.2.1.89	6753	Arabinogalactan endo-1,4-β-mannosidas	2.0E-49	*Erwinia carotovora*
Other saccharide-degrading enzymes				
3.2.1.74	8559	Glucan 1,4-β-glucosidase	8.0E-178	*Xanthomonas axonopodis*

Polysaccharide metabolism

S. cellulosum So ce56 is in common with other *Sorangium* strains, a potent degrader of rotting plant material. Analysis of the genome identifies classical pathways for degradation of cellulose, hemicellulose and pectin.

Cellulose

Strains of *S. cellulosum* are one among the rare aerobic cellulose degrading bacteria that grow on cellulose as a sole carbon source (**Fig. 1**); other Gram negative degraders of cellulose include *Cytophaga* and *Sporocytophaga*. Cellulases are distinguished from other glycoside hydrolases by their ability to hydrolyse β-1,4-glucosidic bonds between glucosyl residues. Anaerobic bacteria often posses unique extracellular multienzyme complexes for cellulose degradation called cellulosomes, in which glycoside hydrolases are grafted onto a macomolecular scaffold[1]. Assembly of the cellulosomes is mediated by interaction of short 'dockerin' domains on the hydrolases with complementary 'cohesin' domains on the scaffold proteins. In contrast, most aerobic bacteria and fungi investigated to date produce numerous individual, extracellular enzymes (non-complexed systems), incorporating binding modules for different conformations of cellulose. Exceptions include the anaerobic bacterium *Clostridium stercorarium* which produces cellulases of the non-complexed type, and members of the facultative anaerobic *Cellulomonas* which utilize an aerobic-type strategy[2].

The typical dockering modules of the cellulosomes could not be detected within the genome of *S. cellulosum* So ce56. Indeed, a *Sorangium* strain has been shown previously to degrade cellulose using extracellular enzymes[3]. Nevertheless *Sorangium* species show a tendency to adhere to crystalline cellulose, although such contact does not appear to be necessary for cellulose utilization (**Fig. 2**). In contrast to *Bacillus licheniformis* where the genes involved in cellulose degradation are clustered[4], the corresponding genes in *S. cellulosum* are distributed throughout the genome. Among them, the glycoside hydrolases can be classified according to the Carbohydrate-Active Enzymes Database

(www.cazy.org./CAZY/fam/acc_fam.html). This classification into families on the basis of structure provides valuable insights that extend and complement the functionally oriented International Union of Biochemistry and Molecular Biology (IUBMB) classification.

The genome of *S. cellulosum* So ce56 contains at least seven endoglucanases belonging to the glycoside hydrolase (GH) families, GH5 (sce902, sce1468, sce4910 and sce5351), GH8 (sce5506 and sce2330) and GH9 (sce2234), as well as one exoglucanase (GH6) (sce8077). Glycosyl hydrolases of the GH5 family are heterogeneous with respect to their activities, and include cellulases from bacteria (archaea as well as aerobic and anaerobic eubacteria), fungi, plants, and animals (i.e. nematodes). In contrast, families GH8 and GH9 contain only bacterial hydrolases. Cellobiohydrolase (EC 3.2.1.91, sce8077) is the only exocellulase in the genome, and acts from the non-reducing ends of cellulose. Its conserved domain structure places it into the GH6 family, found only in bacteria. In the environment, fungi are believed to compete directly for cellulose with *Sorangium* species. However, the enzymes responsible for cellulose degradation in *S. cellulosum* So ce56 are not related to the fungal glycosyl hydrolases, but instead to those from aerobic and anaerobic eubacteria.

Hemicellulose and pectin

Both in the primary and in the secondary cell wall of plants, cellulose microfibrils are embedded in an amorphous ground substance, the matrix. The matrix is a heteropolymer, constructed from two different components, pectin and hemicellulose. A hemicellulose is one of several polymers consisting of xylose, glucose, galactose, arabinose and mannose. Classification is based on which sugar predominates in the polymer (e.g. xylans, galactans, or arabinogalactans). In contrast to crystalline cellulose, hemicellulose can be readily hydrolyzed by a number of hemicullulases belonging to the family of *O*-glycoside hydrolases, as well as by members of the glycosyltransferase family of enzymes. Full decomposition requires the concerted action of several different enzymes, including endoxylanase (EC 3.2.1.8), β-xylosidase (EC 3.2.1.37), α-glucoronidase (EC 3.2.1.139), alpha-

arabinofuranosidase (EC 3.2.1.55) and acetylxylan esterase (EC 3.1.1.6), all of which were identified in the genome of *S. cellulosum* So ce56. Xylanases (sce7089 and sce2188) belong to family GH10, which contains exclusively bacterial enzymes. The four β-xylosidases (sce0125, sce1485, sce2693, and sce4884) are members of family GH43; gene sce0125 shows very high identity to an enzyme found in *Caulobacter crescentus*. Similarly, the α-glucoronidase gene (sce0996), which belongs to the GH67 family, also has a strong homolog in *C. cerscentus*. The two α-L-arabinofuranosidases present in the genome (sce1246 and sce7850) are members of family GH62, and both show similarities to enzymes from *Streptomyces* species.

Hemicelluloses appear to be important substrates for *Sorangium*, as mannose[5] and arabinose (Gerth, unpublished results) are superior sources of carbon relative to glucose. Xylose can be used by some *Sorangium* strains, for example So ce12[6], but it does not support growth of So ce56. Thus, it is surprising that the So ce56 genome contains enzymes which mediate the conversion of xylose to xylulose (xylose isomerase, sce5429) and xylulose to xylulose-5P (xylulokinase, sce9296), as well as ABC transporters most likely exhibiting specificity for xylose (sce2221–sce2223).

Pectin is a polymer of D-galacturonic acid incorporating varying amounts of D-galactose, L-arabinose, and L-rhamnose sugars. The initial step in pectin degradation is accomplished by a pectinesterase (EC 3.1.1.11) to yield pectate, which is then further broken down by pectate lyases (EC 4.2.2.2) to yield oligosaccharides with 4-deoxy-α-D-galact-4-enuronosyl groups at their non-reducing ends. The genome contains two enzymes putatively involved in pectin metabolism, the pectate lyases sce4816 and sce5832.

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Figures

Figure 1. Consumption of cellulose by *S. cellulosum*. A swarm colony of *S. cellulosum* (grown on an agar block (yellow)) has completely consumed a piece of filter paper. Fruiting bodies have formed at the original edge of the filter paper, where the carbon source became limiting.

Figure 2. Liquid culture of *S. cellulosum* grown using crystalline cellulose as a sole carbon source. Aggregates of cellulose and clumps of cells are visible, although at later stages, the cellulose will become completely metabolized.