

Sequence Analysis of the Genome of the Unicellular Cyanobacterium *Synechocystis* sp. Strain PCC6803. II. Sequence Determination of the Entire Genome and Assignment of Potential Protein-coding Regions

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(Received 19 June, 1996)

Abstract

The sequence determination of the entire genome of the *Synechocystis* sp. strain PCC6803 was completed. The total length of the genome finally confirmed was 3,573,470 bp, including the previously reported sequence of 1,003,450 bp from map position 64% to 92% of the genome. The entire sequence was assembled from the sequences of the physical map-based contigs of cosmid clones and of λ clones and long PCR products which were used for gap-filling. The accuracy of the sequence was guaranteed by analysis of both strands of DNA through the entire genome. The authenticity of the assembled sequence was supported by restriction analysis of long PCR products, which were directly amplified from the genomic DNA using the assembled sequence data. To predict the potential protein-coding regions, analysis of open reading frames (ORFs), analysis by the GeneMark program and similarity search to databases were performed. As a result, a total of 3,168 potential protein genes were assigned on the genome, in which 145 (4.6%) were identical to reported genes and 1,257 (39.6%) and 340 (10.8%) showed similarity to reported and hypothetical genes, respectively. The remaining 1,426 (45.0%) had no apparent similarity to any genes in databases. Among the potential protein genes assigned, 128 were related to the genes participating in photosynthetic reactions. The sum of the sequences coding for potential protein genes occupies 87% of the genome length. By adding rRNA and tRNA genes, therefore, the genome has a very compact arrangement of protein- and RNA-coding regions. A notable feature on the gene organization of the genome was that 99 ORFs, which showed similarity to transposase genes and could be classified into 6 groups, were found spread all over the genome, and at least 26 of them appeared to remain intact. The result implies that rearrangement of the genome occurred frequently during and after establishment of this species.

Key words: *Synechocystis* PCC6803; genome sequencing; potential protein genes

1. Introduction

The cyanobacteria, which are capable of photosynthetic growth, have been used as a model organism for the study of oxygenic photosynthesis of higher plants because they have relatively simple genetic systems compared with higher plants in which both the nuclear and chloroplast genomes are involved. The availability of genetic engineering technology based on the transformable

characteristics also facilitated the wide use of these microorganisms for elucidation of gene function.¹ To gain a whole set of genetic information necessary for oxygenic photosynthesis as well as the general genetic complement carried by a single microorganism, we began the project of sequencing the entire genome of a unicellular cyanobacterium *Synechocystis* sp. strain PCC6803. The sequence of the entire genome has so far been reported for *Haemophilus influenzae* Rd (1.83 Mb)² and *Mycoplasma genitalium* (0.58 Mb),³ but both are heterotrophic microorganisms. We first constructed a fine physical map of the *Synechocystis* genome, and estimated its genome size

Communicated by Mituru Takanami

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to be 3.6 Mb.⁴ Then, the contigs of cosmid clones were localized on the physical map,⁵ and sequence analysis was started from several different points. In the previous report, we described sequence features in the 1,003,450-bp region corresponding to the map positions of 64% to 92%.^{6,7} We now completed the sequence determination of the entire genome by sequencing the rest of the genome. We describe here the assignment of the potential protein-coding regions on the entire *Synechocystis* genome. This is the first paper reporting the entire genomic sequence of a photosynthetic autotroph.

2. Materials and Methods

2.1. DNA sources

The cosmid and λ clones and the long PCR products used for sequence analysis were prepared as described previously.⁶ The regions covered by respective clones and PCR products are given on the physical map in the Supplement section.

2.2. DNA sequencing and data assembly

The methods of template preparation used for DNA sequencing and the systems used for sequencing and data assembly were essentially the same as those in the previous paper.⁶

2.3. Sequencing strategy

The same strategy that was used for analysis of the 1-Mb region from map positions 64% to 92% was applied to the entire genome.⁶ In brief, the sequence was assembled from the sequence data of partially overlapped cosmid and λ clones and of long PCR products, which have been assigned on the physical map of the genome.⁵ For the sequence deduction of the respective clones, the "bridging shotgun" method was adopted. Two shotgun libraries, one with inserts of approximately 700 bp (element clones) and the other with inserts of about 2.5 kb (bridge clones), were prepared, and the sequence data on element clones were assembled using the information on the terminal sequences of bridge clones. The assembled sequence was confirmed by additional sequencing which excludes any ambiguity, and both strands of the entire genome were sequenced. Finally, the authenticity of the assembled sequence was confirmed by analysis of long PCR products directly amplified from the genomic DNA using the assembled sequence data.

3. Results and Discussion

3.1. Sequence determination of the entire genome

As the sequence of 1,003,450 bp from map positions 64% to 92% of the genome has already been determined, we deduced the sequence of the remaining parts which

span map positions 0% to 64% and 92% to 100%. The total length of the genome finally confirmed was 3,573,450 bp long. The nucleotide position was numbered from the junction of the *Asc* I-E and *Asc* I-F fragments according to the physical map of the genome.^{5,6} Nucleotide position 1 of the previously deduced 1,003,450-bp sequence corresponds to nucleotide position 2,267,260 in the entire genome.

As described in the Methods section, the deduced sequence was confirmed by analysis of both strands, and its authenticity was supported by analysis of long PCR products based on the deduced sequence. Therefore, we believe that the sequence of the entire genome virtually 100% accurate. The distribution of ACGT along the strand was A: 26.1%, C: 23.8%, G: 23.9% and T: 26.2%, which results in a GC content of 47.7%.

3.2. Assignment of potential protein-coding regions

The potential protein-coding regions (protein genes) were assigned as follows. First the open reading frames (ORFs) which consist of longer than 50 sense codons starting with ATG or GTG were searched, and named with a three-letter code which represents the species name (s), ORF length (l: longer than 100 codons, s: less than 100 codons), and the reading direction (l or r), as in the previous paper.⁶ All the ORFs were then translated into amino acid sequences and subjected to similarity search using the FASTA and MPSRCH programs against GenBank/Genpept (release 95.0), EMBL (release 47.0) and SWISS-PROT databases (release 32.0). For the anticipation of gene function, an MPSRCH score of higher than 200 was taken into account for longer ORFs (>100 codons), and a score of higher than 130 for shorter ORFs (50 to 100 codons), and these ORFs were listed as having similarity. The degree of similarity was further compared with query-match percentages, and those having relatively high values are referred to homologues. All the ORFs were assigned on the genome, and if two ORFs overlapped on either strand, those showing similarity to known genes were preferentially taken, and the longer one was chosen unless the function of the shorter one could reasonably be anticipated. Finally, the DNA stretches between the ORFs assigned as above were searched in the databases for similarity. The mini-ORFs (shorter than 50 codons), which showed similarity and had query-match percentages higher than 40%, were taken and indicated by placing (m) next to the second letter of the three-letter ORF name.

In parallel with ORF analysis, the entire genomic sequence was searched for coding potential using the computer program GeneMark.^{7,8} Approximately 90% of the ORFs assigned as above were identified by GeneMark as likely genes, although about one-fourth of them were predicted to start at more internal positions than assigned.

In this paper, however, we listed the largest ORFs as a measure of the coding potentiality. GeneMark did not support the remaining 10% of the assigned ORFs, but this is probably because genes of different phylogenetic origin escape detection by GeneMark which uses a matrix trained by a single organism.⁷ There were only two protein genes newly predicted by GeneMark from the mini-ORFs, and these genes have a (g) next to the second letter of the ORF name.

The total ORFs thus assigned along the genomic sequence totalled 3,168, including those in the previously reported 1-Mb region, which were re-evaluated under the above criterion. It should be borne in mind, however, that the ORFs assigned in this paper merely represent the coding potentiality of protein under the defined assumptions, and the real ORF assignment should be validated experimentally. According to the direct analysis of the N-terminal sequences of proteins which were resolved by two-dimensional gel electrophoresis, TTG and ATT start codons have been identified in addition to the major initiation codons, ATG and GTG, and among the proteins so far analyzed, some were shown to initiate at positions internal to those assigned by ORF analysis (T. Sazuka and O. Ohara, personal communication).

3.3. Similarity search of potential genes

Similarity search of the 3,168 potential protein genes against the databases indicated that 145 (4.6%) genes have already been reported in this *Synechocystis* species, 933 (29.4%) were homologues to known genes, and 324 (10.2%) and 340 (10.8%) showed similarity to known and hypothetical genes, respectively. The remaining 1,426 (45.0%) showed no significant similarity to any registered genes.

The putative genes whose function could be anticipated were grouped into 14 categories with respect to different biological roles, according to the principle of Riley,⁹ and listed in Table 1. On the physical map of the Supplement section, the location, length and direction of these ORFs were indicated, with color codes corresponding to functional categories.

3.4. Characteristics of the genome and unique genes

3.4.1. Gene density

The assigned potential protein genes as a whole occupied 87.0% of the genome length, corresponding to a gene density of approximately one gene per 1.1 kb. An average length of the putative gene products was 326 amino acid residues, and the longest one consisted of 4,199 residues (slr0408). As reported previously,⁵ the genome contained two copies of ribosomal RNA gene clusters, which consisted of the identical 5,028-bp sequences but with the reverse orientation at map positions 68% and 93% of the genome. Forty-two putative transfer RNA genes were

also found by computer search using the tRNA-scan program (manuscript in preparation). It is therefore apparent that the *Synechocystis* genome has a very compact arrangement of protein- and RNA-coding regions.

3.4.2. Genes relating to photosynthesis

A variety of genes relating to oxygenic photosynthesis have been studied using various photosynthetic autotrophs including cyanobacteria, and 71 such genes have been isolated from the *Synechocystis* species. As listed in Table 1, we now know that the *Synechocystis* genome contained a total of 126 genes, including the 71 reported genes, which were reported as those relating to the various processes of oxygenic photosynthesis: photosystems I and II, phycobilisome formation, ATP synthesis, CO₂ fixation, and electron transport systems. However, *psaG*, *psaH* and *psaN* for the subunits of photosystem I and *psbP*, *psbQ*, *psbR*, *psbS*, *psbT* and *psbW* for the subunits of photosystem II, which were commonly present in the nuclear genomes of higher plants,^{10,11} were not identified in the *Synechocystis* genome.

3.4.3. Transposases

A notable feature regarding the gene organization of the genome was that a total of 99 ORFs, which showed significant similarity to putative bacterial transposases, were found spread all over the genome (see Table 1). These ORFs could be classified into 6 groups on the basis of similarity, and each of them appeared to be located within a stretch which constitutes an IS-like element. Interestingly, only 26 of them seemed to hold the coding capacity of functional transposases with intact lengths. The remaining ORFs have apparently been disrupted by mutations such as frame-shift and deletion and by insertion of other IS-like elements, as judged by sequence similarity. The presence of a large number of intact and disrupted IS-like elements strongly suggests that rearrangement of the genome frequently occurred during and after establishment of this ancient microorganism. Detailed structural features of these transposases and the corresponding IS-like elements will be published elsewhere.

3.4.4. Eukaryote-type genes

We previously reported that the *Synechocystis* genome harbored the genes for proteins containing typical Trp-Asp(WD)-repeats, which were originally reported as conserved repeats specifically contained in the regulatory proteins of eukaryotes.¹² Recently, another example of bacterial genes carrying the WD-repeats was reported.¹³ In the entire genome of *Synechocystis*, 5 genes (sll0163, sll1491, slr1409, slr1410 and slr0143) were found to contain the typical repeats. Gene disruption experiments are currently underway to elucidate the functional role of these genes. Other eukaryote-type

genes identified so far are slr1106 (prohibitin), slr1251 (cyclophilin-type peptidyl-prolyl cis-trans isomerase), sll1540 (dolichol phosphate mannose synthase, yeast), slr1975 (renin-binding protein, mammalian), slr1705 (aspartoacylase, human), ssl2296 (pterin-4a-carbinolamine dehydratase, vertebrate), slr0813 (ceramide glucosyltransferase, human), sll0045 (sucrose phosphate synthase, plant), sll0626 (meiosis-specific Lim17, plant), and slr0473 (phytochrome, plant). The phylogenetical aspect between cyanobacteria and plant will also be discussed elsewhere, as a considerable number of protein and tRNA genes with significant similarity to plant nuclear and plastid genes were predicted in the *Synechocystis* genome.

The data presented in this paper and additional information on the *Synechocystis* genome are provided in Cyanobase (<http://www.kazusa.or.jp/cyano/cyano.html>).

Acknowledgments: We thank Dr. M. Takanami for his support and encouragement to carry out this project, and Dr. K. Isono for valuable discussion on GeneMark analysis. This work was supported by the Kazusa DNA Research Institute Foundation.

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Table 1. List of open reading frames with known or predicted function.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
Amino acid biosynthesis							
Aromatic amino acid family							
slr0444	2,088,680	2,090,023	447	X75325	100.0	3-phosphoshikimate 1-carboxyvinyltransferase	
slr2130	1,643,682	1,644,767	361	Z19601	34.8	3-dehydroquinate synthase	<i>aroA</i>
slr1747	922,637	921,549	362	X67516	100.0	chorismate synthase	<i>aroB</i>
slr1559	3,367,417	3,368,289	290	D84432	21.8	shikimate 5-dehydrogenase	<i>aroC</i>
slr0109#	2,966,537	2,966,154	127	M32278	33.5	chorismate mutase	<i>aroE</i>
slr1669	260,271	259,702	189	X63560	30.3	shikimate kinase	<i>aroH</i>
slr1112	903,606	903,148	152	U32724	40.1	carbonic 3-dehydroquinase	<i>aroK</i>
slr0652	3,319,281	3,320,051	256	X61207	42.5	phosphorybosilformimino-5-amino- phosphorybosil-4-imidazoleboxamideisomerase	<i>aroQ</i>
slr0500#	2,906,797	2,907,429	210	L10036	79.6	imidazoleglycerol-phosphate dehydratase	<i>hisB</i>
slr10084#	2,879,771	2,879,286	161	X03416	19.5	imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase	<i>hisB</i>
slr1713	970,820	969,762	352	M80245	10.1	histidinol-phosphate aminotransferase	<i>hisC</i>
slr1958	1,412,098	1,410,995	367	D14440	24.0	histidinol phosphate aminotransferase	<i>hisC</i>
slr0682	420,502	421,731	409	M90760	11.6	histidinol dehydrogenase	<i>hisD</i>
slr1848	555,642	556,946	434	M90760	27.5	histidinol dehydrogenase	<i>hisD</i>
slr1893	1,772,243	1,771,458	261	X61207	52.5	cyclase	<i>hisF</i>
slr0900#	3,233,809	3,233,177	210	M90760	17.2	ATP phosphoribosyltransferase	<i>hisG</i>
slr0084#	2,890,566	2,891,198	210	U30821	51.8	<i>N</i> -acetyl-glutamate-gamma-semialdehyde dehydrogenase	<i>hisH</i>
slr0608	3,569,627	3,570,319	230	M90760	35.9	phosphoribosyl-ATP pyrophosphohydrolase:phosphoribosyl-AMP cyclohydrolase	<i>hisI</i>
slr1662	271,369	270,476	297	M73971	20.4	chorismate mutase / prephenate dehydratase	
slr0966	326,150	326,944	264	U18993	54.2	tryptophan synthase alpha chain	<i>trpA</i>
slr0543#	3,213,272	3,214,510	412	L14596	99.8	tryptophan synthase beta subunit	<i>trpB</i>
slr0546#	3,240,181	3,241,068	295	U18770	46.7	indole-3-glycerol phosphate synthase	<i>trpC</i>
slr1867	1,206,947	1,207,993	348	X17149	31.5	anthranilate phosphoribosyltransferase	<i>trpD</i>
slr0738	127,186	128,712	508	D00399	31.4	anthranilate synthetase alpha-subunit	<i>trpE</i>
slr1979	1,800,387	1,801,844	485	M34053	23.5	anthranilate synthetase component I	<i>trpE</i>
slr0356	2,155,172	2,154,516	218	M34485	16.2	5'-phosphoribosyl anthranilate isomerase	<i>trpF</i>
slr0055#	2,577,552	2,578,043	163	U30821	57.5	anthranilate synthetase component II	<i>trpG</i>
slr2081	1,539,677	1,540,516	279	X78413	13.5	prephenate dehydrogenase	<i>tyrA</i>
Aspartate family							
slr0549#	3,248,484	3,249,326	280	D49540	34.9	aspartate beta-semialdehyde dehydrogenase	<i>asd</i>
slr0402#	2,559,989	2,558,820	389	M59430	43.9	aspartate aminotransferase	<i>aspC</i>
slr0006#	2,495,389	2,494,205	394	M59430	12.3	aspartate aminotransferase	<i>aspC</i>
slr0366#	3,160,717	3,161,886	389	D50624	14.4	aspartate aminotransferase	<i>aspC</i>
slr0550#	3,249,386	3,250,291	301	Z68126	50.4	dihydrodipicolinate synthase	<i>dapA</i>
slr1058	77,407	76,580	275	L47709	34.6	dihydrodipicolinate reductase	<i>dapB</i>
slr1665	3,471,003	3,471,842	279	U00077	29.0	diaminopimelate epimerase	<i>dapF</i>
slr0212#	2,751,026	2,754,613	1195	U00006	13.8	5-methyltetrahydrofolate--homocysteine methyltransferase	<i>metH</i>
slr0455#	2,627,874	2,626,573	433	M23217	34.2	homoserine dehydrogenase	<i>thrA</i>
slr1760	1,236,056	1,235,136	306	Y00522	52.4	homoserine kinase	<i>thrB</i>
slr1688	1,304,596	1,303,295	433	Z29562	15.0	threonine synthase	<i>thrC</i>
slr1172	1,874,846	1,873,698	382	X04603	48.4	threonine synthase	<i>thrC</i>
Branched chain family							
slr2072	911,357	912,883	508	U40630	62.5	L-threonine deaminase	
slr1981	1,558,127	1,556,475	550	X98092	91.9	acetolactate synthase	<i>ilvA</i>
slr1363	3,318,804	3,317,701	367	L03181	58.2	ketol-acid reductoisomerase	<i>ilvB</i>
slr0452	3,498,903	3,500,588	561	X87611	41.8	dihydroxyacid dehydratase	<i>ilvD</i>
slr0032#	3,156,760	3,157,677	305	M32253	19.7	branched-chain amino acid aminotransferase	<i>ilvE</i>
slr2088	1,548,873	1,550,738	621	M75906	72.5	acetohydroxy acid synthase	<i>ilvG</i>
slr0065#	2,575,910	2,575,344	188	U38804	65.1	acetolactate synthase	<i>ilvN</i>
slr0186#	2,338,636	2,340,237	533	Z46907	78.4	2-isopropylmalate synthase	<i>leuA</i>
slr1564	1,961,079	1,959,436	547	Z46907	9.1	alpha-isopropylmalate synthase	<i>leuA</i>
slr1517	1,608,232	1,609,320	362	M75903	74.0	3-isopropylmalate dehydrogenase	<i>leuB</i>
slr1470	3,407,822	3,406,416	468	U32936	80.2	3-isopropylmalate dehydratase	<i>leuC</i>
slr1444	1,890,474	1,889,872	200	X02528	24.0	3-isopropylmalate dehydratase	<i>leuD</i>
slr0504#	3,207,103	3,205,694	469	L09228	29.8	diaminopimelate decarboxylase	<i>lysA</i>
Glutamate family / Nitrogen assimilation							
slr0100#	2,982,190	2,981,009	393	X74289	27.1	<i>N</i> -acyl-L-amino acid amidohydrolase	<i>ama</i>
slr1898	848,074	848,967	297	M94625	59.2	<i>N</i> -acetylglutamate kinase	<i>argB</i>
slr0080#	2,890,320	2,889,265	351	X52834	36.0	<i>N</i> -acetyl-gamma-glutamyl-phosphate reductase	<i>argC</i>
slr1022	640,737	642,026	429	X78854	70.9	<i>N</i> -acetylmethionine aminotransferase	<i>argD</i>
slr0902#	3,227,266	3,226,340	308	Z26919	42.3	ornithine carbamoyltransferase chain f	<i>argF</i>
slr0585	3,533,844	3,535,046	400	Z49111	42.7	argininosuccinate synthetase	<i>argG</i>
slr1133	783,379	784,764	461	U13259	37.4	L-argininosuccinate lyase	<i>argH</i>
slr1883	1,792,676	1,791,417	419	L06036	32.4	ornithine acetyltransferase	<i>argJ</i>
slr0899#	2,770,857	2,771,306	149	M17891	29.5	cyanate lyase	<i>cynS</i>
slr0710#	3,112,516	3,113,802	428	X77454	100.0	glutamate dehydrogenase (NADP ⁺)	<i>gdhA</i>
slr1756	531,446	532,867	473	X69199	96.6	glutamate-ammonia ligase	<i>glnA</i>
slr0707	2,152,548	2,152,291	85	M62447	86.9	nitrogen regulatory protein P-II	<i>glnB</i>
slr0288	2,128,767	2,130,941	724	X76719	99.6	glutamate-ammonia ligase	<i>glnN</i>
slr1502	482,320	477,668	1550	X80485	100.0	glutamate synthase (ferredoxin)	<i>gltB</i>
slr1499	3,358,862	3,354,192	1556	D78371	100.0	ferredoxin-dependent glutamate synthase	<i>gltD</i>
slr1027	221,463	219,979	494	D85230	82.4	NADH-glutamate synthase small subunit	<i>narB</i>
slr1454	1,004,777	1,002,633	714	X89445	65.0	nitrate reductase	<i>nirA</i>
slr0898#	2,769,125	2,770,633	502	D31732	72.3	ferredoxin-nitrite reductase	<i>proA</i>
slr0373#	2,710,385	2,709,084	433	X86778	35.7	gamma-glutamyl phosphate reductase	

Table 1. Continued.

ORF No.	Initiation	Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll0461#	2,607,357	2,606,095	420	X82929	14.0	gamma-glutamyl phosphate reductase	
sll2035	571,440	572,567	375	D29973	33.2	glutamate 5-kinase	<i>proA</i>
sll0661	3,338,682	3,339,485	267	J01665	36.3	pyrroline carboxylate reductase	<i>proB</i>
Serine family / Sulfur assimilation							
sll0676	414,871	415,404	177	M86936	39.6	adenylylsulfate 3'-phosphotransferase	<i>cysC</i>
sll1348	1,743,443	1,744,192	249	D13777	99.1	serine acetyltransferase	<i>cysE</i>
sll1791	257,426	258,175	249	M84476	63.9	3'-phosphoadenosine-5'-phosphosulfate sulfotransferase	<i>cysH</i>
sll1842	960,099	961,094	331	X81698	54.3	cysteine synthase	<i>cysK</i>
sll0712	101,771	100,794	325	U19395	48.2	cysteine synthase	<i>cysM</i>
sll1931	604,726	603,443	427	Z38002	57.1	serine hydroxymethyltransferase	<i>gyrA</i>
sll1165	1,931,139	1,932,311	390	U07353	21.7	sulfate adenylyltransferase	<i>metJ</i>
sll1908	1,434,640	1,432,976	554	L47648	33.9	phosphoglycerate dehydrogenase	<i>serA</i>
sll0963	321,699	323,606	635	Z11755	58.5	ferredoxin-sulfite reductase	<i>sir</i>
Biosynthesis of cofactors, prosthetic groups, and carriers							
Biotin							
sll1364	1,107,242	1,108,330	362	D14084	27.4	biotin synthetase	<i>bioB</i>
sll0917#	2,791,688	2,793,001	437	U10482	38.4	7-keto-8-aminopalargonic acid synthetase	<i>bioF</i>
sll1365	1,108,314	1,108,967	217	M29292	12.6	BioY protein	<i>bioY</i>
sll1655	280,951	280,127	274	L47709	11.9	biotin [acetyl-CoA-carboxylase] ligase	<i>birA</i>
Carotenoid							
sll1255	1,399,298	1,400,311	337	X69172	100.0	phytoene synthase	<i> crtB</i>
sll1254	1,397,819	1,399,237	472	X62574	100.0	phytoene desaturase	<i>crtD</i>
sll0611	3,573,271	772	323	M37111	59.6	geranylgeranyl pyrophosphate synthase	<i>crtE</i>
sll0739	128,802	129,710	302	U30821	58.4	geranylgeranyl pyrophosphate synthase	<i>crtE</i>
sll0088#	2,894,946	2,896,574	542	M87280	4.6	phytoene dehydrogenase	<i>crtE</i>
sll0940	2,004,626	2,006,095	489	X38550	60.5	zeta-carotene desaturase precursor	<i>crtQ</i>
sll1125	86,159	87,418	419	D90087	17.1	zeaxanthin glucosyl transferase	<i>crtX</i>
Cobalamin, heme, phycobilin and porphyrin							
ssr2049	1,042,306	1,042,557	83	Z11165	20.5	protochlorophyllide reductase 57 kD subunit	<i>bchB</i>
sll0905#	2,777,447	2,778,946	499	Z11165	12.7	Mg-protoporphyrin IX monomethyl ester oxidative cyclase 66 kD subunit	<i>bchE</i>
sll1055	508,515	512,510	1331	U29131	97.9	Mg-chelatase subunit	<i>bchH</i>
sll1777	232,008	234,038	676	X70810	14.9	Mg chelatase subunit	<i>bchI/bchD</i>
sll1501	486,247	484,799	482	L12006	22.8	cobyric acid a,c-diamide synthase	<i>cblA</i>
sll1925	2,213,707	2,214,735	342	L12006	22.1	CbiB protein	<i>cblB</i>
sll0916	2,002,894	2,002,241	217	L12006	12.2	precorrin isomerase	<i>cblC</i>
sll1538	976,748	977,842	364	L12006	8.3	CbiD protein	<i>cblD</i>
sll0099#	2,983,566	2,982,289	425	M59301	10.3	precorrin-6y methylase	<i>cblE</i>
sll0239	141,648	142,442	264	L12006	30.8	precorrin methylase	<i>cblH</i>
sll0969	331,144	333,027	627	L12006	12.4	precorrin methylase	<i>cblL</i>
sll1879	1,233,784	1,234,512	242	L12006	10.9	S-adenosyl-methionine: precorrin-2 methyltransferase	<i>cblM</i>
sll0383#	2,693,724	2,693,080	214	U00085	16.7	CbiM protein	<i>cblP</i>
sll0618#	2,954,506	2,956,089	527	L12006	28.9	cobyric acid synthase	<i>cblT</i>
sll1368	1,119,826	1,120,509	227	L12006	12.1	precorrin decarbocylase	<i>chIL</i>
sll0772#	2,395,103	2,396,629	508	X04465	73.2	protochlorophyllide reductase ChlB subunit	<i>chIB</i>
sll1030	658,262	659,335	357	U35144	98.3	Mg-protoporphyrin IX	<i>chII</i>
sll0749	3,415,989	3,416,924	311	D10474	99.8	light-independent protochlorophyllide reductase iron protein ChlL	<i>chIL</i>
sll0525#	3,182,315	3,183,007	230	L47126	99.7	Mg-protoporphyrin IX methyl transferase	<i>chIM</i>
sll0750	3,417,442	3,418,851	469	D10474	100.0	protochlorophyllide reductase subunit ChlN	<i>chIN</i>
sll0260	1,507,481	1,508,092	203	M62866	42.7	cob(I)alamin adenosyltransferase	<i>cobA</i>
sll0794**	3,058,328	3,057,216	370	U33192	7.1	mercuric resistance operon regulatory protein/precorrin isomerase	<i>merR/cobH</i>
sll1211	893,984	897,262	1092	M62866	36.8	CobN protein	<i>cobN</i>
sll1180	1,777,537	1,776,983	184	M62866	23.7	CobN protein	<i>cobN</i>
sll0216#	2,508,477	2,509,034	185	L12006	14.8	cobinamide kinase / cobinamide phosphate guanylyltransferase	<i>cobU</i>
sll0502#	2,911,990	2,913,048	352	M62866	41.8	CobW protein	<i>cobW</i>
sll0378#	2,701,735	2,700,944	263	M62881	42.5	uroporphyrin-III C-methyltransferase	<i>cysG</i>
sll0056#	2,578,187	2,579,161	324	U19382	59.9	chlorophyll synthase 33 kD subunit	<i>G4</i>
sll1808	1,284,552	1,285,943	463	M84218	92.2	transfer RNA-Gln reductase	<i>hemA</i>
sll1994	1,643,271	1,642,288	327	X70434	83.8	porphobilinogen synthase	<i>hemB</i>
sll1887	1,247,192	1,248,154	320	X04808	42.8	porphobilinogen deaminase	<i>hemC</i>
sll0166#	2,319,627	2,318,011	538	X70966	20.9	uroporphyrin-III synthase	<i>hemD</i>
sll0536#	3,198,731	3,199,783	350	Z11705	76.0	uroporphyrinogen decarboxylase	<i>hemE</i>
sll1185	316,904	315,882	340	X75413	41.5	coproporphyrinogen III oxidase	<i>hemF</i>
sll0839#	2,849,096	2,850,259	387	D26106	47.3	ferrochelatase	<i>hemH</i>
sll1237	1,653,296	1,652,397	299	Z49782	11.6	protoporphyrinogen oxidase	<i>hemK</i>
sll0017#	2,473,189	2,471,954	411	X53695	82.4	glutamate-1-semialdehyde 2,1- aminomutase	<i>hemL</i>
sll1876	1,804,142	1,802,742	466	D16509	42.6	oxygen independent coproporphyrinogen III oxidase	<i>hemN</i>
sll1917	770,291	769,053	412	X82073	6.6	oxygen independent coproporphyrinogen III oxidase	<i>ho</i>
sll1184	317,849	317,127	240	U38804	55.3	heme oxygenase	<i>ho</i>
sll1875	1,805,155	1,804,403	250	U38804	39.8	heme oxygenase	<i>ho</i>
sll0506#	2,914,828	2,915,796	322	L37783	98.2	protochlorophyllide oxido-reductase	<i>pcr</i>
sll1099	195,685	196,305	206	M68935	20.8	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	<i>ubiX</i>
sll1091	1,935,386	1,934,307	359	X97972	100.0	391 aa (43 kD) bacteriochlorophyll synthase subunit	
sll1784	243,158	244,144	328	M81681	7.6	biliverdin reductase	
sll1906	1,440,941	1,439,487	484	Z11165	5.1	428 aa (44.5 kD) bacteriochlorophyll synthase subunit	
Folic acid							
sll1612	1,462,101	1,460,815	428	L04520	15.3	folyl-polyglutamate synthetase	<i>folC</i>

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll0753#	2,418,461	2,417,577	294	U32689	41.4	methylenetetrahydrofolate dehydrogenase /methylenetetrahydrofolate cyclohydrolase	<i>folD</i>
sll0426#	2,718,050	2,718,754	234	M58364	51.1	GTP cyclohydrolase I	<i>folE</i>
sll1093	189,128	189,715	195	U00069	25.6	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	<i>folK</i>
sll2026	771,651	772,520	289	D26185	37.6	dihydropteroate pyrophosphorylase	<i>folP</i>
Lipoate							
sll1598	462,809	463,678	289	L24124	47.2	lipoic acid synthetase	<i>lipA</i>
sll0868	1,151,033	1,150,122	303	L24124	35.8	lipoic acid synthetase	<i>lipA</i>
sll0994	2,263,827	2,264,510	227	L07636	11.3	LipB protein	<i>lipB</i>
Menaquinone and ubiquinone							
sll1518	1,609,826	1,610,749	307	U00074	7.8	menaquinone biosynthesis protein	<i>menA</i>
sll1127	1,053,754	1,052,927	275	U32724	61.4	naphthoate synthase	<i>menB</i>
sll0603#	2,671,902	2,670,115	595	M74538	14.8	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	<i>menD</i>
sll0492#	2,623,414	2,624,907	497	U51132	4.7	O-succinylbenzoic acid-CoA ligase	<i>menE</i>
sll0926#	3,228,712	3,229,590	292	X69522	18.9	4-hydroxybenzoate-octaprenyl transferase	<i>ubiA</i>
sll1300	301,110	302,354	414	D90281	14.3	UbiH protein	<i>ubiH</i>
Molybdopterin							
sll0901#	2,772,470	2,773,453	327	Z48047	20.7	molybdenum cofactor biosynthesis protein A	<i>moaA</i>
sll0902#	2,773,454	2,774,497	347	X92502	12.6	molybdenum cofactor biosynthesis protein C	<i>moaC</i>
sll0903#	2,774,732	2,775,169	145	X70420	23.0	molybdopterin (MPT) converting factor, subunit 2	<i>moaE</i>
sll0900#	2,771,322	2,772,494	390	U34309	9.0	molybdopterin biosynthesis MoeA	<i>moeA</i>
sll1536	2,041,458	2,040,280	392	M21151	18.2	molybdopterin biosynthesis MoeB protein	<i>moeB</i>
Nicotinate and nicotinamide							
sll0936	1,998,460	1,999,347	295	U20508	29.0	nicotinate-nucleotide pyrophosphorylase	<i>nadC</i>
sll1691	1,983,982	1,985,658	558	X59399	27.8	NH ₃ ⁺ -dependent NAD ⁺ synthetase	<i>nadE</i>
Pantothenate							
sll0250	1,515,338	1,514,130	402	U32722	25.6	pantothenate metabolism flavoprotein	<i>dfp</i>
sll0526#	3,183,014	3,183,796	260	L17086	32.0	alpha-ketopantoate hydroxymethyl transferase	<i>panB</i>
sll1249*	1,742,375	1,740,834	513	U44896	43.9	pantothenate synthetase/cytidylate kinase	<i>panC/ky</i>
sll0892#	2,795,375	2,794,938	145	L47709	30.2	aspartate 1-decarboxylase	<i>panD</i>
Pyridoxine							
sll0660#	3,118,090	3,117,041	349	M68521	18.0	pyridoxal phosphate biosynthetic protein PdxA	<i>pdxA</i>
sll1440	1,897,561	1,896,869	230	M29288	40.6	pyridoxamine 5'-phosphate oxidase	<i>pdxH</i>
sll1779	237,660	238,325	221	M74526	51.9	pyridoxal phosphate biosynthetic protein PdxJ	<i>pdxJ</i>
Quinolinate							
sll0622	3,346,817	3,345,861	318	M37111	66.7	quinolinate synthetase	<i>nadA</i>
sll0631	3,321,736	3,320,075	553	U17232	27.9	L-aspartate oxidase	<i>nadB</i>
Riboflavin							
sll1894	1,770,418	1,768,748	556	X51510	39.3	GTP cyclohydrolase II	<i>ribA</i>
sll3000#	2,280,947	2,280,267	226	L27202	27.8	riboflavin synthase alpha chain	<i>ribC</i>
sll0066#	2,594,055	2,595,161	368	U27202	27.2	riboflavin biosynthesis protein	<i>ribG</i>
sll1282	1,095,143	1,094,649	164	U27202	44.0	riboflavin synthase beta subunit	<i>ribH</i>
Thiamin							
sll0118#	2,999,181	3,000,560	459	U26178	55.8	ThiC protein	<i>thiC</i>
sll0635	444,944	443,913	343	X78824	16.7	thiamin biosynthetic bifunctional enzyme	<i>thiE</i>
sll0633#	2,653,153	2,655,123	656	Z67753	22.3	ThiG protein	<i>thiG</i>
Thioredoxin, glutaredoxin, and glutathione							
sll1269	1,859,816	1,861,372	518	M28722	8.9	gamma-glutamyltranspeptidase	<i>ggt</i>
ssr2061	1,050,812	1,051,078	88	U00039	52.9	glutaredoxin 3	<i>grxC</i>
sll1562	3,369,699	3,370,028	109	X77150	22.4	glutaredoxin	<i>grxC</i>
sll1238	1,051,159	1,052,121	320	U14408	60.4	glutathione synthetase	<i>gstB</i>
sll0067#	2,574,203	2,573,649	184	D17673	16.1	glutathione S-transferase	<i>gstI</i>
sll1545	3,468,696	3,467,881	271	L05915	11.1	glutathione S-transferase	<i>gstL</i>
sll1057	77,874	77,494	126	X80888	24.0	thioredoxin M	<i>trx</i>
sll0623#	2,961,120	2,961,443	107	X80486	100.0	thioredoxin	<i>trxA</i>
sll1139	794,362	794,691	109	M22997	53.4	thioredoxin	<i>trxA</i>
sll0233#	2,537,521	2,537,838	105	X87899	43.2	thioredoxin M	<i>trzM</i>
sll1992	1,436,699	1,437,163	154	X89866	34.1	glutathione peroxidase	
sll1171	1,938,985	1,939,494	169	Z38061	46.9	glutathione peroxidase	
Others							
ssl2296	1,393,906	1,393,616	96	L41559	40.5	pterin-4a-carbinolamine dehydratase	<i>dcoH</i>
sll1706	733,401	734,432	343	Z18277	7.3	dihydroflavonol 4-reductase	<i>dfrA</i>
Cell envelope							
Membranes, lipoproteins, and porins							
sll0819	1,707,317	1,708,876	519	U32825	5.8	apolipoprotein N-acyltransferase	<i>int</i>
sll1187	315,106	314,255	283	U35773	26.1	prolipoprotein diacylglycerol transferase	<i>lgt</i>
sll0993	2,260,429	2,262,576	715	L07869	5.7	lipoprotein NlpD	<i>nlpD</i>
ssl3177	1,012,888	1,012,616	90	U32797	20.8	rare lipoprotein A	<i>repA</i>
sll0423#	2,706,733	2,707,698	321	U32797	14.0	rare lipoprotein A	<i>rlpA</i>
sll0495#	2,628,002	2,628,742	246	L22883	18.6	lipopeptide antibiotics iturin A biosynthesis protein	
Murein sacculus and peptidoglycan							
sll0827#	2,831,881	2,833,083	400	M19142	20.4	alanine racemase	<i>alr</i>
sll1910	613,801	614,817	338	D10388	16.4	N-acetyl muramoyl-L-alanine amidase	<i>amiA</i>
sll0891	1,159,029	1,160,804	591	D10388	5.1	N-acetyl muramoyl-L-alanine amidase	<i>amiA</i>
sll1744	1,332,429	1,334,378	649	D10388	7.9	N-acetyl muramoyl-L-alanine amidase	<i>amiA</i>
sll0804	1,684,928	1,685,872	314	X64790	10.0	D-alanyl-D-alanine carboxypeptidase	<i>dacB</i>
sll0646#	2,674,736	2,676,196	486	Z34883	6.7	penicillin-binding protein 4	<i>dacB</i>

Table 1. Continued.

ORF No.	Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll1874	1,224,777	1,225,841	354	U00457	31.3	D-alanine:D-alanine ligase-related protein	<i>ddlA</i>
sll1833	624,123	622,300	607	X59628	13.4	penicillin-binding protein	<i>ftsI</i>
sll0899#	3,235,186	3,233,816	456	Z50023	28.9	UDP-N-acetylglucosamine pyrophosphorylase	<i>glmU</i>
sll0191#	2,722,431	2,724,038	535	M87645	5.1	amidase enhancer	<i>lytB</i>
sll0016#	2,474,796	2,473,645	383	U32224	8.9	membrane-bound lytic transglycosylase A	<i>mltA</i>
sll0657#	3,123,068	3,121,971	365	Z15056	26.3	phospho-N-acetylumuramoyl-pentapeptide-transferase	<i>mraY</i>
sll1434	1,905,977	1,904,025	650	U00086	14.9	penicillin-binding protein 1B	<i>mrcA</i>
sll1710	739,682	741,931	749	U00086	8.0	penicillin-binding protein 1B	<i>mrcB</i>
sll1267	1,858,609	1,859,790	393	U30821	34.2	rod-shape-determining protein	<i>mrdB</i>
sll1423	3,279,390	3,280,907	505	U00081	12.3	UDP-N-acetylumuramate-alanine ligase	<i>mrcC</i>
sll2010	1,258,263	1,256,905	452	Z15056	16.5	UDP-N-acetylumuramoylalanine-D-glutamate ligase	<i>mrdC</i>
sll0528#	3,184,733	3,186,250	505	Z15056	25.7	UDP-MurNac-tripeptid synthetase	<i>mreE</i>
sll1351	1,749,146	1,750,510	454	X62437	99.6	UDP-N-acetylumuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase	<i>mrfF</i>
sll1656	3,458,282	3,459,397	371	U00081	16.2	UDP-N-acetylglucosamine--N-acetylumuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	<i>mugG</i>
sll1746	1,334,522	1,335,361	279	D29627	29.6	glutamate racemase	<i>murl</i>
sll0017#	2,486,607	2,487,923	438	Z11835	40.5	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	<i>muzZ</i>
sll1167	1,884,573	1,883,329	414	L10629	5.6	penicillin-binding protein 4	<i>pbp</i>
sll0002#	2,503,878	2,501,221	885	M97208	11.4	penicillin-binding protein 1A	<i>ponA</i>
sll0534#	3,193,999	3,196,542	847	U14003	5.2	soluble lytic transglycosylase	<i>slt</i>
sll1678	244,708	244,160	182	L09228	31.3	spore maturation protein A	
sll1677	245,436	244,783	217	L09228	33.4	spore maturation protein B	
sll1708	734,985	736,220	411	M15686	6.9	lysostaphin	
sll1924	2,212,505	2,213,707	400	X05109	9.2	D-alanyl-D-alanine carboxypeptidase	
Surface polysaccharides, lipopolysaccharides and antigens							
sll1875	1,225,928	1,226,566	212	M61753	12.1	exopolysaccharide synthesis protein ExoD	<i>exoD</i>
sll0083#	2,880,549	2,879,965	194	U32590	25.1	phosphoheptose isomerase	<i>gmaH</i>
sll1724	950,536	949,397	379	X90711	6.2	LPS glycosyltransferase IcsA	<i>icsA</i>
sll0847#	2,867,372	2,867,851	159	M60670	44.0	KdtB protein	<i>kdtB</i>
sll0379#	2,699,145	2,698,258	295	Z25462	30.2	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine o-acyltransferase	<i>lpxA</i>
sll0015#	2,483,643	2,484,827	394	U38802	100.0	lipid A disaccharide synthase	<i>lpxB</i>
sll1508	468,666	467,836	276	U00081	22.1	UDP-3-O-acyl N-acetylglucosamine deacetylase	<i>lpxC</i>
sll0207#	2,513,648	2,512,467	393	Y00459	39.1	glucose-1-phosphate thymidylyltransferase	<i>rfaA</i>
sll0809	1,689,948	1,690,934	328	Z49239	62.5	dTDP-glucose 4,6-dehydratase	<i>rfaB</i>
sll0836#	2,843,714	2,844,742	342	L23941	53.0	dTDP-glucose 4,6-dehydratase	<i>rfaB</i>
sll0985	355,424	355,993	189	L14842	24.6	dTDP-6-deoxy-L-mannose-dehydrogenase	<i>rfaC</i>
sll1933	2,227,829	2,228,377	182	X56793	56.9	dTDP-4-dehydrorhamnose 3,5-epimerase	<i>rfaD</i>
sll1395	56,511	55,669	280	U09876	36.2	dTDP-6-deoxy-L-mannose-dehydrogenase	<i>rfaE</i>
sll1615	360,030	361,166	378	X59554	26.7	perosamine synthetase	<i>rfaF</i>
sll0983	353,552	354,322	256	L33181	74.1	alpha-D-glucose-1-phosphate cytidylyltransferase	<i>rfaG</i>
sll0984	354,323	355,405	360	L01777	41.7	CDP-glucose 4,6-dehydratase	<i>rfaG</i>
sll1457	997,806	996,850	318	X71970	22.7	RfbJ protein	<i>rfaJ</i>
sll1370	1,846,898	1,845,795	367	D43637	21.8	GDP-mannose pyrophosphorylase	<i>rfaM</i>
sll1535	2,043,838	2,043,107	243	U35434	33.7	galactosyl-1-phosphate transferase	<i>rfaP</i>
sll1064	367,807	368,910	367	D43637	12.6	Mannosyltransferase B	<i>rfaU</i>
sll0344#	2,429,543	2,430,964	473	X61917	8.9	mannosyl transferase	<i>rfaW</i>
sll0380#	2,698,248	2,697,151	365	X61917	11.9	mannosyl transferase	<i>rfaW</i>
sll1118	67,606	68,361	251	M87049	12.2	UDP-N-acetyl-D-mannosaminuronic acid transferase	<i>rffM</i>
sll1271	1,863,247	1,863,987	246	M95047	12.1	UDP-N-acetyl-D-mannosaminuronic acid transferase	<i>rffM</i>
sll2116	1,629,604	1,630,434	276	X73124	8.4	spore coat polysaccharide biosynthesis protein SpsA	<i>spsA</i>
sll2114	1,626,981	1,628,018	345	X73124	28.8	spore coat polysaccharide biosynthesis protein SpsC	<i>spsC</i>
sll1072	375,470	376,432	320	U18320	36.6	GDP-D-mannose dehydratase	<i>yefA</i>
Surface structures							
sll0163	2,204,476	2,205,372	298	M32066	27.4	pilin biogenesis protein	<i>pilC</i>
sll2043	583,680	584,696	338	U38702	9.9	adhesion protein	
Cellular processes							
Cell division							
sll1604	471,080	472,930	616	D26185	48.1	cell division protein FtsH	<i>ftsH</i>
sll1390	695,975	697,972	665	M83138	35.3	cell division protein FtsH	<i>ftsH</i>
sll1463	991,603	989,717	628	D26185	40.1	cell division protein FtsH	<i>ftsH</i>
sll0228#	2,529,009	2,530,892	627	D26185	40.5	cell division protein FtsH	<i>ftsH</i>
sll2102	1,570,209	1,571,723	504	X04398	22.8	cell division protein FtsY	<i>ftsY</i>
sll1633	1,014,337	1,013,045	430	U14408	64.4	cell division FtsZ protein	<i>ftsZ</i>
sll0905	2,028,744	2,028,157	195	L08793	13.3	maf protein	<i>maf</i>
sll0288#	3,008,966	3,008,508	152	M95582	19.1	septum site-determining protein MinC	<i>minC</i>
sll0289#	3,008,431	3,007,631	266	M95582	49.0	septum site-determining protein MinD	<i>minD</i>
sll0546#	3,007,573	3,007,280	97	J03153	18.7	septum site-determining protein MinE	<i>minE</i>
sll1223	1,025,423	1,026,442	339	U00081	21.3	cell division inhibitor	
sll0374#	2,375,539	2,377,044	501	U37587	8.2	cell division cycle protein	
Cell killing							
sll1180	1,853,742	1,850,707	1011	X61112	25.0	HlyB family	<i>hlyB</i>
sll1651	3,449,928	3,452,129	733	L12148	14.0	haemolysin secretion ATP-binding protein	<i>hlyB</i>
sll1181	1,850,550	1,848,799	583	X14199	6.1	HlyD family of secretion proteins	<i>hlyD</i>
sll1951	1,427,651	1,422,426	1741	U13767	2.0	hemolysin	
sll1254	1,731,206	1,730,166	346	U00072	13.3	hemolysin	
sll0260	2,127,589	2,126,243	448	X73141	11.4	hemolysin	
sll0721	3,447,386	3,443,514	1290	M27399	2.7	leukotoxin (LtA)	

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll0720	3,448,158	3,447,715	147	X73117	15.5	apxIC gene product hemolysin activation protein	
Chaperones							
sll0897#	3,238,258	3,237,125	377	L08110	36.3	DnaJ protein	<i>dnaJ</i>
sll1666	265,938	265,414	174	L08110	14.2	DnaJ protein	<i>dnaJ</i>
sll1933	600,833	599,910	307	D29968	18.2	DnaJ protein	<i>dnaJ</i>
sll0093#	2,900,980	2,901,978	332	D29968	16.0	DnaJ protein	<i>dnaJ</i>
sll1932	603,308	600,942	788	D29968	58.1	DnaK protein	<i>dnaK</i>
sll0170#	2,314,574	2,312,664	636	M57518	100.0	DnaK protein	<i>dnaK</i>
sll0058#	2,588,650	2,586,572	692	D28550	54.7	DnaK protein	<i>dnaK</i>
sll2076	915,721	917,346	541	D12677	99.8	60kD chaperonin 1	<i>groEL</i>
sll0416#	2,540,658	2,539,000	552	M57517	98.6	60kD chaperonin 2	<i>groEL-2</i>
sll2075	915,304	915,624	106	D12677	97.0	10kD chaperonin	<i>groES</i>
sll0057#	2,589,633	2,588,884	249	D28550	37.3	heat shock protein GrpE	<i>grpE</i>
sll0430	3,516,208	3,514,232	658	M38777	12.1	heat shock protein	<i>hspG</i>
Chemotaxis							
sll0322#	2,271,581	2,274,868	1095	X82645	8.1	chemotaxis protein CheA	<i>cheA</i>
sll0073#	2,869,752	2,870,699	315	U28962	10.1	chemotaxis protein CheA	<i>cheA</i>
sll0043#	3,148,420	3,144,212	1402	M57894	6.5	chemotaxis protein CheA	<i>cheA</i>
sll1296	687,334	684,560	924	U30501	8.8	chemotaxis protein CheA	<i>cheA</i>
sll0039#	3,153,314	3,152,955	119	L22036	35.1	chemotaxis protein CheY	<i>cheY</i>
sll0038#	3,154,660	3,153,452	402	M87501	10.6	chemotaxis protein CheY	<i>cheY</i>
sll1044	492,130	494,739	869	L22036	12.8	methyl-accepting chemotaxis protein	<i>mcpA</i>
sll1294	690,252	687,391	953	L22036	10.5	methyl-accepting chemotaxis protein (MCP) homologue	<i>pilJ</i>
sll0042#	3,148,928	3,148,437	163	X61367	27.4	methyl-accepting chemotaxis protein II	<i>kar</i>
sll0041#	3,151,649	3,148,974	891	L22036	13.1	methyl-accepting chemotaxis protein I	<i>tsr</i>
Detoxification							
sll0946	2,012,231	2,012,626	131	M80565	26.5	arsenate reductase	<i>arsC</i>
sll1987	1,546,978	1,544,714	754	M29876	62.3	catalase hpi	<i>katG</i>
sll1516	1,607,353	1,607,952	199	U17612	63.7	superoxide dismutase	<i>sodB</i>
sll1615	1,457,123	1,455,753	456	X62539	33.4	thiophen and furan oxidation protein	<i>thdF</i>
sll0755#	2,416,693	2,416,091	200	Z34917	61.1	thiol-specific antioxidant protein	
Protein and peptide secretion							
sll1531	1,899,700	1,901,148	482	X92071	71.4	signal recognition particle protein	<i>ffh</i>
sll1277	1,868,645	1,871,002	785	X66504	3.6	general secretion pathway protein D	<i>gspD</i>
sll0063#	2,589,851	2,591,869	672	M96172	23.3	general secretion pathway protein E	<i>gspE</i>
sll0079#	2,881,378	2,883,819	813	U18997	8.5	general secretion pathway protein E	<i>gspE</i>
sll0162	2,204,157	2,204,654	165	M32613	19.2	general secretion pathway protein F	<i>gspF</i>
sll1120	74,995	75,804	269	U20255	24.2	type 4 prepilin peptidase	<i>hofD</i>
sll1695	1,296,894	1,296,382	170	L39904	16.3	general secretion pathway protein G	<i>hofG</i>
sll1694	1,297,499	1,296,993	168	L39904	20.4	general secretion pathway protein G	<i>hofG</i>
sll0716	99,199	98,609	196	X81990	47.9	leader peptidase I	<i>lepB</i>
sll1377	672,291	672,947	218	X81990	49.6	leader peptidase I	<i>lepB</i>
sll1366	1,108,967	1,109,452	161	U00079	15.4	lipoprotein signal peptidase	<i>lspA</i>
sll1667	265,316	264,516	266	X53735	9.8	mitochondrial outer membrane 72K protein	<i>mom72</i>
sll0616#	2,650,184	2,647,386	932	U38892	82.5	preprotein translocase SecA subunit	<i>secA</i>
sll0774#	2,400,914	2,402,332	472	U00071	17.1	protein-export membrane protein SecD	<i>secD</i>
sll3335	926,558	926,313	81	D17464	18.8	secretory protein SecE	<i>secE</i>
sll0775#	2,402,393	2,403,340	315	U00071	17.1	protein-export membrane protein SecF	<i>secF</i>
sll1814	833,719	832,391	442	X68056	66.7	preprotein translocase SecY subunit	<i>secY</i>
sll0533#	3,247,816	3,246,401	471	J04180	7.3	trigger factor	<i>tig</i>
sll1456	3,302,812	3,303,339	175	X62666	13.4	general secretion pathway protein G	
Transformation							
sll1929	608,594	606,465	709	L15202	3.3	comE ORF3	<i>comEc</i>
sll0197#	2,727,047	2,728,708	553	L15202	4.2	comE ORF1	
Central intermediary metabolism							
Amino sugars							
sll0220	163,663	161,768	631	U17352	35.0	L-glutamine:D-fructose-6-P amidotransferase	<i>glmS</i>
Phosphorus compounds							
sll1622	2,034,102	2,034,803	233	X64200	32.5	inorganic pyrophosphatase	<i>ppa</i>
sll0290#	3,006,640	3,004,454	728	U16262	31.2	polyphosphate kinase	<i>ppk</i>
sll1546	3,465,289	3,463,667	540	L06129	9.0	exopolyphosphatase	<i>ppx</i>
Polysaccharides and glycoproteins							
sll0518#	2,931,476	2,932,009	177	U38661	17.9	arabinofuranosidase	<i>abfB</i>
sll1176	3,516,539	3,517,858	439	M83556	96.9	ADP-glucose pyrophosphorylase	<i>agg</i>
sll0323#	2,274,868	2,277,996	1042	M57547	8.0	alpha-mannosidase	<i>amsI</i>
sll1540	2,034,123	2,032,951	390	Z54162	11.8	dolichyl-phosphate-mannose synthase	<i>dpm1</i>
sll1943	2,245,636	2,246,631	331	J04184	7.1	dolichol phosphate mannose synthase	<i>dpm1</i>
sll1393	58,815	57,340	491	X95759	18.2	glycogen (starch) synthase	<i>glgA</i>
sll0945	2,266,646	2,265,213	477	Z25795	20.7	glycogen synthase	<i>glgA</i>
sll0158#	2,333,817	2,331,505	770	M31544	72.5	1,4-alpha-glucan branching enzyme	<i>glgB</i>
sll1356	1,075,629	1,073,080	849	J03544	44.9	glycogen phosphorylase	<i>glgP</i>
sll1367	1,117,107	1,119,674	855	M32598	45.5	glycogen phosphorylase	<i>glgP</i>
sll0237	138,295	140,535	746	U18908	24.8	glycogen operon protein GigX	<i>glgX</i>
sll1857	1,194,653	1,196,776	707	U18908	31.7	glycogen operon protein GigX	<i>glgX</i>
sll1676	247,019	245,502	505	L37874	36.7	4-alpha-glucanotransferase	<i>malQ</i>
sll0842	1,360,372	1,358,846	508	M28138	26.8	neopullulanase	<i>nplT</i>
sll1566	1,948,824	1,947,325	499	U15187	18.6	alpha,alpha-trehalose-phosphate synthase	<i>otsA</i>
sll0726	3,433,020	3,431,317	567	L24077	57.6	phosphoglucomutase	<i>pgm</i>

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
slr1830	933,157	934,293	378	S54369	46.8	poly(3-hydroxyalcanoate) synthase	
slr0820	1,709,232	1,710,668	478	X85787	14.4	glucosyltransferase	
slr0897#	2,765,554	2,768,766	1070	M64644	15.7	endo-1,4-beta-glucanase	
Other							
slr1256	1,401,059	1,401,361	100	M36068	75.7	urease gamma subunit	<i>ureA</i>
slr0420	2,096,040	2,095,723	105	X74600	63.1	urease beta subunit	<i>ureB</i>
slr1750	561,170	559,461	569	S69145	73.2	urease alpha subunit	<i>ureC</i>
slr1639	547,278	546,553	241	L03307	14.8	urease accessory protein D	<i>ureD</i>
slr1219	1,019,155	1,019,583	142	M36068	23.2	urease accessory protein E	<i>ureE</i>
slr1899	849,095	849,748	217	M31834	16.4	urease accessory protein F	<i>ureF</i>
slr0643	431,044	430,424	206	L03308	70.0	urease accessory protein G	<i>ureG</i>
slr0784#	3,071,320	3,070,280	346	D11425	27.1	nitrilase	
Energy metabolism							
Amino acids and amines							
slr1234	1,659,788	1,658,511	425	Z50174	53.0	S-adenosylhomocysteine hydrolase	<i>ahcY</i>
slr0573	3,545,133	3,544,207	308	X14693	47.2	carbamate kinase	<i>arcC</i>
slr1683	236,356	234,905	483	X58433	32.0	lysine decarboxylase	<i>ad</i>
slr1498	3,362,006	3,360,732	424	U38804	47.0	carbamoyl-phosphate synthetase subunit A	<i>carA</i>
slr0107#	2,972,095	2,971,475	206	U32799	22.6	4-hydroxy-2-oxoglutarate aldolase	<i>ata</i>
slr0370#	2,369,282	2,370,646	454	M88334	21.5	succinate-semialdehyde dehydrogenase (NADP ⁺)	<i>gabD</i>
slr1641	544,871	543,468	467	U10034	45.3	glutamate decarboxylase	<i>gad</i>
slr0879	1,138,210	1,138,608	132	Z37529	38.1	glycine decarboxylase complex H-protein	<i>gcvH</i>
slr0293	2,134,202	2,137,153	983	X59773	54.1	P protein of glycine cleavage complex	<i>gcvP</i>
slr0171#	2,312,495	2,311,377	372	D82370	37.4	aminomethyltransferase	<i>gcvT</i>
slr1877	1,228,237	1,229,067	276	Z37980	21.0	5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase/isomer	<i>hpcE</i>
slr0657	3,333,244	3,335,046	600	M93419	30.9	aspartate kinase	<i>lysC</i>
slr0229#	2,532,823	2,533,695	290	M84911	18.2	3-hydroxyisobutyrate dehydrogenase	<i>mmsB</i>
slr0090#	2,897,634	2,898,653	339	D31628	12.2	4-hydroxyphenylpyruvic acid dioxygenase (HPD)	<i>ppd</i>
slr1561	1,969,118	1,966,146	990	U05212	12.6	delta-1-pyrroline-5-carboxylate dehydrogenase	<i>putA</i>
slr1312	8,492	10,471	659	Z37540	27.4	arginine decarboxylase	<i>speA</i>
slr0662	3,342,857	3,344,944	695	M31770	27.3	arginine decarboxylase	<i>speA</i>
slr1077	801,206	800,034	390	L15470	14.9	arginine ureohydrolase	<i>speB</i>
slr0228	148,942	148,022	306	M34778	11.2	arginase	
slr1682	237,438	236,356	360	L20916	49.9	alanine dehydrogenase	
slr0938	329,181	328,006	391	X93600	8.4	aspartate transaminase	
slr0422	2,093,508	2,092,519	329	Z34884	10.1	asparaginase	
Glycolate pathway							
slr1349	1,093,590	1,092,925	221	U33322	25.6	phosphoglycolate phosphatase	<i>cbbZp</i>
slr0404#	2,555,439	2,553,961	492	L43490	40.2	glycolate oxidase subunit GlcD	<i>glcD</i>
slr1189	309,418	308,114	434	L43490	8.1	glycolate oxidase subunit GlcE	<i>glcE</i>
slr1831	626,281	624,899	460	L43490	13.5	glycolate oxidase subunit, (Fe-S)protein	<i>glcF</i>
Glycolysis							
slr0018#*	2,471,670	2,470,591	359	U29134	64.8	fructose-1,6-bisphosphate aldolase	<i>cbbA</i>
slr0752	3,420,416	3,421,714	432	L29475	53.3	enolase	<i>eno</i>
slr0952*	2,022,028	2,023,071	347	U33282	79.2	fructose 1,6-bisphosphatase	<i>fba</i>
slr0943*	2,007,850	2,008,752	300	X71729	57.7	fructose-bisphosphate aldolase	<i>fba</i>
slr0884	1,147,034	1,148,098	354	X86375	95.1	glyceraldehyde 3-phosphate dehydrogenase	<i>gapI</i>
slr0593#	2,946,137	2,945,070	355	M60615	13.7	glucokinase	<i>glk</i>
slr1124	85,058	86,107	349	U14003	7.5	phosphoglycerate mutase	<i>gpmB</i>
slr1196	294,963	293,878	361	U31277	34.7	phosphofructokinase	<i>pfkA</i>
slr0745#	3,126,198	3,125,044	384	U31277	13.8	phosphofructokinase	<i>pfkA</i>
slr1349	1,744,498	1,746,093	531	D13777	100.0	glucose-6-phosphate isomerase	<i>pgi</i>
slr0394*	2,139,271	2,140,395	374	Z48977	71.7	phosphoglycerate kinase	<i>pgk</i>
slr1275	1,104,058	1,102,283	591	D13095	38.2	pyruvate kinase	<i>pykF</i>
slr0587#	2,959,487	2,958,036	483	U256334	34.5	pyruvate kinase	<i>pykF</i>
slr0783#*	2,423,621	2,424,349	242	X66129	42.8	triosephosphate isomerase	<i>tpi</i>
slr1945	2,248,578	2,250,176	532	U38804	49.9	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	<i>vibO</i>
Pentose phosphate pathway							
slr1479	3,395,718	3,394,954	254	U14553	54.8	glucose 6-P-dehydrogenase	<i>devB</i>
slr1709	1,276,982	1,276,236	248	D10625	13.6	glucose dehydrogenase	<i>gdh</i>
slr1608	483,326	484,564	412	X15871	6.7	glucose dehydrogenase-B	<i>gdhB</i>
slr0329#	2,388,872	2,387,424	482	M55002	62.6	6-phosphogluconate dehydrogenase	<i>gnd</i>
slr1734	1,316,227	1,317,654	475	L32796	49.2	OxPPCycle gene	<i>opcA</i>
slr0194**	2,725,326	2,726,033	235	L35034	35.4	ribose 5-phosphate isomerase	<i>rpiA</i>
slr1793	260,463	261,638	391	L47327	63.0	transaldolase	<i>talB</i>
slr1070*	819,979	817,967	670	Z50099	60.7	transketolase	<i>tktA</i>
slr1843	961,201	962,730	509	U33282	77.3	glucose 6-phosphate dehydrogenase	<i>zwf</i>
Pyruvate and acetyl-CoA metabolism							
slr1299	678,286	677,045	413	L17320	34.7	acetate kinase	<i>ackA</i>
slr0542#	2,821,855	2,819,894	653	M97217	51.2	acetyl-coenzyme A synthetase	<i>acs</i>
slr1019	399,214	398,441	257	X90999	23.1	glyoxalase II	<i>HAGH1</i>
slr0721	99,402	100,793	463	M19485	50.3	malic enzyme	<i>me</i>
slr0920	1,997,251	1,994,147	1034	M11198	55.4	phosphoenolpyruvate carboxylase	<i>ppc</i>
slr0301#	3,011,671	3,014,127	818	X59381	49.8	phosphoenolpyruvate synthase	<i>ppsA</i>
slr2132	1,250,442	1,252,535	697	D17576	24.7	phosphotransacetylase	<i>pta</i>
slr0091#	2,898,710	2,900,080	456	U10868	38.9	aldehyde dehydrogenase	
Pyruvate dehydrogenase							
slr1841	2,252,958	2,251,657	433	D10655	21.3	dihydrolipoamide acetyltransferase component (E2)	<i>odhB</i>

Table 1. Continued.

ORF No.	Initiation	Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll1721	955,427	954,453	324	U38804	79.2	pyruvate dehydrogenase E1 beta subunit	<i>pdhB</i>
srl1096	192,870	194,306	478	Z48564	99.3	dihydrolipoamide dehydrogenase	<i>pdhD</i>
srl1934	2,230,487	2,231,515	342	U38804	67.6	pyruvate dehydrogenase E1 component, alpha subunit	
Sugars							
sll1538	2,038,527	2,036,911	538	L19954	14.4	beta-glucosidase	<i>bgI</i>
srl1448	1,089,400	1,090,323	307	U37838	18.4	fructokinase	<i>cscK</i>
srl1078	382,949	383,266	105	M38175	41.5	UDP-glucose 4-epimerase	<i>galE</i>
srl1067	371,487	372,509	340	Z25478	42.4	UDP-glucose 4-epimerase	<i>galE</i>
sll0244	1,522,226	1,521,210	338	X58126	44.4	UDP-glucose 4-epimerase	<i>galE</i>
srl2074	914,052	914,441	129	M77127	45.0	mannose-6-phosphate isomerase	<i>manA</i>
sll1231	1,663,505	1,662,306	399	D43637	15.3	mannosyltransferase B	<i>mfB</i>
sll1212	6,622	5,534	362	L11721	39.8	GDP-D-mannose dehydratase	<i>rfdD</i>
srl0493#	2,625,095	2,625,481	128	M14037	50.9	phosphomannose isomerase	<i>rfdM</i>
ssl2153	1,923,087	1,922,791	98	Z38002	30.6	ribose phosphate isomerase B	<i>rpiB</i>
sll0045#	3,142,874	3,140,712	720	M97550	21.3	sucrose phosphate synthase	<i>sps</i>
srl1299	299,522	300,883	453	X79772	27.0	UDP-glucose dehydrogenase	
srl0942	2,006,824	2,007,807	327	J04794	36.5	aldehyde reductase	
sll1558	1,977,965	1,976,799	388	U24437	7.7	mannose-1-phosphate guanyltransferase	
sll1496	3,365,797	3,363,266	843	U19608	7.3	mannose-1-phosphate guanyltransferase	
TCA cycle							
sll0891#	2,796,400	2,795,426	324	X90527	44.5	2-ketoacid dehydrogenase	<i>citH</i>
srl1233	1,040,531	1,042,258	575	U02603	35.7	succinate dehydrogenase flavoprotein subunit	<i>frdA</i>
srl0018#	2,488,028	2,489,428	466	X78576	58.1	fumarase	<i>fumC</i>
sll0401#	2,561,305	2,560,112	397	L75931	47.5	citrate synthase	<i>gltA</i>
srl1289	283,060	284,487	475	X77654	82.8	isocitrate dehydrogenase (NADP ⁺)	<i>icd</i>
sll1625	1,320,541	1,319,546	331	X01070	19.3	succinate dehydrogenase iron-sulphur protein subunit	<i>sdhB</i>
sll0823#	2,861,838	2,861,101	245	X01070	21.7	succinate dehydrogenase iron-sulfur protein	<i>sdhB</i>
sll1023	393,104	391,899	401	X54073	11.4	succinate-CoA ligase	<i>sucC</i>
sll1557	1,979,039	1,978,131	302	X56033	21.0	succinyl-CoA synthetase	<i>sucD</i>
Fatty acid, phospholipid and sterol metabolism							
sll0728	3,426,518	3,425,538	326	U38804	56.7	acetyl-CoA carboxylase alpha subunit	<i>accA</i>
srl0435#	2,550,059	2,550,523	154	L14863	44.9	biotin carboxyl carrier protein of acetyl-CoA carboxylase	<i>accB</i>
sll0053#	2,599,197	2,597,851	448	L14862	78.0	biotin carboxylase	<i>accC</i>
sll0336#	2,373,229	2,372,249	326	D10004	100.0	acetyl-CoA carboxylase beta subunit	<i>accD</i>
ssl2084	821,783	821,550	77	U32810	64.7	acyl carrier protein	<i>acp</i>
srl1369	1,120,643	1,121,524	293	D83536	12.7	phosphatidate cytidylyltransferase	<i>cdsA</i>
srl0574#	2,817,862	2,819,196	444	X87367	11.9	cytochrome P450	<i>cyp</i>
sll0262	2,121,146	2,120,067	359	L11421	100.0	delta-6 desaturase	<i>des6</i>
sll0541#	2,823,535	2,822,579	318	D16547	100.0	acyl-CoA desaturase 1	<i>des9</i>
srl1350	1,746,308	1,747,363	351	X53508	100.0	fatty acid desaturase	<i>desA</i>
sll1441	1,896,599	1,895,520	359	D13780	99.8	delta 15 desaturase	<i>desB</i>
srl0054#	2,576,889	2,577,416	175	U00006	16.6	diacylglycerol kinase	<i>dgkA</i>
srl1051	503,883	504,719	278	M31806	39.3	enoyl-[acyl-carrier-protein] reductase	<i>envM</i>
srl0089#	2,896,657	2,897,610	317	X89867	8.4	delta(24)-sterol C-methyltransferase	<i>erg6</i>
srl2023	766,727	767,608	293	U32810	22.6	malonyl coenzyme A-acyl carrier protein transacylase	<i>fabD</i>
sll1069	821,352	820,102	416	Z43979	46.5	beta ketoacyl-acyl carrier protein synthase	<i>fabF</i>
srl1332	1,670,650	1,671,864	404	Z43979	15.0	beta ketoacyl-acyl carrier protein synthase	<i>fabG</i>
srl0886	1,152,549	1,153,292	247	X64566	62.5	3-oxoacyl-[acyl-carrier protein] reductase	<i>fabG</i>
srl1994	1,438,704	1,439,426	240	U39441	33.9	3-ketoacyl-acyl carrier protein reductase	<i>fabG</i>
sll0330#	2,384,728	2,383,949	259	M84991	18.6	3-ketoacyl-acyl carrier protein reductase	<i>fabG</i>
srl1511	1,598,065	1,598,928	287	U38804	51.2	beta ketoacyl-acyl carrier protein synthase III	<i>fabH</i>
sll1605	1,470,347	1,469,847	166	M19334	36.8	(3R)-hydroxymyristoyl acyl carrier protein dehydrase	<i>fabZ</i>
srl1167	1,935,912	1,937,069	385	U08463	17.7	glycerol dehydrogenase	<i>gldA</i>
srl1085	1,947,179	1,945,518	553	U36310	15.0	glycerol-3-phosphate dehydrogenase	<i>gldP</i>
srl1672	1,952,323	1,953,810	495	M34393	39.2	glycerol kinase	<i>gldP</i>
srl1755	529,696	530,688	330	L47648	27.1	NAD+-dependent glycerol-3-phosphate dehydrogenase	<i>gpsA</i>
srl0776#	2,403,473	2,404,507	344	D83536	17.3	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	<i>lpxD</i>
sll1522	2,076,507	2,075,968	179	D50064	27.8	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	<i>pgsA</i>
srl1510	1,596,795	1,597,841	348	M96793	22.7	PlsX protein	<i>plsX</i>
srl2033	569,141	569,488	115	M81168	22.8	rubredoxin	<i>rub</i>
srl2089	1,550,952	1,552,895	647	M73834	31.9	squalene-hopene-cyclase	<i>shc</i>
srl1020	636,372	637,523	383	M89780	31.6	sulfolipid biosynthesis protein SqdB	<i>sqdB</i>
srl1993	1,437,373	1,438,602	409	L37761	33.8	acetyl coenzyme A acetyltransferase (thiolase)	<i>thl</i>
srl1609	487,287	489,377	696	U32795	8.9	long-chain-fatty-acid CoA ligase	
srl0418	2,097,574	2,096,618	318	X89867	7.5	sterol-C-methyltransferase	
Photosynthesis and respiration							
ATP synthase							
sll1326	174,525	173,014	503	X58128	100.0	ATP synthase a subunit	<i>atpA</i>
srl1329	1,666,932	1,668,383	483	X58129	100.0	ATP synthase b subunit	<i>atpB</i>
sll1327	172,883	171,939	314	X58128	100.0	ATP synthase g subunit	<i>atpC</i>
sll1325	175,143	174,586	185	X58128	100.0	ATP synthase d subunit	<i>atpD</i>
srl1330	1,668,444	1,668,941	165	X58129	80.7	ATP synthase e subunit	<i>atpE</i>
sll1324	175,682	175,143	179	X58128	98.9	ATP synthase subunit b	<i>atpF</i>
sll1323	176,139	175,708	143	X58128	100.0	ATP synthase subunit b'	<i>atpG</i>
ssl2615	176,501	176,256	81	X58128	100.0	ATP synthase subunit c	<i>atpH</i>
sll1322	177,523	176,693	276	X58128	100.0	ATP synthase subunit a	<i>atpI</i>
CO₂ fixation							

Table 1. Continued.

ORF No.	Initiation	Termination	Accession No.	QryMatch (%)	Product	
sll0018#*	2,471,670	2,470,591	U29134	64.8	fructose-1,6-bisphosphate aldolase	<i>cbbA</i>
sll0934	335,623	334,568	D26444	84.8	carboxysome formation protein	<i>ccmA</i>
sll1029	219,077	218,742	M96929	84.3	carbon dioxide concentrating mechanism protein CcmK	<i>ccmK</i>
sll1028	219,517	219,206	M96929	89.1	carbon dioxide concentrating mechanism protein CcmK	<i>ccmK</i>
sir1838	955,805	956,116	M96929	45.5	carbon dioxide concentrating mechanism protein CcmK	<i>ccmK</i>
sir1839	956,275	956,613	M96929	46.6	carbon dioxide concentrating mechanism protein CcmK	<i>ccmK</i>
sir0436#	2,550,753	2,551,646	M96929	11.9	carbon dioxide concentrating mechanism protein CcmK	<i>ccmK</i>
sll1030	218,709	218,407	M96929	59.4	carbon dioxide concentrating mechanism protein CcmL	<i>ccmL</i>
sll1031	218,327	216,264	M96929	32.6	carbon dioxide concentrating mechanism protein CcmM	<i>ccmM</i>
sll0807	1,713,256	1,712,564	Z50098	66.8	pentose-5-phosphate-3-epimerase	<i>cfxE</i>
sir0952*	2,022,028	2,023,071	U33282	79.2	fructose 1,6-bisphosphatase	<i>fbp</i>
sir0943*	2,007,850	2,008,752	X71729	57.7	fructose-bisphosphate aldolase	<i>fba</i>
sll1342	3,279,135	3,278,122	X86376	99.8	glyceraldehyde-3-phosphate dehydrogenase (NADP ⁺)	<i>gap2</i>
sir1347	1,742,434	1,743,369	U45962	87.6	carbonic anhydrase	<i>icfa</i>
sir0051#	2,568,182	2,568,973	U41190	28.6	carbonic anhydrase	<i>icfa</i>
sir0394*	2,139,271	2,140,395	Z48977	71.7	phosphoglycerate kinase	<i>pgk</i>
sll1525	2,066,999	2,066,001	M77134	99.7	phosphoribulokinase	<i>prk</i>
sir0009#	2,478,414	2,479,826	X65960	100.0	ribulose bisphosphate carboxylase large subunit	<i>rbcL</i>
sll0030#	3,168,801	3,167,887	D11141	47.1	ribulose operon transcriptional regulator	<i>rbcR</i>
sll1594	1,488,395	1,487,445	D11141	45.4	ribulose operon transcriptional regulator	<i>rbcR</i>
sir0012#	2,480,477	2,480,818	X65960	100.0	ribulose bisphosphate carboxylase small subunit	<i>rbcS</i>
sir0194#*	2,725,326	2,726,033	L35034	35.4	ribose 5-phosphate isomerase	<i>rpiA</i>
sll1070*	819,979	817,967	Z50099	60.7	transketolase	<i>tktA</i>
sir0783#*	2,423,621	2,424,349	X66129	42.8	triosephosphate isomerase	<i>tpi</i>
Cytochrome <i>b</i>/<i>f</i> complex						
sll1317	1,166,073	1,165,087	X58532	100.0	apocytochrome <i>f</i>	<i>petA</i>
sir0342#	2,428,010	2,428,678	Z31580	100.0	cytochrome <i>b</i> ₆	<i>petB</i>
sll1316	1,166,764	1,166,186	X58532	100.0	plastoquinol--plastocyanin reductase	<i>petC</i>
sir1185	3,527,045	3,527,581	J03855	43.5	cytochrome <i>b</i> / <i>f</i> -complex iron-sulfur protein	<i>petC</i>
sll1182	1,848,702	1,848,301	M74514	21.4	cytochrome <i>b</i> / <i>f</i> complex iron-sulfur protein	<i>petC</i>
sir0343#	2,428,809	2,429,291	X58522	100.0	cytochrome <i>b</i> / <i>f</i> complex subunit 4	<i>petD</i>
smr0010	1,823,570	1,823,686	U30821	80.8	PetG subunit of the cytochrome <i>b</i> / <i>f</i> complex	<i>petG</i>
smr0003#	3,118,191	3,118,301	U36401	34.0	cytochrome <i>b</i> / <i>f</i> /complex subunit PetM	<i>petM</i>
NADH dehydrogenase						
sir1743	1,330,930	1,332,144	V00306	7.0	NADH dehydrogenase	<i>ndh</i>
sir0851	1,337,299	1,338,636	V00306	7.1	NADH dehydrogenase	<i>ndh</i>
sll1484	3,391,602	3,390,028	Z47071	4.7	NADH dehydrogenase	<i>ndh</i>
sll0519#	3,270,196	3,269,078	X62517	100.0	NADH dehydrogenase subunit 1	<i>ndhA</i>
sll0223	158,615	157,050	D90288	99.6	NADH dehydrogenase subunit 2	<i>ndhB</i>
sir1279	1,875,129	1,875,491	X17439	99.4	NADH dehydrogenase subunit 3	<i>ndhC</i>
sir0331#	2,287,948	2,289,525	X65170	100.0	NADH dehydrogenase subunit 4	<i>ndhD</i>
sir2007	747,575	749,038	U14130	5.2	NADH dehydrogenase subunit 4	<i>ndhD</i>
sll1733	938,276	936,768	X65170	25.0	NADH dehydrogenase subunit 4	<i>ndhD</i>
sll0027#	3,178,066	3,176,543	X65170	25.8	NADH dehydrogenase subunit 4	<i>ndhD</i>
sir1291	286,164	287,843	U14130	78.1	NADH dehydrogenase subunit 4	<i>ndhD2</i>
sll0522#	3,267,555	3,267,244	X62517	100.0	NADH dehydrogenase subunit 5	<i>ndhE</i>
sir0844#	2,857,874	2,859,919	M99378	75.0	NADH dehydrogenase subunit 5	<i>ndhF</i>
sir2009	749,550	751,037	U27296	5.2	NADH dehydrogenase subunit 5	<i>ndhF</i>
sll1732	940,240	938,393	U47419	12.4	NADH dehydrogenase subunit 5	<i>ndhF</i>
sll0026#	3,180,135	3,178,231	U27296	14.1	NADH dehydrogenase subunit 5	<i>ndhF</i>
sll0521#	3,268,291	3,267,695	X62517	85.3	NADH dehydrogenase subunit 6	<i>ndhG</i>
sir0261	1,509,990	1,511,174	X60650	100.0	NADH dehydrogenase subunit 7	<i>ndhH</i>
sll0520#	3,268,967	3,268,386	X62517	100.0	NADH dehydrogenase subunit Ndhl	<i>ndhI</i>
sir1281	1,876,302	1,876,841	X17439	89.2	NADH dehydrogenase subunit I	<i>ndhJ</i>
Photosystem I						
sir1834	941,686	943,941	X58825	100.0	P700 apoprotein subunit Ia	<i>psaA</i>
sir1835	944,187	946,382	X58825	99.9	P700 apoprotein subunit Ib	<i>psaB</i>
ssl0563#	2,287,579	2,287,334	X65170	100.0	photosystem I subunit VII	<i>psaC</i>
sir0737	126,639	127,064	J04195	100.0	photosystem I subunit II	<i>psaD</i>
ssr2831	1,982,049	1,982,273	J05079	98.2	photosystem I subunit IV	<i>psaE</i>
sll0819	1,688,053	1,687,556	L20938	100.0	photosystem I subunit III	<i>psaF</i>
smr0004	3,458,023	3,458,145	L24773	100.0	photosystem I subunit VIII	<i>psaI</i>
smr0008	1,687,448	1,687,326	L20938	100.0	photosystem I subunit IX	<i>psaJ</i>
ssr0390	156,391	156,651	U38804	39.9	photosystem I subunit X	<i>psaK</i>
sll0629	3,322,763	3,322,377	X63764	25.7	photosystem I subunit X	<i>psaL</i>
sir1655	3,457,459	3,457,932	L11649	100.0	photosystem I subunit XI	<i>psaM</i>
smr0005	467,201	467,296	X59760	81.7	photosystem I PsAM subunit	<i>psaM</i>
Photosystem II						
sll0247	1,518,604	1,517,576	L26530	97.2	iron-stress chlorophyll-binding protein	<i>isiA</i>
sir1181	3,523,717	3,524,799	Y00885	98.9	photosystem II D1 protein	<i>psbA1</i>
sir1311	7,229	8,311	X13547	100.0	photosystem II D1 protein	<i>psbA2</i>
sll1867	1,819,997	1,818,915	X13547	100.0	photosystem II D1 protein	<i>psbA3</i>
sir0906#	2,779,510	2,781,033	M17109	100.0	photosystem II P680 chlorophyll A apoprotein	<i>psbB</i>
sll0851	1,348,892	1,347,474	M21538	99.7	photosystem II 44kD reaction center protein	<i>psbC</i>
sll0849	1,349,898	1,348,840	M21538	100.0	photosystem II D2 protein	<i>psbD</i>
sir0927#	3,229,780	3,230,838	M21538	100.0	photosystem II D2 protein	<i>psbE</i>
ssr3451	570,658	570,903	M33897	100.0	cytchrome b559 a subunit	<i>psbF</i>
smr0006	570,940	571,074	M33897	100.0	cytchrome b559 b subunit	<i>psbG</i>
sir1280	1,875,563	1,876,309	X17439	100.0	NADH-ubiquinone oxidoreductase subunit PsbG	<i>psbG</i>

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product
ssl2598	1,167,247	1,167,053	64	X58532	100.0	photosystem II PsbH protein
sml0001#	2,350,256	2,350,140	38	U28040	100.0	photosystem II PsbI protein
smr0008	571,236	571,355	39	X15767	70.7	photosystem II PsbJ protein
smr0005	553,202	553,065	45	M74841	100.0	photosystem II PsbK protein
smr0007	571,084	571,203	39	M33897	100.0	photosystem II PsbL protein
smr0003	146,831	146,724	35	X04465	67.8	photosystem II PsbM protein
smr0009	1,167,333	1,167,464	43	X58532	100.0	photosystem II PsbN protein
sll0427	2,087,129	2,086,305	274	X07986	100.0	photosystem II manganese-stabilizing polypeptide
smr0001#	2,414,584	2,414,679	31	U38804	64.3	photosystem II PsbT protein
sll1194	297,888	297,493	131	D84098	99.3	photosystem II 12 kD extrinsic protein
sll0258	2,132,098	2,131,616	160	D45178	99.5	cytochrome c550
sml0002#	2,613,600	2,613,481	39	U38804	65.9	photosystem II PsbX protein
sll1398	50,231	49,893	112	D82937	100.0	photosystem II 13 kD protein
srl1645	2,070,975	2,071,382	135	D82936	99.3	photosystem II 11 kD protein
Phycobilisome						
srl2067	1,430,419	1,430,904	161	M77135	100.0	allophycocyanin a chain
srl1986	1,431,000	1,431,485	161	M77135	100.0	allophycocyanin b chain
ssr3383	1,431,698	1,431,901	67	L02308	100.0	phycobilisome Lc linker polypeptide
sll0928	339,625	339,140	161	Y00539	76.3	allophycocyanin-B
srl0335#	2,292,188	2,294,878	896	L02309	97.6	phycobilisome Lcm core-membrane linker polypeptide
srl1459	3,304,872	3,305,381	169	U21853	74.8	phycobilisome core component
sll1578	726,837	726,349	162	U34930	100.0	phycocyanin a subunit
sll1577	727,466	726,948	172	U34930	99.6	phycocyanin b subunit
sll1580	725,367	724,492	291	M75599	66.3	phycocyanin associated linker protein
sll1579	726,234	725,413	273	M94218	62.9	phycocyanin associated linker protein
ssl3093	724,345	724,094	83	M93569	56.2	phycocyanin associated linker protein
srl1878	1,229,120	1,229,938	272	M93569	58.2	phycocyanin alpha phycocyanobilin lyase CpcE
sll1051	88,661	88,017	214	M93569	43.3	phycocyanin alpha phycocyanobilin lyase CpcF
srl2051	596,540	597,247	235	X57251	45.9	phycobilisome rod-core linker polypeptide CpcG
sll1471	3,404,306	3,403,557	249	X57251	45.4	phycobilisome rod-core linker polypeptide CpcG
ssl0453	1,523,709	1,523,527	60	U38804	27.2	phycobilisome degradation protein NblA
ssl0452	1,523,984	1,523,796	62	U05044	24.2	phycobilisome degradation protein NblA
Soluble electron carriers						
sll1245	1,751,067	1,750,681	128	X82563	83.9	cytochrome CytM
sll0554#	2,804,584	2,804,228	118	X74881	67.7	ferredoxin-thioredoxin reductase, catalytic chain
ssr0330#	2,745,934	2,746,161	75	M54196	62.1	ferredoxin-thioredoxin reductase, variable chain
sll0248	1,517,171	1,516,659	170	L25881	100.0	flavodoxin
sll0199#	2,526,207	2,525,827	126	X54105	100.0	plastocyanin
srl0150	2,180,577	2,180,888	103	U33848	54.0	ferredoxin
ssl0020#	2,485,183	2,484,890	97	U38802	100.0	ferredoxin
srl1828	931,639	931,959	106	X05302	51.6	ferredoxin
sll1382	1,831,929	1,831,561	122	X05302	38.3	ferredoxin
ssr3184	1,239,156	1,239,383	75	U38804	72.6	ferredoxin
srl1643	2,067,522	2,068,763	413	X94297	98.0	ferredoxin-NADP oxidoreductase
sll1796	846,328	845,966	120	L25252	100.0	cytochrome c553
srl1239	1,053,955	1,055,547	530	X66086	54.3	pyridine nucleotide transhydrogenase alpha subunit
srl1434	1,056,985	1,058,427	480	X66086	63.3	pyridine nucleotide transhydrogenase beta subunit
Cytochrome oxidase						
sll1899	1,758,542	1,757,592	316	D13960	100.0	cytochrome c oxidase folding protein
srl1136	790,719	791,717	332	X53746	94.3	cytochrome c oxidase subunit II
sll0813	1,697,913	1,697,011	300	X53746	18.4	cytochrome c oxidase subunit II
srl1137	791,806	793,461	551	X53746	89.6	cytochrome c oxidase subunit I
srl2082	1,540,650	1,542,284	544	D16254	49.8	cytochrome c oxidase subunit I
srl1138	793,509	794,210	233	X53746	90.9	cytochrome c oxidase subunit III
srl2083	1,542,341	1,542,937	198	D16254	28.3	cytochrome c oxidase subunit III
srl1379	673,889	675,340	483	J03939	18.3	cytochrome oxidase d subunit I
srl1380	675,344	676,354	336	J03939	13.3	cytochrome oxidase d subunit II
Purines, pyrimidines, nucleosides, and nucleotides						
Interconversions and salvage of nucleosides and nucleotides						
sll1430	1,579,243	1,578,725	172	U22442	42.5	adenine phosphoribosyltransferase
sll1776	1,208,697	1,208,020	225	U32737	32.1	deoxyribose-phosphate aldolase
sll1852	2,234,753	2,234,304	149	U10283	69.9	nucleoside diphosphate kinase
sll0469#	2,939,631	2,938,630	333	D14994	83.8	ribose-phosphate pyrophosphokinase
sll1035	210,546	209,896	216	X73329	34.3	uracil phosphoribosyltransferase
Purine ribonucleotide biosynthesis						
sll1059	76,500	75,955	181	X17524	26.8	adenylate kinase
sll1815	832,265	831,702	187	M88104	33.4	adenylate kinase
sll0398#	2,681,872	2,680,550	440	U42435	8.7	dGTP triphosphohydrolase
srl1123	84,122	84,697	191	M84400	39.6	guanylate kinase
srl0213#	2,504,415	2,506,043	542	M83691	50.1	GMP synthetase
srl0172#	2,304,094	2,304,561	155	L07487	16.3	IMP dehydrogenase
srl1722	1,475,555	1,476,718	387	X02209	9.9	IMP dehydrogenase subunit
srl1164	1,928,323	1,930,626	767	K02927	10.7	ribonucleotide reductase subunit alpha
sll1823	825,831	824,584	415	D26185	41.9	adenylosuccinate synthetase
sll0421	2,094,924	2,093,629	431	J02732	52.1	adenylosuccinate lyase
srl1226	1,030,195	1,030,989	264	J02732	39.4	phosphoribosyl aminoimidazole succinocarboxamide synthetase
srl1159	1,920,660	1,921,919	419	X54200	42.0	glycynamide ribonucleotide synthetase
sll0901#	3,227,909	3,227,379	176	M37264	58.4	phosphoribosylaminoimidazole carboxylase

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll0757#	2,414,313	2,412,826	495	U33211	66.1	amidophosphoribosyltransferase	
sll0597	3,553,851	3,555,512	553	J02732	39.4	phosphoribosyl aminoimidazole carboxy formyl formyltransferase/inosinemonophosphate cyclohydrolase (PUR-H(J))	<i>purF</i> <i>purH</i>
sll0578	3,537,630	3,536,464	388	M91187	41.2	phosphoribosyl aminoimidazole carboxyformyl transferase	
sll1056	80,800	78,467	777	J02732	41.4	phosphoribosylformyl gycinamide synthetase II	<i>purK</i>
sll0520#	2,932,510	2,933,184	224	J02732	48.6	phosphoribosylformyl gycinamide synthase	<i>purL</i>
sll0838#	2,847,323	2,848,348	341	J02732	44.4	phosphoribosylformyl gycinamide cyclo-ligase	<i>purM</i>
sll0477#	2,613,717	2,614,370	217	J02732	31.0	phosphoribosylgycinamide formyltransferase	<i>purN</i>
sll0861	1,352,256	1,353,431	391	L36958	100.0	gycinamide ribonucleotide transformylase	<i>purT</i>
sll0070#	2,568,091	2,567,237	284	U00024	37.3	phosphoribosylgycinamide formyltransferase	<i>purU</i>
sll0509#	3,200,838	3,199,930	302	M60265	7.7	Ap-4-A phosphorylase II	
Pyrimidine ribonucleotide biosynthesis							
sll0370#	2,716,688	2,713,371	1105	J01597	52.0	carbamoyl-phosphate synthase, pyrimidine-specific, large chain	<i>carB</i>
sll1237	1,047,005	1,048,357	450	X63656	7.0	cytosine deaminase	<i>codA</i>
sll1249*	1,742,375	1,740,834	513	U44896	43.9	pantothenate synthetase/cytidylate kinase	<i>panC/kcy</i>
sll1476	1,834,508	1,835,503	331	M97253	31.7	aspartate carbamoyltransferase	<i>pyrB</i>
sll0406	2,157,442	2,158,470	342	X04469	46.4	dihydroorotate	<i>pyrC</i>
sll1018	400,600	399,275	441	L19649	11.2	dihydroorotate	<i>pyrD</i>
sll1418	3,270,451	3,271,596	381	X80778	23.2	dihydroorotate dehydrogenase	<i>pyrE</i>
sll0838	1,364,532	1,363,837	231	X05382	31.5	orotidine 5' monophosphate decarboxylase	<i>pyrF</i>
sll1443	1,892,119	1,890,461	552	M22039	59.5	CTP synthetase	<i>pyrG</i>
sll0144	2,193,450	2,192,668	260	D83536	44.7	uridine monophosphate kinase	<i>pyrH</i>
sll0185#	2,336,427	2,337,023	198	J03626	15.3	uridine 5'-monophosphate synthase	<i>umpS</i>
Regulatory functions							
sll0447	2,098,921	2,100,261	446	M43175	13.2	negative aliphatic amidase regulator	<i>amiC</i>
sll1957	1,412,551	1,412,237	104	U38947	27.1	arsenical resistance operon repressor	<i>arsA</i>
sll1766	1,231,167	1,229,971	398	M31938	9.5	putative arylsulfatase regulatory protein	<i>aslB</i>
sll0789#	3,065,609	3,064,911	232	L05176	30.0	regulatory components of sensory transduction system	<i>copR</i>
sll0646	427,738	425,468	756	D55650	4.5	adenylate cyclase	<i>cyaA</i>
sll1991	1,435,645	1,436,658	337	M55650	8.7	adenylate cyclase	<i>cyaA</i>
sll1666	3,472,053	3,473,210	385	M29002	38.5	pleiotropic regulatory protein	<i>degT</i>
sll0698	126,443	124,452	663	X72856	100.0	drug sensory protein A	<i>dfr</i>
sll2041	579,646	580,194	182	U13765	14.0	cell division response regulator DivK	<i>divK</i>
sll0321#	2,270,624	2,271,571	315	U18532	39.3	GTP-binding protein Era	<i>Era</i>
sll0567	3,552,954	3,552,457	165	L41065	37.1	ferric uptake regulation protein	<i>fur</i>
sll1937	583,573	583,157	138	M85154	16.5	ferric uptake regulation protein	<i>fur</i>
sll1860	1,197,262	1,199,166	634	X75568	94.7	ICFG protein	<i>ICFG</i>
sll1626	1,319,330	1,318,719	203	J01643	13.6	SOS function regulatory protein	<i>lexA</i>
sll0709	106,539	105,151	462	U17233	5.8	2nd component required for Lla1 restriction activity	<i>lla1.2</i>
sll1872	1,808,724	1,807,333	463	M87645	7.3	membrane bound protein LytR	<i>lytR</i>
sll0701#	3,091,243	3,091,656	137	U18997	24.2	mercuric resistance operon regulatory protein	<i>merR</i>
sll0794#*	3,058,328	3,057,216	370	U33192	7.1	mercuric resistance operon regulatory protein/precorrin isomerase	<i>merR/cobH</i>
sll1416	182,354	183,298	314	X96434	31.6	MorR protein	<i>morR</i>
sll0835#	2,842,772	2,843,683	303	X96434	27.0	MoxR protein	<i>moxR</i>
sll1708	1,278,122	1,277,442	226	M24910	24.8	nitrate/nitrite response regulator protein	<i>narL</i>
sll1305	309,649	312,171	840	Y00525	4.4	nitrogen fixation positive activator protein	<i>nifL</i>
sll1423	1,590,061	1,589,384	225	X71607	100.0	global nitrogen regulator	<i>nicA</i>
sll0395	2,140,664	2,141,593	309	D16303	36.8	transcriptional activator protein NtcB	<i>nicB</i>
sll0564#	2,287,067	2,286,798	89	U30821	26.6	transcriptional regulatory protein	<i>ompR</i>
sll1594	451,735	452,922	395	M87501	8.2	PatA protein	<i>patA</i>
sll1041	489,722	490,888	388	M87501	9.1	PatA protein	<i>patA</i>
sll1205	21,595	20,615	326	L11657	13.2	regulatory protein PchR	<i>pchR</i>
sll1489	38,644	39,636	330	L11657	12.1	regulatory protein PchR	<i>pchR</i>
sll1408	29,030	27,990	346	L11657	14.0	regulatory protein PcrR	<i>pcrR</i>
sll1435	1,903,996	1,902,437	519	A04970	39.5	PET112 protein	<i>pet112</i>
sll0649	423,509	422,772	245	X67676	34.6	regulatory components of sensory transduction system	<i>phoP</i>
sll0741	131,116	131,790	224	D45195	15.5	a negative regulator of pho regulon	<i>phoU</i>
sll1225	1,027,844	1,029,331	495	U00484	16.3	protein kinase PknA	<i>pknA</i>
sll0776#	3,083,667	3,082,150	505	U00484	26.2	eukaryotic protein kinase	<i>pknA</i>
sll1443	1,078,657	1,080,501	614	U41664	6.9	protein kinase	<i>pknA</i>
sll1697	1,991,550	1,993,274	574	U00484	19.5	eukaryotic protein kinase	<i>pknA</i>
sll1798	271,600	273,357	585	L42554	5.5	PleD gene product	<i>pleD</i>
sll0687	431,350	432,795	481	X96983	6.3	PleD gene product	<i>pleD</i>
sll1047	496,450	497,844	464	L42554	8.4	PleD gene product	<i>pleD</i>
sll0829#	2,833,378	2,835,867	829	L42554	3.3	PleD gene product	<i>pleD</i>
sll0302#	3,014,389	3,016,695	768	L42554	6.3	PleD gene product	<i>pleD</i>
sll1657	3,459,781	3,460,608	275	L42554	12.6	PleD gene product	<i>pleD</i>
sll0883	1,144,728	1,146,173	481	U42211	6.9	regulation of penicillin binding protein 5 production	<i>psr</i>
sll0368#	2,717,713	2,717,177	178	X76083	42.3	pyrimidine operon regulatory protein PyrR	<i>pyrR</i>
sll0640	436,158	434,320	612	U47541	14.2	sulfur deprivation response regulator	<i>SacI</i>
sll2014	1,253,982	1,253,269	237	D26562	29.0	sugar fermentation stimulation protein	<i>sfsA</i>
sll0792#	3,061,204	3,060,806	132	X64585	44.0	transcriptional repressor SmtB	<i>smtB</i>
sll0724	110,392	110,724	110	M30178	22.2	Hfq suppressor protein	<i>sohA</i>
sll1325	1,656,043	1,658,325	760	M24503	28.9	(p)ppGpp 3'-pyrophosphohydrolase	<i>spoT</i>
sll1383	1,831,491	1,830,628	287	M34828	23.9	extragenic suppressor SuhB	<i>suhB</i>
sll0329#	2,283,794	2,284,777	327	A00033	10.5	xylene repressor	<i>xylR</i>
sll0947	2,012,781	2,013,485	234	U30821	80.1	regulatory components of sensory transduction system	<i>ycf27</i>
sll0115#	2,995,908	2,996,633	241	U30821	33.1	regulatory components of sensory transduction system	<i>ycf27</i>

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product
sll0998	631,592	630,555	345	U38804	67.1	LysR transcriptional regulator
sll1234	1,042,609	1,042,953	114	M34833	69.9	protein kinase C inhibitor
sll1871	1,216,281	1,217,168	295	U31464	17.8	transcriptional regulator
sll1245	1,383,828	1,384,736	302	X89816	21.4	transcriptional regulator
sll1975	1,793,852	1,795,027	391	J05399	24.3	renin-binding protein
sll0312#	3,034,782	3,035,411	209	M23558	30.7	nitrate/nitrite response regulator protein
sll0449	3,482,568	3,483,284	238	D50019	19.8	DNR protein
sll0593	3,548,402	3,549,706	434	L03357	6.7	cAMP protein kinase regulatory chain
sll1090	397,037	398,143	368	U18997	37.1	GTP-binding protein
sll1005	516,897	516,088	269	D00937	17.4	regulatory protein for beta-lactamase
sll1575	731,358	730,108	416	D26539	8.0	serine/threonine protein kinase
sll2031	781,653	783,011	452	L35574	7.7	sigma factor SibG regulation protein RsbU
sll1213	899,937	900,662	241	U35231	13.5	LumQ gene product
sll1214	901,197	902,315	372	M87501	10.0	PatA protein
sll1371	1,845,266	1,844,568	232	M13772	11.4	catabolite gene activator protein
sll1529	1,892,918	1,895,425	835	X63841	3.3	nitrogen assimilation regulatory protein
sll1694	1,988,385	1,988,837	150	L42555	16.0	activator of photopigment and puc expression
sll0152	2,182,063	2,183,958	631	D26539	6.9	serine/threonine protein kinase
sll0594#	2,944,889	2,944,272	205	Z47212	24.8	transcriptional regulatory protein
sll0782#	3,074,737	3,073,628	369	A08709	6.8	putative protein kinase
sll0779#	3,078,549	3,075,895	884	L42554	4.5	PleD gene product
sll1329	3,296,443	3,295,580	287	X92429	8.2	monophosphatase
sll0599	3,557,481	3,559,088	535	U00484	31.7	eukaryotic protein kinase
sll0609	3,570,424	3,571,575	383	D90216	15.2	47 kD protein
sll1393	701,343	704,267	974	L09228	5.2	sensory transduction histidine kinase
sll1147	811,489	812,793	434	D29633	14.7	sensory transduction histidine kinase
sll1124	866,377	862,262	1371	M98873	2.8	sensory transduction histidine kinase
sll1228	1,666,699	1,664,798	633	X52948	12.9	sensory transduction histidine kinase
sll1888	1,783,355	1,782,057	432	D10888	16.6	sensory transduction histidine kinase
sll1871	1,810,946	1,808,922	674	M80477	12.2	sensory transduction histidine kinase
sll0337#	2,372,110	2,370,818	430	S77740	22.3	sensory transduction histidine kinase
sll0750#	2,422,687	2,421,536	383	D14056	33.4	sensory transduction histidine kinase
sll0210#	2,747,604	2,748,857	417	M91449	13.7	sensory transduction histidine kinase
sll0533#	3,192,683	3,193,900	405	D14054	15.5	sensory transduction histidine kinase
sll1414	179,734	181,047	437	M23549	7.4	sensory transduction histidine kinase
sll1672	255,629	253,125	834	D10888	8.8	sensory transduction histidine kinase
sll1003	520,272	518,287	661	U42597	4.5	sensory transduction histidine kinase
sll1759	533,086	537,474	1462	L30101	7.4	sensory transduction histidine kinase
sll1353	1,087,753	1,084,757	998	U53189	9.0	sensory transduction histidine kinase
sll1805	1,278,293	1,280,542	749	D14056	4.4	sensory transduction histidine kinase
sll1687	1,309,348	1,306,436	970	L42554	5.0	sensory transduction histidine kinase
sll1905	1,444,046	1,441,002	1014	L30101	9.4	sensory transduction histidine kinase
sll1590	1,492,686	1,491,634	350	L09228	11.3	sensory transduction histidine kinase
sll2098	1,563,115	1,566,900	1261	U30858	10.5	sensory transduction histidine kinase
sll2104	1,572,849	1,575,701	950	U30858	10.5	sensory transduction histidine kinase
sll1324	1,653,402	1,654,664	420	X53315	8.8	sensory transduction histidine kinase
sll1969	1,777,729	1,779,981	750	U30858	6.7	sensory transduction histidine kinase
sll0222#	2,518,321	2,521,857	1178	D78193	4.3	sensory transduction histidine kinase
sll0484#	2,618,067	2,620,094	675	D78193	7.2	sensory transduction histidine kinase
sll0640#	2,661,959	2,663,284	441	M23549	9.5	sensory transduction histidine kinase
sll0474#	2,929,700	2,927,280	806	M80477	9.1	sensory transduction histidine kinase
sll0311#	3,032,495	3,034,774	759	L15444	5.0	sensory transduction histidine kinase
sll0798#	3,050,265	3,048,901	454	M23549	11.8	sensory transduction histidine kinase
sll0790#	3,064,924	3,063,548	458	M23549	11.6	sensory transduction histidine kinase
sll1475	3,400,350	3,399,457	297	D78193	14.6	sensory transduction histidine kinase
sll1783	242,246	243,094	282	U30821	27.9	regulatory components of sensory transduction system
sll1042	491,006	491,449	147	U01971	26.2	regulatory components of sensory transduction system
sll1760	537,471	538,418	315	L42554	13.3	regulatory components of sensory transduction system
sll1037	667,447	667,842	131	M16775	34.0	regulatory components of sensory transduction system
sll1291	692,576	691,371	401	M87501	9.1	regulatory components of sensory transduction system
sll1837	953,752	954,456	234	X83541	29.4	regulatory components of sensory transduction system
sll1592	1,491,363	1,490,683	226	A08709	24.9	regulatory components of sensory transduction system
sll1229	1,664,690	1,663,554	378	L42554	10.1	regulatory components of sensory transduction system
sll1982	1,811,130	1,811,501	123	U13765	32.5	regulatory components of sensory transduction system
sll1983	1,811,746	1,813,557	603	X75568	18.5	regulatory components of sensory transduction system
sll1555	1,981,471	1,980,365	368	X62579	11.3	regulatory components of sensory transduction system
sll0921	1,994,045	1,993,377	222	A08709	26.2	regulatory components of sensory transduction system
sll0396#	2,683,226	2,682,552	224	U01971	37.0	regulatory components of sensory transduction system
sll0081#	2,885,022	2,885,810	262	D13172	51.4	regulatory components of sensory transduction system
sll0797#	3,050,966	3,050,262	234	M95680	25.3	regulatory components of sensory transduction system
sll1330	3,295,250	3,294,498	250	L41661	21.4	transcriptional regulatory protein
sll1584	3,404,545	3,405,249	234	M95680	47.5	regulatory components of sensory transduction system
sll1673	253,116	251,758	452	U01831	8.8	regulatory components of sensory transduction system
sll1400	402,290	403,432	380	D26185	10.7	regulatory components of sensory transduction system
sll1909	613,102	613,743	213	U38804	28.0	regulatory components of sensory transduction system
sll1292	691,264	690,899	121	D14054	25.0	regulatory components of sensory transduction system
sll2024	767,890	768,432	180	X80027	16.5	regulatory component of sensory transduction system
sll2099	1,566,990	1,568,090	366	L42554	11.2	regulatory components of sensory transduction system
sll2100	1,568,317	1,569,423	368	L42554	11.4	regulatory components of sensory transduction system
sll1693	1,987,100	1,988,242	380	M87501	7.7	regulatory components of sensory transduction system

Table 1. Continued.

ORF No.	Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product
sll1544	3,474,199	3,473,513	228	A08709	10.7	regulatory components of sensory transduction system
DNA replication, restriction, modification, recombination, and repair						
sll0848	1,351,579	1,350,236	447	L36958	97.2	chromosomal replication initiator protein DnaA
sll0833#	2,839,957	2,842,575	872	D26185	17.8	replicative DNA helicase
sll1572	737,811	736,435	458	U32703	17.4	DNA polymerase III alpha subunit
sll0603	3,561,946	3,564,639	897	D83536	25.4	DNA polymerase III alpha subunit
sll1868	1,818,762	1,816,855	635	X94247	42.1	DNA primase
sll0965	324,831	326,006	391	U33322	55.0	DNA polymerase III beta subunit
sll0446	2,097,643	2,098,602	319	L42622	9.4	DNA polymerase III subunit
sll1360	1,069,010	1,065,660	1116	D26185	6.2	DNA polymerase III subunit
sll0204#	2,518,184	2,516,814	456	L27797	39.5	glucose inhibited division protein A
sll0202#	2,523,737	2,521,830	635	X62539	43.3	glucose inhibited division protein A
sll0072#	2,868,767	2,869,561	264	D26185	13.4	glucose inhibited division protein B
sll1941	579,768	576,934	944	D26185	25.7	DNA gyrase A subunit
sll0417#	2,687,952	2,690,534	860	D26185	46.4	DNA gyrase A subunit
sll2005	1,267,564	1,264,328	1078	D26185	21.6	DNA gyrase B subunit
sll1209	12,631	10,622	669	U10483	39.5	DNA ligase
sll1583	716,153	714,465	562	M30255	6.7	DNA ligase
sll1803	1,274,352	1,275,281	309	D13968	30.3	adenine-specific DNA methylase
sll0377#	2,705,530	2,701,931	1199	D26185	24.7	transcription-repair coupling factor
sll1199	880,147	881,838	563	Z11831	8.5	DNA mismatch repair protein MutL
sll1689	1,982,308	1,983,171	287	X53930	25.8	formamidopyrimidine-DNA glycosylase
sll1772	1,219,624	1,217,156	822	D63810	3.4	DNA mismatch repair protein MutS
sll1165	1,375,193	1,372,455	912	M63007	27.1	DNA mismatch repair protein
sll1045	96,228	95,818	136	L07579	23.3	mutator MutT protein
sll1822	1,310,575	1,311,234	219	U22181	39.9	endonuclease III
sll0854	1,339,656	1,341,122	488	U51943	97.6	deoxyribopyrimidine photolyase
sll1629	1,314,639	1,313,278	453	M94110	13.4	DNA photolyase
sll0707#	3,104,141	3,107,101	986	U32713	19.9	DNA polymerase I
sll0270	2,110,159	2,107,664	831	D00616	17.2	primosomal protein N'
sll0569	3,551,020	3,549,956	354	M29495	78.1	RecA gene product
sll1277	1,100,368	1,099,214	384	D26185	25.8	RecF protein
sll0020#	2,497,726	2,500,221	831	Z49988	25.3	DNA recombinase
sll1354	1,084,716	1,082,437	759	M54884	9.0	single-strand-DNA-specific exonuclease RecJ
sll1520	2,080,120	2,078,366	584	M30297	18.0	DNA repair protein RecN
sll1536	974,053	975,489	478	M30198	19.7	ATP-dependent DNA helicase RecQ
sll1426	3,283,467	3,284,165	232	X17014	44.2	recombination protein
sll0876	1,132,899	1,132,264	211	D83138	21.0	Holliday junction DNA helicase RuvA
sll0613#	2,652,951	2,651,866	361	Z138892	100.0	Holliday junction DNA helicase RuvB
sll0925#	3,228,010	3,228,375	121	X65079	22.3	single-stranded DNA-binding protein
sll2058	1,414,126	1,416,822	898	X72391	42.1	DNA topoisomerase I
sll0790#	3,048,284	3,048,634	116	U13633	34.1	UmuC protein
sll1844	962,888	965,800	970	X15867	50.1	excinuclease ABC subunit A
sll0459#	2,612,715	2,610,706	669	M80215	54.7	excinuclease ABC subunit B
sll0865	1,158,909	1,157,029	626	L29642	22.6	excinuclease ABC subunit C
sll1143	1,024,659	1,022,278	793	M63176	25.1	DNA helicase II
sll0733	120,719	121,660	313	U00076	8.1	integrase-recombinase protein
sll1854	2,233,864	2,233,037	275	D26185	15.7	exodeoxyribonuclease III
sll1543	980,276	981,694	472	L02362	11.4	DNA-damage-inducible protein
sll0214#	2,506,131	2,507,405	424	U06424	33.6	cytosine-specific methyltransferase
sll1366	3,308,773	3,305,654	1039	Z36114	9.8	helicase of the snf2/rad54 family
Transcription						
Degradation of RNA						
sll130	95,236	95,808	190	D83536	27.9	ribonuclease HII
sll1290	695,211	693,211	666	X67913	3.5	ribonuclease II
sll1646	2,071,379	2,072,074	231	D64044	19.2	ribonuclease III
sll0346#	2,431,704	2,432,438	244	D64116	13.8	ribonuclease III
sll0320#	2,437,888	2,437,235	217	U32831	10.6	ribonuclease D
sll1129	93,128	95,152	674	U38804	28.0	ribonuclease E
sll0080#	2,884,357	2,884,839	160	D83536	37.3	ribonuclease H
RNA synthesis, modification, and DNA transcription						
sll0083#	2,887,644	2,889,122	492	M63288	32.8	ATP-dependent RNA helicase DeaD
sll0743	132,483	133,859	458	Z48001	21.4	N utilization substance protein
sll0271	2,105,770	2,104,943	275	U00082	9.6	N utilization substance protein B
sll1742	926,033	925,416	205	X72627	100.0	transcription antitermination protein NusG
sll1043	98,481	96,325	718	U29668	45.5	polyribonucleotide nucleotidyltransferase
sll1818	830,085	829,141	314	U38804	60.1	RNA polymerase alpha subunit
sll1787	860,866	857,558	1102	U38804	66.1	RNA polymerase beta subunit
sll1265	1,854,102	1,855,982	626	M60831	81.1	RNA polymerase gamma-subunit
sll1789	857,450	853,497	1317	U30821	36.3	RNA polymerase beta prime subunit
sll2012	1,255,739	1,254,783	318	D78583	61.8	RNA polymerase sigma factor
sll1689	1,302,780	1,301,671	369	D10973	38.6	RNA polymerase sigma factor
sll0306#	2,270,163	2,269,126	345	D78583	66.4	RNA polymerase sigma factor
sll0184#	2,732,774	2,731,560	404	M95759	60.2	RNA polymerase sigma factor
sll0653	3,323,275	3,324,552	425	D50318	71.4	RNA polymerase sigma factor
sll1545	983,804	984,475	223	U15180	20.6	RNA polymerase sigma-E factor
sll0856	1,342,612	1,342,052	186	U00075	17.5	RNA polymerase sigma-E factor

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
slr1564	3,371,247	3,372,023	258	M13927	17.1	RNA polymerase sigma-37	<i>rpoF</i>
Translation							
Aminoacyl tRNA synthetases and tRNA modification							
slr0362	2,144,246	2,141,613	877	X95571	38.0	alanyl-tRNA synthetase	<i>alaS</i>
slr0502#	3,210,452	3,208,698	584	X15320	37.2	arginyl-tRNA synthetase	<i>argS</i>
slr0495#	3,224,017	3,222,476	513	X68192	49.8	asparaginyl-tRNA synthetase	<i>asnS</i>
slr1720	1,472,149	1,473,948	599	X70943	42.6	aspartyl-tRNA synthetase	<i>aspS</i>
slr0958	2,026,675	2,028,126	483	D26185	35.8	cysteinyl-tRNA synthetase	<i>cysS</i>
slr0070#	2,600,705	2,601,697	330	X63666	26.3	methionyl-tRNA formyltransferase	<i>fmt</i>
slr0179#	2,743,125	2,741,674	483	D26185	31.0	glutamyl-tRNA synthetase	<i>gltX</i>
slr0638#	2,659,905	2,660,804	299	U00039	59.1	glycyl-tRNA synthetase alpha chain	<i>glyQ</i>
slr0220#	2,513,806	2,515,974	722	U00078	21.7	glycyl-tRNA synthetase beta chain	<i>glyS</i>
slr0357#	2,456,935	2,458,278	447	U38804	47.1	histidyl-tRNA synthetase	<i>hisS</i>
slr1560	3,368,416	3,369,621	401	L35476	40.4	histidyl tRNA synthetase	<i>hisS</i>
slr1362	1,065,204	1,062,238	988	X74219	33.8	isoleucyl-tRNA synthetase	<i>ileS</i>
slr11074	809,325	806,716	869	U00078	35.8	leucyl-tRNA synthetase	<i>leuS</i>
slr1550	995,275	996,807	510	D26185	49.9	lysyl-tRNA synthetase	<i>lysS</i>
slr0649#	2,678,140	2,679,738	532	X57925	36.1	methionyl-tRNA synthetase	<i>metS</i>
slr0927	340,966	339,737	409	U36379	51.3	S-adenosylmethionine synthetase	<i>metX</i>
slr0817	1,693,538	1,692,627	303	U14003	22.9	tRNA delta-2-isopentenylpyrophosphate (IPP) transferase	<i>miaA</i>
slr0454#	2,630,266	2,629,271	331	U01668	51.2	phenylalanyl-tRNA synthetase alpha chain	<i>pheS</i>
slr1553	1,991,266	1,988,834	810	X94345	47.3	phenylalanyl-tRNA synthetase	<i>pheT</i>
slr1425	1,587,062	1,585,209	617	D83536	33.2	proline-tRNA ligase	<i>proS</i>
slr0922#	2,797,422	2,798,006	194	X61941	24.3	peptidyl-tRNA hydrolase	<i>pth</i>
slr0467#	2,941,666	2,940,566	366	M37702	30.2	queuosine biosynthesis protein QueA	<i>queA</i>
slr1703	722,570	723,862	430	D26185	41.1	seryl-tRNA synthetase	<i>serS</i>
slr0713#	3,118,390	3,119,514	374	D26469	36.0	transfer RNA-guanine transglycosylase	<i>tgt</i>
slr0078#	2,893,012	2,891,201	603	M36594	39.3	threonyl-tRNA synthetase	<i>thrS</i>
slr1198	293,485	292,790	231	X74933	38.7	tRNA(m1G37)methyltransferase	<i>trmD</i>
slr1884	1,243,154	1,244,287	377	U00075	36.1	tryptophanyl-tRNA synthetase	<i>trpS</i>
slr1820	828,695	827,868	275	X02743	22.2	pseudouridine synthase I	<i>truA</i>
slr0457	3,508,111	3,509,001	296	X13775	22.0	tRNA pseudouridine 55 synthase	<i>truB</i>
slr1031	659,370	660,584	404	U00085	32.5	tyrosyl tRNA synthetase	<i>tyrS</i>
slr1720	662,952	663,188	78	U00085	23.2	tyrosyl tRNA synthetase	<i>tyrS</i>
slr0557#	3,264,290	3,267,022	910	X77239	41.4	valyl-tRNA synthetase	<i>valS</i>
Degradation of proteins, peptides, and glycopeptides							
slr1343	3,277,923	3,275,314	869	U35646	4.9	aminopeptidase	<i>ape2</i>
slr1641	2,062,905	2,065,523	872	U20646	75.9	ClpB protein	<i>clpB</i>
slr0156	2,194,405	2,197,101	898	U20646	61.3	ClpB protein	<i>clpB</i>
slr0020#	2,468,872	2,466,407	821	U16134	89.4	ATP-dependent Clp protease regulatory subunit	<i>clpC</i>
slr0164	2,205,774	2,206,451	225	U16135	28.4	ATP-dependent Clp protease proteolytic subunit	<i>clpP</i>
slr0165	2,206,551	2,207,159	202	U16135	56.8	ATP-dependent Clp protease proteolytic subunit	<i>clpP</i>
slr0542#	3,212,598	3,213,194	198	U16135	75.6	ATP-dependent protease ClpP	<i>clpP</i>
slr0534#	3,246,101	3,245,421	226	U16135	63.9	ATP-dependent Clp protease proteolytic subunit	<i>clpP</i>
slr0535#	3,245,416	3,244,079	445	X95306	53.5	ATP-dependent protease ATPase subunit	<i>ctpA</i>
slr0008#	2,476,853	2,478,136	427	L25250	100.0	carboxyl-terminal processing protease	<i>ctpB</i>
slr0257	168,533	169,921	462	X96490	99.3	carboxyl-terminal protease	<i>ctpB</i>
slr0807	1,688,213	1,689,259	348	U32844	28.6	sialoglycoprotease	<i>gcp</i>
slr1679	242,047	240,863	394	U07351	23.5	protease HhoA	<i>hhoA</i>
slr1427	1,584,499	1,583,249	416	U32853	21.2	protease HhoB	<i>hhoB</i>
slr1204	886,184	887,542	452	U32853	24.3	serine protease HtrA	<i>htrA</i>
slr0136	2,208,695	2,207,370	441	D00398	34.7	aminopeptidase P	<i>pepP</i>
slr1751	1,015,511	1,016,782	423	X96490	38.5	carboxyl-terminal protease	<i>prc</i>
slr0659	3,336,407	3,338,548	713	M84574	35.1	oligopeptidase A	<i>prlC</i>
slr1703	1,283,193	1,281,361	610	U32775	18.8	protease IV	<i>sppA</i>
slr0021#	2,500,322	2,501,155	277	L27482	16.3	protease IV	<i>sppA</i>
slr1331	1,669,101	1,670,642	513	U27560	4.8	processing protease	<i>ymxG</i>
slr2009	1,259,751	1,258,444	435	L08471	10.0	processing protease	
slr2008	1,261,052	1,259,760	430	L43135	9.3	processing protease	
slr0055#	2,596,566	2,595,280	428	L12965	10.3	processing protease	
slr0535#	3,196,783	3,198,624	613	L29506	13.5	serine proteinase	
Nucleoproteins							
slr0517#	3,182,013	3,181,708	101	L47126	100.0	RNA binding protein	<i>rpbA</i>
slr1712	971,289	970,882	135	S78244	47.4	DNA binding protein HU	
slr1480	1,135,337	1,135,588	83	L20890	82.3	RNA-binding protein	
slr0193#	2,724,648	2,725,103	151	L15080	20.8	RNA-binding protein	
slr1120	873,270	869,668	1200	D50617	3.9	chromosome segregation protein SMC1	
Protein modification and translation factors							
slr0869	1,150,067	1,149,471	198	L10383	17.3	Leu/Phe-tRNA-protein transferase	<i>aaT</i>
slr1251	1,392,972	1,393,487	171	U31077	72.0	peptidyl-prolyl cis-trans isomerase	<i>cyp</i>
slr1549	994,343	994,906	187	U00075	22.0	polypeptide deformylase	<i>def</i>
slr0434#	2,549,388	2,549,951	187	X61676	39.7	elongation factor P	<i>efp</i>
slr0145	2,192,681	2,192,133	182	D83536	45.2	ribosome releasing factor	<i>frr</i>
slr1098	1,918,608	1,916,533	691	X15646	82.4	elongation factor EF-G	<i>fus</i>
slr1463	3,313,667	3,315,754	695	X65159	99.8	elongation factor EF-G	<i>fus</i>
slr1105	204,604	206,397	597	U41261	8.7	elongation factor EF-G	<i>fus</i>
slr0830#	2,847,189	2,845,180	669	X16278	21.5	elongation factor EF-G	<i>fus</i>
slr13441	831,558	831,355	67	X04465	79.8	initiation factor IF-1	<i>infA</i>

Table 1. Continued.

ORF No.	Position	Length (aa)	Accession No.	QryMatch (%)	Product	
Ribosomal proteins: synthesis and modification						
sll0744	134,437	137,442	1001 X04399	30.8	initiation factor IF-2	<i>infB</i>
sll0974	343,026	343,559	177 U38804	72.6	initiation factor IF-3	<i>infC</i>
sll2001	1,619,653	1,618,127	508 X63444	37.2	leucine aminopeptidase	<i>lap</i>
sll0555#	2,804,283	2,803,366	305 D00619	35.6	methionine aminopeptidase	<i>map</i>
sll0786#	3,042,788	3,043,612	274 X55778	39.8	methionine aminopeptidase	<i>map</i>
sll0918#	2,793,159	2,793,920	253 X55778	46.9	methionine aminopeptidase	<i>map</i>
sll1394	57,224	56,556	222 U37150	60.5	peptide methionine sulfoxide reductase	<i>msrA</i>
sll1795	263,321	263,965	214 U14003	27.8	peptide methionine sulfoxide reductase	<i>msrA</i>
sll1865	2,215,551	2,214,685	288 U32746	40.2	peptide chain release factor	<i>pfbB</i>
sll1435	1,058,537	1,059,820	427 U14003	6.4	PmbA protein	<i>pmbA</i>
sll0227	149,683	148,943	246 D42050	12.9	peptidyl-prolyl cis-trans isomerase B	<i>ppiB</i>
sll1110	3,521,694	3,520,597	365 Z49782	44.4	peptide chain release factor	<i>pfrA</i>
sll1228	1,033,902	1,035,545	547 U00087	39.6	peptide-chain-release factor 3	<i>pfrC</i>
sll1980	1,559,611	1,559,069	180 U05044	43.1	thiol:disulfide interchange protein TrxA	<i>trxA</i>
sll1261	1,722,006	1,721,350	218 U38804	65.0	elongation factor TS	<i>tsf</i>
sll1099	1,916,473	1,915,274	399 U30821	81.8	protein synthesis elongation factor Tu	<i>tufA</i>
sll0328#	2,283,232	2,283,705	157 L33929	28.8	low molecular weight phosphotyrosine protein phosphatase	
Transport and binding proteins						
sll1909	1,432,898	1,431,996	300 S67010	15.8	ribosomal protein L11 methyltransferase, PrmA	<i>prmA</i>
sll0853	1,339,155	1,339,631	158 X06117	17.0	ribosomal-protein-alanine acetyltransferase	<i>rml</i>
sll1744	924,802	924,086	238 X73005	100.0	50S ribosomal protein L1	<i>rpl1</i>
sll1802	840,952	840,122	276 Z67753	65.1	50S ribosomal protein L2	<i>rpl2</i>
sll1799	842,613	841,972	213 X17498	62.7	50S ribosomal protein L3	<i>rpl3</i>
sll1800	841,932	841,300	210 U38804	52.6	50S ribosomal protein L4	<i>rpl4</i>
sll1808	836,954	836,352	200 X16548	68.3	50S ribosomal protein L5	<i>rpl5</i>
sll1810	835,799	835,260	179 M30487	58.6	50S ribosomal protein L6	<i>rpl6</i>
sll1244	1,751,829	1,751,311	172 D10716	100.0	50S ribosomal protein L9	<i>rpl9</i>
sll1745	923,839	923,318	173 X53178	100.0	50S ribosomal protein L10	<i>rpl10</i>
sll1743	925,314	924,889	141 X73005	100.0	50S ribosomal protein L11	<i>rpl11</i>
sll1746	923,230	922,844	128 X53178	100.0	50S ribosomal protein L12	<i>rpl12</i>
sll1821	827,803	827,348	151 U38804	62.5	50S ribosomal protein L13	<i>rpl13</i>
sll1806	837,717	837,349	122 U38804	79.8	50S ribosomal protein L14	<i>rpl14</i>
sll1813	834,264	833,821	147 M31102	40.3	50S ribosomal protein L15	<i>rpl15</i>
sll1805	838,637	838,218	139 M30487	77.6	50S ribosomal protein L16	<i>rpl16</i>
sll1819	829,063	828,713	116 M26414	43.0	50S ribosomal protein L17	<i>rpl17</i>
sll1811	835,256	834,894	120 M30487	71.8	50S ribosomal protein L18	<i>rpl18</i>
sll1740	927,228	926,860	122 X72627	100.0	50S ribosomal protein L19	<i>rpl19</i>
sll0767#	2,404,968	2,404,615	117 U30821	72.5	50S ribosomal protein L20	<i>rpl20</i>
sll1678	1,957,758	1,958,132	124 Z67753	45.4	50S ribosomal protein L21	<i>rpl21</i>
sll1803	839,795	839,430	121 Z67753	57.6	50S ribosomal protein L22	<i>rpl22</i>
sll1801	841,307	841,002	101 U38804	46.4	50S ribosomal protein L23	<i>rpl23</i>
sll1807	837,348	837,001	115 M87838	52.4	50S ribosomal protein L24	<i>rpl24</i>
ssr2799	1,958,240	1,958,503	87 M75731	62.8	50S ribosomal protein L27	<i>rpl27</i>
ssr1604	318,661	318,897	78 X68078	56.9	50S ribosomal protein L28	<i>rpl28</i>
ssl3436	838,215	837,994	73 U38804	46.2	50S ribosomal protein L29	<i>rpl29</i>
ss13445	826,882	826,637	81 U38804	70.9	50S ribosomal protein L31	<i>rpl31</i>
ssr1736	502,042	502,215	57 U38804	54.5	50S ribosomal protein L32	<i>rps32</i>
ssl1398#	2,831,106	2,831,303	65 Z67753	72.4	50S ribosomal protein L33	<i>rpl33</i>
smr0011	1,826,764	1,826,901	45 Z35718	51.4	50S ribosomal protein L34	<i>rpl34</i>
ssl1426#	2,405,312	2,405,109	67 U30821	48.6	50S ribosomal protein L35	<i>rpl35</i>
smr0006	831,217	831,101	38 U30821	83.2	50S ribosomal protein L36	<i>rpl36</i>
sll1356	1,097,077	1,098,063	328 D28752	78.2	30S ribosomal protein S1	<i>rps1</i>
sll1984	1,815,454	1,816,371	305 D28752	27.8	30S ribosomal protein S1	<i>rps1</i>
sll1260	1,722,969	1,722,160	269 U38804	61.9	30S ribosomal protein S2	<i>rps2</i>
sll1804	839,400	838,678	240 M30487	67.2	30S ribosomal protein S3	<i>rps3</i>
sll0469#	2,603,947	2,604,555	202 U38804	73.1	30S ribosomal protein S4	<i>rps4</i>
sll1812	834,854	834,333	173 U38804	75.0	30S ribosomal protein S5	<i>rps5</i>
sll1767	1,227,932	1,227,591	113 D26185	28.1	30S ribosomal protein S6	<i>rps6</i>
sll1097	1,919,285	1,918,815	156 X15646	79.9	30S ribosomal protein S7	<i>rps7</i>
sll1809	836,260	835,859	133 U38804	65.0	30S ribosomal protein S8	<i>rps8</i>
sll1822	827,348	826,935	137 U38804	61.0	30S ribosomal protein S9	<i>rps9</i>
sll1101	1,915,135	1,914,818	105 Z21676	96.3	30S ribosomal protein S10	<i>rps10</i>
sll1817	830,586	830,194	130 U30821	78.9	30S ribosomal protein S11	<i>rps11</i>
sll1096	1,919,816	1,919,436	126 U30821	91.6	30S ribosomal protein S12	<i>rps12</i>
sll1816	831,018	830,635	127 U30821	71.2	30S ribosomal protein S13	<i>rps13</i>
ssl0628#	2,644,795	2,645,097	100 D85103	74.9	30S ribosomal protein S14	<i>rps14</i>
ssl1784	336,582	336,313	89 Z37726	49.8	30S ribosomal protein S15	<i>rps15</i>
ssl0482	2,127,879	2,128,127	82 U30821	63.1	30S ribosomal protein S16	<i>rps16</i>
ssl3437	837,986	837,741	81 U38804	61.0	30S ribosomal protein S17	<i>rps17</i>
ssl1399#	2,831,400	2,831,615	71 U30821	73.0	30S ribosomal protein S18	<i>rps18</i>
ssl3432	840,089	839,811	92 U30821	80.5	30S ribosomal protein S19	<i>rps19</i>
ssl2233	862,166	861,873	97 U30821	41.3	30S ribosomal protein S20	<i>rps20</i>
ssl0601#	2,448,404	2,448,222	60 D17710	61.1	30S ribosomal protein S21	<i>rps21</i>

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll1768	1,224,646	1,223,666	326	U20909	24.4	oligopeptide transport system permease protein	<i>appB</i>
sll0312#	2,456,768	2,455,755	337	U20909	27.2	oligopeptide transport system permease protein	<i>appB</i>
sll0324#	2,277,989	2,278,873	294	U20909	27.3	oligopeptide transport system permease protein	<i>appC</i>
sll0833#	2,838,910	2,837,795	371	D85103	60.9	oligopeptide transport system permease protein	<i>appC</i>
sll2057	1,412,923	1,413,666	247	U38664	49.1	water channel protein	<i>apqZ</i>
sll0242	144,061	144,543	160	U32820	36.9	bacterioferritin comigratory protein	<i>bcp</i>
sll0221	161,642	161,088	184	M63654	17.1	bacterioferritin comigratory protein	<i>bcp</i>
sll1890	822,837	823,367	176	M83692	46.3	bacterioferritin	<i>bfr</i>
sll1341	3,282,912	3,282,442	156	M83692	46.2	bacterioferritin	<i>bfr</i>
sll0467#	2,601,733	2,602,536	267	D90223	30.7	high-affinity branched-chain amino acid transport ATP-binding protein	<i>braF</i>
sll0374#	2,709,006	2,708,257	249	D90223	26.4	high-affinity branched-chain amino acid transport ATP-binding protein	<i>braG</i>
sll0797#	3,058,410	3,060,338	642	M90750	31.8	cadmium-transporting ATPase	<i>cadA</i>
sll0798#	3,061,356	3,063,521	721	L46864	35.3	cadmium-transporting ATPase	<i>cadA</i>
sll1457	3,303,481	3,304,680	399	J05278	16.8	chromate transport protein	<i>chrA</i>
sll1455	3,301,555	3,302,622	355	J04512	60.1	sulfate transport system permease protein	<i>cysA</i>
sll0895#	3,239,748	3,238,873	291	M80795	9.5	ammonium transport protein	<i>cysQ</i>
sll1453	3,299,716	3,300,576	286	X67911	82.2	sulfate transport system permease protein	<i>cysT</i>
sll1454	3,300,563	3,301,393	276	M65247	59.0	sulfate transport system permease protein	<i>cysW</i>
sll0794#	3,051,771	3,054,935	1054	M26073	22.4	cation efflux system protein	<i>czcA</i>
sll1314	1,170,187	1,169,078	369	X63974	10.1	C4-dicarboxylase binding protein	<i>dctP</i>
sll0817	1,704,375	1,705,799	474	X82644	16.0	isochorismate synthase	<i>entC</i>
sll0923	347,806	345,536	756	U17898	3.6	exopolysaccharide export protein	<i>epsB</i>
sll1404	33,544	32,912	210	U28377	11.8	biopolymer transport ExbB protein	<i>exbB</i>
sll0677	415,562	416,245	227	U28377	10.9	biopolymer transport ExbB protein	<i>exbB</i>
sll1319	16,740	17,687	315	X87208	22.1	iron(III) dicarboxylate transport system permease protein FecB	<i>fecB</i>
sll1491	42,405	43,397	330	X87208	9.9	iron(III) dicarboxylate-binding periplasmic protein	<i>fecB</i>
sll1492	43,571	44,506	311	X87208	8.0	iron(III) dicarboxylate-binding periplasmic protein	<i>fecB</i>
sll1316	13,498	14,529	343	X93092	36.8	iron(III) dicarboxylate transport system permease protein FecC	<i>fecC</i>
sll1317	14,626	15,675	349	X93092	32.3	iron(III) dicarboxylate transport system permease protein FecD	<i>fecD</i>
sll1318	15,937	16,743	268	X87208	52.9	iron(III) dicarboxylate transport system permease protein FecE	<i>fecE</i>
sll1392	698,970	700,814	614	X71063	10.7	ferrous iron transport protein B	<i>feoB</i>
sll1409	27,857	25,266	863	M12486	7.7	ferrichrome-iron receptor	<i>fhuA</i>
sll1406	32,454	29,968	828	M12486	6.2	ferrichrome-iron receptor	<i>fhuA</i>
sll1490	39,802	42,363	853	M12486	8.9	ferrichrome-iron receptor	<i>fhuA</i>
sll0771#	2,400,616	2,399,210	468	X16472	100.0	glucose transport protein	<i>glcP</i>
sll1104	1,912,786	1,911,896	296	M61017	15.9	glutamine-binding protein	<i>glnH</i>
sll1270	1,116,021	1,114,429	530	X77636	13.5	glutamine-binding periplasmic protein/glutamine transport system permease protein	<i>glnH/glnP</i>
sll1145	809,450	810,658	402	L10328	34.6	glutamate permease	<i>gltS</i>
sll1581	721,247	719,733	504	U22511	6.3	GumB protein	<i>gumB</i>
sll0327#	2,281,509	2,283,182	557	S72674	7.1	iron utilization protein	<i>hitB</i>
ssr1386	1,700,893	1,701,135	80	M73833	100.0	inorganic carbon transport protein	<i>ictA</i>
sll1206	20,408	17,853	851	X97499	16.1	ferri-aerobactin receptor	<i>iutA</i>
sll1728	1,493,025	1,494,701	558	K02670	29.9	potassium-transporting ATPase A chain	<i>kdpA</i>
sll1729	1,494,758	1,496,830	690	K02670	50.1	potassium-transporting ATPase B chain	<i>kdpB</i>
sll1730	1,497,306	1,497,878	190	K02670	27.0	potassium-transporting ATPase C chain	<i>kdpC</i>
sll1731	1,498,110	1,499,222	370	M36066	29.6	potassium-transporting ATPase D chain	<i>kdpD</i>
sll2107	1,620,973	1,621,881	302	S36795	8.3	polysialic acid transport protein KpsM	<i>kpsM</i>
sll2108	1,621,978	1,623,093	371	L11870	24.5	polysialic acid transport ATP-binding protein KpsT	<i>kpsT</i>
sll1202	884,635	885,531	298	X66596	20.5	lactose transport system permease protein LacF	<i>lacF</i>
sll1723	1,476,845	1,477,657	270	X66092	27.8	lactose transport system permease protein LacG	<i>lacG</i>
sll1881	1,239,490	1,240,212	240	D90223	39.2	high-affinity branched-chain amino acid transport ATP-binding protein BraG	<i>livF</i>
sll0764#	2,408,686	2,407,565	373	J05516	17.2	high-affinity branched-chain amino acid transport ATP-binding protein	<i>livG</i>
sir0949	2,017,104	2,017,964	286	D90223	14.4	high-affinity branched-chain amino acid transport permease protein	<i>livH</i>
sir1200	882,023	883,189	388	D12589	6.7	high-affinity branched-chain amino acid transport protein	<i>livH</i>
sir1224	1,026,511	1,027,737	408	U00006	31.6	cytoplasmic membrane protein for maltose uptake	<i>malK</i>
sll1374	1,842,690	1,841,056	544	L10328	8.6	melibiose carrier protein	<i>melB</i>
sir0014#	2,481,984	2,482,688	234	U38802	100.0	Mg ²⁺ transport ATPase	<i>mgtC</i>
srl1216	904,115	905,506	463	U18744	22.4	Mg ²⁺ transporter	<i>mgtE</i>
sll1599	1,482,162	1,481,380	260	L34630	100.0	Mn transporter MntA	<i>mntA</i>
sll1600	1,481,383	1,480,463	306	L34630	99.7	Mn transporter MntB	<i>mntB</i>
sll1598	1,483,253	1,482,261	330	L34630	100.0	Mn transporter MntC	<i>mntC</i>
sll0738#	3,135,996	3,135,184	270	S32789	27.5	molybdate-binding periplasmic protein	<i>modA</i>
sll0747	3,410,761	3,411,852	363	U12007	41.8	ATP binding protein responsible for multiple sugar import	<i>mskK</i>
sir0415#	2,684,959	2,687,055	698	M81961	5.5	Na ⁺ /H ⁺ antiporter	<i>napA</i>
sll0796#	3,055,813	3,057,150	445	L31491	15.2	nickel resistance	<i>nreB</i>
sll1450	1,010,574	1,009,234	446	Z19598	65.4	nitrate transport 45kD protein	<i>nrtA</i>
sir0040#	3,169,054	3,170,412	452	M32999	60.3	nitrate transport 45kD protein	<i>nrtA</i>
sll1451	1,009,148	1,008,321	275	Z19598	61.3	nitrate transport protein NrtB	<i>nrtB</i>
sir0041#	3,170,475	3,171,317	280	D26358	67.8	nitrate transport protein NrtB	<i>nrtB</i>
sll1452	1,008,246	1,006,234	670	D26358	55.8	nitrate transport protein NrtC	<i>nrtC</i>
sir0043#	3,173,335	3,175,338	667	D26358	73.0	nitrate transport protein NrtC	<i>nrtC</i>
sll1453	1,006,179	1,005,181	332	D26358	60.6	nitrate transport protein NrtD	<i>nrtD</i>
sir0044#	3,175,411	3,176,259	282	D26358	78.9	nitrate transport protein NrtD	<i>nrtD</i>
sll1082	796,732	795,932	266	X61625	33.4	nitrate transport protein NrtD	<i>nrtD</i>
sll1509	1,595,285	1,596,619	444	D17462	24.8	Na ⁺ -ATPase subunit J	<i>ntpJ</i>
sll1927	744,732	742,780	650	D14438	22.2	oligopeptide transport ATP-binding protein OppF	<i>oppF</i>
sll0753	3,423,032	3,424,381	449	M99564	8.8	P protein	<i>p</i>
sll1076	806,384	803,466	972	D16436	20.8	cation-transporting P-ATPase	<i>pacL</i>

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll0822	1,713,409	1,716,270	953	D16436	47.8	cation-transporting ATPase PacL	<i>pacL</i>
sll0672#	3,101,565	3,098,728	945	D16436	53.0	cation-transporting ATPase PacL	<i>pacL</i>
sll1614	1,459,930	1,457,213	905	X71022	95.9	H ⁺ -transporting ATPase	<i>pmaL</i>
sll1249	1,391,050	1,391,922	290	X02723	31.2	phosphate transport system permease protein PstA	<i>pstA</i>
sll0682#	2,639,441	2,638,578	287	U32764	30.0	phosphate transport system permease protein PstA	<i>pstA</i>
sll1250	1,391,976	1,392,791	271	D45195	50.0	phosphate transport ATP-binding protein PstB	<i>pstB</i>
sll0684#	2,637,628	2,636,828	266	D45195	52.1	phosphate transport ATP-binding protein PstB	<i>pstB</i>
sll0683#	2,638,552	2,637,743	269	U15182	50.9	phosphate transport ATP-binding protein PstB	<i>pstB</i>
sll1248	1,390,059	1,391,045	328	X02723	30.1	phosphate transport system permease protein PstC	<i>pstC</i>
sll0681#	2,640,580	2,639,627	317	U32764	33.7	phosphate transport system permease protein PstC	<i>pstC</i>
sll1247	1,388,912	1,389,913	333	X71359	24.1	periplasmic phosphate binding protein	<i>pstS</i>
sll0680#	2,641,813	2,640,662	383	U32764	26.7	phosphate-binding periplasmic protein precursor (PBP)	<i>pstS</i>
sll0574	3,542,936	3,542,121	271	L31775	12.9	integral membrane O-antigen translocator protein	<i>rfbA</i>
sll0575	3,542,108	3,541,344	254	U36795	34.2	ATP-binding protein	<i>rfbB</i>
sll0982	352,263	353,555	430	U36795	22.0	ABC transporter	<i>rfbB</i>
sll1452	3,298,326	3,299,384	352	X67911	99.6	sulfate binding protein SbpA	<i>sbpA</i>
sll0679#	2,643,145	2,642,135	336	D26161	38.4	SphX protein precursor	<i>sphX</i>
sll1295	291,626	292,708	360	M33815	15.3	iron transport protein	<i>sufA</i>
sll0075#	2,873,258	2,874,028	256	U30821	66.3	ABC transporter subunit	<i>ycf16</i>
sll0074#	2,871,674	2,873,116	480	U30821	79.0	ABC transporter subunit	<i>ycf24</i>
sll1740	1,327,367	1,329,115	582	Y00142	4.1	extracellular solute-binding protein family	
sll1428	1,581,810	1,580,932	292	X12458	12.3	P3 protein	
sll0142	2,200,959	2,197,732	1075	M26073	8.0	cation efflux system protein CzcA	
sll1735	1,317,712	1,318,470	252	M61017	56.7	ABC transporter	
sll0146	2,192,051	2,190,933	372	D90223	7.3	high-affinity branched-chain amino acid transport protein BraE	
sll1776	228,866	230,566	566	X82256	16.2	high affinity sulfate transporter	
sll1864	2,219,175	2,216,476	899	Z56277	3.2	chloride channel protein	
sll0834#	2,837,510	2,835,816	564	X82454	5.3	low affinity sulfate transporter	
sll0096#	2,902,831	2,904,501	556	X82454	5.2	low affinity sulfate transporter	
sll0530#	3,189,929	3,190,768	279	X66596	14.5	membrane bound sugar transport protein	
sll0531#	3,190,768	3,191,664	298	U15180	15.5	membrane bound sugar transport protein	
sll1087	1,942,087	1,940,549	512	L77077	32.7	sodium-coupled permease	
sll11920	766,538	764,301	745	D16437	54.4	cation-transporting ATPase	
sll1336	1,723,452	1,724,570	372	U36603	31.3	H ⁺ /Ca ²⁺ exchanger	
sll0273	2,104,391	2,102,769	540	U00006	5.1	Na ⁺ /H ⁺ exchanger	
sll1950	2,254,112	2,256,454	780	U04356	33.9	cation-transporting P-type ATPase	
sll0689#	2,633,509	2,632,124	461	U17283	16.5	Na ⁺ /H ⁺ -antiporter protein	
sll1595	453,214	454,446	410	X73329	6.6	Na ⁺ /H ⁺ -antiporter protein	
sll0993	640,613	639,516	365	U24196	7.6	potassium channel	
sll1727	1,488,843	1,490,426	527	U00006	9.0	eukaryotic Na ⁺ /H ⁺ exchanger	
sll0513#	2,924,779	2,925,819	346	X64857	9.8	periplasmic iron-binding protein	
sll0671#	3,102,961	3,101,819	380	U15180	12.1	magnesium and cobalt transport protein	
sll0507#	3,203,862	3,202,699	387	U15180	9.3	magnesium and cobalt transport protein	
sll0401	2,150,247	2,151,401	384	M64519	6.9	spermidine/putrescine-binding periplasmic protein	
sll1488	36,721	38,538	605	U00069	11.4	ABC transporter	
sll0251	154,703	155,461	252	M58480	53.0	ABC transporter	
sll1041	186,554	185,772	260	J04512	22.2	ABC transporter	
sll1001	523,798	523,016	260	U18997	23.0	ABC transporter	
sll2044	584,674	585,543	289	U30821	20.9	ABC transporter	
sll2019	761,482	763,263	593	Z49782	24.2	ABC transporter	
sll149	813,799	815,604	601	Z49782	20.7	ABC transporter	
sll1901	850,605	851,585	326	U30873	18.2	ABC transporter	
sll1725	949,343	947,511	610	Z49782	19.9	ABC transporter	
sll1276	1,102,014	1,100,410	534	Z49782	27.0	ABC transporter	
sll1623	1,322,523	1,321,852	223	Z34795	18.8	ABC transporter	
sll0864	1,360,434	1,362,158	574	U18997	21.8	ABC transporter	
sll0240	1,532,957	1,532,301	218	M33815	32.5	ABC transporter	
sll1878	1,798,658	1,797,552	368	M93239	29.1	ABC transporter	
sll1870	1,814,234	1,813,554	226	U00075	20.2	ABC transporter	
sll0912	2,016,818	2,014,908	636	U32755	24.2	ABC transporter	
sll0759#	2,412,110	2,411,067	347	L06249	24.7	ABC transporter	
sll0354#	2,447,491	2,448,123	210	M32101	16.9	ABC transporter	
sll0415#	2,541,885	2,540,821	354	X53676	16.1	ABC transporter	
sll0385#	2,692,382	2,691,528	284	U34795	21.6	ABC transporter	
sll0489#	2,906,510	2,905,482	342	L20573	18.3	ABC transporter	
sll0484#	2,911,859	2,911,122	245	X75422	59.2	ABC transporter	
sll0615#	2,946,344	2,948,086	580	L08627	19.8	ABC transporter	
sll0739#	3,135,137	3,133,290	615	J04512	12.7	ABC transporter	
sll1494	44,948	46,789	613	Z67882	6.9	ABC transporter	
sll1113	60,524	61,522	332	U00039	17.4	ABC transporter	
sll0977	349,468	350,298	276	U36795	17.7	ABC transporter	
ssr2802	1,961,439	1,961,600	53	U36795	39.7	ABC transporter	
sll0182#	2,737,791	2,735,806	661	U32798	17.5	ABC transporter	
sll0778#	3,081,209	3,078,837	790	X77589	6.0	ABC transporter	
sll0544#	3,217,855	3,218,655	266	U32776	30.3	ABC transporter	
sll11081	797,631	796,789	280	D64043	16.3	integral membrane components of other binding-protein-dependent transport system	

Other categories

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
Adaptations and atypical conditions							
ssr1169#	3,084,345	3,084,584	79	U00966	26.9	salt-stress induced hydrophobic peptide	<i>ESI3</i>
slr1212	897,354	899,888	844	L24119	3.3	ethylene response sensor protein	<i>ETR1</i>
ssr1789	398,188	398,361	57	U12333	29.4	high light inducible protein	<i>hliA</i>
ssl2542	701,350	701,138	70	U12333	32.3	high light-inducible protein	<i>hliA</i>
ssr2595	982,968	983,180	70	U12333	31.5	high light inducible protein	<i>hliA</i>
ssl1633	1,142,015	1,141,803	70	U30821	36.7	CAB/ELIP/HLIP superfamily	<i>hliA</i>
ssl0947	2,263,380	2,262,805	191	L29194	73.9	light repressed protein	<i>lrtA</i>
slr0875	1,131,810	1,132,247	145	U08371	19.1	large-conductance mechanosensitive channel	<i>mscL</i>
slr2047	593,257	594,243	328	D10391	22.0	phosphate starvation-inducible protein	<i>phoH</i>
ssl0473#	2,607,812	2,610,058	748	Z32538	12.5	phytochrome	<i>phy</i>
ssl1214	4,268	3,192	358	U37437	56.7	phytochrome-regulated gene	<i>AT103</i>
ssl1874	1,806,296	1,805,220	358	U38232	46.0	phytochrome-regulated gene	<i>AT103</i>
slr0746	3,409,355	3,410,623	422	U32936	100.0	salt tolerance protein A	<i>stpA</i>
ssl2922	474,432	474,205	75	L22308	36.9	virulence associated protein B	<i>vapB</i>
ssl2923	474,204	473,953	83	L22308	39.4	virulence associated protein C	<i>vapC</i>
ssl0690#	2,631,608	2,631,207	133	L22308	24.9	virulence associated protein C	<i>vapC</i>
slr0545#	3,220,162	3,221,106	314	X56267	7.4	auxin-induced protein	
Drug and analog sensitivity							
slr0454	3,504,240	3,506,969	909	M94248	7.0	acriflavine resistance protein	<i>acrB</i>
slr2131#	1,644,905	1,648,090	1061	X57948	36.1	acriflavine resistance protein	<i>acrF</i>
ssl0319#	3,041,493	3,042,407	304	L07945	61.2	beta-lactamase	<i>blaOXA-3</i>
slr1719	1,471,414	1,472,019	201	L29426	89.4	DrgA gene product	<i>drgA</i>
ssl0369#	2,365,930	2,369,181	1083	X57948	27.7	acriflavine resistance protein	<i>envD</i>
ssl0708	108,325	107,471	284	U32845	20.1	dimethyladenosine transferase	<i>ksgA</i>
slr0648	424,566	423,490	358	D21131	21.4	lipophilic protein	<i>lim</i>
ssl1154	1,388,296	1,387,040	418	S74031	7.3	quinolone resistance protein Nora	<i>nora</i>
ssl1910	779,411	777,066	781	X80179	98.1	protein conferring resistance to acetazolamide, Zam	<i>zam</i>
ssl0378#	2,378,981	2,381,095	704	M11436	14.1	7-beta-(4-carboxybutanamido)cephalosporanic acid acylase	
Radiation sensitivity							
ssl0766#	2,406,140	2,405,409	243	M96343	26.8	RadC protein	<i>radC</i>
slr0448	2,100,463	2,101,980	505	X63155	30.3	sms protein	<i>sms</i>
WD repeat proteins							
slr1409	1,182,665	1,183,645	326	L28125	11.6	beta transducin-like protein	
slr1410	1,183,660	1,184,664	334	Z50728	8.1	beta transducin-like protein	
slr0143	2,173,197	2,176,772	1191	X85125	19.9	beta transducin-like protein	
ssl0163#	2,324,636	2,319,555	1693	L28125	5.7	beta transducin-like protein	
ssl1491	3,374,765	3,373,719	348	L28125	18.8	beta transducin-like protein	
Hydrogenase							
ssl1221	1,677,967	1,676,366	533	X79285	64.8	hydrogenase subunit	<i>hoxF</i>
ssl1226	1,673,495	1,672,071	474	X79285	66.3	hydrogenase large subunit	<i>hoxH</i>
ssl1223	1,675,660	1,674,944	238	X79285	66.5	hydrogenase subunit	<i>hoxU</i>
ssl1224	1,674,898	1,674,350	182	X79285	62.9	hydrogenase small subunit	<i>hoxY</i>
slr2135	1,261,217	1,261,993	258	X52974	9.1	hydrogenase accessory protein	<i>hupE</i>
slr1675	1,955,221	1,955,562	113	X52974	23.8	hydrogenase expression/formation protein HypA	<i>hypA</i>
ssl1079	799,535	798,846	229	L23970	40.7	hydrogenase expression/formation protein HypB	<i>hypB</i>
ssl1432	1,908,621	1,907,764	285	L24513	33.2	hydrogenase isoenzymes formation protein HypB	<i>hypB</i>
ssl3580	1,757,514	1,757,284	76	X70183	36.9	hydrogenase expression/formation protein HypC	<i>hypC</i>
ssl1498	54,533	55,657	374	X52974	40.4	hydrogenase isoenzymes formation protein HypD	<i>hypD</i>
ssl1462	992,772	991,735	345	L23970	41.4	hydrogenase expression/formation protein HypE	<i>hypE</i>
ssl0322#	2,434,762	2,432,459	767	U29579	24.0	transcriptional regulatory protein HypF	<i>hypF</i>
ssl1559	1,974,765	1,973,611	384	X17482	72.8	soluble hydrogenase 42 kD subunit	
ssl1220	1,678,565	1,678,044	173	U07229	28.5	potential NAD-reducing hydrogenase subunit	
ssl3044	1,975,874	1,975,575	99	U09760	16.9	hydrogenase component	
Transposon-related functions							
ssl1397	53,108	52,260	282	U38915	98.9	transposase	
ssl0700	123,995	123,501	164	U38915	98.3	transposase	
ssl0699	124,348	123,989	119	U38915	84.9	transposase	
ssl0426	141,416	141,123	97	U38915	85.9	transposase	
slr1075	379,065	379,913	282	U38915	98.9	transposase	
ssl0651	422,259	421,765	164	U38915	98.3	transposase	
ssl0650	422,612	422,253	119	U38915	84.2	transposase	
ssl2699	473,414	473,662	82	U38915	88.2	transposase	
ssl1922	521,169	520,918	83	U38802	61.1	transposase	
ssl1920	521,357	521,076	93	U38802	80.2	transposase	
ssl3452	572,736	572,909	57	X60383	41.5	transposase	
ssl2036	573,494	574,510	338	U38915	52.1	transposase	
ssl1930	606,035	605,541	164	U38915	96.7	transposase	
ssl1792	852,898	852,470	142	U38915	28.0	transposase	
ssl1791	853,281	852,895	128	U38915	36.8	transposase	
ssl1716	968,352	967,567	261	U38799	99.3	transposase	
ssl1357	1,098,323	1,099,171	282	U38915	98.4	transposase	
ssl1780	1,201,392	1,200,376	338	U38915	54.0	transposase	
ssl1710	1,276,157	1,275,372	261	U38799	98.9	transposase	
ssl0856	1,346,197	1,346,556	119	U38915	84.2	transposase	
ssl0857	1,346,550	1,347,044	164	U38915	98.3	transposase	
ssl2078	1,384,824	1,385,084	86	M98778	31.8	transposase	
ssl1246	1,385,212	1,385,748	178	M98777	12.9	transposase	
ssl2062	1,420,940	1,422,142	400	U21215	33.4	transposase	

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product
sll1715	1,463,455	1,463,814	119	U38915	84.9	transposase
sll1716	1,463,808	1,464,302	164	U38915	98.3	transposase
ssr2898	1,483,397	1,483,603	68	U38802	97.8	transposase
sll0265	1,513,225	1,514,010	261	U38799	98.3	transposase
sll1985	1,553,960	1,553,601	119	X60383	23.1	transposase
sll1984	1,554,423	1,553,929	164	U38915	98.3	transposase
sll1983	1,554,776	1,554,417	119	U38915	84.9	transposase
sll1982	1,555,774	1,555,061	237	X60383	50.5	transposase
ssl2789	1,580,801	1,580,586	71	X02590	21.9	resolvase
sll1522	1,614,572	1,615,648	358	X60383	42.4	transposase
sll1523	1,615,869	1,616,528	219	U30714	19.2	transposase
sll1524	1,616,904	1,617,419	171	U38915	79.9	transposase
sll1999	1,623,648	1,623,130	172	U38915	88.3	transposase
sll1998	1,624,571	1,623,723	282	U38915	98.7	transposase
sll1997	1,625,095	1,624,628	155	U38915	97.6	transposase
ssf2227	1,679,517	1,679,804	95	X65471	19.3	transposase
sll1507	1,711,014	1,710,814	66	U38915	68.3	transposase
sll0808	1,711,659	1,711,093	188	U38915	52.3	transposase
sll1257	1,725,925	1,725,431	164	U38915	98.3	transposase
sll1256	1,726,278	1,725,919	119	U38915	84.9	transposase
sll1255	1,730,028	1,729,012	338	U38915	53.6	transposase
sll1282	1,877,208	1,877,567	119	U38915	50.3	transposase
sll1283	1,877,582	1,878,055	157	U38915	68.4	transposase
sll1437	1,901,879	1,901,385	164	U38915	98.3	transposase
sll1436	1,902,232	1,901,873	119	U38915	84.9	transposase
sll1094	1,923,472	1,923,170	100	U38915	27.8	transposase
sll1560	1,971,968	1,970,952	338	U38915	53.9	transposase
sll1682	1,970,581	1,970,988	135	X60383	39.6	transposase
sll1683	1,972,154	1,972,549	131	X60383	43.5	transposase
sll1684	1,972,609	1,973,061	150	X60383	20.0	transposase
sll1635	2,048,497	2,049,513	338	U38915	54.0	transposase
ssr0256	2,210,451	2,210,705	84	U38799	72.5	transposase
sll0166	2,210,626	2,210,928	100	U38915	77.4	transposase
sll1861	2,226,530	2,225,766	254	U38799	71.8	transposase
sll1860	2,227,404	2,226,619	261	U38802	100.0	transposase
sll1936	2,235,561	2,235,920	119	U38915	84.9	transposase
sll1937	2,235,914	2,236,408	164	U38915	98.3	transposase
sll0180#	2,327,013	2,328,029	338	U38915	54.0	transposase
sll0161#	2,328,695	2,328,393	100	U38915	76.7	transposase
ssl0296#	2,328,870	2,328,616	84	U38799	73.8	transposase
sll0350#	2,441,098	2,441,883	261	U38802	100.0	transposase
sll0317#	2,443,859	2,443,461	132	U38915	100.0	transposase
sll0315#	2,445,426	2,444,743	227	U38915	82.1	transposase
sll0352#	2,443,999	2,444,847	282	U38915	99.3	transposase
sll0012#	2,483,528	2,482,743	261	U38802	100.0	transposase
sll0201#	2,525,067	2,524,573	164	U38915	98.3	transposase
sll0200#	2,525,420	2,525,061	119	U38915	84.9	transposase
sll0230#	2,534,106	2,534,954	282	U38915	98.5	transposase
ssl0769#	2,558,617	2,558,423	64	U22370	27.6	transposase
ssr0871#	2,921,446	2,921,604	52	X60383	60.8	transposase
sll0511#	2,921,660	2,922,439	259	U38799	97.9	transposase
sll0099#	2,968,169	2,969,188	339	X60383	45.8	transposase
sll0172#	2,998,080	2,997,811	89	X60383	30.2	transposase
sll0092#	2,998,925	2,998,239	228	X60383	51.8	transposase
sll0799#	3,066,428	3,066,751	107	U38915	36.6	transposase
sll0800#	3,066,748	3,067,176	142	U38802	25.7	transposase
sll0677#	3,094,692	3,093,907	261	U38802	100.0	transposase
sll1277#	3,094,969	3,094,772	65	M60971	30.4	transposase
sll1175#	3,096,047	3,096,331	94	U38915	95.4	transposase
sll0703#	3,096,387	3,097,172	261	U38802	100.0	transposase
sml0002#	3,097,274	3,097,378	34	U38915	89.0	transposase
sll0704#	3,097,435	3,098,283	282	U38915	98.5	transposase
ssl1176#	3,098,424	3,098,717	97	U38915	100.0	transposase
sll0667#	3,109,694	3,109,035	219	X60383	53.8	transposase
sll0666#	3,110,151	3,109,732	139	U38802	84.6	transposase
sll0665#	3,110,559	3,110,215	114	U38915	98.3	transposase
sll1474	3,401,418	3,400,402	338	U38915	54.0	transposase
sll1585	3,405,462	3,405,848	128	U38915	46.0	transposase
sll1586	3,405,991	3,406,311	106	U38915	62.2	transposase
sll0460	3,511,818	3,512,291	157	X60383	54.7	transposase
ssr0817	3,513,229	3,513,441	70	X60383	34.2	transposase
sll0462	3,513,516	3,514,040	174	X60383	18.9	transposase
sll2112	1,626,165	1,626,524	119	U38915	84.2	transposase
sll2113	1,626,518	1,627,012	164	U38915	98.3	transposase
sll0431	3,513,163	3,512,315	282	U38915	98.9	transposase
Other						
sll1900	1,757,223	1,756,594	209	D13960	100.0	acetyltransferase
sll1653	3,453,175	3,454,425	416	X74289	29.6	N-acyl-L-amino acid amidohydrolase
sll1109	221,742	223,067	441	X69063	6.4	erythroid ankyrin
sll1705	732,418	733,284	288	S67156	17.6	aspartoacylase, ASP

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product	
sll0119#	3,000,786	3,001,742	318	U12276	12.6	serum resistance locus BrkB	<i>brkB</i>
sll1764	542,803	543,342	179	M36176	15.5	cAMP binding protein	<i>capA</i>
sll1869	1,815,304	1,814,231	357	U00692	8.2	3-chlorobenzoate-3,4-dioxygenase	<i>cbaB</i>
sll1513	461,960	460,956	334	U30821	44.0	c-type cytochrome synthesis protein	<i>ccsA</i>
sll2143	1,271,069	1,272,274	401	M32324	8.3	isopenicillin N epimerase	<i>cefD</i>
sll1298	679,023	678,283	246	M15201	12.8	diene lactone hydrolase	<i>clcD</i>
sll1704	1,281,337	1,280,567	256	M29288	10.2	cell signal signaling protein, C-factor	<i>csgA</i>
sll1556	3,359,578	3,360,579	333	U00069	49.8	2-hydroxyaciddehydrogenase	<i>dih</i>
sll0621	3,347,656	3,346,910	248	U14003	10.2	thiol:disulfide interchange protein DsbD	<i>dsbD</i>
sll1636	549,701	549,129	190	M82832	27.8	ferripyochelin binding protein	<i>fbp</i>
sll0298#	3,009,462	3,010,094	210	U14553	40.8	heterocyst to vegetative cell connection protein	<i>frhH</i>
sll1009	508,027	506,252	591	L06299	7.1	iron-regulated protein	<i>frpC</i>
sll2136	1,262,049	1,263,260	403	U00072	21.4	GcpE protein	<i>gcpE</i>
sll1653	282,223	281,507	238	M80245	21.1	spore germination protein c2	<i>gerC</i>
sll2097	1,562,468	1,562,842	124	D13920	37.6	cyanoglobin	<i>glbN</i>
sll2094	1,560,387	1,561,424	345	M97678	30.2	GlpX protein	<i>glpX</i>
sll0201#	2,733,081	2,733,986	301	X81133	17.0	heterodisulfide reductase subunit B	<i>hdrB</i>
sll1521	1,612,797	1,614,401	534	U14003	25.4	GTP-binding protein HflX	<i>hflX</i>
sll1519	1,610,727	1,611,464	245	L42525	17.4	HgIK	<i>hgIK</i>
sll1514	460,690	460,250	146	M94510	20.6	spore protein sp21	<i>hspA</i>
sll1227	1,031,202	1,033,787	861	L36858	3.7	chloroplast import-associated channel IAP75	<i>IAP75</i>
sll0617#	2,646,074	2,645,271	267	M73744	40.5	chloroplast membrane-associated 30 kD protein	<i>im30</i>
sll1188	3,529,323	3,529,994	223	M73744	24.1	chloroplast membrane-associated 30 kD protein	<i>im30</i>
sll0604	3,564,838	3,566,649	603	X91655	67.9	LepA gene product	<i>lepA</i>
sll0626	3,340,969	3,339,500	489	D21823	12.6	LIM17 protein	<i>lim17</i>
sll0862	1,354,094	1,355,074	326	X79146	7.2	LmbP protein	<i>lmbP</i>
sll1849	557,423	558,979	518	L29436	21.6	mercuric reductase	<i>merA</i>
sll0873	1,141,660	1,140,497	387	D31783	17.2	carboxyhoerspermidine decarboxylase	<i>napC</i>
sll0741#	3,131,985	3,128,386	1199	L14925	68.4	pyruvate oxidoreductase	<i>nifJ</i>
sll0704	117,693	116,518	391	U00072	24.6	NifS protein	<i>nifS</i>
sll0387#	2,391,547	2,392,707	386	M98808	43.1	NifS protein	<i>nifS</i>
sll0077#	2,875,593	2,876,855	420	U00013	31.7	NifS protein	<i>nifS</i>
sll0450	3,482,141	3,479,829	770	U28078	4.8	cytochrome b subunit of nitric oxide reductase	<i>norB</i>
sll0656	410,184	404,545	1879	L76304	2.7	extracellular nuclease	<i>nucH</i>
sll0828#	2,851,851	2,850,331	506	D26094	13.0	6-aminohexanoate-cyclic-dimer hydrolase	<i>nyIA</i>
sll1253	1,737,210	1,734,382	942	L39923	3.1	polyA polymerase	<i>pcnB</i>
sll0825#	2,857,410	2,856,160	416	L39923	7.2	polyA polymerase	<i>pcnB</i>
sll1106	210,781	211,629	282	S85655	15.6	prohibitin	<i>phb</i>
sll0222	159,737	158,757	326	X56656	24.5	alkaline phosphatase	<i>phoA</i>
sll1274	1,865,658	1,866,761	367	L28837	8.8	membrane protein	<i>pilM</i>
sll1533	2,046,364	2,045,078	428	S72391	29.6	twitching mobility protein	<i>pilT</i>
sll0161	2,202,944	2,204,053	369	M55524	42.4	twitching motility protein	<i>pilT</i>
sll1297	684,156	683,140	338	X78823	6.9	phenoxybenzoate dioxygenase	<i>pobA</i>
sll0915	2,004,465	2,002,891	524	L41335	7.7	protease	<i>pqqE</i>
sll0829#	2,848,983	2,848,345	212	X86780	11.9	methyltransferase	<i>rpxQ</i>
sll0011#	2,480,028	2,480,444	138	D13971	45.4	unknown function	<i>rbcX</i>
sll0451	3,493,885	3,496,905	1006	L13469	6.6	antiviral protein	<i>ski2</i>
sll1639	2,050,948	2,051,412	154	D12501	35.8	small protein	<i>smpB</i>
sll1283	712,783	711,608	391	M20331	12.1	sporulation protein SpoIID	<i>spoID</i>
sll1673	1,953,791	1,954,615	274	L10328	10.4	rRNA methylase	<i>spoU</i>
sll1897	846,509	847,810	433	L41665	50.2	SrtA	<i>srrA</i>
sll1959	1,410,990	1,410,187	267	U00078	10.1	exogenous suppressor	<i>suhB</i>
sll1129	1,050,407	1,049,517	296	M64080	9.0	2-hydroxy-6-oxohexa-2,4-dienoate hydrolase	<i>tdfF</i>
sll1761	538,415	539,020	201	U41441	31.1	FKBP-type peptidyl-prolyl cis-trans isomerase	<i>ytfC</i>
sll0245	146,980	147,894	304	D10463	9.8	acetyl/polyamine aminohydrolase	
sll0644	429,614	428,619	331	L38252	11.3	esterase	
sll2046	587,228	593,125	1965	X87241	4.7	Fat protein	
sll0992	644,379	643,549	276	U00007	53.4	esterase	
sll0990	645,497	644,388	369	X73835	87.4	formaldehyde dehydrogenase (glutathione)	
sll1284	711,595	710,981	204	S70419	46.4	serine esterase	
sll1568	742,688	742,080	202	X71952	12.5	fibrillin	
sll1198	879,408	880,043	211	U40818	43.2	rehydrin	
sll1735	935,236	934,835	133	M33916	26.1	secreted protein MPB70	
sll2250	1,044,693	1,044,517	58	M27176	29.1	glycoprotein 64	
sll0877	1,135,716	1,137,167	483	U49269	41.1	amidase	
sll1886	1,245,395	1,245,859	154	Z15063	19.7	putative ioap protein	
sll1621	1,325,404	1,324,835	189	U32848	43.0	membrane protein	
sll2123	1,635,746	1,636,702	318	L21027	18.7	D-isomer specific 2-hydroxyacid dehydrogenase family	
sll2124	1,636,705	1,637,454	249	X73124	20.7	short-chain alcohol dehydrogenase family	
sll0813	1,698,811	1,699,980	389	D50840	9.9	ceramide glucosyltransferase	
sll0615#	2,650,997	2,650,377	206	M23568	30.5	transmembrane protein FT27	
sll0915#	2,791,074	2,791,526	150	U10482	100.0	putative endonuclease	
sll0095#	2,902,007	2,902,669	220	U24657	40.2	O-methyltransferase	
sll0314#	3,036,233	3,037,063	276	M84990	59.0	bromoperoxidase	
sll0788#	3,045,876	3,047,264	462	U02020	34.2	pre-B cell enhancing factor	
sll1483	3,392,187	3,391,645	180	M77349	25.2	transforming growth factor induced protein	
sll1192	3,532,600	3,533,610	336	U14003	45.7	zinc-containing alcohol dehydrogenase family	
sll0576	3,541,264	3,540,326	312	D25537	20.8	HrEpIB	
sll1128	91,517	92,482	321	X91043	14.2	erythrocyte band 7 integral membrane protein, protein 7.2B, stomatin	
sll0654	414,544	410,315	1409	M77507	28.0	alkaline phosphatase	

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product
sll1916	619,618	620,469	283	U12537	8.6	esterase
sll1919	627,572	629,272	566	Z28353	10.0	ABC1-like
sll1140	794,764	795,900	378	U33059	10.2	3-amino-5-hydroxybenzoic acid synthase
sll1208	891,276	893,249	657	D90316	5.7	short-chain alcohol dehydrogenase family
sll0880	1,138,702	1,140,474	590	M33916	26.1	secreted protein MPB70 precursor
sll0889	1,154,857	1,156,083	408	Z28353	13.7	ABC1-like
ssr1499	1,156,234	1,156,503	89	Z28353	22.3	ABC1-like
sll1770	1,222,230	1,220,473	585	Z28353	11.2	ABC1-like
sll1468	1,826,259	1,826,708	149	U34350	33.3	tymocyte protein cThy28kD
sll1471	1,827,753	1,828,907	384	U32727	10.0	inner membrane protein
sll1178	1,857,917	1,856,070	615	L22756	10.1	nodulation protein
sll1541	2,032,473	2,031,001	490	S65040	7.0	lignostilbene-alpha,beta-dioxygenase
sll0005#	2,497,538	2,495,493	681	Z28353	7.9	ABC1-like
sll0095#	2,990,510	2,988,807	567	Z28353	11.5	ABC1-like
sll0309#	3,026,235	3,027,656	473	D37877	4.9	P-methylase
sll2667	3,317,593	3,317,363	76	L04499	47.7	NifU protein
Hypothetical						
sll1321	178,038	177,592	148	X58128	80.3	hypothetical protein
sll1032	216,229	215,504	241	M30808	20.1	hypothetical protein
sll0527#	3,183,756	3,184,571	271	Z50189	15.3	ExsB protein
sll0679	417,201	418,541	446	U18997	15.8	fmu and fmv protein
sll0823	1,716,379	1,716,900	173	U30821	72.6	hypothetical protein
sll0226	150,455	149,889	188	Z27404	97.9	hypothetical protein
sml0004	160,093	160,004	29	U38804	76.2	hypothetical protein
sll1281	1,095,571	1,095,248	107	U30821	30.2	hypothetical protein
sll1685	231,839	230,658	393	X78945	11.1	heme binding protein precursor
ssr2142	290,902	291,174	90	X62578	25.6	hypothetical protein
sll1509	465,561	465,232	109	U38804	25.4	hypothetical protein
sll1797	844,032	843,613	139	U30821	28.6	hypothetical protein
sll1002	522,853	521,483	456	U38804	8.1	hypothetical protein
sll0751#	2,419,894	2,419,385	169	U38804	18.4	hypothetical protein
sll2032	566,059	566,805	248	M86239	35.5	hypothetical protein
sml0007	1,268,308	1,268,189	39	Z67753	47.9	hypothetical protein
sll1417#	2,417,466	2,417,266	66	U30821	41.5	hypothetical protein
ssr1425#	2,857,507	2,857,755	82	U38804	35.6	hypothetical protein
sll0661#	3,116,358	3,115,972	128	U38804	44.2	hypothetical protein
sll0584#	2,963,227	2,962,706	173	U38804	31.0	hypothetical protein
sll0171#	2,303,507	2,304,034	175	U30821	30.7	hypothetical protein
ssr0102#	2,564,175	2,564,390	71	Z67753	26.1	hypothetical protein
sll0194#	2,532,430	2,531,666	254	U38804	47.9	hypothetical protein
sll2087	1,547,182	1,548,558	458	Z67753	33.5	hypothetical protein
sll0692	442,164	443,933	589	U38804	47.0	hypothetical protein
sll0480#	2,615,100	2,616,599	499	U38804	53.4	hypothetical protein
sll3307	2,250,241	2,250,474	77	U38804	36.2	hypothetical protein
sll0612	937	1,494	185	U32698	38.0	hypothetical protein
sll0558	2,873	2,172	233	U38804	28.3	hypothetical protein
sll1054	82,259	81,696	187	D84432	23.1	hypothetical protein
sll1053	83,853	82,291	520	U00039	5.0	hypothetical protein
sll0711	102,831	101,884	315	D26185	22.7	hypothetical protein
sll0725	110,808	111,224	138	U18997	40.1	hypothetical protein
sll0732	117,869	118,336	155	X89445	37.5	hypothetical protein
sll0230	145,529	145,164	121	Z26494	25.2	hypothetical protein
sll0219	165,821	164,037	594	U29579	10.0	potential FMN-protein
sll0216	170,566	169,934	210	U00081	33.1	hypothetical protein
sll1417	183,493	183,849	118	U38804	53.3	hypothetical protein
sll1780	238,344	238,745	133	U38804	36.8	hypothetical protein
sll1680	240,829	240,299	176	L23646	25.4	hypothetical protein
sll1671	256,305	255,823	160	D38582	19.7	hypothetical protein
sll1790	256,647	257,279	210	L76097	16.3	hypothetical protein
ssr2998	261,863	262,060	65	X70432	67.6	hypothetical protein
sll0967	327,100	327,552	150	L42525	22.2	hypothetical protein
sll0936	331,060	329,555	501	M87049	28.3	hypothetical protein
sll0926	342,139	341,135	334	U00075	50.5	hypothetical protein
sll0980	351,036	351,467	143	D85735	31.7	hypothetical protein
sll1611	357,245	357,697	150	D85735	22.2	hypothetical protein
sll1765	382,392	382,646	84	U24159	19.5	hypothetical protein
sll0681	418,963	420,264	433	U18997	18.9	hypothetical protein
sll1512	462,554	462,147	135	D26185	24.3	hypothetical protein
sll1045	494,828	495,619	263	U38804	46.3	hypothetical protein
sll1011	501,990	501,178	270	L42525	14.1	hypothetical protein
sll1640	546,556	545,591	321	X87299	12.2	hypothetical protein
ssr3122	554,289	554,546	85	U18997	32.3	hypothetical protein
sll1846	554,727	555,050	107	U38804	59.3	hypothetical protein
sll1847	555,262	555,606	114	M38777	24.7	hypothetical protein
sll1945	568,905	566,983	640	D84432	39.1	hypothetical protein
sll2034	569,544	570,572	342	U30821	46.5	hypothetical protein

Table 1. Continued.

ORF No.	Position	Length (aa)	Accession No.	QryMatch (%)	Product
	Initiation	Termination			
slr2045	585,497	586,342	281	L11577	24.7 hypothetical protein
slr1019	632,213	633,157	314	X79146	10.7 hypothetical protein
slr0996	636,247	634,892	451	U32796	31.4 hypothetical protein
ssr1698	637,666	637,956	96	U32713	16.8 hypothetical protein
slr1894	843,105	843,575	156	D01016	32.1 hypothetical protein
slr1896	845,482	845,874	130	X59279	54.3 hypothetical protein
sll1786	861,737	860,952	261	D26185	29.1 hypothetical protein
slr1194	874,693	875,361	222	U47055	24.8 hypothetical protein
slr1118	878,890	878,564	108	M82881	34.1 hypothetical protein
slr1203	885,641	886,078	145	D85735	39.1 hypothetical protein
slr11967	910,994	909,603	463	U29580	10.4 hypothetical protein
slr2077	917,816	920,014	732	X63841	9.6 hypothetical protein
slr2078	920,331	920,915	194	D84432	12.9 hypothetical protein
sll1738	930,843	930,148	231	U44761	32.7 hypothetical protein
sll1737	931,389	930,907	160	U38804	18.2 hypothetical protein
slr1840	956,673	957,788	371	U18997	24.1 hypothetical protein
slr1542	979,685	980,170	161	U32175	44.0 hypothetical protein
ssl2823	987,967	987,740	75	U00071	24.9 hypothetical protein
sll11464	989,505	988,072	477	X17300	14.6 hypothetical protein
slr11459	994,213	993,536	225	U32699	12.4 hypothetical protein
slr1748	1,011,975	1,012,619	214	Z70692	12.8 hypothetical protein
sll1144	1,018,517	1,017,600	305	Z68230	28.7 hypothetical protein
slr1229	1,035,593	1,037,089	498	D84213	47.6 hypothetical protein
sll1355	1,077,019	1,076,474	181	U38537	19.3 hypothetical protein
sll1348	1,094,495	1,093,626	289	U14003	28.6 hypothetical protein
slr0861	1,164,338	1,163,421	305	U00077	38.3 hypothetical protein
sll1773	1,216,151	1,215,453	232	U18997	46.1 hypothetical protein
sll1771	1,220,418	1,219,654	254	Z70722	15.0 hypothetical protein
sll1758	1,238,988	1,237,543	481	U00083	24.5 hypothetical protein
slr1882	1,240,448	1,241,302	284	M35367	25.4 hypothetical protein
slr1888	1,248,284	1,250,176	630	L21902	26.5 hypothetical protein
sll2011	1,256,751	1,256,125	208	U29580	12.5 hypothetical protein
sll1702	1,283,702	1,283,190	170	U30821	22.9 hypothetical protein
slr1811	1,290,478	1,290,957	159	D85735	21.9 hypothetical protein
slr1812	1,291,080	1,291,556	158	D85735	20.5 hypothetical protein
slr1813	1,291,631	1,292,092	153	D85735	22.8 hypothetical protein
slr1814	1,292,215	1,292,679	154	D85735	20.6 hypothetical protein
slr1693	1,298,965	1,297,643	440	X05302	5.2 hypothetical protein
slr1692	1,300,166	1,299,729	145	D85735	40.2 hypothetical protein
slr1819	1,300,661	1,301,656	331	L42525	20.2 hypothetical protein
sll1631	1,312,803	1,312,309	164	X52144	33.4 hypothetical protein
slr0855	1,344,130	1,342,775	451	D26562	29.3 hypothetical protein
slr1260	1,404,839	1,405,372	177	X79285	17.7 hypothetical protein
slr1261	1,405,436	1,405,975	179	D84432	14.8 hypothetical protein
sll1956	1,419,573	1,418,995	192	U38537	38.9 hypothetical protein
slr2000	1,445,874	1,446,839	321	X67694	36.2 hypothetical protein
sll1902	1,452,518	1,451,319	399	U44977	42.0 hypothetical protein
sll1606	1,469,801	1,469,013	262	U00086	10.3 hypothetical protein
sll1601	1,478,891	1,477,647	414	U00024	10.6 hypothetical protein
slr0249	1,516,424	1,515,669	251	X14577	27.8 hypothetical protein
slr0267	1,519,114	1,519,953	279	U39731	10.5 hypothetical protein
slr0245	1,521,100	1,520,009	363	D26185	58.3 hypothetical protein
sll1988	1,544,665	1,543,757	302	D26185	30.0 hypothetical protein
sll1973	1,576,592	1,575,924	222	U28379	12.0 hypothetical protein
slr2128	1,640,786	1,641,238	150	D85735	19.9 hypothetical protein
sll1232	1,662,285	1,661,722	187	U38537	60.8 hypothetical protein
slr0818	1,692,332	1,691,493	279	U18997	37.7 hypothetical protein
slr0821	1,712,080	1,712,409	109	Z73902	33.8 hypothetical protein
sll0803	1,718,789	1,718,310	159	D85735	35.8 hypothetical protein
slr0802	1,719,263	1,718,820	147	D85735	41.7 hypothetical protein
slr1344	1,738,184	1,739,035	283	U38804	40.4 hypothetical protein
sll1250	1,740,774	1,740,388	128	U38537	48.4 hypothetical protein
slr1972	1,783,855	1,784,934	359	D26185	32.5 hypothetical protein
slr1974	1,788,550	1,789,908	452	L47648	36.6 hypothetical protein
sll1880	1,795,564	1,795,121	147	U00006	24.5 hypothetical protein
sll1866	1,820,837	1,820,238	199	Z38002	17.6 hypothetical protein
slr1278	1,872,656	1,873,648	330	U38804	19.0 hypothetical protein
slr1152	1,910,499	1,911,494	331	L42525	17.2 hypothetical protein
sll1095	1,920,548	1,919,913	211	U44977	10.9 hypothetical protein
slr1166	1,932,354	1,933,418	354	X70433	23.2 hypothetical protein
ssl2803	1,961,625	1,961,876	83	D85735	39.0 hypothetical protein
sll1556	1,980,193	1,979,144	349	M87280	39.6 hypothetical protein
slr0944	2,010,218	2,011,369	383	D32216	22.7 hypothetical protein
slr0913	2,014,787	2,014,182	201	U38537	38.0 hypothetical protein
slr0950	2,017,964	2,018,788	274	D84432	37.8 hypothetical protein
slr0951	2,021,252	2,021,944	230	L14580	24.0 hypothetical protein
slr0954	2,024,549	2,024,980	143	X70431	39.4 hypothetical protein
slr0955	2,024,993	2,026,147	384	D26185	24.0 hypothetical protein
slr1626	2,039,078	2,039,530	150	M34053	24.4 hypothetical protein
slr1629	2,041,999	2,042,982	327	D50832	29.5 hypothetical protein

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product
sll1534	2,045,074	2,043,938	378	X61917	38.9	hypothetical protein
sll2982	2,048,374	2,048,144	76	U38804	61.1	hypothetical protein
sll1649	2,075,381	2,075,971	196	M95288	25.3	hypothetical protein
sll0284	2,123,646	2,123,996	116	U37580	21.1	hypothetical protein
sll0291	2,131,105	2,131,539	144	D85735	24.8	hypothetical protein
sll0257	2,134,022	2,133,549	157	L19346	17.4	hypothetical protein
sll0402	2,151,606	2,152,190	194	U28377	29.5	hypothetical protein
sll0407	2,158,543	2,159,355	270	M29297	17.7	hypothetical protein
sll0135	2,209,758	2,208,778	326	Z54366	29.2	hypothetical protein
sll1923	2,211,283	2,212,479	398	U14553	50.3	hypothetical protein
sll0989	2,257,203	2,257,964	253	D83138	34.9	hypothetical protein
sll0992	2,259,402	2,259,863	153	Z46432	32.9	hypothetical protein
sll0296#	2,286,746	2,286,186	186	U38537	51.4	unidentified open reading frame
sll0154#	2,338,450	2,337,062	462	M57692	25.6	hypothetical 35.6 kD protein
sll0359#	2,340,322	2,344,056	1244	Z00027	6.3	hypothetical protein
sll0361#	2,345,797	2,346,546	249	L09228	23.9	hypothetical protein
sll0362#	2,346,573	2,347,127	184	D84432	16.9	hypothetical protein
sll0335#	2,374,788	2,373,343	481	U00016	44.1	hypothetical protein
sll0381#	2,383,241	2,383,636	131	U06949	62.5	hypothetical protein
sll0769#	2,393,493	2,394,107	204	D84432	13.3	hypothetical protein
sll0765#	2,406,966	2,406,130	278	U02603	30.9	hypothetical protein
sll0780#	2,414,833	2,415,318	161	D28752	61.1	hypothetical protein
sll0754#	2,417,207	2,416,806	133	U00082	29.7	hypothetical protein
sll0348#	2,439,092	2,440,312	406	X54945	5.8	hypothetical protein
sll0001#	2,464,527	2,465,009	160	L19521	72.7	hypothetical protein
sll0019#	2,470,429	2,469,245	394	U00077	30.3	hypothetical protein
sll0007#	2,494,153	2,493,578	191	U38537	38.5	hypothetical protein
sll0210#	2,508,362	2,507,382	326	U00017	16.3	hypothetical protein
sll0232#	2,536,824	2,537,480	218	U00011	12.9	hypothetical protein
sll0050#	2,564,465	2,565,445	326	D84432	35.9	hypothetical protein
sll0053#	2,576,285	2,576,824	179	D84432	16.1	hypothetical protein
sll0064#	2,591,953	2,593,107	384	L47838	16.5	hypothetical protein
sll0067#	2,596,787	2,597,848	353	X55791	33.9	put. ATPase
sll0051#	2,600,491	2,600,012	159	X52144	18.6	hypothetical protein
sll0636#	2,657,850	2,658,632	260	Z70283	9.8	hypothetical protein
sll0639#	2,660,854	2,661,744	296	X14436	28.2	hypothetical protein
sll0644#	2,669,089	2,670,156	355	Z37984	27.8	hypothetical protein
sll0601#	2,677,755	2,676,937	272	U19102	21.6	hypothetical protein
sll0650#	2,679,884	2,680,489	201	D63898	22.4	hypothetical protein
sll0395#	2,684,081	2,683,443	212	Z70692	11.3	hypothetical protein
sll0331#	2,750,816	2,750,577	79	U32727	46.9	hypothetical protein
sll0904#	2,775,767	2,777,296	509	U32737	36.6	hypothetical protein
sll0923#	2,798,072	2,798,410	112	U38804	62.4	hypothetical protein
sll0550#	2,808,932	2,807,211	573	Z29579	11.0	flavoprotein
sll0546#	2,812,720	2,812,385	111	U32747	26.0	hypothetical protein
sll0580#	2,823,646	2,824,893	415	D10020	27.6	hypothetical protein
sll0540#	2,826,641	2,825,718	307	D84432	9.1	hypothetical protein
sll0846#	2,862,558	2,863,031	157	U32831	26.7	hypothetical protein
sll0086#	2,878,035	2,876,845	396	U09867	35.6	hypothetical protein
sll0078#	2,880,766	2,881,155	129	Z29579	29.6	hypothetical protein
sll0082#	2,886,182	2,887,513	443	U00019	17.0	hypothetical protein
sll0487#	2,909,383	2,908,175	402	X05302	54.0	hypothetical protein
sll0503#	2,913,111	2,914,124	337	X04465	13.8	hypothetical protein
sll0482#	2,917,076	2,915,853	407	Z50177	5.7	hypothetical protein
sll0509#	2,918,957	2,919,574	205	Z29065	28.6	alkaline phosphatase like protein
sll0510#	2,919,706	2,921,223	505	U32813	10.3	hypothetical protein
sll0516#	2,926,783	2,927,283	166	L42525	29.4	hypothetical protein
sll0586#	2,960,756	2,959,530	408	U00039	10.7	hypothetical protein
sll0585#	2,962,647	2,961,619	342	D63706	10.0	hypothetical protein
sll0624#	2,963,397	2,964,512	371	Z22516	39.6	hypothetical protein
sll0626#	2,966,735	2,967,931	398	X70966	36.4	hypothetical protein
sll0098#	2,984,747	2,983,695	350	L49434	28.8	hypothetical protein
sll0120#	3,002,075	3,002,797	240	U32831	18.6	hypothetical protein
sll0286#	3,022,407	3,021,892	171	U38804	48.8	hypothetical protein
sll0315#	3,037,309	3,038,043	244	M67471	46.2	hypothetical protein
sll0697#	3,084,676	3,088,434	1252	Z68166	27.1	hypothetical protein
sll0709#	3,111,995	3,112,387	130	D26185	48.9	hypothetical protein
sll0743#	3,127,845	3,127,363	160	D85735	20.6	hypothetical protein
sll0742#	3,128,312	3,127,863	149	D85735	25.1	hypothetical protein
sll0031#	3,154,910	3,156,664	584	U21853	54.7	hypothetical protein
sll0506#	3,204,743	3,203,994	249	U00078	38.3	hypothetical protein
sll0551#	3,250,985	3,252,907	640	X95649	21.7	hypothetical protein
sll0553#	3,253,809	3,254,414	201	U48808	29.3	hypothetical protein
sll0554#	3,254,560	3,257,670	1036	D13972	26.0	hypothetical protein
sll0556#	3,261,406	3,262,062	218	D50472	26.8	hypothetical protein
sll1004#	3,262,749	3,262,471	92	U05590	17.9	hypothetical protein
sll0524#	3,264,162	3,262,819	447	Z73101	12.3	hypothetical protein
sll1419	3,271,699	3,272,178	159	L37353	15.8	hypothetical protein
sll1424	3,280,979	3,281,932	317	M31827	23.3	hypothetical protein
sll1336	3,287,168	3,285,051	705	Z47358	11.0	hypothetical protein

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product
ssr2439	3,299,421	3,299,714	97	M65247	19.9	hypothetical protein
sll1461	3,308,878	3,309,474	198	Z73902	25.7	hypothetical protein
sll0665	3,348,690	3,351,296	868	D26562	55.3	hypothetical protein
sll1565	3,372,152	3,372,493	113	X71865	27.1	hypothetical protein
sll0755	3,428,383	3,428,940	185	Z46907	69.0	hypothetical protein
sll1547	3,463,341	3,462,883	152	U46071	21.4	hypothetical protein
sll0451	3,479,683	3,479,219	154	Z68166	17.8	hypothetical protein
sll179	3,519,431	3,520,561	376	U00077	15.1	hypothetical protein
sll1108	3,523,260	3,522,433	275	U29579	20.0	hypothetical protein
sll1184	3,526,097	3,526,591	164	D84432	14.8	hypothetical protein
sll0605	3,566,761	3,567,720	319	U18997	63.8	hypothetical protein
sll1213	5,389	4,451	312	U42580	22.3	hypothetical protein
sll1204	23,121	21,838	427	U46844	5.5	hypothetical protein
sll1392	59,650	59,039	203	J01830	11.6	hypothetical protein
sll0722	108,290	109,201	303	D84432	9.9	hypothetical protein
sll0217	168,152	166,416	578	U29579	11.4	potential FMN-protein
sll1039	191,954	190,815	379	U00016	11.7	hypothetical protein
sll1102	197,624	200,185	853	Z00027	7.5	hypothetical protein
sll1103	200,405	202,525	706	Z00027	9.2	hypothetical protein
sll1104	202,554	204,395	613	Z00027	8.6	hypothetical protein
sll1787	247,619	248,713	364	U00082	12.3	hypothetical protein
sll1670	259,363	258,227	378	M84964	14.8	hypothetical protein
sll1794	262,177	263,265	362	U09867	9.9	hypothetical protein
sll1298	295,076	297,343	755	U32787	3.9	hypothetical protein
sll0964	323,805	324,731	308	X73124	7.8	hypothetical protein
sll1610	355,909	357,210	433	X60379	8.4	hypothetical protein
sll1063	365,716	367,785	689	U00085	3.6	hypothetical protein
sll0634	445,924	445,061	287	Z69383	15.8	hypothetical protein
sll1592	449,166	450,041	291	U32811	8.1	hypothetical protein
sll1593	450,740	451,651	303	Z00027	25.8	hypothetical protein
sll1596	456,975	458,297	440	U38804	29.7	hypothetical protein
sll1597	459,200	460,096	298	X62539	8.6	hypothetical protein
sll1763	540,863	542,065	400	X60379	10.6	hypothetical protein
sll1851	562,557	563,045	162	L42525	30.7	hypothetical protein
sll2048	594,454	595,650	398	M29495	8.8	hypothetical protein
sll2049	595,733	596,311	192	M95288	23.4	hypothetical protein
sll1300	676,929	676,351	192	U39718	12.0	hypothetical protein
sll1924	755,602	754,877	241	U21853	13.1	hypothetical protein
sll1143	802,207	803,238	343	U17054	8.9	hypothetical protein
sll1197	877,325	878,521	398	U32725	16.9	hypothetical protein
sll1723	951,774	950,533	413	X56793	11.5	hypothetical protein
sll1363	1,105,666	1,107,168	500	D12973	6.8	hypothetical protein
sll0878	1,137,375	1,138,112	245	M77039	13.0	hypothetical protein
sll1308	1,180,672	1,179,926	248	Z49939	11.3	hypothetical protein
sll3364	1,242,989	1,242,765	74	X79285	40.1	hypothetical protein
sll1885	1,244,731	1,245,309	192	D84432	19.3	hypothetical protein
sll2013	1,254,623	1,254,036	195	M86238	16.5	hypothetical protein
sll1821	1,309,482	1,310,582	366	D83536	9.9	hypothetical protein
sll1624	1,321,839	1,320,835	334	X81642	8.9	hypothetical protein
sll0844	1,357,626	1,356,550	358	U32811	28.2	hypothetical protein
sll0863	1,355,162	1,356,553	463	U32784	10.1	hypothetical protein
sll1259	1,404,085	1,404,783	232	Z68493	21.2	hypothetical protein
sll0264	1,512,016	1,513,125	369	U18997	6.3	hypothetical protein
sll1424	1,589,374	1,587,899	491	L10036	12.3	hypothetical protein
sll1415	1,603,405	1,602,482	307	U00021	12.2	hypothetical protein
sll1414	1,604,159	1,603,437	240	U42580	10.2	hypothetical protein
sll1322	1,650,889	1,652,358	489	U18997	16.5	hypothetical protein
sll0816	1,694,661	1,693,546	371	X78503	7.2	hypothetical protein
sll1263	1,720,576	1,719,644	310	L19201	15.0	hypothetical protein
sll12471	1,740,349	1,740,188	53	U38537	37.7	hypothetical protein
sll11895	1,766,925	1,764,835	696	Z00027	10.1	hypothetical protein
sll11882	1,793,608	1,792,784	274	S44426	8.8	hypothetical protein
sll1170	1,879,682	1,878,099	527	U00015	7.4	hypothetical protein
sll1287	1,885,136	1,886,146	336	X05302	38.7	hypothetical protein
sll1166	1,888,262	1,887,159	367	U32819	7.6	hypothetical protein
sll1446	1,889,740	1,888,778	320	L42525	18.4	hypothetical protein
sll1433	1,907,744	1,906,170	524	U00020	7.8	hypothetical protein
sll1103	1,914,113	1,912,776	445	U32809	13.7	hypothetical protein
sll1162	1,924,999	1,925,943	314	U04356	7.9	hypothetical protein
sll1690	1,983,147	1,983,932	261	U00010	12.5	hypothetical protein
sll1692	1,985,874	1,986,872	332	U32936	26.3	hypothetical protein
sll0910	2,020,344	2,019,253	363	S44426	7.3	hypothetical protein
sll1627	2,039,541	2,040,161	206	L27528	12.3	hypothetical protein
sll1524	2,069,694	2,068,855	279	L10328	12.2	hypothetical protein
sll1521	2,078,340	2,076,547	597	U29579	10.7	hypothetical protein
sll0267	2,115,877	2,111,141	1578	U00039	4.8	hypothetical protein
sll0400	2,149,333	2,150,250	305	U00069	16.1	hypothetical protein
sll0141	2,202,550	2,201,147	467	X58632	7.3	hypothetical protein
sll1938	2,237,134	2,238,189	351	U40828	13.6	hypothetical protein
sll0175#	2,308,472	2,306,850	540	L04468	10.6	putative; ORF1

Table 1. Continued.

ORF No.	Position Initiation	Position Termination	Length (aa)	Accession No.	QryMatch (%)	Product
slr0782#	2,420,030	2,421,445	471	S45812	15.4	hypothetical protein
slr0784#	2,424,368	2,425,390	340	U00039	7.0	hypothetical protein
sll0023#	2,463,555	2,462,212	447	U28377	6.9	hypothetical protein
sll00414#	2,542,724	2,541,864	286	L42525	10.9	hypothetical protein
slr0069#	2,599,315	2,599,974	219	U04356	13.1	hypothetical protein
slr0483#	2,617,440	2,617,889	149	U19925	16.9	hypothetical protein
slr0719#	2,643,403	2,644,569	388	L42525	7.9	hypothetical protein
slr0642#	2,664,403	2,665,887	494	L25643	5.0	integral membrane protein
slr0427#	2,718,963	2,720,213	416	U56238	25.9	hypothetical protein
slr0199#	2,730,649	2,731,563	304	Z71467	12.4	hypothetical protein
ssl0353#	2,734,323	2,734,030	97	D50472	14.8	hypothetical protein
sll0183#	2,735,301	2,734,522	259	L42525	12.3	hypothetical protein
ssr1513#	2,760,435	2,760,632	65	U00017	25.3	hypothetical protein
sll0886#	2,762,953	2,762,114	279	S44426	9.7	hypothetical protein
slr0896#	2,763,867	2,765,252	461	U32781	14.1	hypothetical protein
slr0545#	2,813,636	2,812,914	240	Z21972	11.0	hypothetical protein
slr0583#	2,828,140	2,829,072	310	U42580	8.1	hypothetical protein
slr0825#	2,829,098	2,831,011	637	U13070	18.7	hypothetical protein
slr0842#	2,854,916	2,856,130	404	Z00027	15.7	hypothetical protein
sll0821#	2,866,923	2,863,093	1276	U00039	6.2	hypothetical protein
slr0848#	2,867,917	2,868,750	277	L19521	9.8	hypothetical protein
slr0076#	2,874,164	2,875,525	453	U00013	8.1	hypothetical protein
slr0092#	2,900,089	2,900,862	257	U44977	9.4	hypothetical protein
sll0597#	2,942,883	2,941,756	375	U32819	6.6	hypothetical protein
slr0616#	2,948,563	2,949,819	418	D37826	6.9	hypothetical protein
slr0104#	2,973,268	2,975,703	811	D84432	9.9	hypothetical protein
slr0110#	2,992,055	2,992,690	211	X62540	11.8	hypothetical protein
slr0305#	3,019,260	3,019,889	209	X04963	11.7	hypothetical protein
slr0317#	3,039,857	3,040,720	287	U14003	12.8	hypothetical protein
sll0036#	3,160,651	3,159,350	433	L38424	13.1	hypothetical protein
sll0505#	3,205,651	3,204,740	303	D84214	16.5	hypothetical protein
slr0541#	3,211,808	3,212,518	236	U11243	14.9	hypothetical protein
sll0493#	3,226,314	3,225,628	228	D37799	27.3	hypothetical protein
ssr1558#	3,232,902	3,233,180	92	Z69795	18.5	hypothetical protein
sll0898#	3,236,855	3,235,746	369	U14003	8.7	hypothetical protein
sll1563	3,370,059	3,370,946	295	X68477	13.7	hypothetical protein
slr1575	3,384,151	3,385,590	479	U32813	9.4	hypothetical protein
slr1588	3,408,051	3,409,316	421	X63841	19.0	hypothetical protein

Assigned ORFs were classified into 14 categories with respect to biological function as suggested by Riley,⁹ and listed in the sections with titles representing categories, and those which showed similarity to the hypothetical genes were listed in the last section. The previously reported ORFs in the 1-Mb region from map positions 62% to 94% were included in this classification, and indicated by a # mark. The ORFs which appeared in two different functional categories were listed in each section marked by asterisks. The right three columns represent the accession number and name of genome products which showed similarity and their genetic symbols. The degree of similarity of the ORFs, which were primarily taken by the MPSRCH score, are shown by query-match percentages in the fifth column from the left.