## Complete Genome Sequence of an Aerobic Thermoacidophilic Crenarchaeon, *Sulfolobus tokodaii* strain7

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#### Abstract

The complete genomic sequence of an aerobic thermoacidophilic crenarchaeon, Sulfolobus tokodaii strain7 which optimally grows at 80°C, at low pH, and under aerobic conditions, has been determined by the whole genome shotgun method with slight modifications. The genomic size was 2.694,756 bp long and the G+C content was 32.8%. The following RNA-coding genes were identified: a single 16S-23S rRNA cluster, one 5S rRNA gene and 46 tRNA genes (including 24 intron-containing tRNA genes). The repetitive sequences identified were SR-type repetitive sequences, long dispersed-type repetitive sequences and There elements. The genome contained 2826 potential protein-coding regions (open reading frames, ORFs). By similarity search against public databases, 911 (32.2%) ORFs were related to functional assigned genes, 921 (32.6%) were related to conserved ORFs of unknown function, 145 (5.1%) contained some motifs, and remaining 849 (30.0%) did not show any significant similarity to the registered sequences. The ORFs with functional assignments included the candidate genes involved in sulfide metabolism, the TCA cycle and the respiratory chain. Sequence comparison provided evidence suggesting the integration of plasmid, rearrangement of genomic structure, and duplication of genomic regions that may be responsible for the larger genomic size of the S. tokodaii strain7 genome. The genome contained eukaryote-type genes which were not identified in other archaea and lacked the CCA sequence in the tRNA genes. The result suggests that this strain is closer to eukaryotes among the archaea strains so far sequenced.

The data presented in this paper are also available on the internet homepage

(http://www.bio.nite.go.jp/ E-home/genome\_list-e.html/).

Key words: aerobic thermoacidophilic crenarchaeon; genome sequencing; whole genome shotgun method; comparative analysis; plasmid

#### 1. Introduction

Among the complete genome sequences of thermophilic archaea reported,<sup>1-5</sup> two genomes were sequenced by our group: *Pyrococcus horikoshii* OT3<sup>1</sup> and *Aeropyrum pernix* K1.<sup>2</sup> These two species are hyper-thermophilic and

<sup>†</sup> The entire genome sequence has been deposited in DDBJ/GenBank/EMBL databases under accession numbers AP000981–AP000990.

optimally grow at over 95°C. While *P. horikoshii* OT3 is an anaerobic euryarchaeon, *A. pernix* K1 is an aerobic crenarchaeon. The entire genomic sequence of *A. pernix* K1 was the first and the only complete genomic data of crenarchaeota. It is also the only known genomic sequence of a strictly aerobic hyperthermophile. To obtain more information about the genomic sequence data of *A. pernix* K1, it is useful to compare the data with data from closely related species.

We therefore selected *Sulfolobus tokodaii* strain7, a species of genus *Sulfolobus* in crenarchaeon for sequencing. This strain was isolated from Beppu hotsprings

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in Kyushu, Japan in 1983.<sup>6</sup> This species grows under aerobic conditions, as does *A. pernix* K1. The optimal growth temperature of *S. tokodaii* strain7 is 80°C and the optimal pH is between 2 and 3. The genomic data of this strain is expected to provide the information on not only the thermostability of proteins but also the characteristics of cells living in an acidic environment. The genomic size of this strain is approximately 2.7 Mbp,<sup>7</sup> 1 Mbp larger than the other two species previously determined by our group: *P. horikoshii* OT3 and *A. pernix* K1. In addition to above genomic features, *S. tokodaii* strain7 has no extra-chromosomal genetic unit<sup>7</sup> and is able to convert hydrogen sulfide to sulfate (personal communication from A. Yamagishi and T. Oshima).

To determine the entire sequence of this genome, the shotgun libraries with short and long inserts were constructed both from the entire genomic DNA and from the restriction fragments of genomic DNA digested with  $Bss{\rm H~II}$ . The raw sequencing data from shotgun clones were assembled using the software PhredPhrap and Consed.<sup>8-10</sup> The remaining sequencing gaps were filled by walking of long insert shotgun clones.

#### 2. Materials and Methods

#### 2.1. Bacterial strains and genomic DNA

The strain, *S. tokodaii* strain7 deposited in the Japan Collection of Microorganisms (JCM number 10545) was used for genome sequencing in this study. These cells were inoculated into 100 ml of the Sulfolobus culture medium<sup>11</sup> which was prepared in 500-ml Erlenmeyer flasks, and cultured at 80°C with vigorous shaking. The genomic DNA was isolated principally based on the method of Yamagishi and Oshima.<sup>12</sup> Escherichia coli DH10B was used for the preparation of plasmid clones.

#### 2.2. Construction of shotgun clones

The *S. tokodaii* strain7 genomic DNA was sonicated for 5, 10, and 20 sec at the L position of a sonicator Biorupter (Cosmo Bio, Tokyo, Japan), followed by size-fractionation by agarose gel electrophoresis. The fractions from 0.8 to 1.2 kb and from 2.0 to 2.5 kb were independently cloned into the *Hinc* II site of pUC118 (Takara Shuzo, Kyoto, Japan). They are referred to as short-fragment and long-fragment shotgun libraries, respectively.

For the construction of the shotgun libraries from restriction fragments, the genomic DNA was prepared in the agarose-plug as described by Kondo et al.,<sup>7</sup> and after complete digestion of DNA in the plugs with BssH II, the digests were resolved in 0.4% low-melting-point agarose gel by electrophoresis. The bands were cut out and the gel was dissolved by incubation at 50°C with Agarase (FMC, Rockland, ME, USA) overnight. The resultant solution containing DNA fragments was sonicated, and the short-fragment shotgun library was prepared as above, except for BssH II fragment A (945 kb) from which both short- and long-fragment shotgun libraries were constructed.

#### 2.3. Sequencing

Plasmid DNA was prepared by an Autogen 740 automatic DNA preparation system (Autogen, Framington, MA, USA). The sequencing reaction was performed using two kinds of cycle sequencing kits, a dye-primer cycle sequencing kit and a dye-terminator cycle sequencing kit. The sequence data were detected by ABI-DNA sequencers (377XL; Perkin-Elmer ABI, Foster City, CA, USA). Also the dye-terminator cycle sequencing kit was used for filling the sequencing gaps. The long-fragment shotgun clones with inserts covering gap regions were used for filling of gaps by walking with synthesized primers.

The raw sequence data were first analyzed with the software Phred.<sup>7</sup> After the elimination of contaminated sequences derived from *E. coli* or vector DNAs, the treated data were assembled into contigs using the software Phrap<sup>8</sup> and Consed.<sup>9</sup> The assembled sequences were split into 30-kbp segments and the sequence in each segment was re-assembled and edited by Sequencher (Gene Codes, Ann Arbor, MI, USA).

#### 2.4. Computational analysis

The criteria used for the assignment of potential protein-coding regions were similar to those used in the previous paper.<sup>1</sup> However, the open reading frames (ORFs) which had neither similarity nor motif sequences completely included within longer ORFs were not assigned as potential protein-coding regions in this work. Similarity search of the assigned ORFs was mainly performed by the Smith-Waterman algolithm.<sup>13</sup> The databases used for similarity search were GenBank release 109, EMBL release 56.0, Swiss-Prot release 38.0, PIR release 62.0, and Owl release 31.4.

#### 3. Results and Discussion

#### 3.1. Determination of entire genome sequence

The physical map of circular genomic DNA of S. tokodaii strain7 has been reported by Kondo et al.<sup>7</sup> According to their observation that the genomic DNA generates six fragments upon digestion with BssH II, these six fragments were used for the construction of fragment-specific shotgun libraries.

The entire genome sequence was determined by the whole genome shotgun method<sup>14</sup> with slight modifications. The two kinds of shotgun libraries, one with approximately 1-kb inserts (short-fragment shotgun library) and the other with approximately 2.2-kb inserts (long-fragment shotgun library), were prepared from the genomic DNA and from BssH II fragment A. From the other BssH II fragments, only short-fragment shotgun libraries were constructed. The clones from the short-fragment shotgun libraries were sequenced from one end whereas the clones from the long-fragment shotgun libraries were sequenced from both ends. A total of 61,000 readings of raw sequencing data were accumulated and assembled using PhredPhrap.<sup>8–10</sup>

As indicated in the following section, a large number of long dispersed repetitive sequences were identified from the consensus sequences of primary contigs generated by PhredPhrap. To avoid the confusion of assembling by these repetitive sequences, the nucleotide sequence of these repetitive units were added in the cross-match database of PhredPhrap and were not used for contig assembling. The resulting contigs were separated into 30-kbp regions and the raw data contained in each region was re-assembled and edited by Sequencher.

To fill the remaining sequencing gaps, the clones carrying the end sequences of contigs were selected from the long-fragment shotgun libraries and sequenced by walking with synthesized primers. The nucleotide sequences of long dispersed repetitive units were also determined by walking the long-fragment shotgun clones which included each repetitive unit with synthesized primers. All the sequences were determined by co-incidence of sequences of at least two clones per base.

To confirm the authenticity of the genomic sequence constructed, the restriction pattern of each 15-kb fragment directly amplified from the genomic DNA by long PCR were compared with those deduced from the sequence data.

The total length of the genome finally confirmed was 2,694,756 bp. The nucleotide position was numbered from the one end of the BssH II restriction site located on the Not I B and Rsr II F fragments in the physical map shown by Kondo et al.<sup>7</sup>

Distribution of ACGT along the strand of the entire genome was 33.4% A, 16.3% C, 16.5% G, and 33.8% T, resulting in a G + C content of 32.8%. Through the processes of genomic sequencing, no evidence was obtained for the presence of an extra-chromosomal unit.

#### 3.2. RNA coding genes

The entire genomic sequence was subjected to similarity search against the rRNA sequences registered in the databases. It was found that the *S. tokodaii* strain7 genome contained a single 16S–23S rRNA cluster and one 5S rRNA. This organization is similar to those of *P. horikoshii* OT3<sup>1</sup> and *A. pernix* K1.<sup>2</sup>

Forty-five tRNA genes were identified by searching with tRNA scan,<sup>15</sup> and one tRNA gene for Leu (GAG) was identified by similarity search. The species of tRNA genes identified are shown in Table 1. Forty-one of these genes were discretely mapped, while the remaining six tRNA genes were mapped as clusters of two tRNA genes. As noted in other microorganisms,<sup>1,2,16</sup> no tRNA genes containing A at the first position of the anticodon were identified. Similar to the archaea genomes already sequenced, the Met-tRNA gene occurred in triplicate. However, the sequences had no similarity to one another, suggesting that the different Met-tRNA species may be used for the translation initiation of different classes of genes.

Twenty-four tRNA genes were found to contain 11to 57-bp long introns. These genes containing introns and the organization of the introns in each gene are summarized in Table 2. In all of the intron-containing tRNA genes except for the tRNA-Leu (GAG), tRNA-Glu (UUC) and tRNA-Glu (CUC) genes, the introns were identified 1 bp downstream from the 3' end of the anticodon triplet. The intron in the tRNA-Leu (GAG) gene had been inserted 4-bp upstream from the 5' end of anticodon region. The 17 bp-long intron portion was assigned within the D-loop of two tRNA-Glu genes. The Insertion position of these introns was similar to that of the tRNA-Thr (UGU) gene identified in the A. pernix K1 genome.<sup>2</sup>

In contrast to tRNA genes in other archaea, most of the tRNA genes identified did not contain the 3' terminal CCA sequence. On the other hand, tRNA nucleotidyltransferase,<sup>17</sup> that catalyzed the addition of the CCA sequence to tRNA transcripts, was found on this genome (ST0952). In bacteria, the 3' CCA is generally encoded on the tRNA genes. The role of *E. coli* tRNA nucleotidyltransferase is the repair of tRNA 3' ends.<sup>18–20</sup> In eukaryotes, where CCA is rarely encoded by tRNA genes, tRNA nucleotidyltransferase is essential.<sup>21</sup> Although the role of tRNA nucleotidyltransferase is unclear in *S. tokodaii* strain7, the structure of tRNA genes and the presence of a CCA-adding enzyme are similar to eukaryotic cells.

The genes for all tRNA synthetases have been identified in the assigned ORFs, except for those for tRNA<sup>Gln</sup> and tRNA<sup>Asn</sup>. Instead, similar to *Bacillus subtilis*<sup>22</sup> and *Deinococcus radiodurans*,<sup>23</sup> the three subunits of Glu-tRNA<sup>Gln</sup> amidotransferase (ST1283, ST0282, and STS140), which were necessary for transamidation of Glu-tRNA<sup>Gln</sup> and Asp-tRNA<sup>Asn</sup>, were identified.

#### 3.3. Repetitive sequences identified

Three types of repeating units including Tn-like elements were found on the genome of *S. tokodaii* strain7.

The first type, named type A, is comprised of repetitive sequences composed of LR and SR segments, and is divided into two subtypes based on the sequences of SR segments. The subtype A-I repetitive unit contained 24 bp-long well-conserved SR segments (GMTAATCCWTAATGGAATTGAAAG) and a

Table 1. Summary of assigned tRNA genes.

UUU (Phe)		UCU (Ser)		UAU (Tyr)		UGU (Cys)	
UUC (Phe)	0	UCC (Ser)	0	UAC (Tyr)	Ø	UGC (Cys)	O
UUA (Leu)	0	UCA (Ser)	0	UAA (End)		UGA (End)	
UUG (Leu)	0	UCG (Ser)	0	UAG (End)		UGG (Trp)	0
CUU (Leu)		CCU (Pro)		CAU (His)		CGU (Arg)	
CUC (Leu)	0	CCC (Pro)	0	CAC (His)	0	CGC (Arg)	O
CUA (Leu)	0	CCA (Pro)	0	CAA (Gln)	0	CGA (Arg)	0
CUG (Leu)	0	CCG (Pro)	0	CAG (Gln)	0	CGG (Arg)	0
AUU (Ile)		ACU (Thr)		AAU (Asn)		AGU (Ser)	
AUC (Ile)	0	ACC (Thr)	0	AAC (Asn)	0	AGC (Ser)	0
AUA (Ile)		ACA (Thr)	0	AAA (Lys)	Ø	AGA (Arg)	0
AUG (Met)	0 *	ACG (Thr)	0	AAG (Lys)	0	AGG (Arg)	0
GUU (Val)	Recordencia	GCU (Ala)	9	GAU (Asp)		GGU (Gly)	
GUC (Val)	0	GCC (Ala)	0	GAC (Asp)	O	GGC (Gly)	0
GUA (Val)	0	GCA (Ala)	0	GAA (Glu)	0	GGA (Gly)	0
GUG (Val)	0	GCG (Ala)	0	GAG (Glu)	0	GGG (Gly)	0

tRNA genes assigned are indicated by  $\bigcirc$  and those with introns by  $\bigcirc$  \*; All three tRNA<sup>Met</sup> possessed the introns

Table 2. The size a	and position of introns in	the intron-containing tRNA genes.
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tRNA-ID	tRNA species	anticodon	gene size	Intron p		Intron size	mature tRNA	
			(nt)	start	end	(nt)	(nt)	
STtRNA02	tRNA-Glu	TTC	91	22**	38	17	74	
STtRNA03	tRNA-Lys	TTT	99	39	63	25	74	
STIRNA04	tRNA-Lys	CTT	101	39	65	27	74	
STtRNA06	tRNA-Cys	GCA	88	38	51	14	74	
STtRNA08	tRNA-Met	CAT	98	39	62	24	74	
STtRNA11	tRNA-Thr	CGT	98	39	62	24	74	
STtRNA15	tRNA-Met	CAT	93	39	57	19	74	
STIRNA16	tRNA-Tyr	GTA	93	39	57	19	74	
STtRNA18	tRNA-Ser	CGA	111	39	64	26	85	
STtRNA19	tRNA-Leu	CAG	101	41	56	16	85	
STtRNA20	tRNA-Glu	CTC	91	22**	38	17	74	
STtRNA21	tRNA-Ser	TGA	95	39	49	11	84	
STtRNA23	tRNA-Phe	GAA	91	39	55	17	74	
STtRNA25	tRNA-Leu	TAG	101	41	56	16	85	
STtRNA26	tRNA-Leu	GAG	104	34**	52	19	85	
STtRNA27	tRNA-Pro	GGG	94	41	58	18	76	
STtRNA29	tRNA-Ile	GAT	90	39	54	16	74	
STtRNA31	tRNA-Thr	TGT	92	40	56	17	75	
STIRNA32	tRNA-Arg	GCG	88	40	52	13	75	
STtRNA33	tRNA-Leu	CAA	97	40	52	13	84	
STtRNA34	tRNA-Met	CAT	87	40	51	12	75	
STtRNA36	tRNA-Arg	CCT	99	40	63	24	75	
STtRNA40	tRNA-Trp	CCA	131	39	95	57**	74	
STtRNA46	tRNA-Arg	TCT	91	40	55	16	75	

\*: Nucleotide positions from the 5' end of tRNA genes.

\*\*: These numerals indicated the unusual position or size of introns.

variable 36- to 169-bp sequence, followed by 223 bp-, 244 bp-, or 310 bp-long LR segments. This type of repetitive unit was present at three different positions with 48, 104, and 119 repeats of SR segments (coordinates: 2,667,399–2,664,097; 2,678,286–2,671,319; and 2,693,179–2,685,053).

The subtype A-II repetitive unit was composed of 73 and 113 repeats of 25-bp-long well-conserved SR seg-

ments (GATGAATCCCAAAAGGAATTGAAAG) and a variable 33- to 45-bp spacer sequence, followed by 228-bp-long LR segments. These repetitive units were identified at two different positions (coordinates: 30,837– 25,997 and 32,475–39,835).

The second type of repetitive sequences was Tn-like elements. This was extracted by analysis of ORFs that are present in repetitive sequences. Out of nine ORFs

type of repetitive sequence	length (nt)	coor	din	nates	direction	
Tn-like element	1779	57900		59678	<	
		660704	=	662475	<	
		1034923		1036702	>	
		1077993	$\Xi$	1079772	>	
		1157568	-	1159339	>	
		1907731	2	1909502	>	
		2562560	÷	2564337	<	
truncated Tn-like element	345	120380	-	120715	>	
		715738	-	716074	>	
		740655	÷.,	740991	<	
		760848	÷	761184	<	
		1115939	$\approx$	1116276	<	
		1146090	$\approx$	1146426	>	
		1623632	Ξ.	1623968	<	
		1777801		1778137	>	
		1784191	÷	1784527	<	
dispersed repetetive unit						
subtype I	1459	1309109	-	1310567	>	
		1367448	5	1368906	<	
subtype II	1322	823496	×	824817	<	
		885027	-	886348	>	
		1164946	-	1166267	<	
		1922728	÷	1924049	<	
subtype III	844	163506	-	164343	<	
1000		269897	-	270739	<	
		833260	-	834103	<	
		1164031	÷	1164874	<	
		2269440	2	2270271	<	
subtype IV	518	2394814	-	2395331	>	
665 C		2396410	-	2396927	<	

Table 3. The lengths and coordinations of the Tn-like elements and dispersed repetitive sequences.

assigned as transposases, seven ORFs with 136 amino acid residues were located within the highly conserved 1779-bp-long sequences. Thus, these regions were assigned as a Tn-like element. However, the inverted repeats, which were generally identified at the border of Tn elements were not found. In addition to this complete Tn-like element, its truncated form was also identified. The end region of each truncated element was identical to the end sequence of the Tn-like element. The size of this element was 352 bp long and the transposase was not found in this truncated element. The position and direction of these Tn-like repetitive elements and truncated form of the Tn-like element are summarized in Table 3.

The third type of repetitive units comprised four subtypes of different repeating units from 518 bp to 1459 bp, and appeared dispersed along the entire genome. The length and coordinate of these four different repetitive sequences are summarized in Table 3. These long repetitive sequences often interfered with the assembly of raw sequencing data, but the problem could be minimized by registration of repetitive sequences into a cross-match database in PhredPhrap. The biological significance of these repeats, except for the Tn-like element, is not known.

# 3.4. Assignment and similarity search of potential protein-coding regions

The assignment of potential protein-coding regions was performed as the previous paper<sup>1</sup> with some modifications. The ORFs which consist of longer than 100 codons starting with ATG or GTG were designated by a two-letter code (ST) plus a four-digit number indicating the ORF position. The ORFs which were entirely included within longer ORF on either strand and showed neither similarity nor motif sequences were not assigned as potential protein-coding regions. There were a total of 2558 ST-class ORFs.

Subsequently, shorter ORFs consisting of 50 to 99 codons were extracted from the regions where no ST-class ORF was assigned plus a neighboring 150-bp region overlapping the next ST-class ORFs. Among these short ORFs, those which possessed significant similarity to either the registered sequences in databases or to protein motifs were taken as potential protein-coding regions and named with a three-letter code (STS) plus a three-digit number indicating the ORF position. The organization of all ORFs assigned among the entire genome is shown in Fig. 1.

Thus, a total of 2826 ORFs were assigned along the entire genomic sequence (ST-class ORFs = 2558, STS-class ORFs = 268). The average size of the ORFs was

Table 4. Summary of functional classification of ORFs.

functional categories	number of ORFs
Amino acid biosynthesis	77
Purines, pyrimidines, nucleosides, and nucleotides	55
Fatty acid and phospholipid metabolism	41
Biosynthesis of cofactors, prosthetic groups, and carriers	53
Central intermediary metabolism	34
Energy metabolism	184
Transport and binding proteins	92
DNA metabolism	45
Transcription	47
Protein synthesis	109
Protein fate	42
Regulatory functions	12
Cell envelope	21
Cellular processes	34
Other categories	23
Unknown function	42
Conserved hypothetical protein	921
to	tal 1832

267 amino acid residues, and the longest one consisted of 1933 residues (ST0620). The 2826 assigned ORFs occupy 83.9% of the entire genome. The G + C content in these coding regions was 33.52%, and that in non-coding regions was 28.51%.

For the assignment of gene function, the products name in public databases with a Zscore greater than or equal to 20, or with over 30% amino acid sequence identity along the entire coding region, were taken for ST-class ORFs. The name of gene products with a Zscore greater than or equal to 12 were also used for STS-class ORFs. Among ST- and STS-class ORFs, there were 911(32.2%) ORFs with assigned function, 921(32.6%)showed significant similarity to registered sequences with unknown function, and 145 (5.1%) contained some motifs. The remaining 849 ORFs showed no significant similarity to the sequences in public databases and protein motif sequence. The predicted products of ORFs with known functions are summarized in Table 11, in which all products predicted are classified according to functional categories.

The ORFs showing similarities to the registered genes with known functions were classified according to the functional categories and are provided in Table 4; the product names are listed in Table 11. As indicated in Table 4, this genome contained a large number of genes related to energy metabolism. This may be due to the heterotrophic feature of this microorganism, which use a large number of compounds as the energy source.

The codon usages of the proteins encoded by the 2826 ORFs are summarized in Table 5. The codons with A or U at the third position appeared to be more frequently used, probably reflecting the relatively low G + C content of this strain.

### 3.5. Other features

### 3.5.1. Genes related to respiration

Since *S. tokodaii* strain7 is aerobic, the genes involved in the TCA cycle were searched, and all of the genes in this cycle were identified on the genome. Two copies of the genes coding for citrate synthase and two subunits of 2-oxoacid:ferredoxin oxidoreductase,<sup>24</sup> which plays the same role in archaea as alpha-ketoglutarate dehydrogenase, were identified in the genome. This result suggests that *S. tokodaii* strain7 has a complete TCA cycle system similar to that found in mitochondria of eukaryotes.

On the other hand, some genes in the respiratory chain which participate in the production of ATP were not identified by similarity searching. In particular, cytochrome c was not identified in this microorganism. This feature is similar to that in *A. pernix* K1. As cytochrome c has an important role in electron transfer to oxygen in eukaryotes, it is likely that this microorganism uses a different molecule for the same function or possesses a different pathway. Participation of Rieske iron-sulfur protein and/or sulfocyanin in place of cytochrome c has been suggested in *Sulfolobus* species.

#### 3.5.2. ORFs related to sulfide metabolism

S. tokodaii strain7 is known to oxidize hydrogen sulfide to sulfate intracellularly, and this feature has been applied for the treatment of industrial waste water (personal communication from A. Yamagishi and T. Oshima). By similarity search of the genes relating to this pathway, a total of eight ORFs were detected as genes related to sulfide metabolism (from hydrogen sulfide to sulfate). These ORFs and their products are summarized in Table 6. These enzymes seem to be enough to oxidize sulfur from hydrogen sulfide to sulfate. Although

No. 4]

Table 5. Codon usages of the predicted proteins coded for by the 2826 ORFs.

UUU (Phe)	24003	31.53	UCU	(Ser)	14563	19.13	UAU	(Tyr)	27402	36.00	UGU	(Cys)	3569	4.69
$UUC \ (\text{Phe})$	10453	13.73	UCC	(Ser)	3715	4.88	UAC	(Tyr)	9701	12.74	UGC	(Cys)	1395	1.83
UUA (Leu)	36642	48.14	UCA	(Ser)	12912	16.96	UAA	(Stop)	1532	2.01	UGA (	Stop)	812	1.07
UUG (Leu)	7685	10.10	UCG	(Ser)	2509	3.30	UAG	(Stop)	482	0.63	UGG	(Trp)	7716	10.14
CUU (Leu)	14179	18.63	CCU	(Pro)	10889	14.31	CAU	(His)	7283	9.57	CGU	(Arg)	1103	1.45
CUC (Leu)	4243	5.57	CCC	(Pro)	3211	4.22	CAC	(His)	2636	3.46	CGC	(Arg)	355	0.47
CUA (Leu)	12512	16.44	CCA	(Pro)	13048	17.14	CAA	(Gln)	11842	15.57	CGA	(Arg)	700	0.92
CUG (Leu)	2916	3.83	CCG	(Pro)	2622	3.44	CAG	(Gln)	3964	5.21	CGG	(Arg)	271	0.36
AUU (Ile)	30581	40.17	ACU	(Thr)	16723	22.00	AAU	(Asn)	26487	34.80	AGU	(Ser)	12679	16.66
AUC (Ile)	6932	9.11	ACC	(Thr)	3368	4.42	AAC	(Asn)	10515	13.81	AGC	(Ser)	4328	5.69
AUA (Ile)	37755	49.60	ACA	(Thr)	12969	17.04	AAA	(Lys)	39298	51.63	AGA	(Arg)	19962	26.22
AUG (Met)	15580	20.47	ACG	(Thr)	3096	4.07	AAG	(Lys)	21379	28.09	AGG	(Arg)	9091	11.94
GUU (Val)	22315	29.32	GCU	(Ala)	19352	25.42	GAU	(Asp)	27892	36.64	GGU	(Gly)	18010	23.66
GUC (Val)	4210	5.53	GCC	(Ala)	3927	5.16	GAC	(Asp)	7224	9.49	GGC	(Gly)	4105	5.39
GUA (Val)	22471	29.52	GCA	(Ala)	15919	20.91	GAA	(Glu)	35726	46.93	GGA	(Gly)	19959	26.22
GUG (Val)	6357	8.35	GCG	(Ala)	2969	3.90	GAG	(Glu)	17583	23.10	GGG	(Gly)	5585	7.34

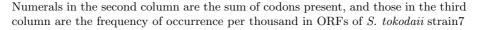


Table 6. List of ORFs related to H<sub>2</sub>S oxidizing reactions.

ORF-ID	Length of ORF (a. a.)	predicted product	predicted function
ST0615	384	sulfide dehydrogenase	$H_2S = Sulfar + H_2$
ST0971	390	sulfide dehydrogenase (flavocytochrome c) flavoprotein chain	$H_2S = Sulfar + H_2$
ST1010	208	sulfite oxidase	$SO_3^{32} + O_2 + H_2O = SO_4^{32} + H_2O_2$
ST1839	270	thiosulfate reductase electron transport protein	$H_2S = S_2O_3^{-2}$
ST2564	293	thiosulfate sulfurtransferase	$S_2O_3^2$ + cyanide = $SO_3^2$ + thiocyanate
ST2566	628	sulfite reductase	$H_2S + 3$ Oxidized Ferredoxin + 3 $H_3O = SO_3^{-2} + 3$ Reduced Ferredoxin
ST2567	239	phosphoadenosine phosphosulfate reductase	$SO_4^{2} + H_2 = SO_3^{2} + H_2O$
ST2568	412	sulfate adenylyltransferase	$ATP + SO_{4}^{2} = PPi + AMP - SO_{4}^{2}$

the products of these ORFs have not yet been isolated, confirmation of their activities would provide the valuable information for sulfide metabolism in this microorganism and facilitate the improvement of this system for industrial applications.

3.5.3. Possible integration of plasmid into chromosome

It has previously been reported that Sulfolobus sp. NOB8H2 contains 41,229 bp long plasmid, pNOB8.<sup>25,26</sup> However, no extra-chromosomal genetic unit was detected in the analysis in the present study, whereas these two strains belong to the same genus. To clarify the possibility that a plasmid had been integrated into this genome, we searched ORF homologues of pNOB8. As indicated in Table 7, a total of 37 gene families, consisting of 66 ORFs, were identified in the *S. tokodaii* strain7 genome, although their organization and the number of genes included in each gene family are variable in the genome. These results imply that a plasmid from an ancestral species was integrated into the *S. tokodaii* strain7 genome, and following rearrangement and duplication of the genome resulted in the variation of the order and

copy number of genes originally encoded by the plasmid. Peng et al. previously showed that pHEN7, a plasmid isolated from *S. islandicus*, was integrated into the host chromosome by integrase encoded by the plasmid itself.<sup>27</sup> The length of the plasmid is very short, 7.83 kb, and the integrase is highly similar to that found in SVV1 virus.<sup>28</sup> Two kinds of integrases were identified in the genome of *S. tokodaii* strain7, one was partially similar to that in SSV1 virus and the other was highly similar to the integrase/recombinase possessed in bacteria. The mechanism of integration in *S. tokodaii* strain7 may be different from that in *S. islandicus*.

Out of the 66 ORFs identified, the functions of only three genes were assigned, and the remaining 63 ORFs were assigned as genes with unknown function. These genes with unknown function may be indispensable for *S. tokodaii* strain7, as these genes have been maintained in the genome until now.

#### 3.5.4. ORFs related to eukaryote-type gene families

Many genes assigned on archaeal genomes are often identified in eukaryotes or eubacteria.  $^{29-31}$  During sim-

Table 7. S. tokodaii ORFs orthologous to genes coded in plasmid pNOB8.

genes in pNOB8	Length (a. a.)	number of identified ORFs		S. tokoda	ii ORF-I	O ortholog	ous to pNG	OB8 genes	ŝ
ORF01	116	3	ST1310	ST0251	ST1317				
ORF02	188	1	ST0159						
ORF03	81	5	ST0758	ST0236	STS156	STS229	ST1340		
ORF04	422	2	ST1308	ST1318					
ORF05	537	2	ST1307	ST2280					
ORF06	72	1	STS202						
ORF07	50	3	STS147	STS180	STS202				
ORF08	406	3	ST1056	ST2325	ST2008				
ORF09	87	1	STS029						
ORF10	1025	1	ST1326						
ORF17	253	2	ST2505	ST1338					
ORF18	94	7	STS156	STS035	STS149	STS148	ST1340	STS157	ST023
ORF19	97	4	STS156	STS149	ST0173	STS035			
ORF20	108	1	ST1342						
ORF22	164	1	ST1344						
ORF23	69	1	STS162						
ORF24	72	2	STS163	STS072					
ORF25	92	1	STS164						
ORF26	101	3	ST1345	STS045	ST2503				
ORF27	439	4	ST1346	ST0313	ST2498	ST0255			
ORF28	80	4	STS146	STS224	ST0837	ST1890			
ORF30	248	3	ST1850	ST1311	ST0254				
ORF31	630	1	ST1312						
ORF34	86	1	ST1479						
ORF37	52	1	STS159						
ORF38	604	1	ST1315						
ORF39	165	1	ST1316						
ORF40	65	2	STS155	STS151					
ORF41	110	3	ST0251	ST1310	ST1317				
ORF42	205	1	ST2077						
ORF43	74	1	ST1343						
ORF44	93	7	STS033	ST1486	STS229	STS148	ST1060	ST1339	ST076
ORF45	470	2	ST1308	ST1318					
ORF46	315	1	ST1320						
ORF48	142	1	ST1321						
ORF50	152	1	ST1316						
ORF52	81	2	STS154	STS152					
	total	81							

Table 8. S. tokodaii ORFs with similarity to the eukaryote-type genes.

ORF-ID	Length of ORFs (aa)	predicted product	distribution
ST0059	462	selenium-binding protein 2	human, mouse, plant, C. elegans
ST0155	353	flug protein.	A. nidulans
ST0233	288	hypothetical protein.	S. cerevisiae
ST0467	548	DNA replication licensing factor	human, mouse, frog, fruit fly, S. pombe
ST0779	583	acylamino-acid-releasing enzyme.	human, rat, pig, C. elegans
ST0940	767	oligosaccharyl transferase stt3 subunit.	human, mouse
ST0945	254	hypothetical protein.	S. cerevisiae , C. elegans
ST1110	386	nonspecific lipid-transfer protein.	mouse, rat
ST1257	108	s100 calcium-binding protein a3.	human, mouse
ST1350	363	nonspecific lipid-transfer protein.	human
ST1603	125	hypothetical protein.	S. cerevisiae
ST1745	565	acylamino-acid-releasing enzyme.	human, rat, pig, C. elegans
ST2082	360	sterol-regulatory element-binding protein.	human, C. griseus
ST2367	297	serine/threonine protein phosphatase pp2a catalytic subunit.	plant, human, mouse, fruit fly, S. cerevisiae

ilarity search of the *S. tokodaii* strain7 ORFs against public databases, we found that 14 ORFs show similarity to gene families that are only identified in eukaryotes. The homologues of these ORFs are not detected either in other archaea or bacteria. These ORFs and predicted gene products are given in Table 8. In addition to these eukaryotic-type genes, this strain contained 37 archaea-specific ORFs and 53 ORFs which are present both in archaea and eukaryotes. Identification of eukaryote-specific genes together with the absence of the CCA sequence in tRNA genes suggests that this strain is closer to eukaryote among archaea that have had their genomes completely sequenced.

number of homologous ORFs* in one group	number of groups	total ORFs
12	1	12
11	1	11
10	1	10
9	4	36
8	6	48
7	11	77
6	14	84
5	25	125
4	56	224
3	94	282
2	281	562
total	494	1471

Table 9. Homologous ORFs identified by sequence comparison among the 2826 ORFs of S. tokodaii strain7.

\*: ORFs with Z score higher than 8 in SW search and amino acid identity higher than 30% in 70% of the entire region were taken.

Table 10. List of the same ORFs identified on the S. tokodaii strain7 genome.

predicted function	length of ORFs (a. a.)							
transposase	136	ST0043 ST2553 ST1048 ST1096 ST1904 ST0680 ST1158						
insertion element protein	242	ST0142 ST1907 ST1139 ST1082 ST0671						
not assigned	235	ST0143 ST0857 ST1165 ST2259 ST1981						
not assigned	330	ST0847 ST0907 ST1167 ST1916 ST2230						
not assigned	240	ST0162 ST1719 ST0798 ST1987						
not assigned	347	ST0041 ST1098 ST1050						
not assigned	108	ST0042 ST1097 ST1049						
not assigned	350	ST0055 ST1957 ST1769						
not assigned	381	ST0152 ST2431 ST2008						
not assigned	168	ST0254 ST1311 ST1850						
not assigned	434	ST0678 ST1160 ST1906						
not assigned	144	ST0679 ST1159 ST1905						
IS hypothetical protein	202	ST1092 ST1939 ST2495						
not assigned	328	ST0046 ST0099						
ferredoxin	104	ST0163 ST1175						
not assigned	123	ST0856 ST1718						
IS element DNA-binding protein	314	ST1122 ST1908						
insertion element protein	100	ST1156 ST2015						
not assigned	470	ST1304 ST1360						
transposase	340	ST1779 ST2430						
not assigned	353	ST1952 ST2181						
sulfocyanin	220	ST2393 ST2394						

#### 3.5.5. Duplication of ORFs

By sequence comparison among the ORFs, 1471 ORFs were grouped into 494 families (Table 9). The result can be interpreted that ORFs in each group were generated by duplication of an ancestral sequence. Such homologous ORFs were present in the genome as either tandem repeats of a single ORF or the repeats of a single or a cluster of ORFs at different locations.

Within these families, we detected 22 families that are composed of ORFs which have over 95% length identity and over 95% amino acid identity. The gene families detected are summarized in Table 10. In addition to transposase and IS-element related proteins, sixteen kinds of proteins which possessed the same sequence were detected at different positions in the genome. This result suggests that rearrangement or duplication of the genome may continue to occur.

#### 3.5.6. Other notable genes

The structure of the operon encoding H<sup>+</sup>-ATPase (ST1435, ST1436, ST1437, ST1438, ST1439, STS172) of this strain has already been reported by Denda et al.<sup>32–35</sup> Data comparison indicated that the length of the delta subunit is 80 amino acids shorter than that of ST1435. Because some subunits which were present in *E. coli*<sup>36</sup> or *Synecococcus*<sup>37</sup> were not identified in the operon cloned from *S. tokodaii* strain7, Denda et al. suggested two possibilities: One is that the operon encodes all of the genes necessary for the whole ATPase complex and the other is that the operon encoding the subunits of

ATPase were split into two (or more) independent operons. Our data suggest that one more ORF (ST1434) upstream of ST1435 may be included in this operon as the subunit of the H<sup>+</sup>-ATPase. It seems reasonable to conclude that this operon in *S. tokodaii* strain7 contains all of the genes of the whole ATPase complex.

The genes containing inteins, defined as the self-splicing portions of a polypeptide sequence,<sup>38,39</sup> have been identified in the genome of *P. horikoshii*  $OT3^1$  and *A. pernix* K1.<sup>2</sup> However, no genes with the intein portion were identified in the *S. tokodaii* strain7 genome. Like all other aerobic organisms, the gene for superoxide dismutase<sup>2,40-42</sup> was also present in this organism (ST2283).

The entire genomic sequence of *S. tokodaii* strain7 is the third sequence from aerobic thermophilic crenarchaeota. The comparison of this genome with other archaea or thermophilic microorganisms may provide important information about the difference between euryarchaeota and crenarchaeota, as well as differences of the thermostability of proteins and the origin or evolution of eukaryotes. More detailed analysis of gene organization and gene structure in comparison with other archaeal genomes is under investigation.

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No. 4]

### Table 11. List of ORFs showing similarities to registered genes with known function.

nino acid	Length (a.a.)	Predicted Product	Locus	Zscore	ig Identity	ORFID	(4.4.)		Lœus	Zscore	9 Ider
		ithesis cid family			ASTREE PS	ST1481 Salarate of	195	uridine 5-monophosphate synthese	Swiss_Prot:OOB359	109.00	61
F2272	352	3-dehydroquinate synthase	Swiss_Prot:P36919	63.75	40.249	Sarvage of ST0485	271	sides and nucleotides 5'-methylthioadenosine phosphorylase	Swiss_Prot:Q13126	\$7.53	48
T2277 T1231	408 345	3-phosphoshikumate 1-carboxyvinyltransferase anthranilate phosphoribosyltransferase	Swiss_Prot:Q57925 Swiss_Prot:P50384	49.00 96.60	31.542 54.810	ST0975 ST0484	237	5'-methylthioadenosine phosphorylase hypoxanthine-guanine phosphoribosyltransferase	Swiss_Prot:P50389 Swiss_Prot:P27605	132.83	67.
F1229	433	anthranilate synthase component I	Swiss_Prot:Q06128	105.03	63.889	ST0803	308	inosine-uridine preferring nucleoside hydrolase	Swiss_Prot:P32986	86.82	52
T1228 T2271	193	anthranilate synthase component II aroA(G) protein	Swiss_Prot:Q06129 Swiss_Prot:P39912	90.42 114.69	76.923	ST2115 ST0551	306	inosine-uridine proferring nucleoside hydrolase	Swiss_Prot:P32986	119.59	71.
T2274	390	chorismate synthase	Swiss_Prot.P23353	79.64	49.157	ST0281	216	purine phosphoribosyltransferase uracil phosphoribosyltransferase	Swiss_Prot:Q64531 Swiss_Prot:P47276	46.23	34
TS222 T1226	50 246	dehydroquinate dehydratase indole-3-glycerol phosphate synthase	OWL:NGU39803 Swiss_Prot:Q06121	8.20 93.62	27.778 58.065	Other ST1018	264		Swiss_Prot:Q03248	29.28	34
T1230	145	N-(5'-phosphoribosyl)anthranilate isomerase	Swiss_Prot:P50386	48.74	44.365	ST1018 ST1121	264	beta-ureidopropionase beta-ureidopropionase	Swiss_Prot:P49954	34.89	27
T0294	202	P-protein (chorismate mutase: prephenate dehydrata		36.38	34.911	ST1116	490	methylmalonate-semialdehyde dehydrogenase	Swiss_Prot:P42412	63.14	48
T2273	260 245	shikimate 5-dehydrogenase tryptophan synthase alpha subunit	Swiss_Prot:Q58484 Swiss_Prot:P50382	45.71	36.742 63.525	ST2490 ST0093	685 762	nicotine dehydrogenase subunit C xanthine dehydrogenase	Swiss_Prot:Q46509 Swiss_Prot:P80457	18,49 30,26	25
T1233	422	tryptophan synthase beta subsmit	Swiss_Prot.P50383	195.87	80.529	ST0094	438	xanthine dehydrogenase	Swiss_Prot:P77165	38.54	41
statate i	449	tryptophan synthase beta subanit	Swisa_Prot:P50383	149.72	51.202	P					
storate i	338	5-methylictrahydroptoroyltrightamatehomocysteir	Swiss_Prot:P80877	50.35	31.928	Bassynthes	is .	ospholipid metabolism			
T0342	415	methyltransferase adenovylhomocysteinase	Swiss Prot P50252	83.54	74.820	ST1352 ST0070	411 253	3-hydroxy-3-methylglutaryl-CoA reductase 3-oxoacyl-[acyl-carrier protein] reductase	Swiss_Prot:008424 Swias_Prot:P51831	106.93	75. 18
T1225	399	aspartate aminotransferase	Swiss_Prot P14909	149.47	63.706	ST1109	250	3-oxoacyl-[acyl-carrier protein] reductase	Swiss_Prot:O67610	46.19	49
ST1242 ST2171	350	aspartate-semialdehyde dehydrogenase aspartate-semialdehyde dehydrogenase	Swiss_Prot:Q57658 Swiss_Prot:Q57658	109.78 93.31	44,737 39,429	ST1868 ST2287	260	3-oxoacyl-[acyl-carrier protein] reductase	Swiss_Prot:P51831 Swiss_Prot:P39333	33.77 20.50	37
T1241	447	aspartokinase	Swiss_Prot:Q57991	70.61	33.120	ST0514	397	3-oxoacyl-[acyl-carrier protein] reductase acetyl-CoA acetyltransferase	Swiss_Prot:P45359	60.78	44
T0506	377 285	cystathionine gamma-synthuse	Swiss_Prot P55217	69.49 47.33	42.059 32.990	ST1349 ST0977	348	acyl carrier protein synthase	Swiss_Prot:P43711	26.36 63.00	30 40
12479	285	dihydrodipicolinate synthase dihydrodipicolinate synthase	Swiss_Prot:Q57695 Swiss_Prot:P06995	30.20	23.958	ST0487	283	diphosphomevalonate decarboxylase isoprenyl diphosphate synthase	Swiss_Prot:P32377 Swiss_Prot:Q53479	27.13	40
T1301	460	homocitrate synthase	Swiss_Prot:Q58787	66.84	41.207	ST2353	386	sulfolipid biosynthesis protein sqdB	Swiss_Prot:P43602	12.95	45
T1519 T0505	312 306	homoserine dehydrogenase	Swiss_Prot P52986 Swiss_Prot Q58504	39.60 76.12	45.517 38,403	Degradatic ST1516	269	3-hydroxybutyryl-CoA dehydratase	Swiss_Prot:P52046	74.06	45
ST1529	382	succinyl-diaminopimelate desuccinylase	Swim_Prot.Q57899	40.29	30.530	ST0069	652	3-hydroxybutyryl-CoA dehydrogenase	Swiss_Prot:P52041	55.78	45
T0960 T1240	337 395	threenine synthase	Swiss_Prot:Q58860	43.88 105.42	30.712 54.103	ST1507 ST2094	318 390	3-hydroxybutyryl-CoA dehydrogenase 3-hydroxybutyryl-CoA dehydrogenase	Swias_Prot:P14755 Swias_Prot:P52041	51.27 67.45	32
lutamate	family	threonine synthase	Swiss_Prot:Q58860			ST2413	278	3-hydroxybutyryl-CoA dehydrogenase	Swiss_Prot:P52041	57.29	44 40
T0194	261	acetylghnamate kinase	Swiss_ProcQ60382	30.67	34.483	ST0066	389	acyl-CoA dehydrogenase	Swins_Prot:P71539	52.18	27
ST0191 ST2549	387 374	acetylomithine aminotransferase acetylomithine deacetylase	Swiss_Prot/O30156 Swiss_Prot/P23908	63.75 22.63	44.142 35.714	ST0076 ST0087	400 360	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Swiss_Prot:P45857 Swiss_Prot:P12007	64.22 38.65	45
ST1502	446	argininosuccinate lyase	Swiss_Prot:Q58201	58.37	35,695	ST0916	358	acyl-CoA dehydrogenase	Swiss_Prot:P45867	47.87	30
T1501 T0100	390 137	argininosoccinate synthase glutamate dehydrogenase	Swisa_Prot:Q60174 Swiss_Prot:P80053	79.83 33.62	47.656 35.514	ST1791 ST1802	404 374	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Swiss_Prot:P45867 Swiss_Prot:P45857	59.72 53.84	38 34
T2241	422	glutamate dehydrogenase	Swiss_Prot.P80053	101.19	76.960	ST2256	379	acyl-CoA dehydrogenase	Swiss_Prot:P45867	57.73	35
T2198 T0156	635 483	glutamate synthase large subunit glutamine synthetase	Swiss_Prot P55038 Swiss_Prot P21154	\$0,47 48,77	40.613 37.566	ST0067 ST0048	372 254	alpha-methylacyl-CoA racemawe enovl-CoA hydratase	Swiss_Prot:P76518 Swiss_Prot:P76082	79.80 55.47	32 35
T0568	429	glutamine synthetase	Swiss_Prot/Q60182	48.99	30.562	ST2416	258	enoyl-CoA hydratase	Swiss_Prot:P34559	75.71	47
T1387	473	glutamine synthetase	Swiss_Prot:P23794 Swiss_Prot:O58496	109.50 89.25	78.981	ST2417 ST0095	250 243	encyl-CoA hydratase fatty-acidCoA dehydratase	Swiss_Prot:P77467 Swiss_Prot:P52046	49.38	33
T1245	305	N-acetyl-gamma-glutamyl-phosphate reductase ornithine carbamoyltransferase	Swiss_Prot:Q51742	58.00	44.160 49.673	\$10095	510	fatty-acidCoA drhydratase fatty-acidCoA ligase	Swiss_Prot:P52046 Swiss_Prot:Q00594	36.91 95.34	35
T0646	259	pyrroline-5-carboxylate reductase	Swiss_Prot:P74572	53.61	38.073	\$10077	536	fatty-acid-CoA ligase	Swiss_Prot:Q00594	71.94	31
yruvale fa	amily 386	2-isopropylmalate sypthase	Swiss_Prot:Q58595	73.79	53.562	ST0669 ST1112	226	glycerophosphoryl diester phosphodiesterase long-chain-fatty-acid-CoA ligase	Swiss_Prot:P54527 Swiss_Prot:P94547	40.89 62.74	34 34
ST2203	522	2-isopropylinalate synthase	Swiss_Prot.Q58787	61.70	32.813	ST1388	454	long-chain-fatty-acidCoA ligase	Swiss_Prot:P31687	36.85	30
T0599	415	3-isopropylmalate dehydratase large subunit 3-isopropylmalate dehydratase small subunit	Swiss_Prot:Q27439 Swiss_Prot:Q58673	91.07 73.95	45.146 53.333	General STS137	90	acylphosphatase	Swiss_Prot:P75877	39.65	52
T0433	337	3-isopropylmalate dehydrogenase*	Owt:D86857	193.59	100.00	ST0592	169	biotin carboxyl carrier protein	Swiss_Prot:P05115	33.38	43
ST0202 ST0752	582 530	acetolactate synthase large subunit acetolactate synthase large subunit	Swiss_Prot:Q02137 Swiss_Prot:O85293	35.88	29.480 27.553	\$T0593 \$T0071	513 303	biotin carboxylase esterase	Swiss_Prot:Q58626 Swiss_Prot:P23872	85.76 32.10	55
ST1447	572	acetolactate synthase large subunit	Swiss_Prot:Q57725	73.53	46.749	ST0079	397	nonspecific lipid-transfer protein	Swiss_Prot:P32020	53.47	30
ST2410 ST2172	531 560	acetolactate synthase large subunit dihydroxy-acid dehydratase	Swiss_Prot:O85293 Swiss_Prot:P51785	23.36	29.630 45.586	ST0096 ST1110	373 386	nonspecific lipid-transfer protein	Swiss_Prot:Q07598 Swiss_Prot:P32020	49.73 21.13	31
ST1445	332	ketol-acid reductoisomerase	Swiss_Prot:P29107	97.60	49.844	ST1799	391	nonspecific lipid-transfer protein nonspecific lipid-transfer protein	Swiss_Prot.P32020 Swiss_Prot.Q07598	32.68	29
\$T0295	404	threonine dehydratase	Swiss_Prot:P05792	85.40	46.795	ST2418	387	nonspecific lipid-transfer protein	Swiss_Proc.Q07598	58.72	33
crine fam	uly 300	cysteine synthuse	Swiss_Prot:P16703	42.65	31.034	Ricecuthen	e at ca	factors, prosthetic groups, and carriers			
T0694	297	D-3-phosphoglycerate dehydrogenase	Swiss_Prot:P45637	26.41	31.923			and cobalamin			
ST1218 ST1354	313 433	D-3-phosphoglycerate dehydrogenase serine hydroxymethyltransferase	Swiss_Prot:Q29445 Swiss_Prot:Q58992	63.26 89.29	44.625 47.794	ST1821 ST1826	354	chiD protein chiG protein	Swiss_Prot/Q60342 Swiss_Prot/Q05631	77.85 17.54	36 30
istidine f	amily					ST2342	269	cobalamin biosynthesis protein cobD	Swiss_Prot:P21634	30.50	39
ST1459 ST1462	283 249	ATP phosphoribosyltransferase hisF protein (cyclase)	Swiss_Prot:O33771 Swiss_Prot:O33774	144.00 87.50	73.239 75.697	ST2344 ST0389	505 437	cobyric acid synthase cobyrinic acid a.e.diamide synthase	Swiss_Prot:Q55860 Swiss_Prot:P29946	64.78 79.78	37
ST1466	197	hisH protein (amidotransferase )	Swiss_Prot:O33777	115.68	65.829	ST0214	336	delta-aminolevulinic acid dehydratase	Swiss_Prot:Q60178	63.73	57
ST1464 ST1458	394 286	histidinol dehydrogenase histidinol-phosphate aminotransferase	Swiss_Prot:O33775 Swiss_Prot:O33770	124.39	61.404 58.246	ST0215 ST0212	304 412	glutamate-1-semialdehyde 2.1-aminomutase glutamy1-tRNA reductase	Swiss_Prot.Q58020 Swiss_Prot.O28304	58.52 34.53	47 39
ST1461	194	imidazoleglycerol-phosphate dehydratase	Swiss_Prot:O33773	97.76	68.421	\$10217	294	porphobilinogen deaminase	Swins_Prot:Q57989	65.84	- 44
ST1465 ST1467	108	phosphoribosyl-AMP cyclohydrolase phosphoribosyl-AMP cyclohydrolase	Swiss_Prot:O33776 Swiss_Prot:O33778	75.67 73.83	68.085 72.840	ST1817 ST1823	222 253	precorrin-2 c20-methyltransferase precorrin-3b c17-methyltransferase	Swiss_Prot:Q58181 Swiss_Prot:Q08590	38.23 78.70	32
ST1460	230	phosphoribosyiformimino-5-aminoimidazole	Swiss_Prot:O33772	107.91	52.155	ST1825	222	precorrin-3b c17-methyltransferase	Swiss_Prot/029534	24.59	29
10.11 J		carboxamide ribotide isomerase				ST1816 ST1819	278 192	precorrin-4 c11-methyltransferase precorrin-8W decarboxylase	Swiss_Prot.Q05630 Swiss_Prot.Q57836	50.97 52.14	40 39
eneral ST0165	323	aminotransferase	Swiss_Prot:Q10503	17.94	32.051	ST1819	333	precorrin-8w decarboxytase precorrin-8x methylmutase	Swiss_Prot.Q58340	46.08	35
ST0735	419	aminotransferase	Swiss_Prot:P94427	50.88	37.736	ST0211	229	siroheme synthase	Swiss_Prot:Q57605	31.91	32
ST1114 ST1011	441	aminotransferase D-hydantoinase	Swiss_Prot:P30268 Swiss_Prot:Q45515	46.92 59.49	32,493 40,000	ST0563	239	uroporphyrin-III C-methyltransferase	Swiss_Prot:P29564	72.20	49
ST1020	413	D-hydantoinase	Swiss_Prot:Q44184	41.28	27.602	Lipcate ST1896	374	lipoate-protein ligase	Swiss_Prot:P54511	22.98	27
ST1118 ST1686	464	D-hydattoinase hydantoin utilization protein	Swiss_Prot:Q45515 Swiss_Prot:Q45515	69.35 98.00	41.189 37.452	Menaquin ST0360	me and 212	ubiquinone	Swiss Proc O57566	72.18	44
	503	N-methylhydantoinase (ATP-hydrolyzing)	Swiss_Prot:Q01262 Swiss_Prot:Q10094	79:16	37.620	ST2204	297	3-octaprenyl-4-hydroxybenzoate carboxy-lyase 4-hydroxybenzoate octaprenyltransferase	Swiss Prot 052366	36.09	26
ST1685						\$1012h \$10127	5// 347	coenzyme POO synthesis protein coenzyme PQQ synthesis protein	Swiss_Prot.1917/82 Swiss_Prot.Q58234	23.99 21.49	29 26
		nes, nucleosides, and nucleotides cotide metabolism ribonucleoside-dipbosphate reductase large subunit		-10-22	100000	ST2412	338	coenzyme PQQ synthesis protein	Swiss_Prot:P27507	24.04	31
rines, pa	bonucă	ribonucleoside-diphosphate reductase large subunit	Swiss Prot: P07742	41.79	27.856	Molybdop ST1383	erin 313	molybdenum cofactor biosynthesis protein A	Swiss_Prot/Q58234	91.14	44
rines, py -Deoxyri ST1259	831	advocide interconnections					323	molyblenum cofactor biosynthesis protein A molyblenum cofactor biosynthesis protein A	Swiss Prot/O57567		
rines, py -Decxyri ST1259 ocleotide ST0408	831 831 and or 180	acleoside interconversions adenylate kinase	Swiss Prot:005982	86.26	59.880	ST2174				63.99	35
rines, py -Deoxyri ST1259 acleotide ST0408 ST0410	831 7 and no 180 197	adenylate kinase adenylate kinase	Swiss_Prot:005982 Swiss_Prot:P35028	128.23	78.238	ST2174 ST2315	178	molybdenum cofactor biosynthesis protein B molybdenum cofactor biosynthesis motein C	Swias_Prot:P30746	63.99 40.94	35 32
rines, py -Decxyri ST1259 acleotids ST0408 ST0410 ST0280 arines	bonucs 831 r and no 180 197 148	adenylate kinase adenylate kinase nucleoside diphosphate kinase	Swiss_Prot:005982 Swiss_Prot:P35028 Swiss_Prot:Q58661	128.23 49.01	78.238 60.741	ST2174 ST2315 ST0472 ST0504	151 545	molybdenum cofactor biosynthesis protein C molybdopterin biosynthesis mocA protein	Swias_Prot:P30746 Swias_Prot:Q58535 Swias_Prot:Q58296	63.99 40.94 80.38 78.79	35 32 59 41
rines, py Decxyri ST1259 acleotide ST0408 ST0410 ST0280 arines ST0288	bonucs 831 r and no 180 197 148 450	adenylate kinase adenylate kinase nucleoside diphosphate kinase adenylosuccinate lyase	Swiss_Prot:005982 Swiss_Ptot:P35028 Swiss_Ptot:Q58661 Swiss_Ptot:058582	128.23 49.01 98.06	78.238 60.741 46.939	ST2174 ST2315 ST0472 ST0504 ST2045	151 545 388	mohybdenum cofactor biosynthesis protein C mohybdopterin biosynthesis mocA protein mohybdopterin biosynthesis mocA protein	Swias_Prot:P30746 Swias_Prot:Q58535 Swias_Prot:Q58296 Swias_Prot:Q58296	63.99 40.94 80.38 78.79 51.33	35 32 59 41 33
rines, py -Deoxyri ST1259 lacleotide ST0408 ST0408 ST0280 urines ST0288 ST0288 ST0281 ST1496	bonucs 831 r and no 180 197 148	adenyiate kinase adenyiate kinase nuckoside diphosphate kinase adenyiosuccimate lyase adenyiosuccimate lyase andicphosphetoiosyittanaterase	Swiss_Prot:O05982 Swiss_Prot:P35028 Swiss_Prot:Q58661 Swiss_Prot:Q57661 Swiss_Prot:Q57981 Swiss_Prot:Q57657	128.23 49.01	78.238 60.741 46.939 49.701 43.534	ST2174 ST2315 ST0472 ST0504	151 545	molybdenum cofactor biosynthesis protein C molybdopterin biosynthesis mocA protein	Swias_Prot:P30746 Swias_Prot:Q58535 Swias_Prot:Q58296	63.99 40.94 80.38 78.79	35 32 59 41 33 27
rines, py -Deoxyri ST1259 acleotide ST0408 ST0408 ST0280 arines ST0288 ST0291 ST1496 ST1497	bonuc5 831 r and no 180 197 148 450 335 443 403	aderylane kinase adenylane kinase neckowide diphosphate kinase adenylosuccinate lyzase adenylosuccinate lyzate amidophosphoribosyltranaferase amidophosphoribosyltranaferase	Swiss_Prot:005982 Swiss_Prot:P35028 Swiss_Prot:Q58661 Swiss_Prot:Q58652 Swiss_Prot:Q57657 Swiss_Prot:Q57657 Swiss_Prot:Q57657	128.23 49.01 98.06 110.86 80.43 65.41	78.238 60.741 46.939 49.701 43.534 41.290	ST2174 ST2315 ST0472 ST0504 ST2045 ST0527 STS230	151 545 388 236 93	molybdenum cofactor biosynthesis protein C molybdopterin biosynthesis mocA protein molybdopterin biosynthesis moc A protein molybdopterin converting factor pterin 4- alpha-carbinolamine dehydratase	Swias_Prot:P30746 Swias_Prot:Q58535 Swias_Prot:Q58296 Swias_Prot:Q58296 Swias_Prot:Q58296 Swias_Prot:P45308 PIR:S74881	63.99 40.94 80.38 78.79 51.33 24.75 51.97	35 32 59 41 33 27 45
rines, py -Deoxyri ST1259 acleotide ST0408 ST0400 BT0280 BT0288 ST0281 ST1496 ST1496 ST1497 ST0296	831 r and us 180 197 148 450 335 443	adenyiate kinase adenyiate kinase nuckoside diphosphate kinase adenyiosuccimate lyase adenyiosuccimate lyase andicphosphetoiosyittanaterase	Swiss_Prot:005982 Swiss_Prot:P55025 Swiss_Prot:Q58661 Swiss_Prot:Q57661 Swiss_Prot:Q57657 Swiss_Prot:Q57657 Swiss_Prot:Q57657	128.23 49.01 98.06 110.86 80.43	78.238 60.741 46.939 49.701 43.534	ST2174 ST2315 ST0472 ST0504 ST2045 ST0527 ST0527 STS230 Pantothem ST0533	151 545 388 236 93 de and 267	molybdepternin cofactor biosynthesia protein C molybdepterin biosynthesia mocA protein molybdepterin biosynthesia mocA protein molybdepterin converting factor perin A- alghe-arbholdanme dehydrataae coenzyne A herebyl-2-oxebutanoate hydroxymethyltransferase	Swias_Prot:P30746 Swias_Prot:Q58535 Swias_Prot:Q58296 Swias_Prot:Q58296 Swias_Prot:Q58296 Swias_Prot:P45308 PIR:S74881	63.99 40.94 80.38 78.79 51.33 24.75	35 32 59 41 33 27 45
rines, py -Deoxyri ST1259 acleotide ST0408 ST0408 ST0410 ST0280 arines ST0288 ST0291 ST1296 ST1291 ST1497 ST1296 ST1497 ST0298 ST1296 ST1297 ST0298 ST2345	bonucs 831 7 and ns 180 197 148 450 335 443 403 171 188 370	adorplane kinase adorplane kinase adorplane kinase adorplane cinate lysane adorplane cinate systematica anaida phosphoribos y brandrater anaida phosphoribos y brandrater (SMF systema) - phosphatase (SMF systema) - phosphatase	Swiss_Prot:005982 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:027657 Swiss_Prot:025165	128.23 49.01 98.06 110.86 80.43 65.41 29.44 35.57 50.89	78.238 60.741 46.939 49.701 43.534 41.290 33.028 32.787 38.222	ST2174 ST2315 ST0472 ST0504 ST2045 ST0527 ST5230 Paetothem ST0533 Riboflavin ST0334	151 545 388 236 93 de and 267 FMN. 157	molybdyenin molydaeth protein C molyddyetri hisoynthesis moch protein molybdyetri hisoynthesis moch protein molybdyprin cowering factor prein – apha-zabioslamine dehydriaae coenzyne A – anethyl – coolotiaaoaie hydroxynethyltransferase an FAD – 6,7-dimethyl - &ribityllamazine synthase	Swias_Prot.P30746 Swias_Prot.Q58355 Swias_Prot.Q58296 Swias_Prot.Q58296 Swias_Prot.Q58296 Swias_Prot.Q5308 PIR:S74881 Swias_Prot.P52996 Swias_Prot.Q57751	63.99 40.94 80.38 78.79 51.33 24.75 51.97 90.16 82.74	35 32 59 41 33 27 45 48 59
rines, py -Deoxyri ST1259 acleotide ST0408 ST0408 ST0280 arinea ST0288 ST0291 ST1291 ST1296 ST1291 ST1497 ST0296 ST1497 ST0296 ST1296 ST12978 ST0295 ST02978 ST02970	bonucs 831 r and nc 180 197 148 450 335 443 403 171 188 370 254	aderplark kinase aderplark kinase uncleoside diphosphate kinase aderploruscinate lyase aderploruscinate synthesis amidsphosphoethosyltranferase amidsphosphoethosyltranferase hist/3-adennyl) triphosphatase GMP synthase ionsiee. <sup>69</sup> monophosphate dehydrogenase	Swiss_Prot:005982 Swiss_Prot:055982 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:057981 Swiss_Prot:057657 Swiss_Prot:058276 Swiss_Prot:058276 Swiss_Prot:028165 Swiss_Prot:028165	128.23 49.01 98.06 110.86 80.43 65.41 29.44 35.57 50.89 40.49	78.238 60.741 46.939 49.701 43.534 41.290 33.028 32.787 38.222 43.697	ST2174 ST2315 ST0472 ST0504 ST2045 ST0527 STS230 Paenothem ST0533 Riboflavin ST0394 ST1385	151 545 388 236 93 de and 267 .FMN. 157 215	mohybdynum ofrator biosynthesia protein C mohybdynetrin biosynthesia mock protein mohybdynetrin biosynthesia mock protein mohybdynetrin ocuverting factor pretra - alpha-carbinolamine dehydrataae coeranyne A - 3-methyl-2-onobutansuste hydroxymethyltransferase and FAD 6,7-dimethyl-K-ribiyliumazine synthase (DP eyckohydratae	Swias_Prot.P30746 Swias_Prot.Q58535 Swias_Prot.Q58296 Swias_Prot.Q58296 Swias_Prot.P45308 PIR:S74881 Swias_Prot.P52996	63.99 40.94 80.38 78.79 51.33 24.75 51.97 90.16	35 32 59 41 33 27 45 48 59
rines, py -Deoxyri ST1259 acleotids ST0408 ST0408 ST0408 ST0280 arines ST0288 ST0291 ST1496 ST1496 ST1497 ST0296 ST1497 ST0296 ST2345 ST0378 ST245 ST0770 ST1498	bonucs 831 7 and ns 180 197 148 450 335 443 403 171 188 370	aderylark kinase aderylark kinase kadrylark kinase aderylarouxcitante lyase aderylarouxcitante lyase aderylarouxcitante yantease amidsphosphothosyltranteferase amidsphosphothosyltranteferase bidy <sup>4</sup> aderouyl) triphosphatase GMP synthase inosites <sup>47</sup> . monophosphate dehydrogenase phosphorbosylamines-ghysiten ligase phosphorbosylamine-ghysiten ligase	Swiss_Prot:005982 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:027657 Swiss_Prot:025165	128.23 49.01 98.06 110.86 80.43 65.41 29.44 35.57 50.89	78.238 60.741 46.939 49.701 43.534 41.290 33.028 32.787 38.222	ST2174 ST2315 ST0472 ST0504 ST2045 ST0527 STS230 Pantothenu ST0333 Riboflavin ST0394 ST1385 Thioredox ST2355	151 545 388 236 93 de and 267 267 215 m. gluta 478	mohybdyatim in orfactor biosynthesis protein C mohybdysterin biosynthesis mock protein mohybdysterin biosynthesis mock protein mohybdysterin overving factor perint - alpha-carbinolamine dehydratase cooraymen A - 3-methyl-3-oxobutassue hybdystymethyltranderase and FAD 6.7-dimethyl-8-mbhyllumatine synthase (TP syckubydoase uerdwin, jolundhoose	Swias, Proc.P30746 Swias, Proc.Q58535 Swias, Proc.Q58296 Swias, Proc.Q58296 Swias, Proc.P5308 PIR:S74881 Swias, Proc.P52996 Swias, Proc.Q57751 Swias, Proc.Q57751 Swias, Proc.Q18956	63.99 40.94 80.38 78.79 51.33 24.75 51.97 90.16 82.74 50.47 32.92	35 32 59 41 33 27 45 48 59 45 28
rines, py -Decxyri \$T1259 acleotidk \$T0408 \$T0408 \$T0280 arines \$T0288 \$T0288 \$T1291 \$T1496 \$T1496 \$T1497 \$T1496 \$T1497 \$T1296 \$T0578 \$T2345 \$T0770 \$T1498 \$T07007	bonucs 831 r and nc 180 197 148 450 335 443 403 171 188 370 254 477 364	adorylark kinase adorylark kinase adorylark kinase adorylosuccinatel yase addrylosuccinate yuthetiase andidytolytochtolythanderase andidytolytochtolythanderase andidytolytochtolytanderase andidytolytochtolytanderase andidytolytochtolytanderase andidytolytochtolytanderase andidytolytochtolytanderase andidytochtolytanderase APDase submit APDase submit	Swiss_Prot:05982 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:057687 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:0581847 Swiss_Prot:0581847 Swiss_Prot:0581847 Swiss_Prot:0581847	128.23 49.01 98.06 110.86 80.43 65.41 29.44 35.57 50.89 40.49 80.80 164.02	78.238 60.741 46.939 49.701 43.534 41.290 33.028 32.787 38.222 43.697 38.526 70.787	ST2174 ST2315 ST0475 ST0504 ST0505 ST0527 STS280 Pantothem ST0394 ST1385 Thiorecket ST2355 ST21223	151 545 388 236 93 de and 267 FMN, 157 215 m, gluta 478 140	mohybdynum corfactor biosynthesis modya mohyddynum in orodoni mohybdydycrin biosynthesis mod A protein mohybdydycrin biosynthesis mod A protein mohybdydycrin ocerwrling factor petrin 4-alpha-carbinelamine drhydratase consymen A - 3-mehyl - 2-cochatasache hydroxymechylr ansferase and A that A that a start a start a start a start A that a start a start A that a start a start a start a start A that a start a start a start a start A that a start a start a start a start A that a start a start a start a start a start A that a start a start a start a start a start a start A that a start a start A that a start a start A that a start a sta	Swiaa, Proc.P30746 Swiaa, Proc.Q58536 Swiaa, Proc.Q58296 Swiaa, Proc.Q58296 Swiaa, Proc.Q58296 Swiaa, Proc.P52996 Swiaa, Proc.Q57751 Swiaa, Proc.Q57751 Swiaa, Proc.P37305	63.99 40.94 80.38 76.79 51.33 24.75 51.97 90.16 82.74 50.47 32.92 35.45	35 32 59 41 33 27 45 48 59 45 28 50
rines, py -Decxyri \$T1259 acleotidk \$T0408 \$T0408 \$T0280 arines \$T0288 \$T0288 \$T1291 \$T1496 \$T1496 \$T1497 \$T1496 \$T1497 \$T1296 \$T0578 \$T2345 \$T0770 \$T1498 \$T07007	bonuc5 831 r and nc 180 197 148 450 335 443 403 171 188 370 254 477	adortylar kinase adortylar kinase adortyloruk vinase adortyloruk vinase adortyloruk vinase amidsphosphorthosyltranferase amidsphosphorthosyltranferase amidsphosphorthosyltranferase bidy adortyloruk GMP synthase inosinet. <sup>69</sup> morophosphate dehydrogenase phosphorthosyl amine-ghysite ligase phosphorthosyltranise-ghysite ligase phosphorthosyltranise-ghysite ligase phosphorthosyltranise-datoryl jase ATPase subsnit phosphorthosyltranisemidadea carboxyl jase	Swiss_Prot:005982 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:058582 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:057657 Swiss_Prot:04057 Swiss_Prot:025165 Swiss_Prot:025165	128.23 49.01 98.06 110.86 80.43 65.41 29.44 35.57 50.89 40.49 80.80	78.238 60.741 46.939 49.701 43.534 41.290 33.028 32.787 38.222 43.607 38.626	ST2174 ST2315 ST0472 ST0504 ST2045 ST0527 STS230 Pantothenu ST0333 Riboflavin ST0394 ST1385 Thioredox ST2355	151 545 388 236 93 de and 267 267 215 m. gluta 478	mohybdyatim incofactor biosynthesis protein C mohybdysterin biosynthesis mock protein mohybdysterin biosynthesis mock protein mohybdysterin overling factor petrin 4-alpha-carbiosalmine dehydratase coexyntin A - 3-methyl-3-oxobutassue hydroxynethyltranderase and FAD 6.7-dimethyl-8-ribhyllumatine synthase (TP syckubylotose aretwin, johanhiote gamma-plannipythase thioredoxin thioredoxin	Swiaa, Prot. P30746 Swiaa, Prot. Q58236 Swiaa, Prot. Q58296 Swiaa, Prot. Q58296 Swiaa, Prot. P45308 PIR: S74881 Swiaa, Prot. P52996 Swiaa, Prot. Q57751 Swiaa, Prot. Q18956 Swiaa, Prot. P18956 Swiaa, Prot. P22231	63.99 40.94 80.38 78.79 51.33 24.75 51.97 90.16 82.74 50.47 32.92 35.45 38.53	35 32 599 41 33 27 45 48 99 45 28 50 48
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Table 11. Continued.

	Length (A.A.)	Predicted Product	Locus	Zscore	4 Identity	ORFID	(44)		Locus	Zacore	4. Ident
T0524 T1909	172 370	inorganic pyrophosphalase* pholl-like protein	PIR-JE0392 Swiss_Prot:P46343	122.67 27.56	100.00 30.178	ST1533 ST1787	300 306	2-ketovalerate ferredoxin oxidoreductase beta-2 2-ketovalerate ferredoxin oxidoreductase beta-2	Swiss_Prot:P52647 Swiss_Prot:Q53046	17.25 23.12	29.0 31.2
lyamine TU352	biosyn 295		Swiss_Prot:Q57757	58.87	36.059	ST1884 ST2305	332 362	acetoin utilization acuC protein acetoin utilization acuC protein	Swiss_Prot:P39067 Swiss_Prot:P39067	33.32 66.35	34.9 40.9
10.346	300	spermidine synthase	Swas_Prot P09158	56.30	35.185	ST2324	129 361	acetoin utilization acuC protein	Swiss_Prot:Q57955	76,90	43.7
fur met f0723	abolian 156	NADH-dependent FMN oxydoeodactase	Swiss_Prot P54990	23.28	28.689	ST1350 ST0050	562	acetyl-CoA synthuse acetyl-CoA synthetase	Swiss_Prot:P22307 Swiss_Prot:P39062	20.64 103.15	41.6
T2567 T2568	239 412	phosphoadenosine phosphosulfate reductase sulfate adenylyltransferase	Swiss_Prot:O05927 Swias_Prot:P08536	77.55 45.03	44.872 35.659	ST0730 ST0783	662 659	acetyl-CoA synthetase acetyl-CoA synthetase	Swiss_Prot:P27095 Swiss_Prot:P27095	90.47 85.44	51.0
12566	628	sulfite reductase	Swiss_Prot:P52673	56.21	30.900	ST1190	497	acetyl-CoA synthetase	Swiss_Prot.P39062	78.21	36.
F1127	311 267	sulfur oxygenase reductase thiosulfate sulfurtransferase	Swiss_Prot:P29082 Swiss_Prot:Q50036	188.56 77.84	68.730 41.481	ST1796 ST1803	609 621	acetyl-CoA synthetase acetyl-CoA synthetase	Swias_Prot:P27095 Swias_Prot:P27095	67.44 70.82	32. 34.
12564	293	thiosoffate sulfurtransferance	Swiss_Prot:O05793	85.62	48.057	ST2019	661	acetyl-CoA synthetase	Swiss_Prot:P27095	90.53	50.
rogen f 12267	287	hexA protein	Swiss_Prot:P30138	42.41	30.508	ST2139 ST2575	576	acetyl-CoA synthetase acetyl-CoA synthetase	Swias_Prot:P27550 Swias_Prot:P39062	54.63 78.23	31. 35.
T2446	276	nodulation ATP-binding protein	Swiss_Prot:P32010	32.91	35.242	ST0038	307	alcohol dehydrogenase	Swias_Prot:P39462	47.81	37.
T1956	504 netaboli	nodulation protein	Swins_Prot:Q58458	63.91	35.133	ST0053 ST0480	344 334	alcohol dehydrogenase alcohol dehydrogenase	Swiss_Prot:P50381 Swiss_Prot:P12311	93.74 40.25	55. 32.
trogen n T1023		cyanate lyase	Swiss_Prot:Q59948	59.35	42.958	ST0569	333	alcohol dehydrogenase	Swias_Prot:P42327	43.15	32
T0478 T2489	396	enantiomer-selective amidase morphine 6-dehydrogenase	Swiss_Prot:O27540 Swiss_Prot:P22045	49.57 35.77	45.783 31.933	ST2056 ST2252	361	alcohol dehydrogenase alcohol dehydrogenase	Swiss_Post:P49645 Swiss_Post:P42328	35.07 30.48	41.
T1414	255	tropinesterase	Swiss_Prot P07383	27.39	30.928	\$72577	347	alcohol dehydrogenase	Swiss_Prot:P39462	135.99	89
T1028 T1029	493 224	urease alpha subunit urease gamma subunit	Swiss_Prot:Q07397 Swiss_Prot:P42822	59.55 56.22	55.070 49.107	ST2605 STS015	330	alcohol dehydrogenase alcohol dehydrogenase	Swiss_Prot:P42328 Swiss_Prot:P12311	38.82	33 46
gradatio	on of an	ino acids				ST2484	730	aldehyde oxidoreductase	Swiss_Prot:P77489	33.83	24
T1010 meral	208	sulfite oxidase	Swiss_Prot:Q07116	24.14	41.333	ST1786 ST0552	252 562	citrate lyase beta subunit coenzyme B12-dependent isobutyryI-CoA mutase	Swiss_Prot:O53078 Swiss_Prot:P22033	46.73 90.21	31 45
T2099	193	2 hydroxy 6 oxo 6 phenylhexa 2.4 dienoate hydrola		22.20	33.621	ST2295	458	D-lactate dehydrogenase	Swias_Prot:P52075	106.82	37
T1705	281 502	2-bydroxyhepta-2,4-diene-1,7-dioate isomenise 4-bydroxyphenylacetate 3-monooxygenase	Swiss_Prot:P34673 PIR:E69291	54.78 170.73	34.375 49.684	\$T0081 \$T0348	973 654	formate dehydrogenase alpha subunit formate dehydrogenase alpha subunit	Swiss_Prot:P06131 Swiss_Prot:P07658	115.46 90.60	40
		large subonit				ST0084	255	formate dehydrogenase subunit fdhD	Swiss_Prot:Q10820	65.14	40
T0344 T0591	350	glycerol dehydrogenase methylmalonyl-CoA decarboxylase alpha sobunit	Swiss_Prot:Q58122 Swiss_Prot:P54541	84.87 99.44	45.745 51.984	ST0823 ST0732	252	glutaconate CoA-transferase subunit A indolepyravate exidereductase subunit A	Swins_Prot:Q59111 Swins_Prot:Q01700	26.55	29
T2096	140	methylmalonyl-CoA mutase alpha subunit	Swiss_Prot:Q05065	40.80	42.424	ST0734	186	indolepyrovate oxidoreductase subunit B	Swina_Prot.P80906	14.94	68
T2055 T1013	208 637	phosphatase quinoline 2-oxidoreductase	Swiss_Prot:O67359 Swiss_Prot:P08793	19.90 13.88	28.824 26.768	ST1811 ST0114	311 414	L-lactate dehydrogenase malate oxidureductase	Swas_Prot:P33572	32.17	28 46
T1571	693	quinoline 2-oxidoreductaire quinoline 2-oxidoreductaire	Swiss_Prot:P08793 Swiss_Prot:P80457	20.99	28.242	ST0278	443	malate exidereductase	Swiss_Prot:P16468 Swiss_Prot:P16468	117.25	47
			0.405			ST0075 ST1531	311 181	NAD-dependent alcohol dehydrogenase pyruvate ferredoxin oxidoreductase	Swiss_Prot:P77280 Swiss_Prot:O05650	24.71 43.56	28 33
ergy me erobic re	spiratic					Glycolysis	/glocin	Rogenesis			
T0109 T0137	529 566	cytochrome b cytochrome b	Swiss_Prot:P39480 Swiss_Prot:P39480	30.48	28.610	ST1212 ST1356	416	enolase	Swiss_Prot:Q60173 Swiss_Prot:P39460	49.17	48
T1667	494	cytochrome b	Swiss_Prot:P39480 Swiss_Prot:P39480	\$7.05	49.038	ST1356 ST2477	343 506	glyceraldehyde 3-phosphate dehydeogenase NADP-dependent glyceraldehyde-3-phosphate	Swiss_Prot:Q59931 Swiss_Prot:Q59931	46.78	34
TS007	55 184	cylochrome b	OWL:AF072619	9,09	27.500 32.450	ST1058	602	dehydrogenase phosphoenolpyruvaie carboxykinase		53.86	33
T0697 T2573	341	NADH dehydrogenase NADH dehydrogenase	Swiss_Prot:O28017 Swiss_Prot:P00393	39.76 21.27	30.612	ST0698	309	phosphoenolpyruvate synthase	Swiss_Prot:P05153 Swiss_Prot:O29548	47.52	31
TS031	86	NADH dehydrogenaie subunit I	OWL:AF004650	10.54	27.536	ST1235	764	phosphoenolpyruvate synthase	Swiss_Prot:P46893	154.87	62
T2219 T2223	353 462	NADH-plastoquinone oxidoreductase subunit 1 NADH-plastoquinone oxidoreductase subunit 2	Swiss_Prot:P42032 Swiss_Prot:P06256	32.45 36.24	31.804 28.337	ST1357 ST1617	415 438	phosphoglycerate kinase pyruvate kinase	Swiss_Prot:P50317 Swiss_Prot:Q57572	100.90 53.96	70 36
T2216	128	NADH-plastoquinone oxidoreductase subunit 3	Swiss_Prot:P06259	16.22	25.610	ST2030	229	triosephosphate isomerase	Swiss_Prot/Q58923	83.89	42
T2218 T2217	392	NADH-plastoquinong oxidoreductase subunit 4 NADH-plastoquinone oxidoreductase subunit 5	Swiss_Prot:Q55220 Swiss_Prot:P19125	64.00 34.73	36.387 31.092	Pentose pl ST1764	hosphate 360	e pathway glucose 1-debydrogenase	Swiss Prot P13203	82.52	44
T2222	1138	NADH-plastoquinone oxidoreductase subunit 5	Swiss_Prot:P26849	23.42	30.894	ST2556	253	glucose 1-dehydrogenase	Swiss_Prot:Q56318	33.28	37
T2221	165	NADH-plastoquinone oxidoreductase subunit 6 NADH-plastoquinone oxidoreductase subunit 9	Swiss_Prot:P26523 Swiss_Prot:P77423	12.06	23.977 34.286	ST1302 ST2268	219	ribose 5-phosphaie isomerase transketolase	Swiss_Prot:P44725 Swiss_Prot:O58094	30.21 84.26	30 43
TS016	59	NADH-ubiquinone oxidoreductase subunit 4L	Swiss_Prot P24874	9.82	26.415	ST2269	313	transketolase	Swiss_Prot:Q58092	76.07	42
T1527 T0136	173	NADH-ubiquinone oxidoreductase subunit K quinol oxidase polypeptide I	Swiss_Prot:O75251 Swiss_Prot:P98004	50.20 149.44	42.958 58.824	Pyruvate o ST1487	452	genase dihydrolipoamide dehydrogenase	Swins_Prot:P11959	46.78	32
T2396	524	quinol exidase polypeptide I	Swiss_Prot:P98004	112.83	50.547	ST1879	437	dihydrolipoamide debydrogenase	Swiss_Prot:P75393	41.24	30
T0103	815	quinol oxidase polypeptide I/III quinol oxidase polypeptide II	Swiss_Prot P39481 Swiss_Prot P39479	85.43 109.79	58.564 64.072	ST0687 ST1865	455 412	lipoamide dehydrogenase lipoamide dehydrogenase	Swiss_Prot P11959 Swiss_Prot P35484	41.52 37.52	31 32
T2395	179	quinol oxidase polypeptide II	Swiss_Prot P39479	32.05	33.714	Sugars ST2525			0.0001.00000000000000000000000000000000		
T0108	244 327	Rieske iron-sulfur protein Rieske iron-sulfur protein	Swiss_Prot:P70758 PIR:S71348	13.17 120.40	55.556 60.500	ST2525 ST0773	641 384	alpha-glucosidase beta-galactosidase	Swiss_Prot:059645 Swiss_Prot:P14288	198.53 57.40	61 36
T1666	326	Rieske iron-sulfur protein	PIR:\$71348	192.70	77.912	ST2366	396	dgoA protein	Swiss_Prot:P31458	60.95	- 34
T0104	197 225	sulfocyanin (blue copper protein)	Swiss_Prot:Q53765 Swiss_Prot:Q53765	94.59 56.46	52.792 49.080	ST2561 ST2572	370 392	dgoA protein dgoA protein	Swiss_Prot:P31458 Swiss Prot:P31458	24.22 55.90	26 30
T2394	217	sulfocyanin (blue copper protein) sulfocyanin (blue copper protein)	Swias_Prot/Q53765	64.41	49,080	ST2478	311	fractokinase	Swins_Prot:P50845	39.48	28
mino aci	ds and	amines 3-hydroxyisobutyrate dehydrogenase	Swiss_Prot:Q55702	48.98	31.142	ST0238 ST0574	223	hexulose-6-phosphate synthase ribokinase	Swiss_Prot:P42405 Swiss_Prot:P36945	54.11	36
10151	318	acetamidase	Swiss_ProcQ07838	28.01	63.830	ST2328	291	ribokinase	Swiss_Prot:P05054	58.81	38
ST1206	346	aminomethyltransforase (glycine cleavage system T protein)	Swiss_Prot:P54261	56,96	33.333	ST2341 TCA evel	339	sorbitol dehydrogenase	Swias_Prot:Q06004	47.51	33
T1031	378	arginine deiminase	Swiss_Prot:P13981	27.43	28.087	ST2435	628	2-oxoacidferredoxin oxidoreductase alpha subunit	PIR:3C4919	196.66	59
ST1205 ST1894	142	glycine cleavage system H protein glycine cleavage system H protein	Swiss_Prot:P23884 Swiss_Prot:Q39733	51.41 33.53	47.458 38.542	ST2300 ST2433	627	<ol> <li>2-oxoacidferredoxin oxidoreductase alpha subunit</li> <li>2-oxoacidferredoxin oxidoreductase beta subunit</li> </ol>	PIR:JC4919 PIR:JC4920	272.62	99 71
T1895	148	glycine cleavage system H protein	Swiss_Prot:P23884	39.01	40.000	ST2298	305	2-oxoacid-ferredoxin oxidoreductase beta subunit*	PTR://C4920	186.58	99
ST1207	449	glycine dehydrogenase subunit 1 (glycine cleavage system P-protein subunit)	Swiss_Prot:P54376	113,23	44.851	ST0833 ST0587	855 373	aconitate hydratase citrate synthase	Swiss_Prot:P37032 Swiss_Prot:Q53554	75.22 65.12	49 51
T1208	505	glycine dehydrogenase subunit 2	Swiss_Prot:P54377	122.33	49.263	ST1805	378	citrate synthase	Swiss_Prot:P80148	96.83	66
T1264	448	(glycine cleavage system P-protein subunit) L-asparaginase	Swiss Prot:Q60331	134.89	46.394	ST2023 ST2166	439 409	fumarate hydratase NADP-dependent isocitrate dehydrogenase	Swiss_Prot:P39461 Swiss_Prot:P08200	136.45 86.12	75
T1827	271	L-asperaginase	Swiss_Prot:P37595	37.07	50.000	ST2090	318	malate dehydrogenase	Swiss_Prot:P16142	65.28	37
ST1108 ST0726	373	mandelate racemane phenol hydroxylase	Swiss_Prot:P31458 PIR:H75574	42.72 70.49	28.966 31.670	ST0497 ST0498	566 320	succinate dehydrogenase subunit A succinate dehydrogenase subunit B	Swiss_Prot:P51054 Swiss_Prot:Q10761	70.21 54.33	45
erobic						ST0499	290	succinate dehydrogenase subunit C	PIR:S76574	74,93	33
ST2279 ST2095	100 474	3-phenylpropionate dioxygenase ferredoxin subunit phenylacetyi-CoA ligase	Swiss_Prot:P77266 PIR:D69501	25.77 41.16	28.889 29.293	ST1870 ST0500	307	succinate dehydrogenase subunit C succinate dehydrogenase subunit D	PIR:B70336 OWL:SASDHABCD+	107.08 82.77	43
ST2420	429	phenylacetyl-CoA ligase	PIR:B69115	102.16	43.287	ST0962	259	succinyl-CoA synthetase alpha subunit	Swiss_Prot:Q58643	70.95	58
naerobie T1789	391	anaerobic dimethyl sulfoxide reductase	Swiss_Prot:P18776	40.04	51.456	ST0963 Biosepithe	272 sis and	succinyl-CoA synthetase beta subunit degradation of polysaccharides	Swiss_Prot:Q57663	68.62	46
ST2369	396	anaerobic glycerol-3-phosphate dehydrogenase	Swiss_Prot:P13034	37,47	28.936			degradation of polysaccharides alpha-amylase	Swiss_Prot:Q10769	64.80	44
T2574	367	subunit C L-camitine dehvdratase	Swiss_Prot:P76518	53.42	32.166	ST0927 ST1008	359 951	alpha-amylaac alpha-mannosidase	Swiss_Prot:Q10769 Swiss_Prot:P21139	71.15 92.45	42
511839	270	thiosulfate reductase electron transport protein phsB	Swiss_Prot:P45015	33.83	35.172	ST2337	235	dolichol monophosphate mannose synthase	Swiss_Prot:Q58619	36.75	32
TP-prot	on moti	re force interconversion ATP synthase protein 8	Swiss Prot/Q34942	10.28	37.838	ST0928 ST0818	716	glycogen debranching enzyme granule-bound starch synthase	Swiss_Prot:Q10767 Swiss_Prot:P54138	160.72 23.11	50 40
STS213	52	ATP synthase protein 8	Swiss_Prot.Q02653	9.17	34.091	haloalkan	e		- 5.0011090100010000000		
factron to	ranspor 468	aldehyde dehydrogenase	Swisa_Prot:Q59931	37.69	35,637	ST1836 ST2570	200	2-haloalkanoic scid dehalogenase 2-haloalkanoic acid dehalogenase	Swiss_Prot:P24070 Swiss_Prot:P24070	20.27 34.07	31 30
ST1664	466	cytochrome h558/566 subunit A	OWL:SAY10108	249,26	75.322	Other					
ST1665	314 569	cytochrome b558/566 subunit B cytochrome c oxidase polypeptide I	OWL:SAY101081 Swiss_Prot:P33518	102.55 28.65	44.333 29.588	ST0045 ST0047	214 560	dehydrogenase dehydrogenase	Swiss_Prot:P17201 Swiss_Prot:Q46509	14.98 21.94	27
TU676	522	cytochrome c oxidase polypeptide I	Swiss_Prot:P33518	29.26	29.020	ST0130	267	dehydrogenase	Swiss_Prot:P30863	34.05	31
ST2053 ST2595	593 590	cytochrome e oxidase polypeptide I cytochrome e oxidase polypeptide I	Swiss_Prot:P33518 Swiss_Prot:Q06473	29,75 33.98	29.389 27.484	ST0561 ST0649	171 440	deltydrogenase glycolate oxidase subunit glcD	Swiss_Prot:P77165 Swiss_Prot:P52075	50.67 55.07	43 27
ST0105	147	cytochrome c oxidase polypeptide II	Swiss_Prot:Q04441	21.71	37.113	ST2296	276	glycolate oxidase subunit glcE	Swiss_Prot:P52073	20.42	27
T1148	367	cytochrome P450	Swiss_Prot/Q55080 Swiss_Prot/P31574	148.59 48.76	63.514 44.828	ST0724	316	metapyrocatechase	Swiss_Prot:P08127	39.01	28
T1793	241	electron transfer flavoprotein alpha subunit electron transfer flavoprotein beta subunit	Swiss_Prot:P97089	46.73	37.056	Transport	and bi	nding proteins			
T1175	104 457	ferredoxin ferredoxin	PIR:JC4907 Swiss_Prot:P00211	108.56 21.06	90.385 37.931	Amino ac ST1757	ids. pep	tides and amines amino acid transporter	Swiss_ProcP46349	18.13	24
ST1837 STS199	457	ferredoxin	Swiss_Prot:P53658	27.49	37.895	\$10700	313	oligopeptide transporter ATP-binding protein	Swiss_Prot:P24137	46.25	45
STS201	89	ferredoxin	Swias_Prot.P53658 PIR:JC4907	25.10	36.047 100.00	ST0701 ST0702	321 482	oligopeptide transporter ATP-binding protein	Swiss_Prot:P76027 Swiss_Prot:P42063	46.16 43.91	45
T0163	104 602	ferredot.in* fixB protein	PIR:JC4907 Swins_Prot:P71153	106.44 62.76	100.00 41.049	ST0704	482 353	oligopeptide transporter permease protein oligopeptide transporter permease protein	Swiss Prot:Q53191	43.91 46.57	26
T1775	384	fixC protein	Swiss_Prot:P10331	52.69	35.474	ST1647	279	peptide transporter ATP-binding protein	Swiaa_Prot:P45289	28.06	28
ST1795 ST1873	406	fixC protein heterodisulfide reductase	Swiss_Prot:P31575 Swiss_Prot:P32009	67.73 12.81	32.840 50.000	ST2536 ST2537	322 312	peptide transporter ATP-binding protein peptide transporter ATP-binding protein	Swiss_Prot:P45095 Swiss_Prot:P45094	37.69 36.74	35
STS260	85	NADH dehydrogenase subunit III	OWL:AF0763741	8.70	27.419	ST2542	294	peptide transporter ATP-binding protein	Swiss_Prot:P26905	45.45	45
STS234 ST0090	94 546	NADH-plastoquinone oxidoreductase subunit 4L oxidoreductase	Swiss_Prot:Q00244 Swiss_Prot:P32382	23.84 69.82	34.091 37.104	ST2543 ST1649	323	peptide transporter ATP-binding protein peptide transporter permease protein	Swiss_Prot:P45094 Swiss_Prot:P45054	41.32 25.47	44 24
STS024	53	photosystem I reaction centre subunit VIII (PSI-I)	Swiss_Prot:P52768	9.85	37.209	ST2532	285	peptide transporter permease protein	Swiss_Prot:P26904	42.74	32
ST0228 ST0092	233	redoxin-like protein reductase	Swiss_Prot:Q57755 Swiss_Prot:P43494	29.17 57.30	38.824 32.479	ST2535 ST2540	333 350	peptide transporter permease protein peptide transporter permease protein	Swiss_Prot:Q07742 Swiss_Prot:P77308	50.54 57.80	30
ST0938	245	reductase	Swiss_Prot:P54554	32.99	36.646	ST2541	358	peptide transporter permease protein	Swiss_Prot:P77463	58.01	39
ST1299 ST2239	265	reductase reductase	Swiss_Prot:O67610 Swiss_Prot:P39640	31.29 31.20	31.034 30.830	ST2576	429	proline/betaine transporter	Swiss_Prot P37643	59.69	33
ST2370	144	rubrerythria	Swiss_Prot:P24931	46.86	36.552	Anions ST1818	103	myoglobin	Swiss_Prot P02163	8.41	28
ST0615	384	sulfide dehydrogenase [flavocytochrome c]	Swiss_Prot:Q06530	23.91	27.823	ST2428	458	phosphate transporter	Swiss_ProcP31679	45.43	26
\$10971	390	flavoprotein subunit sulfide dehydrogenase [flavocytochrome c]	Swies_Prot P81540	43.11	72.917	ST2033 Carbohyd	272 rates, o	sulfate transporter permease protein rganic alcohols, and acids	Swiss_Prot:P18795	39.38	31
		flavoprotein subunit				ST2618	445	4-methyl-o-phthalate/phthalate permease	Swim_Prot:P77228	41.53	33
		terminal exidase small hydrophobic subunit	OWL:AADOXP84B3	62.16	71.429	ST0644	374	oxalate:formate antiporter oxalate:formate antiporter	Swiss_Prot:P05715	127.14	- 44
STS219 crimenta	56 tion	settime or one stress should be be a stress				ST1853	364		Swiss Prot:P05715	114.08	-42

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### Complete Genome Sequence of S. tokodaii strain7

### Table 11. Continued.

ORF ID Lengt		Locus	Zacore	st. Identity	ORF ID		Predicted Product	Locus	Zecore	4. Identity
ST1788 398 ST2557 459		Swiss_Prot:O05651 Swiss_Prot:P46333	101.45 50.03	43.363 33.021	ST2454 ST2261	473	sugar transporter DNA-directed RNA polymerase subunit M	Swiss_Prot:P37514 Swiss_Prot:Q07271	27.67 78.07	23,739 68,750
Cations ST0561 S18		Swiss Proc O26759	84.91	41.058	STS221	66	DNA-directed RNA polymerase subunit N	Swiss_Prot.P39472	74,45	77,273
ST1785 155 ST1715 740	bacterioferritin comigratory protein	Swiss_Prot.P23480	37.46 57.48	36.641	Transcripti ST2114 ST1054	141	ferric uptake regulator	Swiss_Prot:P44561	25.42	32.308
ST2208 260	crythrocyte hand 7 integral membrane protein	Swiss_Prot:P32113 Swiss_Prot:Q58237	65.68	47.594	ST1275	166	sugar fermentation stimulation protein TATA-box binding protein	Swiss_Prot/P18273 Swiss_Prot/Q55031	26.62 95.63	31.000 88.957
ST1436 591 ST1437 465		Swiss_Prot P09639 Swiss_Prot P13052	101.01 80.36	99.662 98.925	STS247 ST0349	54 308	transcription factor transcription initiation factor IIB	OWL:ATZ95790 Swiss_Prot:P50387	9,90 158.42	27.500
ST1439 101 ST1435 194	membrane-associated ATPase c subunit*	Swiss_Prot:P23040 Swiss_Prot:P22722	92.04 112.67	100.000	ST1271 ST2236	295 137	transcription initiation factor IIB	Swiss_Prot:Q51731	75.90 15.00	36.735
STS172 59	membrane-associated ATPase epsilon subunit*	Swiss_Prot:P23039	64.36	190,000	ST1369	152	transcription repressor transcription termination-antitermination factor	Swiss_Prot.Q57988 Swiss_Prot.P27341	107.80	73.02
ST1438 216 ST0638 399		Swiss_Prot:P22721 Swiss_Prot:P26235	168.15	100.000 27.301	ST0684 ST1007	205	transcriptional activator transcriptional activator	Swiss_Prot/P25052 Swiss_Prot/P25052	24.94	25.00
ST0728 386 ST1861 500	Na(+)/H(+) antiportor	Swiss_Prot.P26235	46.92	29.538	ST0193 ST0489	140	transcriptional regulator	Swiss_Prot:P42180	30.77	38.31
ST2443 383	nickel transporter	Swiss_Prot:P26235 Swiss_Prot:P23516	100.60	45.734	\$10749	151 123	transcriptional regulator transcriptional regulator	Swiss_Prot:P44337 Swiss_Prot:Q58482	18.34	33.33
ST1846 271 ST2555 285		Swiss_Prot:P46218 Swiss_Prot:P46218	146.09 82.20	63.636 44.074	ST0980 ST1022	107	transcriptional regulator transcriptional regulator	Swiss_Prot.Q58482 Swiss_Prot.Q57615	14.98 34.20	29.47/ 30.872
	rines and pyrimidines allantoin permease		54.66	28.875	ST1076 ST1473	128	transcriptional regulator	Swiss_Prot:P37374	31.50 33.43	39.50 29.06
ther		Swiss_Pnst:P94575			ST1710	146	transcriptional regulator transcriptional regulator	Swiss_Prot:Q57615 Swiss_Prot:P40676	20.24	26.119
ST10.34 266 ST0666 478		Swiss_Prot:P52218 Swiss_Prot:P39886	27.60 46.44	36.054 26.142	ST1867 ST1889	127	transcriptional regulator transcriptional regulator	Swiss_Prot.Q58898 Swiss_Prot.Q58958	12.70	29.167
ST0707 560 ST1006 473	multidrug resistance protein	Swiss_Prot:Q00538 Swiss_Prot:P54585	35.64 47.42	26.905 25.743	ST1890 ST2050	135	transcriptional regulator	Swiss_Prot/P27245 Swiss_Prot/O58898	13.41	30.556
ST1670 468	multidrug resistance protein	Swiss_Prot:P54585 Swiss_Prot:P54585	47.42	25.743 27.586	ST2084	128 515	transcriptional regulator transcriptional regulator	Swiss_Prot:P06153	15.18 22.93	22.000
T1852 415		Swiss_Prot:P39886 Swiss_Prot:P27173	35.60	23.126 25.773	ST2562 ST5086	213	transcriptional regulator transcriptional regulator	Swiss_Prot.005494 PIR:E71028	49.77	33.668
T2604 480		Swiss_Prot P39886	31.62	22.798	STS042	83	transcriptional regulator and	PIR.E71108	45.01	49.33
nknown substr T0265 233	ABC transporter ATP-binding protein	Swisa_Prot.P19844	30.81	30.594	ST0173 RNA more	116	transcriptional regulator Lzs14	Swiss_Pnit:Q58898	13.19	18.26
T0595 240 T0608 294	ABC transporter ATP-binding protein	Swisa_Pnit:Q57855	43.80 33.40	42.601 37.611	ST0343	637	cleavage and polyadenylation specificity factor	Swiss_Prot.Q58633	176.41	47,961
T0756 224	ABC transporter ATP-binding protein	Swiss_Prot:P36879 Swiss_Prot:P46903	31.69	44.203	ST2188	422	large subunit cleavage and polyadenylation specificity factor	Swiss_Prot Q60355	97.63	36.941
T0842 219 T0902 232	ABC transporter ATP-binding protein	Swiss_Prot:Q58429 Swiss_Prot:Q58206	23.18 43.60	33.803 50.442	ST0856	123	small subunit cryptogene protein G4	PIR:551910	11.27	26.54
T1099 851	ABC transporter ATP-binding protein	Swise_Prot.Q11047	38.52	32.400	ST0570	339	RNA 3-terminal phosphate cyclase	Swim_Prot/O59198	90.01	46.061
T1106 367 T1136 471	ABC transporter ATP-binding protein	Swiss_Prot:P94360 Swiss_Prot:P40755	45.65 33.74	42.582 38.265	STS030 RNA mod	90 ficatio	unall nuclear ribonucleoprotein 1	PIR:C69186	26.95	41.333
T1201 248	ABC transporter ATP-binding protein	Swiss_Prot.P80866	64.31 28.18	49,590	ST0456		rRNA adenine N-6-methyltransferase	Swiss_Prot P02979	18.83	27.059
T1672 331	ABC transporter ATP-binding protein	Swiss_Prot:P19844 Swiss_Prot:P42332	33.95	36.937	Protein syr					
T1730 268 T1735 298	ABC transporter ATP-binding protein	Swiss_Prot:Q58429 Swiss_Prot:P54592	27.12 37.59	31.905 39.269	tRNA ami ST0167		alanyl-tRNA synthetase	Swiaa_Prot:Q57984	32.02	34.884
T1772 334	ABC transporter ATP-binding protein	Swiss_Prot:P32010	41.24	39.677 44.693	ST1364	904	slaryl-tRNA synthetase	Swiss_Prot:Q57984	122.24 40.55	40.541
T2035 203	ABC transporter ATP-binding protein	Swiss_Prot P37009 Swiss_Prot Q58762	33.51 28.78	34.426	ST1258 ST0205	429	arginyl tRNA synthetase aspartyl-tRNA synthetase	Swiss_Prot:Q57689 Swiss_Prot:Q58950	87.06	29.821 49.42
T2437 301 T2473 287	ABC transporter ATP-binding protein	Swiss_Prot P19844 Swiss_Prot P42332	36.96 30.46	40.278 35.610	ST2244 ST1283	471 476	cysteinyl-tRNA synthetase glutamyl-tRNA (gln) amidotransferase subunit A	Swiss_Prot:O29836 Swiss_Prot:P56114	82.93 90.54	42.911 47.901
T2509 234	ABC transporter ATP-binding protein	Swiss_Prot:P56344	28.47	32.569	ST0282	479	glutamyl-tRNA (gln) amidotransferase subunit B	Swiss_Prot:Q57624 PIR:D70484	97.74	42.029
ST0841 325 ST1104 214	ABC transporter permease protein	Swiss_ProcQ57130 Swiss_Prot:P18812	46.32 41.98	27.152 39.752	STS140 ST1423	97 566	glutamyl-tRNA (gln) amidotransferase subunit C glutamyl-tRNA synthetase	Swiss_Prot.P95968	34.18 152.28	37.500 63.874
T1105 297 T1918 547	ABC transporter permease protein ABC transporter permease protein	Swiss_Prot:O58760 Swiss_Prot:P40979	35.14 28.62	35.135 31.200	ST0353 ST0323	571 426	glycyl-iRNA synthetase histidyl-tRNA synthetase	Swiss_Prot.Q57681 Swiss_Prot.Q58406	106.24 73.65	42.483
TU535 244	ATP-hinding transporter	Swiss_Prot:P54592	32.44	38.967	ST0431	907	isoleucyl-tRNA synthetase	Swiss_Prot:P46215	104.54	76,92
T1582 274 T0054 442		Swiss_Prot:P72335 Swiss_Prot:P30848	32.11 45.10	38/914 24.096	ST0625 ST1455	945 894	leucyl-tRNA synthetase leucyl-tRNA synthetase	Swiss_Prot:O30250 Swiss_Prot:O30250	117.86	33.11/
T0065 465	transporter	Swina_Prot.P37514	38.31	24.714	ST2083 ST1432	444	lysyl-tRNA synthetase	Swiss_Prot:P95970	127.19	\$2.023
T0091 418 T0339 365	transporter	Swiss_Prot.P31679 Swiss_Prot.P76350	57.73 24.74	29.454 27.795	ST1432 ST1492	113	methionyl-tRNA synthetase methionyl-tRNA synthetase	Swiss_Prot:O26687 Swiss_Prot:O33925	86.00 42.26	40.194
CT0691 446 CT0713 478		Swiss_Prot:P31679 Swisa_Prot:P37514	27.14 40.26	29.834	ST1416 ST1415	469 540	phenylalanyl-tRNA synthetase alpha subunit phenylalanyl-tRNA synthetase beta subunit	Swiss_Prot:P95961 Swiss_Prot:O13432	168.95	58,925
ST0852 425	transporter	Swiss_Prot.Q10858	39.33	28.289	ST1440	483	prolyi-tRNA synthetase	Swiss_Prot:Q58635	125.27	57.44
ST0861 379 ST0934 321	transporter	Swiss_Prot:P39352 Swiss_Prot:P39352	22.26 23.73	21.854	ST1469 ST0966	540	seryl-tRNA synthetase throonyl-tRNA synthetase	Swiss_Prot:O28244 Swiss_Prot:P18256	104.51 67.54	55.531 44.541
T1117 533 T1134 103		Swiss_Prot:P94575 Swiss_Prot:Q43932	60.80 17.75	26.971 30.137	ST2187 ST0169	267 406	threonyl-tRNA synthetase tryptophanyl-tRNA synthetase	Swiss_Prot:Q58597 Swiss_Prot:P23381	30.96 90.28	36.975 50.84
ST1170 448	transporter	Swiss_Prot:P37514	60,45	31.313	ST2074	294	tyrosyl-tRNA synthetase	Swiss_ProcP95982	152:01	68.687
ST1828 401 ST2363 494		Swina_Prot:P44699 Swina_Prot:P25297	29.22 38.62	28.646 31.027	ST1224 Nucleopro	742	valyl-tRNA synthetase	Swiss_Prot:Q58413	99.10	41.44
ST2422 388 ST2476 648	transporter	Swiss_Prot:P39352 Swiss_Prot:P27837	27.72 19.63	24.781 31.034	ST2363 Ribosomal	182	histone macroH2A.1	Swiss_Prot Q02874	36.13	32.31
		and a procession	10.00	31.0.57	ST1424	126	30S ribosomal protein HS6	Swiss_Prot:P55858	90.19	86.508
NA metabolism NA renlication					ST0268 ST2068	102 135	30S ribosomal protein \$10 30S ribosomal protein \$11	Swiss_Prot.P17199 Swiss_Prot.P39469	84.86 74.78	88.235 92.424
T2024 151 T0401 911	<ul> <li>recombination, and repair</li> <li>7,8-dihydro-8-oxoguanine triphosphatase</li> <li>ATP-dependent helicuae</li> </ul>	Swiss_Prot:P36639 Swiss_Prot:P95949	41.98 66.67	43.590 33.448	ST0272 ST0384	147 153	30S ribosomal protein S12 30S ribosomal protein S13	Swiss_Prot:P11524 Swiss_Prot:P54012	83.91 68.52	93.662
STS044 51	copy number control protein copG	PIR:T00008	17.30	50.000	5T2070	172	30S ribosomal protein S13	Swiss_Prot:P95986	98.77	75.316
STS109 72 ST0573 353	dbh protein	PIR:T00008 Swiss_Prot:Q47155	21.57 58.51	54.839 35.484	STS059 STS121	57 63	30S ribosomal protein S14 30S ribosomal protein S15	OWL:SSSPCOPER3 Swisa_Prot/P21473	72.08 9.42	85.185
ST0889 432 ST0223 600	deoxyribodipyrimidine photolyase	Swiss_Prot:Q04449 Swiss_Prot:Q02093	61.65	41.262	ST0423 STS046	116	30S ribosomal protein S17	Swim_Prot:O26120 PIR-C69207	52.88 29.85	51.575
ST0297 324	DNA repair protein radA	Swins_Prot:Q55075	113.20	85.443	ST0426	140	305 ribosomal protein 517 305 ribosomal protein 519	Swiss_Prot:O26114	64.36	60.902
ST0467 548 ST1216 664	DNA replication licensing factor mem	Swiss_Prot P41389 Swiss_Prot P46799	49.49 42.93	46.387 28.032	ST1375 ST2063	153	30S ribosomal protein \$19 30S ribosomal protein \$2	Swiss_Prot:O27653 Swiss_Prot:P95993	55.25 97.91	46.095
STS226 64	DNA-binding protein 7e	Swiss_Prot P13125	64.48	#5.246	ST0362	120	30S ribosomal protein S24	Swiss_Prot:P14249	22,41	25.773
T1426 876 T1680 540	DNA-directed DNA polymerase II	Swiss_Prot:O50607 Swiss_Prot:Q07635	182.51 208.79	99.533 67.754	ST0372 STS173	109 55	305 ribosomal protein 525 305 ribosomal protein 526e	Swiss_Prot P07282 Swiss_Prot P39938	16.24 13.62	27.05/
T2076 781 TS189 88	DNA-directed DNA polymerase II	Swiss_Prot:O05706 Swiss_Prot:Q07635	108.89 49.02	44.586 72.727	STS051 STS105	66 66	305 ribosomal protein 527 305 ribosomal protein 527	PIR:H69388 Swiss_Prot:P54028	24.91 45.01	51.163 52.543
ST2238 220	DNA-directed DNA polymerase, hacteriophage-type	Swiss_Prot.P30314	22.12	31.765	STS040	83	30S ribosomal protein 528	PIR C71025	63.04	71.014
ST1401 224 ST1910 241	exodeoxyribonuclease	Swiss_Prot:P44319 Swiss_Prot:P37454	35.14 65.01	35.519 37.302	ST0424 ST0453	225 193	305 ribosomal protein \$3 305 ribosomal protein \$3	Swiss_Prot:P54034 Swiss_Prot:P54059	66.81 77.03	45.109 41.530
T0210 304 T0590 704	flap endonaclease	Swiss_Prot:P39748 Swiss_Prot:P53327	63.21 30.60	37.457 28.293	STS139 ST0421	55	30S ribosomal protein \$30 30S ribosomal protein \$4	Swiss_Prot/Q05472 Swiss_Prot/O05634	21.71	48.780
TS236 71	integraie	Swiss_Prot:P20214	20.87	50.000	ST2069	177	30S ribosomal protein S4	Swiss Proc P39467	98.54	86.093
ST1393 284 ST0967 156		Swiss_Prot P21891 Swiss_Prot P19220	26.21 32.08	36.196 36.607	ST0414 ST0382	214	30S ribosomal protein S5 30S ribosomal protein S6	Swiss_Prot:O28374 Swiss_Prot:O26360	70.50	56.545
ST2243 146	6 mulT protein	Swiss_Prot:P32056 OWL_SIU930824	19.87	42.105	ST0270	194	30S ribosomal protein S7	Swiss_Prot:P17198	91.54	\$7.625
GTS110 59 GTS248 55	plaunid copy-number control protein cop-6	Swiss_Prot:P25921	48.26	74.510 29.545	ST0419 ST0188	133 128	30S ribosomal protein 58 30S ribosomal protein 58e	Swiss_Prot:O05636 Swiss_Prot:P54055	91.30 66.15	79,695 53.488
T0387 245 5T0397 248	proliferating cell nuclear antigen	Swiss_Prot:Q57697 Swiss_Prot:Q57697	46.16 31.30	24.691	ST2064 ST1367	137	305 ribosomal protein 89 505 ribosomal protein L1	Swiss_Prot:P39468 Swiss_Prot:P35024	94.65	82.30
ST0944 246	5 proliferating cell nuclear antigen	Swiss_Prot:Q57697	36.37	26.556	ST2264	179	50S ribosomal protein L10	Swiss_Prot:Q57963	63.32	50.000
ST0002 579 ST0473 413		Swiss_Prot:P55577 Swiss_Prot:P35600	47.68 21.12	37.004 29.717	ST1368 ST1365	170 108	50S ribosomal protein L11 50S ribosomal protein L12	Swiss_Prot:P96037 Swiss_Prot:P08055	90.90 69.63	78.916 81.905
TD475 327	7 replication factor C small subunit	Swiss_Prot:P40937 Swiss_Prot:Q08582	72.70 243.93	42.628 61.213	ST2065 STS087	146	50S ribosomal protein L13	Swiss_Prot:P39473	90.87 12.41	68.750 35.088
ST1290 1156	i reverse gyrase	Swiss_Prot:Q08582	129.79	32.478	ST0422	141	505 ribosomal protein L13e 505 ribosomal protein L14	OWL:RLAJ3198 Swias_Prot:P54037	55.34	62.500
TS141 99 T0299 353		OWL:SSHTOPR1 Swiss Prot:Q60343	108.78	93.750 50.673	STS054 ST0412	96 144	50S ribosomal protein L14 50S ribosomal protein L15	Swiss_Prot.P54054 Swiss_Prot.O05643	58.34 112.16	66.265
T0683 370	) sun protein	Swiss Prot P94464	39.41	30.370	ST0450	215	50S ribosomal protein L15	Swiss_Prot/O58706	68.92	62.941
T1390 349 T2423 342	2 sun protein	Swiss_Prot:P36929 Swiss_Prot:P94464	31.90 30.74	30.189 36.818	ST0415 ST2066	196 118	50S ribosomal protein 1.18 50S ribosomal protein L18	Swiss_Prot:O05640 Swiss_Prot:P39474	108.23 80.54	68.205 74.528
T1522 448	6 tldD protein	Swiss_Prot:O26944	73.50 203.19	35.692 83.247	ST0416 ST0427	151 241	50S ribosomal protein L19	Swins_Prot:O05639	82.03 64.39	64.667 54.274
GT1295 387 GT1294 532		Swiss_Prot:O05208 Swiss_Prot:O05207	203.19 195.40	83.247 71.012	ST0459	103	505 ribosomal protein L2 505 ribosomal protein L21	Swiss_Prot:O28357 Swiss_Prot:P54013	58.29	55.31
	lification	Swiss_Prot.P15005	20.42	33.088	ST0425 STS062	156 82	50S ribosomal protein 1.22 50S ribosomal protein 1.23	Swiss_Prot:O28359 PIR:E71187	57.34 51.01	45.39
ST1153 683	3 5-methylcytosine-specific restriction enzyme	Swins_Prot:P15005	15.72	27.778	ST\$0.39	61	50S tibosomal protein L24	PIR:F69345	50.64	64.70
sT0335 322	2 modification methylase *	Swiss_Prot.Q57983	99.58	48.710	STS060 STS061	85	508 ribosomal protein L24 508 ribosomal protein L29	OWL:SSSPCOPER PIR:A71671	61.66 13.72	73.23
					ST0429 ST0274	343	508 ribosomal protein L3	Swiss_Prot:P54014	82.36 75.79	47.18
anscription	RNA 8 ribonuclease HII	Swiss_Prot Q57599	50.03	40.367	ST0413	106 158	50S ribosomal protein 1,30 50S ribosomal protein 1,30	Swiss_Prot:P11522 Swiss_Prot:O05642	95.57	58.86
egradation of 1 \$T0519 208	7 ribonuclease PH	Swiss_Prot.Q17533	57.41	35.160	STS168 ST0417	88	50S ribosomal protein L31 50S ribosomal protein L32	Swiss_Prot:P38618 Swiss_Prot:O05638	78.32	77.907
egradation of 1 \$T0519 208 \$T0443 247								Swiss_Proc.005981	83.84	72.414
egradation of 1 ST0519 208 ST0443 247 NA-dependent ST0276 884	t RNA polymerase 4 DNA-directed RNA polymerase subunit A'	Swiss_Prot:P11512	127.95	83.068	STS058	87	50S ribosomal protein L34			
egradation of 1 \$T0519 208 \$T0443 247 NA-dependent \$T0276 884 \$T0275 398	t RNA polymerase 4 DNA-directed RNA polymerase subunit A' 8 DNA-directed RNA polymerase subunit A"	Swim_Prot:P11514	127.95 135.13 141.21	83.068 75.573 84.889	STS058 STS049 STS063	87 61 70	50S ribosomal protein 1.37	PIR:B69186 PIR:B71204	59.31 35.22	73.333
Regradation of 1           \$\$T0519         208           \$\$T0443         247           \$\$NA-dependent         \$\$T0276           \$\$T0276         884           \$\$T0275         398           \$\$T0277         1126           \$\$T2067         264	t RNA polymerase 4 DNA-directed RNA polymerase subunit A' 8 DNA-directed RNA polymerase subunit A" 5 DNA-directed RNA polymerase subunit D 10 DNA-directed RNA polymerase subunit D	Swiss_Prot.P11514 Swiss_Prot.P11513 Swiss_Prot.P39471	135.13 141.21 141.11	75.573 84.889 75.573	STS049 STS063 STS169	61 70 51	505 ribosomal protein L37 505 ribosomal protein L37 505 ribosomal protein L39	PIR:B69186 PIR:B71204 OWL:RL39_SULSO	59.31 35.22 53.91	73.333 50.746 68.000
ST0443 247 NA-dependen ST0276 884 ST0275 398 ST0277 1126 ST0277 264 ST0379 183 STS052 67	ERA polymerase DNA-directed RNA polymerase subunit A' DNA-directed RNA polymerase subunit A" DNA-directed RNA polymerase subunit B DNA-directed RNA polymerase subunit E DNA-directed RNA polymerase subunit E ONA-directed RNA polymerase subunit E	Swiaz_Prot.P11514 Swiaz_Prot.P11513 Swiaz_Prot.P39471 Swiaz_Prot.P39466 Swiaz_Prot.P39466	135.13 141.21 141.11 126.25 29.90	75.573 84.889 75.573 74.863 55.769	STS049 STS063 STS169 ST0428 ST5025	61 70 51 269 56	505 ribosomal protein L37 505 ribosomal protein L37 505 ribosomal protein L39 505 ribosomal protein L4 505 ribosomal protein L40	PIR:B69186 PIR:B71204 OWL:RL39_SULSO Swiss_Proc:O59420 Swiss_Proc:O26653	59.31 35.22 53.91 80.56 19.98	73.333 50.746 68.000 52.778 39.535
Pegradation of 1 ST0519 208 ST0443 247 INA-dependent ST0276 884 ST0275 398 ST0277 1126 ST0267 264 ST0379 183	ERX polymerase I DNA-directed RNA polymerase urbanit A' 5 DNA-directed RNA polymerase urbanit A" 6 DNA-directed RNA polymerase urbanit B 4 DNA-directed RNA polymerase urbanit D DNA-directed RNA polymerase urbanit E DNA-directed RNA polymerase urbanit E DNA-directed RNA polymerase urbanit E	Swim_Prot.P11514 Swim_Prot.P11513 Swim_Prot.P39471 Swim_Prot.P39466 Swim_Prot.P39466 Swim_Prot.P11521	135.13 141.21 141.11 126.25	75.573 84,889 75.573 74,863 55.769 79.762	STS049 STS063 STS169 ST0428 ST5025 ST5106	61 70 51 269	508 ribosomal protein L37 508 ribosomal protein L37 508 ribosomal protein L39 508 ribosomal protein L40 508 ribosomal protein L40 508 ribosomal protein L44 508 ribosomal protein L5	PIR:B69186 PIR:B71204 OWL:RL39_SULSO Swias_Prot:O59420 Swias_Prot:O26653 OWL:PFMAL3P28	59.31 35.22 53.91 80.56	73.333 50.746 68.000 52.778 39.535 49.451
gradation of 1 [0519 208 [0443 247 A-dependent [0276 884 [0277 3988 [0277 1126 [0379 183 [S052 67 [S038 99]	E RNA aphymerase DNA-directed RNA polymerase subunit A" 5 DNA-directed RNA polymerase subunit B 5 DNA-directed RNA polymerase subunit B 1 DNA-directed RNA polymerase subunit E 1 DNA-directed RNA polymerase subunit E 1 DNA-directed RNA polymerase subunit E 1 DNA-directed RNA polymerase subunit H 5 DNA-directed RNA polymerase subunit H 5 DNA-directed RNA polymerase subunit H	Swiaz_Prot.P11514 Swiaz_Prot.P11513 Swiaz_Prot.P39471 Swiaz_Prot.P39466 Swiaz_Prot.P39466	135.13 141.21 141.11 126.25 29.90 82.43	75.573 84.889 75.573 74.863 55.769	STS049 STS063 STS169 ST0428 ST5025	61 70 51 269 56 95	505 ribosomal protein L37 505 ribosomal protein L37 505 ribosomal protein L39 505 ribosomal protein L4 505 ribosomal protein L40	PIR:B69186 PIR:B71204 OWL:RL39_SULSO Swiss_Proc:O59420 Swiss_Proc:O26653	59.31 35.22 53.91 80.56 19.98 39.27	73.333 50.746 68.000 52.778 39.535

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#### Table 11. Continued.

WEID 1		Predicted Product	Locus	Zscore	g. Identity	ORFID	1.00	Predicted Product	Locus	Zscore	44 Identi
T1472 T1366	101 337	DNA-directed RNA polymerase subunit M acidic ribosomal protein p0	Swiss_Prot:Q58548 Swiss_Prot:P35023	18.91	49.091 73.414	STS167 Cellular pr	80	505 ribowanal protein LX	Swiss_Prot P38613	63.35	Identi 62.3
osome a	semble	P)				Cell divisio	at .	5 			
T2459 bosomal	357 protein	ATP-dependent RNA helicase deaD a modification	Swiss_Prot:Q58083	44.86	41.390	ST1215 ST1711	369 587	cell division control protein cell division control protein	Swiss_Prot:Q09803 Swiss_Prot:Q58556	35.78 42.90	42.63
T1505 NA mod		ribosomal protein \$6 modification protein	Swiss_Prot:P17116	27.46	26.761	ST2584 ST0305	700	cell division control protein	Swiss_Prot:Q58556	57.57	49.23
T1266		n fibrillarin-like pre-rRNA processing protein	Swiss_Prot:P35553	72.79	49.778	ST0402	237	cell division control protein 6 centromere/microtubule binding protein cbf5	Swiss_Prot:P29570 Swiss_Prot:O30001	61.79	46.38
NA mod T1269	fication 374	6 N2.N2-dimethylguanosine tRNA methyltransferase	Swiss_Prot:P20300	36.31	55.263	STS055 ST2078	84 341	centromerc/microtubule binding protein cb85 DOM34 protein	PIR:D71044 Swiss_Prot:Q57638	33.15	55.7 36.15
10952	413	tRNA nucleotidyltransforme	Swiss_Prot:P77978	172.28	57.282	ST2367	297	serine/threonine protein phosphatase	Swiss_Prot:P48726	30.84	39.75
anslation T0269	factors 435	elongation factor 1-alpha	Swiss_Prot:P17196	50.70	88 276	Chemotaxi ST2518	s and n 306	otility flagellin	Swiss_Prot:P17603	21.86	48.3
TS027	91	elongation factor 1-beta	Swisa_Prot:Q64214	92.08	79.121	ST0155	353	fluG protein	Swiss_Prot:P38094	28.95	29.3
T0437 T0483	724 340	elongation factor 2 eukaryotic peptide chain release factor subunit 1	Swiss_Prot:P23112 Swiss_Prot:Q58239	114.41 86.36	87.155 42.905	Detoxificat ST0610	252	cyclohex-1-ene-1-carboxyl-CoA hydratase	Swiss Prot:P31551	27.25	28.1
T0941	263	translation initiation factor 2 alpha subunit (eIF-2-alp	Swiss_Prot:Q57581	74.40	40.000	ST1638	327	maleylacetate reductase	Swiss_Prot:O30847	35.74	33.6
T0516 T0381	165	translation initiation factor 2 beta subunit (eIF-2-beta translation initiation factor 2 gamma subunit (eIF-2- $_{\rm F}$		44.91 94.50	36.296 55.718	ST2247 ST1285	440	NADH oxidase periplasmic divalent cation tolerance protein	Swiss_Prot:Q58065 Swiss_Prot:P36654	83.40 36.26	33.3
T0922	362	translation initiation factor 2b alpha subunit (eIF-2b-	Swias_Prot:O29877	90.70	47.661	ST0584	215	peroxiredoxin	Swiss Prot:033665	101.26	78.0
T1296 T1372	131 223	translation initiation factor 5a (eIF-5a) translation initiation factor 6 (eIF-6)	Swiss_Prot:P28461 Swiss_Prot:P38619	104.12	85.496 72.906	ST2442 ST0602	212 389	peroxiredoxin serinepyruvate aminotransferase	Swiss_Prot:P95895 Swiss_Prot:P43567	109.15	89.1
FO811		translational inhibitor protein	Swiss_Prot:O58584	72.27	69.106	ST1217	372	serine-pyruvate aminotransferase	Swiss_Prot:P14776	55,10	30.8
tein fate						ST2283 ST2102	211 150	supercoulde disentatase thioredoxin peroxidase	Swins_Prot:P80857 Swins_Prot:P23480	86.86 30.62	87.5
	peptid	e secretion and trafficking preprotein translocase secY subunit	2007/2012/02/		227773			and resistance			
10411 F1297	463	preprotein translocase secY aubunit signal recognition particle protein	Swiss_Prot:P49978 Swiss_Prot:O27376	186.89 58.51	75.594 53.097	ST0377 ST1813	413	3-phosphonopyruvate decarboxylase bacitracin resistance protein	Swiss_Prot:Q59007 Swiss_Prot:P31054	132.70 19.59	46.
1370	103	signal recognition particle protein	Swisa_Prot:P27414	68.30	77.670	ST1808	248	carboxyvinyl-carboxyphosphonate phosphorylmutas	Swiss_Prot:P54528	99.55	52.1
tein mo (1293	dificate 311	on and repair deoxyhypusine synthase	Swiss Prot P49366	66.89	35 827	ST2140 ST1075	371 456	isopenicillin N epimerase mercuric reductase	Swiss_Prot:P42253 Swiss_Prot:P08663	44.77	26. 40.3
11278	254	diphthine synthase	Swiss_Prot:P32469	33.90	34.524	STS211	84	rRNA adenine N-6-methyltransferase	Swiss_Prot:P06699	13.16	30,1
F1419 F0258	297	methionine aminopeptidase N-terminal acetyltransferase	Swiss_Prot:P95963 Swiss_Prot:P41227	121.55 38.83	63.176 39.103	DNA trans STI 397	fer 474	virB11 protein	Paris Barrowallin	52.09	16.4
10940	767	oligosaccharyl transferase	Swiss_Prot:P46977	25.39	19.820	Adaptation	s to ally	pical conditions	Swiss_Prot:Q58310		
0182	211 234	protein-L-isoaapartate O-methyltransferase protein-L-isoaapartate O-methyltransferase	Swiss_Prot:Q57636 Swiss_Prot:Q57636	44.22 50.07	41.358 40.609	ST1441 Cell killing	336	stress-inducible protein	Swiss_Prot:026762	78.53	60.;
		d stabilization				ST1374	118	apoptosis protein	Swiss_Prot Q58103	41.64	45
0836	311 233	heat shock protein peptidyl prolyl cis-trans isomerase	Swiss_Prot:Q58235 Swiss_Prot:Q58235	43.88	34.831 33.810	Inhibition of	of spore	lation soj protein	Swiss_Prot:P37522	26.34	30.5
1253	559	thermosome, alpha subanit*	Swins_Prot:024734	86.53	100.000	Registant f	or muta	tion	1001012010000000000000		
0321 10820	552 545	thermosome, beta subanit* thermosome, unidentified subunit	Swiss_Prot:O24735 Swiss_Prot:O24734	81.64 57.91	100.000 58.519	ST0365 Host cell at		ham1 protein	Swiss_Prot:Q57679	82.03	47.
radatio	n of pro	steins, peptides, and glycopeptides				STS254	65	sepZ protein	OWL ECSEPZGEN	13.44	35
10330 10779	205 583	26S protease regulatory subanit acylamino-acid-releasing enzyme	Swiss_Prot:O28303 Swiss_Prot:P13676	40.38	63.351 30.288	General ST2108	882	purine NTPase	Swiss_Prot:P25386	12.21	19.
1737	536	acylamino-acid-releasing enzyme	Swiss_Prot:P34422	32.35	30.876	STS205	61	T-cell receptor alpha subunit	OWL-HUMT1414TR	7.71	30.
1745	565 781	acylamino-acid-releasing enzyme aminopeptidase	Swiss_Prot:P13676 Swiss_Prot:P37898	29.26 65.86	28.821 36.743	Other cates	or the second				
1746	786	aminopeptidase	Swass_Prot:P32454	64.30	37.013	Plasmid fu	nctions				
1650 1063	490 292	carboxypeptidase microsomal dipeptidase	Swiss_Prot:P50848 Swiss_Prot:P43477	111.63 25.09	35.569 31.343	ST0849 ST0913	202 166	pepK protein pepK protein	PIR: T00006 Swims_Prot:Q58354	44.90	53.
0920	310	mucD	Swiss_Prot:P45129	50.10	38.202	Transposor ST0547	functi	MIN			
10363	336	O-sialoglycoprotein endopeptidase pG1 protein	Swiss_Prot:O27476 PIR-A44803	98.00 8.99	47.892 27.500			extragenic suppressor protein subB related functions	Swiss_Prot/Q57573	29.88	27.
10690	173	protease I	Swiss_Prot:Q51732	80.70	52.096	ST1908	316	insertion element DNA-binding protein	Swina_Prot P19780	19.25	26.
m446 r0324	235 197	proteasome alpha subunit proteasome beta subunit	Swiss_Prot:O29760 Swiss_Prot:O29769	57.69 52.77	51.542	ST0142 ST0671	242	insertion element protein insertion element protein	Swins_Prot:P03829 Swins_Prot:P03829	22.33 21.75	33. 32.
10477	207	proteasome beta subunit	Swiss_Prot:O29769	58.77	45.109	ST1082	244	insertion element protein	Swins_Prot.P03829	22.04	32.
	1301 1288	pseudomonapepsin pseudomonapepsin	Swiss_Prot:P42790 Swiss_Prot:P42790	24.38 20.41	34.259 32.287	ST1092 ST1139	205	insertion element protein insertion element protein	Swiss_Prot:Q60329 Swiss_Prot:P03829	73.32 22.22	41.
F2082	360	S2P metalloprotease	Swim_Prot:O54862	21.81	31.731	ST1156	100	insertion element protein	Swias_Prot:P03829	20.79	32.
T0894 T2475	598	thermopsin thermopsin	Swiss_Prot:P17118 Swiss_Prot:P17118	50.85 44.84	35.922 35.565	ST1907 ST2015	244 100	insertion element protein insertion element protein	Swina_Prot P03829 Swina_Prot P03829	22.30 23.03	33.
12615	1062	thermopsia	Swiss_Prot:P17118	49.57	32.967	ST0306	102	integrase	Swiss_Prot P20214	24.01	52.
12626 10908	738	thermopain tricom protease	Swiss_Prot:P17118 PIR:S73091	59.12 106.06	36.162	ST0043 ST0680	136	transposase transposase	PIR:072205 PIR:072205	79.29	58/
T1168	854	tricom protease	PIR:\$73091	321.91	74.070	ST0854	386	transposase	Swiss_Prot:P19780	21.76	35.
F1384 F2323	359 353	X-Pro dipeptidase X-Pro dipeptidase	Swiss_Prot:P46545 Swiss_Prot:P54518	65.89 67.65	33.238 38.496	ST1048 ST1096	136	transposase transposase	PIR:D72205 PIR:D72205	80.00	59. 58
18190	58	xylX protein	OWL-COU51165	24.26	46.000	ST1158	136	transposase	PIR. 072205	76.48	58.
elatory	formation in					ST1904 ST2430	136	transposase transposase	PIR:D72205 Swiss_Prot:Q56897	78.96	58. 36.
ncin info	raction	16			10000000	ST2553	136	transposase	PIR:D72205	79.29	58.
C1518 CS263	301 58	cytochrome o ubiquinol oxidase assembly factor degradation enzyme regulation protein degQ	Swiss_Prot:Q04444 Swiss_Prot:P06532	53.42 9.71	29.286 26.087	Neurotrans ST1411	missics 400	kynurenine/alpha-aminoadipate aminotransferase	Swina_Prot P39389	53.55	25
10575	452	TATA-binding protein-interacting protein	PIR:E72723	120.87	55.479	10.0000			3444_140433383	2000	
F1027 F1026	159	urease accessory protein ureE urease accessory protein uroF	Swiss_ProcQ55055 Swiss_ProcP44395	13.25	28.155 25.234	Unknown f ST1651	unction 1136	antibiotic transport-associated protein	Swins_Prot:Q10773	26.52	26.
r1025	209	urease accessory protein areG	Swiss_Prot:Q09066	63.52	53.171	ST1678	842	antibiotic transport-associated protein	Swins_Prot/Q10773	23.11	20
12318	460	sides and nucleotides succinoglycan biosynthesis regulator (exsB)	Swiss_Prot:Q58873	13.03	45.000	ST1914 ST0656	837 223	antibiotic transport-associated protein arylmalonate decarboxylase	Swiss_Prot:Q10773 Swiss_Prot:Q05115	32.19	32 23
A stabil	lity		Balling Strange			ST0721	154	bacterioferritin comigratory protein	Swias_Prot:P55979	37.54	44.
f0317 ulation	603	RNase L inhibitor	Swiss_Prot:Q58129	152.61	52.437	ST2117 ST0404	584 401	bps2 protein clock-controlled gene-9	Swiss_Prot.P32985 Swiss_Prot.Q11152	153.63	51 35
ulation F0872	199	Trp repressor binding protein	Swiss_Prot:P30849	53.14	40.104	ST0303	307	cytosolic acyl-CoA thioester hydrolase	Swiss_Prot:P49851	33.59	27
ier [20399	211	diphtheria toxis repressor	Swiss_Prot P33120	31.76	34.848	STS077 ST0948	64 293	DNA-binding protein 7e elaC protein	Swiss_Prot P13125 Swiss_Prot Q58897	64.48 63.98	85. 39.
F1115	151	leucine-responsive regulatory protein	Swiss_Prot.Q57615	30.42	31.544	ST0451	400	GTP-binding protein	Swiss_Prot P42042	69.59	36
1587	256	leucine-responsive regulatory protein	Swiss_Proc/Q58133	18.84	38.333	ST0520 ST0557	359	GTP-binding protein GTP-binding protein	Swiss_Prot:P32235 Swiss_Prot:Q17045	28.28	44.
envelo						ST1449	265	GTP-binding protein	Swins_Prot:P53742	38.36	33.
face str IS112	s2	structural protein VP1	Swiss_Prot:P20223	42.96	74.074	ST1491 ST0332	334	GTP-binding protein GTP-binding protein hftX	Swiss_Prot/O25505 Swiss_Prot/P25519	16.69 39.63	32 30
synthes	is and	degradation of surface polysaccharides and lipopolysa	ccharides			ST1471	141	histidine triad nucleotide-binding (HINT) protein	Swiss_Prot/Q58276	61.98	54
F1969 F1970	176	dTDP-4-dehydrorhamose 3,5-epimerase dTDP-4-dehydrorhamose reductase	Swiss_Prot:P37780 Swiss_Prot:P26392	68.43 33.75	45.882 41.104	ST2152 ST0976	150	histidine triad nucleotide-binding (HINT) protein interferon-gamma inducible protein	Swiss_Prot:P47378 Swiss_Prot:P39651	44.44 38.66	36. 31.
F1972	320	dTDP-glucose 4,6-dehydratase	Swiss_Prot:P29782	60.08	41.509	ST1421	395	interferon-gamma inducible protein	Swins_Prot:P39651	44.15	30
T0968 T0816	228 419	GDP-mannose pyrophosphorylase glucose-1-phosphate nucleotidyltransferase	Swiss_Prot:P41940 Swiss_Prot:P39122	38.76	35.776	ST1983 ST2164	422	interferon-gamma inducible protein M protein	Swiss_Prot:P39651 Swiss_Prot:P50468	39.59	34. 29
10452	401	glucose-1-phosphate thymidylyltransferase	Swiss_Prot P08075	41.36	30.030	ST1550	230	methyltransferase	Swiss_Prot:P49016	20.00	25
F1071 F2352	344 258	glucose-1-phosphate thymidylyltransferase glucose-1-phosphate thymidylyltransferase	Swias_Prot:P08075 Swias_Prot:P08075	95.04 30.68	47.222 31.944	ST1810 ST2179	431 348	mmge protein mu crystallin	Swiss_Prot:P45859 Swiss_Prot:O54983	30.13 39.46	29. 29.
10929	704	glycosyltransferase	Swiss_Prot:Q10768	64.46	32.160	ST2334	348 311	mu-crystallin	Swina_Prot:Q28488	33.46	29.
12021	415	by aluronan synthase	Swiss_Prot.Q07755	19.65 87.41	30.120	STS185	85	nitrogen fixation protein nifW	OWL:APU470557	10.92	21.
T2284 T0242	455	mannose-1-phosphate guanylyltransferase phospho-sugar mutase	Swiss_Prot:P37820 Swiss_Prot:Q58500	83.70	64.286 34.136	ST1265 ST0174	409 298	nucleolar protein nucleotide-binding protein	Swiaa_Prot:Q58105 Swias_Prot:Q57731	97.46 83.93	48.
10187	306	UDP-glucose 4-epimerase	Swias_Prot:Q57664	55.98	33.117	ST2404	294	Pizin	Swiss_Prot:P46852	23.74	50.
12057	328	UDP-N-acetylglucosaminedolichyl-phosphate N-acetylglucosaminephosphotransferase	Swiss_Prot:P39465	176.51	73.171	ST0440 ST1752	125	protein KE2 repeat motif-containing gene protein	Swiss_Prot:Q58394 Swiss_Prot:Q28758	45.02	45. 17.
10189		undecaprenyl pyrophosphate synthetase	Swian_Proc:O59258	73.63	44.141	ST0209	689	SAV protein	Swiss_Prot/Q07590	72.35	65
and the state of t		ombrane other-linked lipids geranylgeranyl pyrophosphate synthetase	Swina_Prot:P39464	131.48	65.138	ST0376 ST0548	747	SAV protein SAV protein	Swiss_Prot:Q07590 Swiss_Prot:Q07590	104.29 48.49	82. 40
	s, lipop	woteins, and porins	100005-2 <del>8</del> 02010-05-05-05			\$100.99	462	selenium-binding protein	Swiss_Prot:Q63836	103.36	40.
T2058 imbrane	10.00	outer membrane protein	OWL:AF005208 Swiss_Prot:P77774	94.34	37.129	ST2554 STS093	674 79	sip1 protein small nuclear ribonacleoprotein	PIR:545033 PIR:C69186	26.70	32.
T2058 embrane T1164											
T2058 imbrane T1164 T2402 her	459	outer membrane protein				ST0630	318	veg136 protein	Swiss_Prot:Q58873	58.14	35. 36.
T2058 Iembrane ST1164	459 329	outer membrane protein ioRS protein transmembrane postein	Swiss_Prot:P54569 Swiss_Prot:P48278	31.54 34.91	37.821 33.133	ST0630 ST1453 ST1943	318 322 133	veg136 protein veg136 protein viralence-associated protein	Swiss_Prot:Q58873 Swiss_Prot:Q58558	58.14 64.00 26.41	

The columns from left to right represent the ORF ID, length of amino acid residues of ORFs, probable gene products, locus of genes which showed the highest similarity to corresponding ORFs, Zscore taken from Smith-Waterman similarity search, and percent identity between the reported genes and assigned ORFs.

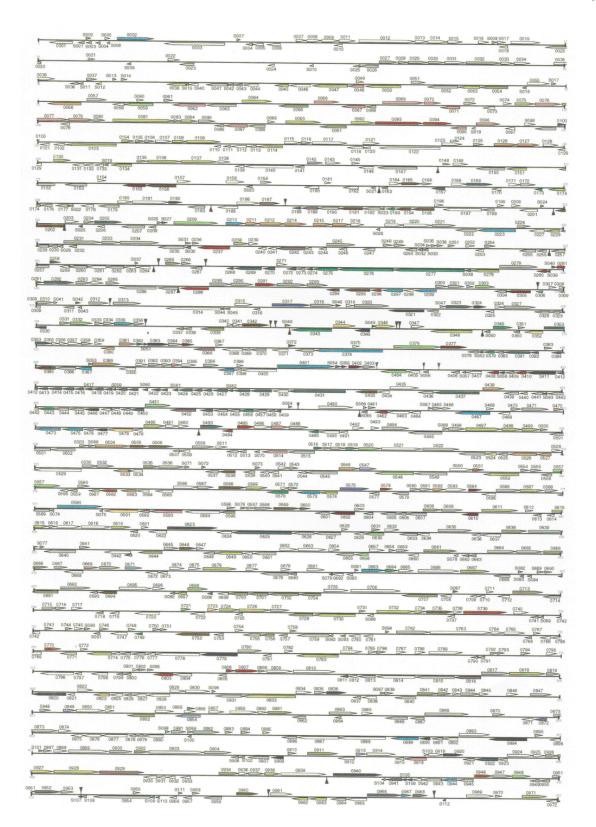


Figure 1. Gene map of the *Sulfolobus tokodaii* strain7 genome. A total of 2826 putatively identified potential protein-coding regions are shown, and the direction of transcription is indicated by arrows. Each line in the figure represents 100,000 bp of sequence in the *S. tokodaii* strain7 genome. Positions are given by numbers above or below the tic marks in each row. The ORFs are color coded by role category as described in the key. ORF ID numbers placed above or below the ORFs correspond to those in Table 11. The rRNA operon and tRNA genes, are labeled.

0974 097	0976	0979 \$113	0981 0	<	-	8 0989 0990		
	1000 1001 1002	0978	0980 0982 0983	994 S114 0996 0665 1006 100	0987		0991 0992	0994 S115 0995 1013 1014 1
0996 0997 0998 0999						1009 1010	1011	
0996 0997 0998 0999 15 1016 1017 1018 0 17 1038	1019 1020	1021	1024 1025 1005 100	7 1028 1029	1030	1032	S118 S119 1033	1034 1035 S120 S121 1
		1044	1024 1025 1026 102 1048 1049 1	7 1028 1029 050 1051 1077 \$124	105 1055	31	1050	1000 1000
		S122 1045 1	046 1047	1051	1052 1054	1057	1059 1	060 1061 1064 1
1067	070 1071 10	1074	1076	1077 S124	1079 1080 1081	1083 1084 1085 1	1067 S125	1089 1090 1088 1091 10
1093 1096 1097	7 1098 1071 10							
1094 1095				1102	1103 1104 110		1108	109 1110 1111 1112
0 1113	1115	11 <sup>1</sup> 11 11 12 12 12 12	1117	1120 1121	S127 1122	1124	1127	-
1131				1118 1119 1141 1142	1122	1123	1125 S128 1126	1128 1129
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     1430         1430         1411           1434         1436         1438           1439         1400         1411           1434         1436         1438           1439         1400         1401           1411         1438         1439           1440         1405         1522           1500         1521         1523           1562         1563         1564           1562         1563         1564           1690         1667         1668           1680         1690         1690           1687         1688         1712           1724         1736         1754           1752         1754         1754</td> <td>847 5171 1398 1413 1414 14 1437 1438 1414 14 1437 1438 51 1414 145 1427 1438 51 1414 145 1427 1438 51 1427 1438 1427 1438 1427 1458 1427 1523 1524 1523 1524 1520 5 1620 1570 1571 1520 5 1620 1670 1620 1670 1620 1670 1620 1670 1621 1670 1620 1670 1775 1670 1775 1670 1775 1670 1775 1670 1775 1670 1775 1770 1775 17700 1775 1770 1775 1770 1775 17700 1775 1770</td> <td>1417           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1000 1000 100		1405 1405 14 1405 1405 14 142 1433 1457 1405 14 1457 1402 15 1457 1402 15 1457 1402 15 1576 1578 15 1577 1578 15 1578 15	100         1410         1412           1430         1430         1411           1434         1436         1438           1439         1400         1411           1434         1436         1438           1439         1400         1401           1411         1438         1439           1440         1405         1522           1500         1521         1523           1562         1563         1564           1562         1563         1564           1690         1667         1668           1680         1690         1690           1687         1688         1712           1724         1736         1754           1752         1754         1754	847 5171 1398 1413 1414 14 1437 1438 1414 14 1437 1438 51 1414 145 1427 1438 51 1414 145 1427 1438 51 1427 1438 1427 1438 1427 1458 1427 1523 1524 1523 1524 1520 5 1620 1570 1571 1520 5 1620 1670 1620 1670 1620 1670 1620 1670 1621 1670 1620 1670 1775 1670 1775 1670 1775 1670 1775 1670 1775 1670 1775 1770 1775 17700 1775 1770 1775 1770 1775 17700 1775 1770	1417           1418           1408           1409           1409           1409           1527           1527           1527           1527           1527           1527           1527           1527           1527           152           152           152           152           152           152           152           152           152           152           152           152           152           152           152           152	1337         1334           1410         1420         1430           1412         1442         1443           1417         1472         1473           1470         1472         1473           1470         1472         1473           1523         1531           1523         1531           1523         1531           1525         1576           1575         1576           1575         1576           1525         1600  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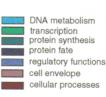
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amino acid biosynthesis

fatty acid and phospholipid metabolism purines, pyrimidines, nucleotides and nucleotides fatty acid and phospholipid metabolism biosynthesis of cofactors, prosthetic groups and carriers central intermediary metabolism energy metabolism tansport and binding proteins



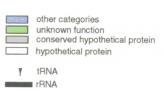


Figure 1. Continued.