Supplementary information of genes annotated for the Fn1 genome

gene_oid	Locus Tag	Source	Cluster Information	Gene Information	E-value
2558669333	DRAFT_00001	Locus_type		CDS	
2558669333	DRAFT_00001	Product_name		hypothetical protein	
2558669333	DRAFT_00001	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669333	DRAFT_00001	Coordinates		3..302(-)	
2558669333	DRAFT_00001	DNA_length		300bp	
2558669333	DRAFT_00001	Protein_length		100aa	
2558669333	DRAFT_00001	GC		0.62	
2558669333	DRAFT_00001	Transmembrane		Yes	
2558669334	DRAFT_00002	KEGG_module	M00254: ABC-2 type transport system		
2558669334	DRAFT_00002	COG_category	[V] Defense mechanisms		
2558669334	DRAFT_00002	COG1131	ABC-type multidrug transport system, ATPase component		1.00E-58
2558669334	DRAFT_00002	pfam00005	ABC_tran		1.20E-25
2558669334	DRAFT_00002	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2558669334	DRAFT_00002	Locus_type		CDS	
2558669334	DRAFT_00002	Product_name		ABC-type multidrug transport system, ATPase component	
2558669334	DRAFT_00002	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669334	DRAFT_00002	Coordinates		299..1240(-)	
2558669334	DRAFT_00002	DNA_length		942bp	
2558669334	DRAFT_00002	Protein_length		313aa	
2558669334	DRAFT_00002	GC		0.63	
2558669335	DRAFT_00003	Locus_type		CDS	
2558669335	DRAFT_00003	Product_name		hypothetical protein	
2558669335	DRAFT_00003	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669335	DRAFT_00003	Coordinates		1770..2261(+)	
2558669335	DRAFT_00003	DNA_length		492bp	
2558669335	DRAFT_00003	Protein_length		163aa	
2558669335	DRAFT_00003	GC		0.46	
2558669336	DRAFT_00004	Locus_type		CDS	

2558669336	DRAFT_00004	Product_name		hypothetical protein		
2558669336	DRAFT_00004	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669336	DRAFT_00004	Coordinates		2258..2431(+)		
2558669336	DRAFT_00004	DNA_length		174bp		
2558669336	DRAFT_00004	Protein_length		57aa		
2558669336	DRAFT_00004	GC			0.53	
2558669337	DRAFT_00005	pfam08445	FR47			3.70E-09
2558669337	DRAFT_00005	Locus_type		CDS		
2558669337	DRAFT_00005	Product_name		Predicted acetyltransferase		
2558669337	DRAFT_00005	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669337	DRAFT_00005	Coordinates		2446..3198(+)		
2558669337	DRAFT_00005	DNA_length		753bp		
2558669337	DRAFT_00005	Protein_length		250aa		
2558669337	DRAFT_00005	GC			0.45	
2558669338	DRAFT_00006	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669338	DRAFT_00006	COG2020	Putative protein-S-isoprenylcysteine methyltransferase			7.00E-14
2558669338	DRAFT_00006	pfam04191	PEMT			9.20E-12
2558669338	DRAFT_00006	Locus_type		CDS		
2558669338	DRAFT_00006	Product_name		Putative protein-S-isoprenylcysteine methyltransferase		
2558669338	DRAFT_00006	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669338	DRAFT_00006	Coordinates		3253..3876(-)		
2558669338	DRAFT_00006	DNA_length		624bp		
2558669338	DRAFT_00006	Protein_length		207aa		
2558669338	DRAFT_00006	GC			0.53	
2558669338	DRAFT_00006	Transmembrane		Yes		
2558669339	DRAFT_00007	Locus_type		CDS		
2558669339	DRAFT_00007	Product_name		hypothetical protein		
2558669339	DRAFT_00007	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669339	DRAFT_00007	Coordinates		3968..4246(-)		
2558669339	DRAFT_00007	DNA_length		279bp		
2558669339	DRAFT_00007	Protein_length		92aa		

2558669339	DRAFT_00007	GC			0.5	
2558669339	DRAFT_00007	Transmembrane		Yes		
2558669340	DRAFT_00008	KEGG_module	M00425: H/ACA ribonucleoprotein complex			
2558669340	DRAFT_00008	Metacyc	RIBOKIN-PWY: ribose degradation			
2558669340	DRAFT_00008	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669340	DRAFT_00008	COG0130	Pseudouridine synthase			4.00E-61
2558669340	DRAFT_00008	pfam08068	DKCLD			7.60E-13
2558669340	DRAFT_00008	pfam01472	PUA			1.70E-17
2558669340	DRAFT_00008	pfam01509	TruB_N			9.20E-18
2558669340	DRAFT_00008	EC:5.4.99.-	Isomerases. Intramolecular transferases (mutases). Transferring other groups.			
2558669340	DRAFT_00008	TIGR00425	rRNA pseudouridine synthase, putative			3.90E-114
2558669340	DRAFT_00008	TIGR00431	tRNA pseudouridine(55) synthase			5.30E-20
2558669340	DRAFT_00008	TIGR00451	uncharacterized domain 2			8.40E-10
2558669340	DRAFT_00008	KO:K11131	H/ACA ribonucleoprotein complex subunit 4 [EC:5.4.99.-]			0.00E+00
2558669340	DRAFT_00008	Locus_type		CDS		
2558669340	DRAFT_00008	Product_name		tRNA pseudouridine synthase B (EC 4.2.1.70)		
2558669340	DRAFT_00008	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669340	DRAFT_00008	Coordinates		4329..5303(-)		
2558669340	DRAFT_00008	DNA_length		975bp		
2558669340	DRAFT_00008	Protein_length		324aa		
2558669340	DRAFT_00008	GC			0.58	
2558669341	DRAFT_00009	KEGG_module	M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP			
2558669341	DRAFT_00009	COG_category	[F] Nucleotide transport and metabolism			
2558669341	DRAFT_00009	COG1102	Cytidylate kinase			1.00E-28
2558669341	DRAFT_00009	pfam13189	Cytidylate_kin2			2.70E-12
2558669341	DRAFT_00009	EC:2.7.4.14	UMP/CMP kinase.			
2558669341	DRAFT_00009	TIGR02173	cytidylate kinase, putative			2.30E-32
2558669341	DRAFT_00009	KO:K00945	cytidylate kinase [EC:2.7.4.14]			1.40E-45
2558669341	DRAFT_00009	Locus_type		CDS		
2558669341	DRAFT_00009	Product_name		Cytidylate kinase		
2558669341	DRAFT_00009	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669341	DRAFT_00009	Coordinates		5320..5880(-)		

2558669341	DRAFT_00009	DNA_length		561bp		
2558669341	DRAFT_00009	Protein_length		186aa		
2558669341	DRAFT_00009	GC			0.56	
2558669342	DRAFT_00010	COG_category	[S] Function unknown			
2558669342	DRAFT_00010	COG1422	Predicted membrane protein			8.00E-19
2558669342	DRAFT_00010	pfam01956	DUF106			3.20E-13
2558669342	DRAFT_00010	Locus_type		CDS		
2558669342	DRAFT_00010	Product_name		Predicted membrane protein		
2558669342	DRAFT_00010	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669342	DRAFT_00010	Coordinates		5894..6826(-)		
2558669342	DRAFT_00010	DNA_length		933bp		
2558669342	DRAFT_00010	Protein_length		310aa		
2558669342	DRAFT_00010	GC			0.56	
2558669342	DRAFT_00010	Transmembrane		Yes		
2558669343	DRAFT_00011	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP			
2558669343	DRAFT_00011	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558669343	DRAFT_00011	COG_category	[F] Nucleotide transport and metabolism			
2558669343	DRAFT_00011	COG2019	Archaeal adenylate kinase			4.00E-43
2558669343	DRAFT_00011	pfam13238	AAA_18			4.40E-12
2558669343	DRAFT_00011	EC:2.7.4.3	Adenylate kinase.			
2558669343	DRAFT_00011	KO:K00939	adenylate kinase [EC:2.7.4.3]			5.60E-42
2558669343	DRAFT_00011	Locus_type		CDS		
2558669343	DRAFT_00011	Product_name		Archaeal adenylate kinase		
2558669343	DRAFT_00011	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669343	DRAFT_00011	Coordinates		6796..7395(-)		
2558669343	DRAFT_00011	DNA_length		600bp		
2558669343	DRAFT_00011	Protein_length		199aa		
2558669343	DRAFT_00011	GC			0.58	
2558669344	DRAFT_00012	KEGG_module	M00335: Sec (secretion) system			
2558669344	DRAFT_00012	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2558669344	DRAFT_00012	COG0201	Preprotein translocase subunit SecY			1.00E-54

2558669344	DRAFT_00012	pfam00344	SecY		1.40E-83
2558669344	DRAFT_00012	pfam10559	Plug_translocon		2.00E-09
2558669344	DRAFT_00012	TIGR00967	preprotein translocase, SecY subunit		2.40E-83
2558669344	DRAFT_00012	KO:K03076	preprotein translocase subunit SecY		0.00E+00
2558669344	DRAFT_00012	ITERM:01964	protein translocase subunit secY/sec61 alpha		
2558669344	DRAFT_00012	Locus_type		CDS	
2558669344	DRAFT_00012	Product_name		protein translocase subunit secY/sec61 alpha	
2558669344	DRAFT_00012	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669344	DRAFT_00012	Coordinates		7400..8854(-)	
2558669344	DRAFT_00012	DNA_length		1455bp	
2558669344	DRAFT_00012	Protein_length		484aa	
2558669344	DRAFT_00012	GC		0.57	
2558669344	DRAFT_00012	Transmembrane		Yes	

2558669345	DRAFT_00013	KEGG_module	M00178: Ribosome, bacteria		
2558669345	DRAFT_00013	KEGG_module	M00179: Ribosome, archaea		
2558669345	DRAFT_00013	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669345	DRAFT_00013	COG0200	Ribosomal protein L15		2.00E-09
2558669345	DRAFT_00013	pfam00828	Ribosomal_L18e		7.00E-22
2558669345	DRAFT_00013	KO:K02876	large subunit ribosomal protein L15		9.60E-30
2558669345	DRAFT_00013	Locus_type		CDS	
2558669345	DRAFT_00013	Product_name		LSU ribosomal protein L15P	
2558669345	DRAFT_00013	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669345	DRAFT_00013	Coordinates		8866..9264(-)	
2558669345	DRAFT_00013	DNA_length		399bp	
2558669345	DRAFT_00013	Protein_length		132aa	
2558669345	DRAFT_00013	GC		0.59	

2558669346	DRAFT_00014	KEGG_module	M00178: Ribosome, bacteria		
2558669346	DRAFT_00014	KEGG_module	M00179: Ribosome, archaea		
2558669346	DRAFT_00014	TIGR01309	50S ribosomal protein L30P, archaeal		1.80E-30
2558669346	DRAFT_00014	KO:K02907	large subunit ribosomal protein L30		2.10E-23
2558669346	DRAFT_00014	ITERM:00257	LSU ribosomal protein L30P		
2558669346	DRAFT_00014	Locus_type		CDS	

2558669346	DRAFT_00014	Product_name		LSU ribosomal protein L30P		
2558669346	DRAFT_00014	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669346	DRAFT_00014	Coordinates		9266..9745(-)		
2558669346	DRAFT_00014	DNA_length		480bp		
2558669346	DRAFT_00014	Protein_length		159aa		
2558669346	DRAFT_00014	GC			0.62	
2558669347	DRAFT_00015	KEGG_module	M00178: Ribosome, bacteria			
2558669347	DRAFT_00015	KEGG_module	M00179: Ribosome, archaea			
2558669347	DRAFT_00015	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669347	DRAFT_00015	COG0098	Ribosomal protein S5			3.00E-32
2558669347	DRAFT_00015	pfam00333	Ribosomal_S5			1.40E-18
2558669347	DRAFT_00015	pfam03719	Ribosomal_S5_C			1.20E-13
2558669347	DRAFT_00015	TIGR01020	ribosomal protein S5(archaeal type)/S2(eukaryote cytosolic type)			1.10E-79
2558669347	DRAFT_00015	KO:K02988	small subunit ribosomal protein S5			0.00E+00
2558669347	DRAFT_00015	ITERM:00284	SSU ribosomal protein S5P			
2558669347	DRAFT_00015	Locus_type		CDS		
2558669347	DRAFT_00015	Product_name		SSU ribosomal protein S5P		
2558669347	DRAFT_00015	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669347	DRAFT_00015	Coordinates		9742..10374(-)		
2558669347	DRAFT_00015	DNA_length		633bp		
2558669347	DRAFT_00015	Protein_length		210aa		
2558669347	DRAFT_00015	GC			0.61	
2558669348	DRAFT_00016	KEGG_module	M00179: Ribosome, archaea			
2558669348	DRAFT_00016	KEGG_module	M00178: Ribosome, bacteria			
2558669348	DRAFT_00016	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669348	DRAFT_00016	COG0256	Ribosomal protein L18			5.00E-22
2558669348	DRAFT_00016	pfam14204	Ribosomal_L18_c			6.40E-07
2558669348	DRAFT_00016	pfam00861	Ribosomal_L18p			5.50E-25
2558669348	DRAFT_00016	KO:K02881	large subunit ribosomal protein L18			9.40E-42
2558669348	DRAFT_00016	Locus_type		CDS		
2558669348	DRAFT_00016	Product_name		Ribosomal protein L18		
2558669348	DRAFT_00016	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		

2558669348	DRAFT_00016	Coordinates		10371..10955(-)		
2558669348	DRAFT_00016	DNA_length		585bp		
2558669348	DRAFT_00016	Protein_length		194aa		
2558669348	DRAFT_00016	GC			0.6	
2558669349	DRAFT_00017	KEGG_module	M00177: Ribosome, eukaryotes			
2558669349	DRAFT_00017	KEGG_module	M00179: Ribosome, archaea			
2558669349	DRAFT_00017	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669349	DRAFT_00017	COG2147	Ribosomal protein L19E			3.00E-26
2558669349	DRAFT_00017	pfam01280	Ribosomal_L19e			1.30E-41
2558669349	DRAFT_00017	KO:K02885	large subunit ribosomal protein L19e			1.30E-27
2558669349	DRAFT_00017	Locus_type		CDS		
2558669349	DRAFT_00017	Product_name		Ribosomal protein L19E		
2558669349	DRAFT_00017	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669349	DRAFT_00017	Coordinates		10952..11386(-)		
2558669349	DRAFT_00017	DNA_length		435bp		
2558669349	DRAFT_00017	Protein_length		144aa		
2558669349	DRAFT_00017	GC			0.58	
2558669350	DRAFT_00018	KEGG_module	M00179: Ribosome, archaea			
2558669350	DRAFT_00018	KEGG_module	M00177: Ribosome, eukaryotes			
2558669350	DRAFT_00018	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669350	DRAFT_00018	COG1717	Ribosomal protein L32E			1.00E-30
2558669350	DRAFT_00018	pfam01655	Ribosomal_L32e			9.90E-38
2558669350	DRAFT_00018	KO:K02912	large subunit ribosomal protein L32e			9.60E-36
2558669350	DRAFT_00018	Locus_type		CDS		
2558669350	DRAFT_00018	Product_name		LSU ribosomal protein L32E		
2558669350	DRAFT_00018	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669350	DRAFT_00018	Coordinates		11370..11798(-)		
2558669350	DRAFT_00018	DNA_length		429bp		
2558669350	DRAFT_00018	Protein_length		142aa		
2558669350	DRAFT_00018	GC			0.58	
2558669351	DRAFT_00019	KEGG_module	M00178: Ribosome, bacteria			

2558669351	DRAFT_00019	KEGG_module	M00179: Ribosome, archaea			
2558669351	DRAFT_00019	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669351	DRAFT_00019	COG0097	Ribosomal protein L6P/L9E			2.00E-29
2558669351	DRAFT_00019	pfam00347	Ribosomal_L6			1.10E-10
2558669351	DRAFT_00019	pfam00347	Ribosomal_L6			4.20E-06
2558669351	DRAFT_00019	TIGR03653	archaeal ribosomal protein L6P			6.80E-61
2558669351	DRAFT_00019	KO:K02933	large subunit ribosomal protein L6			0.00E+00
2558669351	DRAFT_00019	Locus_type		CDS		
2558669351	DRAFT_00019	Product_name		LSU ribosomal protein L6P		
2558669351	DRAFT_00019	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669351	DRAFT_00019	Coordinates		11801..12331(-)		
2558669351	DRAFT_00019	DNA_length		531bp		
2558669351	DRAFT_00019	Protein_length		176aa		
2558669351	DRAFT_00019	GC			0.54	

2558669352	DRAFT_00020	KEGG_module	M00178: Ribosome, bacteria			
2558669352	DRAFT_00020	KEGG_module	M00179: Ribosome, archaea			
2558669352	DRAFT_00020	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669352	DRAFT_00020	COG0096	Ribosomal protein S8			2.00E-34
2558669352	DRAFT_00020	pfam00410	Ribosomal_S8			5.30E-24
2558669352	DRAFT_00020	KO:K02994	small subunit ribosomal protein S8			5.00E-39
2558669352	DRAFT_00020	Locus_type		CDS		
2558669352	DRAFT_00020	Product_name		Ribosomal protein S8		
2558669352	DRAFT_00020	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669352	DRAFT_00020	Coordinates		12336..12728(-)		
2558669352	DRAFT_00020	DNA_length		393bp		
2558669352	DRAFT_00020	Protein_length		130aa		
2558669352	DRAFT_00020	GC			0.56	

2558669353	DRAFT_00021	KEGG_module	M00178: Ribosome, bacteria			
2558669353	DRAFT_00021	KEGG_module	M00179: Ribosome, archaea			
2558669353	DRAFT_00021	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669353	DRAFT_00021	COG0199	Ribosomal protein S14			4.00E-05
2558669353	DRAFT_00021	pfam00253	Ribosomal_S14			2.80E-16

2558669353	DRAFT_00021	KO:K02954	small subunit ribosomal protein S14		5.00E-14
2558669353	DRAFT_00021	Locus_type		CDS	
2558669353	DRAFT_00021	Product_name		SSU ribosomal protein S14P	
2558669353	DRAFT_00021	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669353	DRAFT_00021	Coordinates		12738..12899(-)	
2558669353	DRAFT_00021	DNA_length		162bp	
2558669353	DRAFT_00021	Protein_length		53aa	
2558669353	DRAFT_00021	GC		0.52	
2558669354	DRAFT_00022	KEGG_module	M00179: Ribosome, archaea		
2558669354	DRAFT_00022	KEGG_module	M00178: Ribosome, bacteria		
2558669354	DRAFT_00022	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669354	DRAFT_00022	COG0094	Ribosomal protein L5		9.00E-39
2558669354	DRAFT_00022	pfam00673	Ribosomal_L5_C		6.80E-22
2558669354	DRAFT_00022	pfam00281	Ribosomal_L5		1.30E-17
2558669354	DRAFT_00022	KO:K02931	large subunit ribosomal protein L5		0.00E+00
2558669354	DRAFT_00022	Locus_type		CDS	
2558669354	DRAFT_00022	Product_name		Ribosomal protein L5	
2558669354	DRAFT_00022	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669354	DRAFT_00022	Coordinates		12896..13423(-)	
2558669354	DRAFT_00022	DNA_length		528bp	
2558669354	DRAFT_00022	Protein_length		175aa	
2558669354	DRAFT_00022	GC		0.58	
2558669355	DRAFT_00023	KEGG_module	M00179: Ribosome, archaea		
2558669355	DRAFT_00023	KEGG_module	M00177: Ribosome, eukaryotes		
2558669355	DRAFT_00023	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669355	DRAFT_00023	COG1471	Ribosomal protein S4E		5.00E-49
2558669355	DRAFT_00023	pfam08071	RS4NT		6.10E-11
2558669355	DRAFT_00023	pfam00900	Ribosomal_S4e		6.10E-16
2558669355	DRAFT_00023	KO:K02987	small subunit ribosomal protein S4e		3.10E-42
2558669355	DRAFT_00023	Locus_type		CDS	
2558669355	DRAFT_00023	Product_name		Ribosomal protein S4E	
2558669355	DRAFT_00023	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	

2558669355	DRAFT_00023	Coordinates		13423..14148(-)		
2558669355	DRAFT_00023	DNA_length		726bp		
2558669355	DRAFT_00023	Protein_length		241aa		
2558669355	DRAFT_00023	GC			0.59	
2558669356	DRAFT_00024	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669356	DRAFT_00024	COG0198	Ribosomal protein L24			2.00E-04
2558669356	DRAFT_00024	pfam00467	KOW			1.20E-05
2558669356	DRAFT_00024	TIGR01080	ribosomal protein L24p/L26e, archaeal/eukaryotic			1.20E-29
2558669356	DRAFT_00024	Locus_type		CDS		
2558669356	DRAFT_00024	Product_name		ribosomal protein L24p/L26e, archaeal/eukaryotic		
2558669356	DRAFT_00024	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669356	DRAFT_00024	Coordinates		14149..14439(-)		
2558669356	DRAFT_00024	DNA_length		291bp		
2558669356	DRAFT_00024	Protein_length		96aa		
2558669356	DRAFT_00024	GC			0.55	
2558669357	DRAFT_00025	KEGG_module	M00179: Ribosome, archaea			
2558669357	DRAFT_00025	KEGG_module	M00178: Ribosome, bacteria			
2558669357	DRAFT_00025	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669357	DRAFT_00025	COG0093	Ribosomal protein L14			1.00E-28
2558669357	DRAFT_00025	pfam00238	Ribosomal_L14			9.20E-34
2558669357	DRAFT_00025	KO:K02874	large subunit ribosomal protein L14			0.00E+00
2558669357	DRAFT_00025	Locus_type		CDS		
2558669357	DRAFT_00025	Product_name		LSU ribosomal protein L14P		
2558669357	DRAFT_00025	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669357	DRAFT_00025	Coordinates		14450..14884(-)		
2558669357	DRAFT_00025	DNA_length		435bp		
2558669357	DRAFT_00025	Protein_length		144aa		
2558669357	DRAFT_00025	GC			0.57	
2558669358	DRAFT_00026	KEGG_module	M00178: Ribosome, bacteria			
2558669358	DRAFT_00026	KEGG_module	M00179: Ribosome, archaea			
2558669358	DRAFT_00026	COG_category	[J] Translation, ribosomal structure and biogenesis			

2558669358	DRAFT_00026	COG0186	Ribosomal protein S17			4.00E-17
2558669358	DRAFT_00026	pfam00366	Ribosomal_S17			4.50E-20
2558669358	DRAFT_00026	TIGR03630	archaeal ribosomal protein S17P			7.70E-45
2558669358	DRAFT_00026	KO:K02961	small subunit ribosomal protein S17			2.80E-27
2558669358	DRAFT_00026	Locus_type		CDS		
2558669358	DRAFT_00026	Product_name		SSU ribosomal protein S17P		
2558669358	DRAFT_00026	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669358	DRAFT_00026	Coordinates		14884..15210(-)		
2558669358	DRAFT_00026	DNA_length		327bp		
2558669358	DRAFT_00026	Protein_length		108aa		
2558669358	DRAFT_00026	GC			0.56	
2558669359	DRAFT_00027	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669359	DRAFT_00027	COG1588	RNase P/RNase MRP subunit p29			1.00E-06
2558669359	DRAFT_00027	pfam01868	UPF0086			1.60E-10
2558669359	DRAFT_00027	Locus_type		CDS		
2558669359	DRAFT_00027	Product_name		RNase P/RNase MRP subunit p29		
2558669359	DRAFT_00027	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669359	DRAFT_00027	Coordinates		15207..15443(-)		
2558669359	DRAFT_00027	DNA_length		237bp		
2558669359	DRAFT_00027	Protein_length		78aa		
2558669359	DRAFT_00027	GC			0.55	
2558669360	DRAFT_00028	KEGG_module	M00179: Ribosome, archaea			
2558669360	DRAFT_00028	KEGG_module	M00178: Ribosome, bacteria			
2558669360	DRAFT_00028	pfam00831	Ribosomal_L29			9.40E-12
2558669360	DRAFT_00028	TIGR00012	ribosomal protein L29			1.40E-13
2558669360	DRAFT_00028	KO:K02904	large subunit ribosomal protein L29			6.90E-08
2558669360	DRAFT_00028	Locus_type		CDS		
2558669360	DRAFT_00028	Product_name		ribosomal protein L29		
2558669360	DRAFT_00028	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669360	DRAFT_00028	Coordinates		15440..15646(-)		
2558669360	DRAFT_00028	DNA_length		207bp		
2558669360	DRAFT_00028	Protein_length		68aa		

2558669360	DRAFT_00028	GC		0.53	
2558669361	DRAFT_00029	KEGG_module	M00179: Ribosome, archaea		
2558669361	DRAFT_00029	KEGG_module	M00178: Ribosome, bacteria		
2558669361	DRAFT_00029	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669361	DRAFT_00029	COG0092	Ribosomal protein S3		2.00E-45
2558669361	DRAFT_00029	pfam07650	KH_2		7.20E-12
2558669361	DRAFT_00029	pfam00189	Ribosomal_S3_C		1.00E-12
2558669361	DRAFT_00029	TIGR01008	ribosomal protein S3, eukaryotic/archaeal type		6.70E-63
2558669361	DRAFT_00029	KO:K02982	small subunit ribosomal protein S3		0.00E+00
2558669361	DRAFT_00029	Locus_type		CDS	
2558669361	DRAFT_00029	Product_name		ribosomal protein S3, eukaryotic/archaeal type	
2558669361	DRAFT_00029	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669361	DRAFT_00029	Coordinates		15603..16277(-)	
2558669361	DRAFT_00029	DNA_length		675bp	
2558669361	DRAFT_00029	Protein_length		224aa	
2558669361	DRAFT_00029	GC		0.57	
2558669362	DRAFT_00030	KEGG_module	M00179: Ribosome, archaea		
2558669362	DRAFT_00030	KEGG_module	M00178: Ribosome, bacteria		
2558669362	DRAFT_00030	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669362	DRAFT_00030	COG0091	Ribosomal protein L22		1.00E-20
2558669362	DRAFT_00030	pfam00237	Ribosomal_L22		9.20E-28
2558669362	DRAFT_00030	TIGR01038	ribosomal protein L22(archaeal)/L17(eukaryotic/archaeal)		2.10E-52
2558669362	DRAFT_00030	KO:K02890	large subunit ribosomal protein L22		4.60E-36
2558669362	DRAFT_00030	ITERM:00245	LSU ribosomal protein L22P		
2558669362	DRAFT_00030	Locus_type		CDS	
2558669362	DRAFT_00030	Product_name		LSU ribosomal protein L22P	
2558669362	DRAFT_00030	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669362	DRAFT_00030	Coordinates		16281..16742(-)	
2558669362	DRAFT_00030	DNA_length		462bp	
2558669362	DRAFT_00030	Protein_length		153aa	
2558669362	DRAFT_00030	GC		0.57	

2558669363	DRAFT_00031	KEGG_module	M00149: Succinate dehydrogenase, prokaryotes		
2558669363	DRAFT_00031	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)		
2558669363	DRAFT_00031	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558669363	DRAFT_00031	COG_category	[C] Energy production and conversion		
2558669363	DRAFT_00031	COG2142	Succinate dehydrogenase, hydrophobic anchor subunit		1.00E-03
2558669363	DRAFT_00031	pfam01127	Sdh_cyt		2.50E-09
2558669363	DRAFT_00031	KO:K00242	succinate dehydrogenase membrane anchor subunit		2.30E-08
2558669363	DRAFT_00031	Locus_type		CDS	
2558669363	DRAFT_00031	Product_name		Succinate dehydrogenase, hydrophobic anchor subunit	
2558669363	DRAFT_00031	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669363	DRAFT_00031	Coordinates		17050..17394(-)	
2558669363	DRAFT_00031	DNA_length		345bp	
2558669363	DRAFT_00031	Protein_length		114aa	
2558669363	DRAFT_00031	GC		0.52	
2558669363	DRAFT_00031	Transmembrane		Yes	
2558669364	DRAFT_00032	KEGG_module	M00149: Succinate dehydrogenase, prokaryotes		
2558669364	DRAFT_00032	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558669364	DRAFT_00032	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)		
2558669364	DRAFT_00032	COG_category	[C] Energy production and conversion		
2558669364	DRAFT_00032	COG2009	Succinate dehydrogenase/fumarate reductase, cytochrome b subunit		2.00E-06
2558669364	DRAFT_00032	pfam01127	Sdh_cyt		1.20E-10
2558669364	DRAFT_00032	TIGR02970	succinate dehydrogenase, cytochrome b556 subunit		3.00E-15
2558669364	DRAFT_00032	KO:K00241	succinate dehydrogenase cytochrome b556 subunit		2.90E-22
2558669364	DRAFT_00032	ITERM:01374	succinate dehydrogenase subunit C (EC 1.3.5.1)		
2558669364	DRAFT_00032	Locus_type		CDS	
2558669364	DRAFT_00032	Product_name		succinate dehydrogenase subunit C (EC 1.3.5.1)	
2558669364	DRAFT_00032	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669364	DRAFT_00032	Coordinates		17394..17855(-)	
2558669364	DRAFT_00032	DNA_length		462bp	
2558669364	DRAFT_00032	Protein_length		153aa	
2558669364	DRAFT_00032	GC		0.54	
2558669364	DRAFT_00032	Transmembrane		Yes	

2558669365	DRAFT_00033	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)		
2558669365	DRAFT_00033	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558669365	DRAFT_00033	KEGG_module	M00149: Succinate dehydrogenase, prokaryotes		
2558669365	DRAFT_00033	Metacyc	P23-PWY: reductive TCA cycle I		
2558669365	DRAFT_00033	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)		
2558669365	DRAFT_00033	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558669365	DRAFT_00033	Metacyc	PWY-5392: reductive TCA cycle II		
2558669365	DRAFT_00033	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558669365	DRAFT_00033	COG_category	[C] Energy production and conversion		
2558669365	DRAFT_00033	COG0479	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit		2.00E-65
2558669365	DRAFT_00033	pfam13183	Fer4_8		2.40E-11
2558669365	DRAFT_00033	pfam13085	Fer2_3		6.50E-26
2558669365	DRAFT_00033	EC:1.3.99.1	Succinate dehydrogenase.		
2558669365	DRAFT_00033	TIGR00384	succinate dehydrogenase and fumarate reductase iron-sulfur protein		4.10E-73
2558669365	DRAFT_00033	KO:K00240	succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]		0.00E+00
2558669365	DRAFT_00033	Locus_type		CDS	
2558669365	DRAFT_00033	Product_name		succinate dehydrogenase and fumarate reductase iron-sulfur protein	
2558669365	DRAFT_00033	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669365	DRAFT_00033	Coordinates		17852..18592(-)	
2558669365	DRAFT_00033	DNA_length		741bp	
2558669365	DRAFT_00033	Protein_length		246aa	
2558669365	DRAFT_00033	GC		0.57	

2558669366	DRAFT_00034	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)
2558669366	DRAFT_00034	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle
2558669366	DRAFT_00034	KEGG_module	M00376: 3-Hydroxypropionate bicycle
2558669366	DRAFT_00034	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)
2558669366	DRAFT_00034	KEGG_module	M00149: Succinate dehydrogenase, prokaryotes
2558669366	DRAFT_00034	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate
2558669366	DRAFT_00034	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)
2558669366	DRAFT_00034	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)
2558669366	DRAFT_00034	Metacyc	P42-PWY: incomplete reductive TCA cycle
2558669366	DRAFT_00034	Metacyc	P23-PWY: reductive TCA cycle I
2558669366	DRAFT_00034	Metacyc	PWY-5392: reductive TCA cycle II

2558669366	DRAFT_00034	COG_category	[C] Energy production and conversion		
2558669366	DRAFT_00034	COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit		0.00E+00
2558669366	DRAFT_00034	pfam00890	FAD_binding_2		6.00E-105
2558669366	DRAFT_00034	pfam02910	Succ_DH_flav_C		6.70E-40
2558669366	DRAFT_00034	EC:1.3.99.1	Succinate dehydrogenase.		
2558669366	DRAFT_00034	TIGR01812	succinate dehydrogenase or fumarate reductase, flavoprotein subunit		0.00E+00
2558669366	DRAFT_00034	KO:K00239	succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]		0.00E+00
2558669366	DRAFT_00034	Locus_type		CDS	
2558669366	DRAFT_00034	Product_name		succinate dehydrogenase subunit A (EC 1.3.5.1)	
2558669366	DRAFT_00034	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669366	DRAFT_00034	Coordinates		18677..20425(-)	
2558669366	DRAFT_00034	DNA_length		1749bp	
2558669366	DRAFT_00034	Protein_length		582aa	
2558669366	DRAFT_00034	GC		0.58	

2558669367	DRAFT_00035	COG_category	[C] Energy production and conversion		
2558669367	DRAFT_00035	COG0822	NifU homolog involved in Fe-S cluster formation		7.00E-28
2558669367	DRAFT_00035	pfam01592	NifU_N		3.10E-32
2558669367	DRAFT_00035	TIGR01994	SUF system FeS assembly protein, NifU family		7.80E-33
2558669367	DRAFT_00035	KO:K04488	nitrogen fixation protein NifU and related proteins		4.60E-40
2558669367	DRAFT_00035	Locus_type		CDS	
2558669367	DRAFT_00035	Product_name		SUF system FeS assembly protein, NifU family	
2558669367	DRAFT_00035	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669367	DRAFT_00035	Coordinates		20581..20979(-)	
2558669367	DRAFT_00035	DNA_length		399bp	
2558669367	DRAFT_00035	Protein_length		132aa	
2558669367	DRAFT_00035	GC		0.54	

2558669368	DRAFT_00036	Metacyc	PWY-6823: molybdenum cofactor biosynthesis		
2558669368	DRAFT_00036	Metacyc	PWY-6891: thiazole biosynthesis II (Bacillus)		
2558669368	DRAFT_00036	Metacyc	PWY-6892: thiazole biosynthesis I (E. coli)		
2558669368	DRAFT_00036	Metacyc	PWY0-1021: alanine biosynthesis III		
2558669368	DRAFT_00036	COG_category	[E] Amino acid transport and metabolism		
2558669368	DRAFT_00036	COG0520	Selenocysteine lyase		0.00E+00

2558669368	DRAFT_00036	pfam00266	Aminotran_5		0.00E+00
2558669368	DRAFT_00036	EC:2.8.1.7	Cysteine desulfurase.		
2558669368	DRAFT_00036	EC:4.4.1.16	Selenocysteine lyase.		
2558669368	DRAFT_00036	TIGR01979	cysteine desulfurases, SufSfamily		0.00E+00
2558669368	DRAFT_00036	KO:K11717	cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]		0.00E+00
2558669368	DRAFT_00036	Locus_type		CDS	
2558669368	DRAFT_00036	Product_name		cysteine desulfurase (EC 2.8.1.7)	
2558669368	DRAFT_00036	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669368	DRAFT_00036	Coordinates		20976..22214(-)	
2558669368	DRAFT_00036	DNA_length		1239bp	
2558669368	DRAFT_00036	Protein_length		412aa	
2558669368	DRAFT_00036	GC		0.58	

2558669369	DRAFT_00037	KEGG_module	M00539: Cumate degradation, p-cumate => 2-oxopent-4-enoate + 2-methylpropanoate		
2558669369	DRAFT_00037	KEGG_module	M00547: Benzene/toluene degradation, benzene => catechol / toluene => 3-methylcatechol		
2558669369	DRAFT_00037	KEGG_module	M00545: Trans-cinnamate degradation, trans-cinnamate => 2-oxopent-4-enoate + fumarate		
2558669369	DRAFT_00037	KEGG_module	M00543: Biphenyl degradation, biphenyl => 2-oxopent-4-enoate + benzoate		
2558669369	DRAFT_00037	COG_category	[R] General function prediction only		
2558669369	DRAFT_00037	COG_category	[P] Inorganic ion transport and metabolism		
2558669369	DRAFT_00037	COG2146	Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxyge		2.00E-19
2558669369	DRAFT_00037	pfam00355	Rieske		6.00E-17
2558669369	DRAFT_00037	KO:K05710	dioxygenase ferredoxin subunit		6.90E-15
2558669369	DRAFT_00037	Locus_type		CDS	
2558669369	DRAFT_00037	Product_name		Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxyg	
2558669369	DRAFT_00037	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669369	DRAFT_00037	Coordinates		22233..22550(-)	
2558669369	DRAFT_00037	DNA_length		318bp	
2558669369	DRAFT_00037	Protein_length		105aa	
2558669369	DRAFT_00037	GC		0.57	

2558669370	DRAFT_00038	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669370	DRAFT_00038	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease		1.00E-70
2558669370	DRAFT_00038	pfam01458	UPF0051		1.30E-57
2558669370	DRAFT_00038	TIGR01981	FeS assembly protein SufD		1.70E-69

2558669370	DRAFT_00038	KO:K09014	Fe-S cluster assembly protein SufB		0.00E+00
2558669370	DRAFT_00038	Locus_type		CDS	
2558669370	DRAFT_00038	Product_name		ABC-type transport system involved in Fe-S cluster assembly, permea	
2558669370	DRAFT_00038	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669370	DRAFT_00038	Coordinates		22547..23959(-)	
2558669370	DRAFT_00038	DNA_length		1413bp	
2558669370	DRAFT_00038	Protein_length		470aa	
2558669370	DRAFT_00038	GC		0.56	
2558669371	DRAFT_00039	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669371	DRAFT_00039	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permeas		2.00E-110
2558669371	DRAFT_00039	pfam01458	UPF0051		1.60E-66
2558669371	DRAFT_00039	TIGR01980	FeS assembly protein SufB		0.00E+00
2558669371	DRAFT_00039	KO:K09014	Fe-S cluster assembly protein SufB		0.00E+00
2558669371	DRAFT_00039	Locus_type		CDS	
2558669371	DRAFT_00039	Product_name		Iron-regulated ABC transporter membrane component SufB	
2558669371	DRAFT_00039	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669371	DRAFT_00039	Coordinates		23987..25399(-)	
2558669371	DRAFT_00039	DNA_length		1413bp	
2558669371	DRAFT_00039	Protein_length		470aa	
2558669371	DRAFT_00039	GC		0.57	
2558669372	DRAFT_00040	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669372	DRAFT_00040	COG0396	ABC-type transport system involved in Fe-S cluster assembly, ATPase c		2.00E-97
2558669372	DRAFT_00040	pfam00005	ABC_tran		5.80E-20
2558669372	DRAFT_00040	TIGR01978	FeS assembly ATPase SufC		1.70E-104
2558669372	DRAFT_00040	KO:K09013	Fe-S cluster assembly ATP-binding protein		0.00E+00
2558669372	DRAFT_00040	Locus_type		CDS	
2558669372	DRAFT_00040	Product_name		FeS assembly ATPase SufC	
2558669372	DRAFT_00040	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669372	DRAFT_00040	Coordinates		25444..26220(-)	
2558669372	DRAFT_00040	DNA_length		777bp	
2558669372	DRAFT_00040	Protein_length		258aa	
2558669372	DRAFT_00040	GC		0.55	

2558669373	DRAFT_00041	COG_category	[T] Signal transduction mechanisms			
2558669373	DRAFT_00041	COG1956	GAF domain-containing protein			1.00E-32
2558669373	DRAFT_00041	pfam13185	GAF_2			3.90E-09
2558669373	DRAFT_00041	KO:K07170	GAF domain-containing protein			5.20E-38
2558669373	DRAFT_00041	Locus_type		CDS		
2558669373	DRAFT_00041	Product_name		GAF domain-containing protein		
2558669373	DRAFT_00041	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669373	DRAFT_00041	Coordinates		26371..26853(-)		
2558669373	DRAFT_00041	DNA_length		483bp		
2558669373	DRAFT_00041	Protein_length		160aa		
2558669373	DRAFT_00041	GC			0.57	

2558669374	DRAFT_00042	KEGG_module	M00174: Methane oxidation, methylotroph, methane => CO2			
2558669374	DRAFT_00042	KEGG_module	M00532: Photorespiration			
2558669374	DRAFT_00042	Metacyc	PWY66-162: ethanol degradation IV			
2558669374	DRAFT_00042	COG_category	[P] Inorganic ion transport and metabolism			
2558669374	DRAFT_00042	COG0753	Catalase			0.00E+00
2558669374	DRAFT_00042	pfam06628	Catalase-rel			3.20E-19
2558669374	DRAFT_00042	pfam00199	Catalase			0.00E+00
2558669374	DRAFT_00042	EC:1.11.1.6	Catalase.			
2558669374	DRAFT_00042	KO:K03781	catalase [EC:1.11.1.6]			0.00E+00
2558669374	DRAFT_00042	Locus_type		CDS		
2558669374	DRAFT_00042	Product_name		Catalase		
2558669374	DRAFT_00042	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669374	DRAFT_00042	Coordinates		27083..28558(+)		
2558669374	DRAFT_00042	DNA_length		1476bp		
2558669374	DRAFT_00042	Protein_length		491aa		
2558669374	DRAFT_00042	GC			0.51	

2558669375	DRAFT_00043	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669375	DRAFT_00043	COG0459	Chaperonin GroEL (HSP60 family)			0.00E+00
2558669375	DRAFT_00043	pfam00118	Cpn60_TCP1			0.00E+00
2558669375	DRAFT_00043	TIGR02339	thermosome, various subunits, archaeal			0.00E+00

2558669375	DRAFT_00043	Locus_type		CDS	
2558669375	DRAFT_00043	Product_name		thermosome subunit	
2558669375	DRAFT_00043	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669375	DRAFT_00043	Coordinates		28648..30303(+)	
2558669375	DRAFT_00043	DNA_length		1656bp	
2558669375	DRAFT_00043	Protein_length		551aa	
2558669375	DRAFT_00043	GC		0.57	

2558669376	DRAFT_00044	Locus_type		CDS	
2558669376	DRAFT_00044	Product_name		hypothetical protein	
2558669376	DRAFT_00044	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669376	DRAFT_00044	Coordinates		30416..30658(-)	
2558669376	DRAFT_00044	DNA_length		243bp	
2558669376	DRAFT_00044	Protein_length		80aa	
2558669376	DRAFT_00044	GC		0.56	

2558669377	DRAFT_00045	COG_category	[S] Function unknown		
2558669377	DRAFT_00045	COG2090	Uncharacterized protein conserved in archaea		5.00E-30
2558669377	DRAFT_00045	pfam04027	DUF371		9.70E-41
2558669377	DRAFT_00045	KO:K09738	hypothetical protein		9.40E-33
2558669377	DRAFT_00045	Locus_type		CDS	
2558669377	DRAFT_00045	Product_name		Uncharacterized protein conserved in archaea	
2558669377	DRAFT_00045	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669377	DRAFT_00045	Coordinates		30931..31338(+)	
2558669377	DRAFT_00045	DNA_length		408bp	
2558669377	DRAFT_00045	Protein_length		135aa	
2558669377	DRAFT_00045	GC		0.59	

2558669378	DRAFT_00046	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway		
2558669378	DRAFT_00046	Metacyc	PWY-922: mevalonate pathway I		
2558669378	DRAFT_00046	IMG_pathway	178: Mevalonate pathway for isopentenyl pyrophopsphate synthesis		
2558669378	DRAFT_00046	COG_category	[I] Lipid transport and metabolism		
2558669378	DRAFT_00046	COG3407	Mevalonate pyrophosphate decarboxylase		1.00E-48
2558669378	DRAFT_00046	EC:4.1.1.33	Diphosphomevalonate decarboxylase.		

2558669378	DRAFT_00046	TIGR01240	diphosphomevalonate decarboxylase		1.40E-45
2558669378	DRAFT_00046	KO:K01597	diphosphomevalonate decarboxylase [EC:4.1.1.33]		2.00E-44
2558669378	DRAFT_00046	ITERM:00468	diphosphomevalonate decarboxylase (EC 4.1.1.33)		
2558669378	DRAFT_00046	Locus_type		CDS	
2558669378	DRAFT_00046	Product_name		diphosphomevalonate decarboxylase (EC 4.1.1.33)	
2558669378	DRAFT_00046	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669378	DRAFT_00046	Coordinates		31335..32279(+)	
2558669378	DRAFT_00046	DNA_length		945bp	
2558669378	DRAFT_00046	Protein_length		314aa	
2558669378	DRAFT_00046	GC		0.59	
2558669379	DRAFT_00047	KEGG_module	M00083: Fatty acid biosynthesis, elongation		
2558669379	DRAFT_00047	KEGG_module	M00572: Pimeloyl-ACP biosynthesis, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP		
2558669379	DRAFT_00047	Metacyc	PWY-5367: petroselinate biosynthesis		
2558669379	DRAFT_00047	Metacyc	PWY-5973: <i>cis</i>-vaccenate biosynthesis		
2558669379	DRAFT_00047	Metacyc	PWY-6282: palmitoleate biosynthesis I		
2558669379	DRAFT_00047	Metacyc	PWY-6951: docosahexanoate biosynthesis II		
2558669379	DRAFT_00047	Metacyc	PWYG-321: mycolate biosynthesis		
2558669379	DRAFT_00047	Metacyc	PWY-6519: 7-keto-8-aminopelargonate biosynthesis I		
2558669379	DRAFT_00047	Metacyc	PWY0-862: <i>cis</i>-dodecenoyl biosynthesis		
2558669379	DRAFT_00047	Metacyc	PWY-7053: docosahexanoate biosynthesis I		
2558669379	DRAFT_00047	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism		
2558669379	DRAFT_00047	COG_category	[I] Lipid transport and metabolism		
2558669379	DRAFT_00047	COG_category	[R] General function prediction only		
2558669379	DRAFT_00047	COG1028	Dehydrogenases with different specificities (related to short-chain alco		9.00E-43
2558669379	DRAFT_00047	pfam00106	adh_short		5.60E-30
2558669379	DRAFT_00047	EC:1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase.		
2558669379	DRAFT_00047	KO:K00059	3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]		0.00E+00
2558669379	DRAFT_00047	ITERM:00597	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)		
2558669379	DRAFT_00047	Locus_type		CDS	
2558669379	DRAFT_00047	Product_name		3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)	
2558669379	DRAFT_00047	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669379	DRAFT_00047	Coordinates		32567..33313(-)	
2558669379	DRAFT_00047	DNA_length		747bp	

2558669379	DRAFT_00047	Protein_length		248aa		
2558669379	DRAFT_00047	GC			0.59	

2558669380	DRAFT_00048	KEGG_module	M00021: Cysteine biosynthesis, serine => cysteine			
2558669380	DRAFT_00048	Metacyc	CYSTSYN-PWY: cysteine biosynthesis I			
2558669380	DRAFT_00048	Metacyc	PWY-6936: seleno-amino acid biosynthesis			
2558669380	DRAFT_00048	COG_category	[E] Amino acid transport and metabolism			
2558669380	DRAFT_00048	COG0031	Cysteine synthase			1.00E-65
2558669380	DRAFT_00048	pfam00291	PALP			2.80E-43
2558669380	DRAFT_00048	EC:2.5.1.47	Cysteine synthase.			
2558669380	DRAFT_00048	KO:K01738	cysteine synthase A [EC:2.5.1.47]			0.00E+00
2558669380	DRAFT_00048	Locus_type		CDS		
2558669380	DRAFT_00048	Product_name		Cysteine synthase		
2558669380	DRAFT_00048	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669380	DRAFT_00048	Coordinates		33666..34538(+)		
2558669380	DRAFT_00048	DNA_length		873bp		
2558669380	DRAFT_00048	Protein_length		290aa		
2558669380	DRAFT_00048	GC			0.53	

2558669381	DRAFT_00049	COG_category	[R] General function prediction only			
2558669381	DRAFT_00049	COG1011	Predicted hydrolase (HAD superfamily)			3.00E-24
2558669381	DRAFT_00049	pfam13419	HAD_2			8.10E-27
2558669381	DRAFT_00049	TIGR01509	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third			5.60E-13
2558669381	DRAFT_00049	TIGR01549	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third			7.70E-11
2558669381	DRAFT_00049	Locus_type		CDS		
2558669381	DRAFT_00049	Product_name		haloacid dehalogenase superfamily, subfamily IA, variant 3 with third		
2558669381	DRAFT_00049	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669381	DRAFT_00049	Coordinates		34722..35486(-)		
2558669381	DRAFT_00049	DNA_length		765bp		
2558669381	DRAFT_00049	Protein_length		254aa		
2558669381	DRAFT_00049	GC			0.54	

2558669382	DRAFT_00050	COG_category	[S] Function unknown			
2558669382	DRAFT_00050	COG0432	Uncharacterized conserved protein			1.00E-39

2558669382	DRAFT_00050	pfam01894	UPF0047			3.30E-35
2558669382	DRAFT_00050	TIGR00149	secondary thiamine-phosphate synthase enzyme			2.10E-36
2558669382	DRAFT_00050	Locus_type		CDS		
2558669382	DRAFT_00050	Product_name		secondary thiamine-phosphate synthase enzyme		
2558669382	DRAFT_00050	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669382	DRAFT_00050	Coordinates		35697..36170(-)		
2558669382	DRAFT_00050	DNA_length		474bp		
2558669382	DRAFT_00050	Protein_length		157aa		
2558669382	DRAFT_00050	GC			0.55	
2558669383	DRAFT_00051	Metacyc	PWY-6482: diphthamide biosynthesis			
2558669383	DRAFT_00051	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669383	DRAFT_00051	COG1798	Diphthamide biosynthesis methyltransferase			3.00E-59
2558669383	DRAFT_00051	pfam00590	TP_methylase			3.50E-20
2558669383	DRAFT_00051	pfam04010	DUF357			3.20E-12
2558669383	DRAFT_00051	EC:2.1.1.98	Diphthine synthase.			
2558669383	DRAFT_00051	TIGR00522	diphthine synthase			2.10E-60
2558669383	DRAFT_00051	KO:K00586	diphthine synthase [EC:2.1.1.98]			0.00E+00
2558669383	DRAFT_00051	Locus_type		CDS		
2558669383	DRAFT_00051	Product_name		diphthine synthase		
2558669383	DRAFT_00051	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669383	DRAFT_00051	Coordinates		36548..37588(+)		
2558669383	DRAFT_00051	DNA_length		1041bp		
2558669383	DRAFT_00051	Protein_length		346aa		
2558669383	DRAFT_00051	GC			0.56	
2558669384	DRAFT_00052	Metacyc	TEICHOICACID-PWY: teichoic acid (poly-glycerol) biosynthesis			
2558669384	DRAFT_00052	COG_category	[I] Lipid transport and metabolism			
2558669384	DRAFT_00052	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558669384	DRAFT_00052	COG0615	Cytidylyltransferase			1.00E-24
2558669384	DRAFT_00052	pfam01467	CTP_transf_2			1.80E-08
2558669384	DRAFT_00052	EC:2.7.7.39	Glycerol-3-phosphate cytidylyltransferase.			
2558669384	DRAFT_00052	TIGR00125	cytidyltransferase-like domain			2.70E-16
2558669384	DRAFT_00052	KO:K00980	glycerol-3-phosphate cytidylyltransferase [EC:2.7.7.39]			2.20E-30

2558669384	DRAFT_00052	Locus_type		CDS	
2558669384	DRAFT_00052	Product_name		cytidyltransferase-like domain	
2558669384	DRAFT_00052	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669384	DRAFT_00052	Coordinates		37591..38190(+)	
2558669384	DRAFT_00052	DNA_length		600bp	
2558669384	DRAFT_00052	Protein_length		199aa	
2558669384	DRAFT_00052	GC		0.56	
2558669385	DRAFT_00053	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669385	DRAFT_00053	COG2178	Predicted RNA-binding protein of the translin family		4.00E-29
2558669385	DRAFT_00053	pfam01997	Translin		3.00E-25
2558669385	DRAFT_00053	KO:K07477	translin		1.10E-40
2558669385	DRAFT_00053	Locus_type		CDS	
2558669385	DRAFT_00053	Product_name		Predicted RNA-binding protein of the translin family	
2558669385	DRAFT_00053	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669385	DRAFT_00053	Coordinates		38187..38819(-)	
2558669385	DRAFT_00053	DNA_length		633bp	
2558669385	DRAFT_00053	Protein_length		210aa	
2558669385	DRAFT_00053	GC		0.58	
2558669386	DRAFT_00054	pfam00892	EamA		6.00E-19
2558669386	DRAFT_00054	pfam00892	EamA		7.40E-18
2558669386	DRAFT_00054	Locus_type		CDS	
2558669386	DRAFT_00054	Product_name		Predicted permease, DMT superfamily	
2558669386	DRAFT_00054	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669386	DRAFT_00054	Coordinates		38910..39842(+)	
2558669386	DRAFT_00054	DNA_length		933bp	
2558669386	DRAFT_00054	Protein_length		310aa	
2558669386	DRAFT_00054	GC		0.59	
2558669386	DRAFT_00054	Transmembrane		Yes	
2558669387	DRAFT_00055	pfam01870	Hjc		1.50E-11
2558669387	DRAFT_00055	KO:K03552	holliday junction resolvase, archaea type		5.10E-06
2558669387	DRAFT_00055	Locus_type		CDS	

2558669387	DRAFT_00055	Product_name		Holliday junction resolvase - archaeal type	
2558669387	DRAFT_00055	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669387	DRAFT_00055	Coordinates		39846..40154(+)	
2558669387	DRAFT_00055	DNA_length		309bp	
2558669387	DRAFT_00055	Protein_length		102aa	
2558669387	DRAFT_00055	GC		0.58	

2558669388	DRAFT_00056	Locus_type		CDS	
2558669388	DRAFT_00056	Product_name		hypothetical protein	
2558669388	DRAFT_00056	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669388	DRAFT_00056	Coordinates		40151..40300(+)	
2558669388	DRAFT_00056	DNA_length		150bp	
2558669388	DRAFT_00056	Protein_length		49aa	
2558669388	DRAFT_00056	GC		0.51	

2558669389	DRAFT_00057	Locus_type		CDS	
2558669389	DRAFT_00057	Product_name		hypothetical protein	
2558669389	DRAFT_00057	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669389	DRAFT_00057	Coordinates		40310..40669(-)	
2558669389	DRAFT_00057	DNA_length		360bp	
2558669389	DRAFT_00057	Protein_length		119aa	
2558669389	DRAFT_00057	GC		0.59	

2558669390	DRAFT_00058	Metacyc	PWY-5386: methylglyoxal degradation I		
2558669390	DRAFT_00058	COG_category	[R] General function prediction only		
2558669390	DRAFT_00058	COG0491	Zn-dependent hydrolases, including glyoxylases		7.00E-20
2558669390	DRAFT_00058	pfam00753	Lactamase_B		1.70E-21
2558669390	DRAFT_00058	EC:3.1.2.6	Hydroxyacylglutathione hydrolase.		
2558669390	DRAFT_00058	KO:K01069	hydroxyacylglutathione hydrolase [EC:3.1.2.6]		2.70E-35
2558669390	DRAFT_00058	Locus_type		CDS	
2558669390	DRAFT_00058	Product_name		Zn-dependent hydrolases, including glyoxylases	
2558669390	DRAFT_00058	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669390	DRAFT_00058	Coordinates		40943..41542(+)	
2558669390	DRAFT_00058	DNA_length		600bp	

2558669390	DRAFT_00058	Protein_length		199aa		
2558669390	DRAFT_00058	GC			0.54	
2558669391	DRAFT_00059	KEGG_module	M00570: Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine			
2558669391	DRAFT_00059	Metacyc	PWY-5437: threonine degradation I			
2558669391	DRAFT_00059	Metacyc	ILEUSYN-PWY: isoleucine biosynthesis I (from threonine)			
2558669391	DRAFT_00059	Metacyc	PWY-5826: hypoglycin biosynthesis			
2558669391	DRAFT_00059	COG_category	[E] Amino acid transport and metabolism			
2558669391	DRAFT_00059	COG1171	Threonine dehydratase			2.00E-86
2558669391	DRAFT_00059	pfam00291	PALP			5.70E-72
2558669391	DRAFT_00059	EC:4.3.1.19	Threonine ammonia-lyase.			
2558669391	DRAFT_00059	KO:K01754	threonine dehydratase [EC:4.3.1.19]			0.00E+00
2558669391	DRAFT_00059	Locus_type		CDS		
2558669391	DRAFT_00059	Product_name		Threonine dehydratase		
2558669391	DRAFT_00059	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669391	DRAFT_00059	Coordinates		41424..42509(-)		
2558669391	DRAFT_00059	DNA_length		1086bp		
2558669391	DRAFT_00059	Protein_length		361aa		
2558669391	DRAFT_00059	GC			0.58	
2558669392	DRAFT_00060	Metacyc	P303-PWY: ammonia oxidation II (anaerobic)			
2558669392	DRAFT_00060	IMG_pathway	437: Archaeal replication elongation			
2558669392	DRAFT_00060	COG_category	[L] Replication, recombination and repair			
2558669392	DRAFT_00060	COG0258	5'-3' exonuclease (including N-terminal domain of PolI)			7.00E-40
2558669392	DRAFT_00060	pfam00752	XPG_N			1.00E-16
2558669392	DRAFT_00060	pfam00867	XPG_I			8.70E-26
2558669392	DRAFT_00060	EC:3.-	Hydrolases.			
2558669392	DRAFT_00060	TIGR03674	flap structure-specific endonuclease			0.00E+00
2558669392	DRAFT_00060	KO:K04799	flap endonuclease-1 [EC:3.-.-.-]			0.00E+00
2558669392	DRAFT_00060	ITERM:00111	flap endonuclease 1 (EC 3.1.-.-)			
2558669392	DRAFT_00060	Locus_type		CDS		
2558669392	DRAFT_00060	Product_name		flap endonuclease 1 (EC 3.1.-.-)		
2558669392	DRAFT_00060	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669392	DRAFT_00060	Coordinates		42497..43522(-)		

2558669392	DRAFT_00060	DNA_length		1026bp	
2558669392	DRAFT_00060	Protein_length		341aa	
2558669392	DRAFT_00060	GC		0.57	
2558669393	DRAFT_00061	Locus_type		CDS	
2558669393	DRAFT_00061	Product_name		hypothetical protein	
2558669393	DRAFT_00061	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669393	DRAFT_00061	Coordinates		43551..43799(-)	
2558669393	DRAFT_00061	DNA_length		249bp	
2558669393	DRAFT_00061	Protein_length		82aa	
2558669393	DRAFT_00061	GC		0.56	
2558669394	DRAFT_00062	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669394	DRAFT_00062	COG2092	Translation elongation factor EF-1beta		1.00E-09
2558669394	DRAFT_00062	pfam00736	EF1_GNE		1.70E-09
2558669394	DRAFT_00062	TIGR00489	translation elongation factor aEF-1 beta		1.30E-18
2558669394	DRAFT_00062	KO:K03232	elongation factor 1-beta		7.10E-11
2558669394	DRAFT_00062	Locus_type		CDS	
2558669394	DRAFT_00062	Product_name		Translation elongation factor EF-1beta	
2558669394	DRAFT_00062	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669394	DRAFT_00062	Coordinates		43874..44158(-)	
2558669394	DRAFT_00062	DNA_length		285bp	
2558669394	DRAFT_00062	Protein_length		94aa	
2558669394	DRAFT_00062	GC		0.55	
2558669395	DRAFT_00063	COG_category	[C] Energy production and conversion		
2558669395	DRAFT_00063	COG0644	Dehydrogenases (flavoproteins)		8.00E-45
2558669395	DRAFT_00063	pfam12831	FAD_oxidored		6.00E-10
2558669395	DRAFT_00063	TIGR02032	geranylgeranyl reductase family		2.60E-49
2558669395	DRAFT_00063	Locus_type		CDS	
2558669395	DRAFT_00063	Product_name		Dehydrogenases (flavoproteins)	
2558669395	DRAFT_00063	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669395	DRAFT_00063	Coordinates		44379..45557(-)	
2558669395	DRAFT_00063	DNA_length		1179bp	

2558669395	DRAFT_00063	Protein_length		392aa		
2558669395	DRAFT_00063	GC			0.6	

2558669396	DRAFT_00064	Metacyc	PWY490-4: asparagine biosynthesis III (tRNA-dependent)			
2558669396	DRAFT_00064	COG_category	[S] Function unknown			
2558669396	DRAFT_00064	COG1990	Uncharacterized conserved protein			6.00E-35
2558669396	DRAFT_00064	pfam01981	PTH2			9.40E-47
2558669396	DRAFT_00064	EC:3.1.1.29	Aminoacyl-tRNA hydrolase.			
2558669396	DRAFT_00064	TIGR00283	peptidyl-tRNA hydrolase			4.50E-47
2558669396	DRAFT_00064	KO:K04794	peptidyl-tRNA hydrolase, PTH2 family [EC:3.1.1.29]			2.00E-31
2558669396	DRAFT_00064	ITERM:02547	peptidyl-tRNA hydrolase (EC 3.1.1.29)			
2558669396	DRAFT_00064	Locus_type		CDS		
2558669396	DRAFT_00064	Product_name		peptidyl-tRNA hydrolase (EC 3.1.1.29)		
2558669396	DRAFT_00064	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669396	DRAFT_00064	Coordinates		45620..45967(+)		
2558669396	DRAFT_00064	DNA_length		348bp		
2558669396	DRAFT_00064	Protein_length		115aa		
2558669396	DRAFT_00064	GC			0.56	

2558669397	DRAFT_00065	COG_category	[S] Function unknown			
2558669397	DRAFT_00065	COG0585	Uncharacterized conserved protein			2.00E-44
2558669397	DRAFT_00065	pfam01142	TruD			5.00E-60
2558669397	DRAFT_00065	EC:5.4.99.27	tRNA pseudouridine(13) synthase.			
2558669397	DRAFT_00065	TIGR00094	tRNA pseudouridine synthase, TruD family			6.30E-53
2558669397	DRAFT_00065	KO:K06176	tRNA pseudouridine13 synthase [EC:5.4.99.27]			0.00E+00
2558669397	DRAFT_00065	Locus_type		CDS		
2558669397	DRAFT_00065	Product_name		Uncharacterized conserved protein		
2558669397	DRAFT_00065	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669397	DRAFT_00065	Coordinates		45964..47232(+)		
2558669397	DRAFT_00065	DNA_length		1269bp		
2558669397	DRAFT_00065	Protein_length		422aa		
2558669397	DRAFT_00065	GC			0.6	

2558669398	DRAFT_00066	Metacyc	THIOREDOX-PWY: thioredoxin pathway			

2558669398	DRAFT_00066	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669398	DRAFT_00066	COG0492	Thioredoxin reductase		2.00E-54
2558669398	DRAFT_00066	pfam07992	Pyr_redox_2		4.20E-18
2558669398	DRAFT_00066	pfam00070	Pyr_redox		4.20E-11
2558669398	DRAFT_00066	EC:1.8.1.9	Thioredoxin-disulfide reductase.		
2558669398	DRAFT_00066	KO:K00384	thioredoxin reductase (NADPH) [EC:1.8.1.9]		0.00E+00
2558669398	DRAFT_00066	Locus_type		CDS	
2558669398	DRAFT_00066	Product_name		Thioredoxin reductase	
2558669398	DRAFT_00066	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669398	DRAFT_00066	Coordinates		47280..48275(+)	
2558669398	DRAFT_00066	DNA_length		996bp	
2558669398	DRAFT_00066	Protein_length		331aa	
2558669398	DRAFT_00066	GC		0.57	
2558669399	DRAFT_00067	KEGG_module	M00179: Ribosome, archaea		
2558669399	DRAFT_00067	KEGG_module	M00177: Ribosome, eukaryotes		
2558669399	DRAFT_00067	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669399	DRAFT_00067	COG1632	Ribosomal protein L15E		1.00E-31
2558669399	DRAFT_00067	pfam00827	Ribosomal_L15e		2.30E-46
2558669399	DRAFT_00067	KO:K02877	large subunit ribosomal protein L15e		1.10E-40
2558669399	DRAFT_00067	ITERM:00233	LSU ribosomal protein L15E		
2558669399	DRAFT_00067	Locus_type		CDS	
2558669399	DRAFT_00067	Product_name		LSU ribosomal protein L15E	
2558669399	DRAFT_00067	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669399	DRAFT_00067	Coordinates		48278..48733(-)	
2558669399	DRAFT_00067	DNA_length		456bp	
2558669399	DRAFT_00067	Protein_length		151aa	
2558669399	DRAFT_00067	GC		0.6	
2558669400	DRAFT_00068	KEGG_module	M00020: Serine biosynthesis, glycerate-3P => serine		
2558669400	DRAFT_00068	Metacyc	SERSYN-PWY: serine biosynthesis		
2558669400	DRAFT_00068	COG_category	[E] Amino acid transport and metabolism		
2558669400	DRAFT_00068	COG_category	[H] Coenzyme transport and metabolism		
2558669400	DRAFT_00068	COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases		4.00E-80

2558669400	DRAFT_00068	pfam02826	2-Hacid_dh_C		4.50E-62
2558669400	DRAFT_00068	pfam00389	2-Hacid_dh		6.60E-30
2558669400	DRAFT_00068	EC:1.1.1.95	Phosphoglycerate dehydrogenase.		
2558669400	DRAFT_00068	TIGR01327	D-3-phosphoglycerate dehydrogenase		2.80E-104
2558669400	DRAFT_00068	KO:K00058	D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]		0.00E+00
2558669400	DRAFT_00068	Locus_type		CDS	
2558669400	DRAFT_00068	Product_name		Phosphoglycerate dehydrogenase and related dehydrogenases	
2558669400	DRAFT_00068	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669400	DRAFT_00068	Coordinates		48784..49716(-)	
2558669400	DRAFT_00068	DNA_length		933bp	
2558669400	DRAFT_00068	Protein_length		310aa	
2558669400	DRAFT_00068	GC		0.58	
2558669401	DRAFT_00069	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669401	DRAFT_00069	COG0012	Predicted GTPase, probable translation factor		4.00E-87
2558669401	DRAFT_00069	pfam08438	MMR_HSR1_C		3.20E-31
2558669401	DRAFT_00069	pfam01926	MMR_HSR1		5.40E-17
2558669401	DRAFT_00069	pfam02824	TGS		5.70E-10
2558669401	DRAFT_00069	Locus_type		CDS	
2558669401	DRAFT_00069	Product_name		GTP-binding conserved hypothetical protein TIGR00650	
2558669401	DRAFT_00069	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669401	DRAFT_00069	Coordinates		49879..51084(+)	
2558669401	DRAFT_00069	DNA_length		1206bp	
2558669401	DRAFT_00069	Protein_length		401aa	
2558669401	DRAFT_00069	GC		0.57	
2558669402	DRAFT_00070	KEGG_module	M00179: Ribosome, archaea		
2558669402	DRAFT_00070	KEGG_module	M00177: Ribosome, eukaryotes		
2558669402	DRAFT_00070	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669402	DRAFT_00070	COG1890	Ribosomal protein S3AE		8.00E-45
2558669402	DRAFT_00070	pfam01015	Ribosomal_S3Ae		2.90E-54
2558669402	DRAFT_00070	KO:K02984	small subunit ribosomal protein S3Ae		0.00E+00
2558669402	DRAFT_00070	Locus_type		CDS	
2558669402	DRAFT_00070	Product_name		Ribosomal protein S3AE	

2558669402	DRAFT_00070	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669402	DRAFT_00070	Coordinates		51064..51687(-)		
2558669402	DRAFT_00070	DNA_length		624bp		
2558669402	DRAFT_00070	Protein_length		207aa		
2558669402	DRAFT_00070	GC			0.55	

2558669403	DRAFT_00071	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2558669403	DRAFT_00071	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2558669403	DRAFT_00071	Metacyc	PWY0-901: selenocysteine biosynthesis I (bacteria)			
2558669403	DRAFT_00071	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558669403	DRAFT_00071	Metacyc	PWY-6281: selenocysteine biosynthesis II (archaea and eukaryotes)			
2558669403	DRAFT_00071	IMG_pathway	352: Bacterial selenocysteine synthesis			
2558669403	DRAFT_00071	IMG_pathway	467: Archaeal/eukaryotic selenocysteine synthesis			
2558669403	DRAFT_00071	IMG_pathway	503: L-serine ligation to tRNA(Ser)			
2558669403	DRAFT_00071	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669403	DRAFT_00071	COG0172	Seryl-tRNA synthetase			0.00E+00
2558669403	DRAFT_00071	pfam02403	Seryl_tRNA_N			2.80E-23
2558669403	DRAFT_00071	pfam00587	tRNA-synt_2b			5.90E-36
2558669403	DRAFT_00071	EC:6.1.1.11	Serine--tRNA ligase.			
2558669403	DRAFT_00071	TIGR00414	seryl-tRNA synthetase			0.00E+00
2558669403	DRAFT_00071	KO:K01875	seryl-tRNA synthetase [EC:6.1.1.11]			0.00E+00
2558669403	DRAFT_00071	ITERM:00388	seryl-tRNA synthetase (EC 6.1.1.11)			
2558669403	DRAFT_00071	Locus_type		CDS		
2558669403	DRAFT_00071	Product_name		seryl-tRNA synthetase (EC 6.1.1.11)		
2558669403	DRAFT_00071	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669403	DRAFT_00071	Coordinates		51722..53002(-)		
2558669403	DRAFT_00071	DNA_length		1281bp		
2558669403	DRAFT_00071	Protein_length		426aa		
2558669403	DRAFT_00071	GC			0.57	

2558669404	DRAFT_00072	Locus_type		CDS		
2558669404	DRAFT_00072	Product_name		hypothetical protein		
2558669404	DRAFT_00072	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669404	DRAFT_00072	Coordinates		53024..53278(-)		

2558669404	DRAFT_00072	DNA_length		255bp	
2558669404	DRAFT_00072	Protein_length		84aa	
2558669404	DRAFT_00072	GC		0.56	
2558669405	DRAFT_00073	COG_category	[L] Replication, recombination and repair		
2558669405	DRAFT_00073	COG0608	Single-stranded DNA-specific exonuclease		3.00E-38
2558669405	DRAFT_00073	pfam01368	DHH		2.40E-10
2558669405	DRAFT_00073	pfam02272	DHHA1		2.30E-10
2558669405	DRAFT_00073	KO:K07463	archaea-specific RecJ-like exonuclease		0.00E+00
2558669405	DRAFT_00073	Locus_type		CDS	
2558669405	DRAFT_00073	Product_name		Single-stranded DNA-specific exonuclease	
2558669405	DRAFT_00073	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669405	DRAFT_00073	Coordinates		53275..54684(-)	
2558669405	DRAFT_00073	DNA_length		1410bp	
2558669405	DRAFT_00073	Protein_length		469aa	
2558669405	DRAFT_00073	GC		0.6	
2558669406	DRAFT_00074	KEGG_module	M00179: Ribosome, archaea		
2558669406	DRAFT_00074	KEGG_module	M00178: Ribosome, bacteria		
2558669406	DRAFT_00074	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669406	DRAFT_00074	COG0184	Ribosomal protein S15P/S13E		8.00E-09
2558669406	DRAFT_00074	pfam00312	Ribosomal_S15		3.60E-12
2558669406	DRAFT_00074	pfam08069	Ribosomal_S13_N		3.70E-23
2558669406	DRAFT_00074	KO:K02956	small subunit ribosomal protein S15		2.20E-43
2558669406	DRAFT_00074	ITERM:00304	SSU ribosomal protein S15P		
2558669406	DRAFT_00074	Locus_type		CDS	
2558669406	DRAFT_00074	Product_name		SSU ribosomal protein S15P	
2558669406	DRAFT_00074	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669406	DRAFT_00074	Coordinates		54702..55151(-)	
2558669406	DRAFT_00074	DNA_length		450bp	
2558669406	DRAFT_00074	Protein_length		149aa	
2558669406	DRAFT_00074	GC		0.59	
2558669407	DRAFT_00075	COG_category	[F] Nucleotide transport and metabolism		

2558669407	DRAFT_00075	COG0127	Xanthosine triphosphate pyrophosphatase		7.00E-40
2558669407	DRAFT_00075	pfam01725	Ham1p_like		2.50E-40
2558669407	DRAFT_00075	EC:3.6.1.19	Nucleoside-triphosphate diphosphatase.		
2558669407	DRAFT_00075	TIGR00042	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family		8.50E-48
2558669407	DRAFT_00075	KO:K02428	dITP/XTP pyrophosphatase [EC:3.6.1.19]		6.60E-40
2558669407	DRAFT_00075	Locus_type		CDS	
2558669407	DRAFT_00075	Product_name		non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family	
2558669407	DRAFT_00075	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669407	DRAFT_00075	Coordinates		55196..55771(-)	
2558669407	DRAFT_00075	DNA_length		576bp	
2558669407	DRAFT_00075	Protein_length		191aa	
2558669407	DRAFT_00075	GC		0.6	
2558669408	DRAFT_00076	Metacyc	SPHINGOLIPID-SYN-PWY: sphingolipid biosynthesis (yeast)		
2558669408	DRAFT_00076	Metacyc	PWY-7077: <i>N</i>-acetyl-D-galactosamine degradation		
2558669408	DRAFT_00076	Metacyc	PWY-6682: dehydrophos biosynthesis		
2558669408	DRAFT_00076	Metacyc	PWY-6626: CDP-2-glycerol biosynthesis		
2558669408	DRAFT_00076	Metacyc	PWY-5107: phytol salvage pathway		
2558669408	DRAFT_00076	Metacyc	PWY-5129: sphingolipid biosynthesis (plants)		
2558669408	DRAFT_00076	Metacyc	LIPA-CORESYN-PWY: Lipid A-core biosynthesis		
2558669408	DRAFT_00076	Metacyc	PWY-6577: farnesylcysteine salvage pathway		
2558669408	DRAFT_00076	COG_category	[T] Signal transduction mechanisms		
2558669408	DRAFT_00076	COG3642	Mn2+-dependent serine/threonine protein kinase		2.00E-46
2558669408	DRAFT_00076	pfam00069	Pkinase		1.10E-11
2558669408	DRAFT_00076	EC:2.7.1.-	Transferases. Transferring phosphorous-containing groups. Phosphotransferases with an alcoh		
2558669408	DRAFT_00076	TIGR03724	Kae1-associated kinase Bud32		1.20E-66
2558669408	DRAFT_00076	KO:K07174	Mn2+-dependent serine/threonine protein kinase [EC:2.7.1.-]		4.20E-40
2558669408	DRAFT_00076	Locus_type		CDS	
2558669408	DRAFT_00076	Product_name		Kae1-associated kinase Bud32	
2558669408	DRAFT_00076	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669408	DRAFT_00076	Coordinates		55755..56378(-)	
2558669408	DRAFT_00076	DNA_length		624bp	
2558669408	DRAFT_00076	Protein_length		207aa	
2558669408	DRAFT_00076	GC		0.58	

2558669409	DRAFT_00077	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669409	DRAFT_00077	COG0533	Metal-dependent proteases with possible chaperone activity			2.00E-86
2558669409	DRAFT_00077	pfam00814	Peptidase_M22			1.70E-70
2558669409	DRAFT_00077	TIGR03722	universal archaeal protein Kae1			0.00E+00
2558669409	DRAFT_00077	TIGR00329	metallohydrolase, glycoprotease/Kae1 family			2.70E-82
2558669409	DRAFT_00077	KO:K15900	tRNA threonylcarbamoyladenosine biosynthesis protein			0.00E+00
2558669409	DRAFT_00077	Locus_type		CDS		
2558669409	DRAFT_00077	Product_name		metallohydrolase, glycoprotease/Kae1 family		
2558669409	DRAFT_00077	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669409	DRAFT_00077	Coordinates		56398..57390(-)		
2558669409	DRAFT_00077	DNA_length		993bp		
2558669409	DRAFT_00077	Protein_length		330aa		
2558669409	DRAFT_00077	GC			0.61	

2558669410	DRAFT_00078	Locus_type		CDS		
2558669410	DRAFT_00078	Product_name		hypothetical protein		
2558669410	DRAFT_00078	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669410	DRAFT_00078	Coordinates		57397..57918(-)		
2558669410	DRAFT_00078	DNA_length		522bp		
2558669410	DRAFT_00078	Protein_length		173aa		
2558669410	DRAFT_00078	GC			0.54	

2558669411	DRAFT_00079	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669411	DRAFT_00079	COG1325	Predicted exosome subunit			4.00E-16
2558669411	DRAFT_00079	pfam01877	RNA_binding			1.40E-20
2558669411	DRAFT_00079	KO:K07581	hypothetical protein			1.70E-08
2558669411	DRAFT_00079	Locus_type		CDS		
2558669411	DRAFT_00079	Product_name		Predicted exosome subunit		
2558669411	DRAFT_00079	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669411	DRAFT_00079	Coordinates		57971..58405(+)		
2558669411	DRAFT_00079	DNA_length		435bp		
2558669411	DRAFT_00079	Protein_length		144aa		
2558669411	DRAFT_00079	GC			0.58	

2558669412	DRAFT_00080	Locus_type		CDS	
2558669412	DRAFT_00080	Product_name		hypothetical protein	
2558669412	DRAFT_00080	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669412	DRAFT_00080	Coordinates		58406..58705(+)	
2558669412	DRAFT_00080	DNA_length		300bp	
2558669412	DRAFT_00080	Protein_length		99aa	
2558669412	DRAFT_00080	GC		0.56	
2558669413	DRAFT_00081	COG_category	[I] Lipid transport and metabolism		
2558669413	DRAFT_00081	COG3255	Putative sterol carrier protein		9.00E-04
2558669413	DRAFT_00081	pfam02036	SCP2		1.00E-11
2558669413	DRAFT_00081	Locus_type		CDS	
2558669413	DRAFT_00081	Product_name		Putative sterol carrier protein	
2558669413	DRAFT_00081	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669413	DRAFT_00081	Coordinates		58689..59066(+)	
2558669413	DRAFT_00081	DNA_length		378bp	
2558669413	DRAFT_00081	Protein_length		125aa	
2558669413	DRAFT_00081	GC		0.54	
2558669414	DRAFT_00082	COG_category	[C] Energy production and conversion		
2558669414	DRAFT_00082	COG1804	Predicted acyl-CoA transferases/carnitine dehydratase		5.00E-82
2558669414	DRAFT_00082	pfam02515	CoA_transf_3		4.00E-49
2558669414	DRAFT_00082	Locus_type		CDS	
2558669414	DRAFT_00082	Product_name		Predicted acyl-CoA transferases/carnitine dehydratase	
2558669414	DRAFT_00082	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669414	DRAFT_00082	Coordinates		59321..60466(-)	
2558669414	DRAFT_00082	DNA_length		1146bp	
2558669414	DRAFT_00082	Protein_length		381aa	
2558669414	DRAFT_00082	GC		0.6	
2558669415	DRAFT_00083	Locus_type		CDS	
2558669415	DRAFT_00083	Product_name		hypothetical protein	
2558669415	DRAFT_00083	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	

2558669415	DRAFT_00083	Coordinates		60579..61244(+)		
2558669415	DRAFT_00083	DNA_length		666bp		
2558669415	DRAFT_00083	Protein_length		221aa		
2558669415	DRAFT_00083	GC			0.49	
2558669415	DRAFT_00083	Transmembrane		Yes		
2558669416	DRAFT_00084	Locus_type		CDS		
2558669416	DRAFT_00084	Product_name		hypothetical protein		
2558669416	DRAFT_00084	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669416	DRAFT_00084	Coordinates		61541..61726(+)		
2558669416	DRAFT_00084	DNA_length		186bp		
2558669416	DRAFT_00084	Protein_length		61aa		
2558669416	DRAFT_00084	GC			0.58	
2558669417	DRAFT_00085	Locus_type		CDS		
2558669417	DRAFT_00085	Product_name		hypothetical protein		
2558669417	DRAFT_00085	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669417	DRAFT_00085	Coordinates		61772..61918(+)		
2558669417	DRAFT_00085	DNA_length		147bp		
2558669417	DRAFT_00085	Protein_length		48aa		
2558669417	DRAFT_00085	GC			0.49	
2558669418	DRAFT_00086	Locus_type		CDS		
2558669418	DRAFT_00086	Product_name		hypothetical protein		
2558669418	DRAFT_00086	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669418	DRAFT_00086	Coordinates		62088..63284(+)		
2558669418	DRAFT_00086	DNA_length		1197bp		
2558669418	DRAFT_00086	Protein_length		398aa		
2558669418	DRAFT_00086	GC			0.56	
2558669419	DRAFT_00087	pfam13414	TPR_11			6.90E-09
2558669419	DRAFT_00087	pfam13414	TPR_11			2.00E-06
2558669419	DRAFT_00087	pfam13414	TPR_11			2.60E-14
2558669419	DRAFT_00087	pfam13289	SIR2_2			3.40E-13

2558669419	DRAFT_00087	Locus_type		CDS		
2558669419	DRAFT_00087	Product_name		SIR2-like domain/TPR repeat		
2558669419	DRAFT_00087	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669419	DRAFT_00087	Coordinates		63400..65409(-)		
2558669419	DRAFT_00087	DNA_length		2010bp		
2558669419	DRAFT_00087	Protein_length		669aa		
2558669419	DRAFT_00087	GC			0.47	
2558669420	DRAFT_00088	Locus_type		CDS		
2558669420	DRAFT_00088	Product_name		hypothetical protein		
2558669420	DRAFT_00088	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669420	DRAFT_00088	Coordinates		65842..66954(-)		
2558669420	DRAFT_00088	DNA_length		1113bp		
2558669420	DRAFT_00088	Protein_length		370aa		
2558669420	DRAFT_00088	GC			0.53	
2558669421	DRAFT_00089	COG_category	[R] General function prediction only			
2558669421	DRAFT_00089	COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold			5.00E-25
2558669421	DRAFT_00089	pfam13483	Lactamase_B_3			8.00E-32
2558669421	DRAFT_00089	Locus_type		CDS		
2558669421	DRAFT_00089	Product_name		Predicted Zn-dependent hydrolases of the beta-lactamase fold		
2558669421	DRAFT_00089	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669421	DRAFT_00089	Coordinates		66909..67577(-)		
2558669421	DRAFT_00089	DNA_length		669bp		
2558669421	DRAFT_00089	Protein_length		222aa		
2558669421	DRAFT_00089	GC			0.55	
2558669422	DRAFT_00090	KEGG_module	M00342: Bacterial proteasome			
2558669422	DRAFT_00090	KEGG_module	M00343: Archaeal proteasome			
2558669422	DRAFT_00090	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669422	DRAFT_00090	COG0638	20S proteasome, alpha and beta subunits			7.00E-37
2558669422	DRAFT_00090	pfam00227	Proteasome			8.60E-42
2558669422	DRAFT_00090	EC:3.4.25.1	Proteasome endopeptidase complex.			
2558669422	DRAFT_00090	TIGR03634	proteasome endopeptidase complex, archaeal, beta subunit			2.20E-62

2558669422	DRAFT_00090	KO:K03433	proteasome beta subunit [EC:3.4.25.1]		0.00E+00
2558669422	DRAFT_00090	Locus_type		CDS	
2558669422	DRAFT_00090	Product_name		20S proteasome, alpha and beta subunits	
2558669422	DRAFT_00090	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669422	DRAFT_00090	Coordinates		67590..68189(-)	
2558669422	DRAFT_00090	DNA_length		600bp	
2558669422	DRAFT_00090	Protein_length		199aa	
2558669422	DRAFT_00090	GC		0.58	
2558669423	DRAFT_00091	COG_category	[A] RNA processing and modification		
2558669423	DRAFT_00091	COG0430	RNA 3'-terminal phosphate cyclase		7.00E-73
2558669423	DRAFT_00091	pfam05189	RTC_insert		2.90E-10
2558669423	DRAFT_00091	pfam01137	RTC		3.40E-66
2558669423	DRAFT_00091	EC:6.5.1.4	RNA-3'-phosphate cyclase.		
2558669423	DRAFT_00091	TIGR03399	RNA 3'-phosphate cyclase		8.10E-97
2558669423	DRAFT_00091	KO:K01974	RNA 3'-terminal phosphate cyclase [EC:6.5.1.4]		0.00E+00
2558669423	DRAFT_00091	Locus_type		CDS	
2558669423	DRAFT_00091	Product_name		RNA 3'-phosphate cyclase	
2558669423	DRAFT_00091	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669423	DRAFT_00091	Coordinates		68254..69288(-)	
2558669423	DRAFT_00091	DNA_length		1035bp	
2558669423	DRAFT_00091	Protein_length		344aa	
2558669423	DRAFT_00091	GC		0.64	
2558669424	DRAFT_00092	Metacyc	NAD-BIOSYNTHESIS-III: NAD biosynthesis III		
2558669424	DRAFT_00092	Metacyc	PWY3O-4106: NAD salvage pathway III		
2558669424	DRAFT_00092	COG_category	[H] Coenzyme transport and metabolism		
2558669424	DRAFT_00092	COG1056	Nicotinamide mononucleotide adenylyltransferase		3.00E-37
2558669424	DRAFT_00092	pfam01467	CTP_transf_2		4.20E-16
2558669424	DRAFT_00092	EC:2.7.7.1	Nicotinamide-nucleotide adenylyltransferase.		
2558669424	DRAFT_00092	TIGR00125	cytidyltransferase-like domain		3.30E-17
2558669424	DRAFT_00092	TIGR01527	nicotinamide-nucleotide adenylyltransferase		1.60E-56
2558669424	DRAFT_00092	KO:K00952	nicotinamide-nucleotide adenylyltransferase [EC:2.7.7.1]		1.20E-43
2558669424	DRAFT_00092	Locus_type		CDS	

2558669424	DRAFT_00092	Product_name		cytidyltransferase-like domain		
2558669424	DRAFT_00092	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669424	DRAFT_00092	Coordinates		69373..69897(+)		
2558669424	DRAFT_00092	DNA_length		525bp		
2558669424	DRAFT_00092	Protein_length		174aa		
2558669424	DRAFT_00092	GC			0.55	
2558669425	DRAFT_00093	COG_category	[E] Amino acid transport and metabolism			
2558669425	DRAFT_00093	COG0075	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferas			1.00E-102
2558669425	DRAFT_00093	pfam00266	Aminotran_5			4.50E-35
2558669425	DRAFT_00093	Locus_type		CDS		
2558669425	DRAFT_00093	Product_name		Serine-pyruvate aminotransferase/archaeal aspartate aminotransfera		
2558669425	DRAFT_00093	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669425	DRAFT_00093	Coordinates		69902..71002(+)		
2558669425	DRAFT_00093	DNA_length		1101bp		
2558669425	DRAFT_00093	Protein_length		366aa		
2558669425	DRAFT_00093	GC			0.59	
2558669426	DRAFT_00094	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669426	DRAFT_00094	COG1047	FKBP-type peptidyl-prolyl cis-trans isomerases 2			1.00E-28
2558669426	DRAFT_00094	pfam00254	FKBP_C			1.80E-08
2558669426	DRAFT_00094	EC:5.2.1.8	Peptidylprolyl isomerase.			
2558669426	DRAFT_00094	KO:K01802	peptidylprolyl isomerase [EC:5.2.1.8]			0.00E+00
2558669426	DRAFT_00094	Locus_type		CDS		
2558669426	DRAFT_00094	Product_name		FKBP-type peptidyl-prolyl cis-trans isomerases 2		
2558669426	DRAFT_00094	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669426	DRAFT_00094	Coordinates		71040..71852(+)		
2558669426	DRAFT_00094	DNA_length		813bp		
2558669426	DRAFT_00094	Protein_length		270aa		
2558669426	DRAFT_00094	GC			0.57	
2558669427	DRAFT_00095	Metacyc	PWY-6349: CDP-archaeol biosynthesis			
2558669427	DRAFT_00095	COG_category	[C] Energy production and conversion			
2558669427	DRAFT_00095	COG0371	Glycerol dehydrogenase and related enzymes			8.00E-83

2558669427	DRAFT_00095	pfam13685	Fe-ADH_2		1.50E-61
2558669427	DRAFT_00095	EC:1.1.1.261	sn-glycerol-1-phosphate dehydrogenase.		
2558669427	DRAFT_00095	KO:K00096	glycerol-1-phosphate dehydrogenase [NAD(P)] [EC:1.1.1.261]		0.00E+00
2558669427	DRAFT_00095	Locus_type		CDS	
2558669427	DRAFT_00095	Product_name		Glycerol dehydrogenase and related enzymes	
2558669427	DRAFT_00095	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669427	DRAFT_00095	Coordinates		71849..72868(-)	
2558669427	DRAFT_00095	DNA_length		1020bp	
2558669427	DRAFT_00095	Protein_length		339aa	
2558669427	DRAFT_00095	GC		0.59	
2558669428	DRAFT_00096	KEGG_module	M00342: Bacterial proteasome		
2558669428	DRAFT_00096	KEGG_module	M00343: Archaeal proteasome		
2558669428	DRAFT_00096	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669428	DRAFT_00096	COG0638	20S proteasome, alpha and beta subunits		1.00E-44
2558669428	DRAFT_00096	pfam00227	Proteasome		1.20E-48
2558669428	DRAFT_00096	EC:3.4.25.1	Proteasome endopeptidase complex.		
2558669428	DRAFT_00096	TIGR03634	proteasome endopeptidase complex, archaeal, beta subunit		3.80E-68
2558669428	DRAFT_00096	KO:K03433	proteasome beta subunit [EC:3.4.25.1]		0.00E+00
2558669428	DRAFT_00096	Locus_type		CDS	
2558669428	DRAFT_00096	Product_name		20S proteasome, alpha and beta subunits	
2558669428	DRAFT_00096	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669428	DRAFT_00096	Coordinates		73147..73821(+)	
2558669428	DRAFT_00096	DNA_length		675bp	
2558669428	DRAFT_00096	Protein_length		224aa	
2558669428	DRAFT_00096	GC		0.55	
2558669429	DRAFT_00097	COG_category	[R] General function prediction only		
2558669429	DRAFT_00097	COG1782	Predicted metal-dependent RNase, consists of a metallo-beta-lactamas		0.00E+00
2558669429	DRAFT_00097	pfam00753	Lactamase_B		2.40E-24
2558669429	DRAFT_00097	pfam10996	Beta-Casp		1.50E-29
2558669429	DRAFT_00097	pfam07521	RMMBL		1.30E-11
2558669429	DRAFT_00097	TIGR03675	arCOG00543 universal archaeal KH-domain/beta-lactamase-domain pr		0.00E+00
2558669429	DRAFT_00097	Locus_type		CDS	

2558669429	DRAFT_00097	Product_name		arCOG00543 universal archaeal KH-domain/beta-lactamase-domain p	
2558669429	DRAFT_00097	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669429	DRAFT_00097	Coordinates		73824..75737(+)	
2558669429	DRAFT_00097	DNA_length		1914bp	
2558669429	DRAFT_00097	Protein_length		637aa	
2558669429	DRAFT_00097	GC		0.56	
2558669430	DRAFT_00098	Metacyc	PWY-5469: sesamin biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)		
2558669430	DRAFT_00098	Metacyc	PWY-7079: geodin biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-6766: salicin biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-5748: γ-coniciene and coniine biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-5987: sorgoleone biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-5479: podophyllotoxin and 6-methoxypodophyllotoxin biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-2821: glucosinolate biosynthesis from phenylalanine		
2558669430	DRAFT_00098	Metacyc	PWY66-388: fatty acid α-oxidation III		
2558669430	DRAFT_00098	Metacyc	PWY-7139: sesaminol glucoside biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-5826: hypoglycin biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-5780: hypericin biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-7186: superpathway of scopolin and esculin biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWY-6326: camptothecin biosynthesis		
2558669430	DRAFT_00098	Metacyc	PWYG-321: mycolate biosynthesis		
2558669430	DRAFT_00098	COG_category	[R] General function prediction only		
2558669430	DRAFT_00098	COG1064	Zn-dependent alcohol dehydrogenases		1.00E-106
2558669430	DRAFT_00098	pfam08240	ADH_N		4.30E-27
2558669430	DRAFT_00098	pfam00107	ADH_zinc_N		4.30E-26
2558669430	DRAFT_00098	EC:1.-	Oxidoreductases.		
2558669430	DRAFT_00098	KO:K13979	uncharacterized zinc-type alcohol dehydrogenase-like protein [EC:1.-.-.		0.00E+00
2558669430	DRAFT_00098	Locus_type		CDS	
2558669430	DRAFT_00098	Product_name		Zn-dependent alcohol dehydrogenases	
2558669430	DRAFT_00098	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669430	DRAFT_00098	Coordinates		76432..77481(+)	
2558669430	DRAFT_00098	DNA_length		1050bp	
2558669430	DRAFT_00098	Protein_length		349aa	

2558669430	DRAFT_00098	GC			0.62
2558669431	DRAFT_00099	Locus_type		CDS	
2558669431	DRAFT_00099	Product_name		hypothetical protein	
2558669431	DRAFT_00099	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669431	DRAFT_00099	Coordinates		77789..79159(+)	
2558669431	DRAFT_00099	DNA_length		1371bp	
2558669431	DRAFT_00099	Protein_length		456aa	
2558669431	DRAFT_00099	GC			0.54
2558669431	DRAFT_00099	Transmembrane		Yes	
2558669432	DRAFT_00100	Locus_type		CDS	
2558669432	DRAFT_00100	Product_name		hypothetical protein	
2558669432	DRAFT_00100	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669432	DRAFT_00100	Coordinates		79113..79463(+)	
2558669432	DRAFT_00100	DNA_length		351bp	
2558669432	DRAFT_00100	Protein_length		116aa	
2558669432	DRAFT_00100	GC			0.52
2558669433	DRAFT_00101	Locus_type		CDS	
2558669433	DRAFT_00101	Product_name		hypothetical protein	
2558669433	DRAFT_00101	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669433	DRAFT_00101	Coordinates		79545..79814(-)	
2558669433	DRAFT_00101	DNA_length		270bp	
2558669433	DRAFT_00101	Protein_length		89aa	
2558669433	DRAFT_00101	GC			0.52
2558669433	DRAFT_00101	Transmembrane		Yes	
2558669434	DRAFT_00102	pfam00339	Arrestin_N		1.10E-05
2558669434	DRAFT_00102	Locus_type		CDS	
2558669434	DRAFT_00102	Product_name		Arrestin (or S-antigen), N-terminal domain	
2558669434	DRAFT_00102	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669434	DRAFT_00102	Coordinates		80038..80634(-)	
2558669434	DRAFT_00102	DNA_length		597bp	

2558669434	DRAFT_00102	Protein_length		198aa		
2558669434	DRAFT_00102	GC			0.55	

2558669435	DRAFT_00103	pfam05048	NosD			1.20E-15
2558669435	DRAFT_00103	pfam05048	NosD			5.60E-22
2558669435	DRAFT_00103	pfam05048	NosD			4.70E-22
2558669435	DRAFT_00103	TIGR03804	parallel beta-helix repeat (two copies)			2.70E-12
2558669435	DRAFT_00103	Locus_type		CDS		
2558669435	DRAFT_00103	Product_name		parallel beta-helix repeat (two copies)		
2558669435	DRAFT_00103	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669435	DRAFT_00103	Coordinates		80955..82871(+)		
2558669435	DRAFT_00103	DNA_length		1917bp		
2558669435	DRAFT_00103	Protein_length		638aa		
2558669435	DRAFT_00103	GC			0.53	
2558669435	DRAFT_00103	Transmembrane		Yes		

2558669436	DRAFT_00104	COG_category	[S] Function unknown			
2558669436	DRAFT_00104	COG2450	Uncharacterized conserved protein			1.00E-07
2558669436	DRAFT_00104	pfam04472	DUF552			6.20E-14
2558669436	DRAFT_00104	KO:K09152	hypothetical protein			1.70E-23
2558669436	DRAFT_00104	Locus_type		CDS		
2558669436	DRAFT_00104	Product_name		Uncharacterized conserved protein		
2558669436	DRAFT_00104	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669436	DRAFT_00104	Coordinates		83043..83339(-)		
2558669436	DRAFT_00104	DNA_length		297bp		
2558669436	DRAFT_00104	Protein_length		98aa		
2558669436	DRAFT_00104	GC			0.58	

2558669437	DRAFT_00105	Locus_type		CDS		
2558669437	DRAFT_00105	Product_name		hypothetical protein		
2558669437	DRAFT_00105	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669437	DRAFT_00105	Coordinates		83282..83410(-)		
2558669437	DRAFT_00105	DNA_length		129bp		
2558669437	DRAFT_00105	Protein_length		42aa		

2558669437	DRAFT_00105	GC			0.44	
2558669438	DRAFT_00106	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669438	DRAFT_00106	COG2016	Predicted RNA-binding protein (contains PUA domain)			2.00E-26
2558669438	DRAFT_00106	pfam01472	PUA			4.80E-16
2558669438	DRAFT_00106	TIGR00451	uncharacterized domain 2			1.00E-26
2558669438	DRAFT_00106	KO:K07575	PUA domain protein			6.30E-28
2558669438	DRAFT_00106	Locus_type		CDS		
2558669438	DRAFT_00106	Product_name		Predicted RNA-binding protein (contains PUA domain)		
2558669438	DRAFT_00106	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669438	DRAFT_00106	Coordinates		83542..84021(-)		
2558669438	DRAFT_00106	DNA_length		480bp		
2558669438	DRAFT_00106	Protein_length		159aa		
2558669438	DRAFT_00106	GC			0.59	
2558669439	DRAFT_00107	COG_category	[K] Transcription			
2558669439	DRAFT_00107	COG1958	Small nuclear ribonucleoprotein (snRNP) homolog			2.00E-11
2558669439	DRAFT_00107	pfam01423	LSM			6.40E-20
2558669439	DRAFT_00107	KO:K04796	small nuclear ribonucleoprotein			1.70E-25
2558669439	DRAFT_00107	Locus_type		CDS		
2558669439	DRAFT_00107	Product_name		Small nuclear ribonucleoprotein, LSM family		
2558669439	DRAFT_00107	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669439	DRAFT_00107	Coordinates		84098..84316(+)		
2558669439	DRAFT_00107	DNA_length		219bp		
2558669439	DRAFT_00107	Protein_length		72aa		
2558669439	DRAFT_00107	GC			0.56	
2558669440	DRAFT_00108	Locus_type		CDS		
2558669440	DRAFT_00108	Product_name		hypothetical protein		
2558669440	DRAFT_00108	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669440	DRAFT_00108	Coordinates		84489..85151(+)		
2558669440	DRAFT_00108	DNA_length		663bp		
2558669440	DRAFT_00108	Protein_length		220aa		
2558669440	DRAFT_00108	GC			0.58	

2558669440	DRAFT_00108	Transmembrane		Yes	
2558669441	DRAFT_00109	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P		
2558669441	DRAFT_00109	KEGG_module	M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP		
2558669441	DRAFT_00109	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)		
2558669441	DRAFT_00109	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)		
2558669441	DRAFT_00109	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)		
2558669441	DRAFT_00109	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)		
2558669441	DRAFT_00109	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle		
2558669441	DRAFT_00109	Metacyc	PWY-5723: Rubisco shunt		
2558669441	DRAFT_00109	Metacyc	P124-PWY: Bifidobacterium shunt		
2558669441	DRAFT_00109	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)		
2558669441	DRAFT_00109	IMG_pathway	341: Oxidative pentose phosphate pathway		
2558669441	DRAFT_00109	IMG_pathway	342: Nonoxidative pentose phosphate pathway		
2558669441	DRAFT_00109	IMG_pathway	343: Reverse ribulose monophosphate pathway		
2558669441	DRAFT_00109	IMG_pathway	527: Calvin cycle		
2558669441	DRAFT_00109	IMG_pathway	535: D-allose conversion to D-fructose 6-phosphate		
2558669441	DRAFT_00109	COG_category	[G] Carbohydrate transport and metabolism		
2558669441	DRAFT_00109	COG0120	Ribose 5-phosphate isomerase		7.00E-49
2558669441	DRAFT_00109	pfam06026	Rib_5-P_isom_A		1.20E-45
2558669441	DRAFT_00109	EC:5.3.1.6	Ribose-5-phosphate isomerase.		
2558669441	DRAFT_00109	TIGR00021	ribose 5-phosphate isomerase		3.10E-60
2558669441	DRAFT_00109	KO:K01807	ribose 5-phosphate isomerase A [EC:5.3.1.6]		3.10E-44
2558669441	DRAFT_00109	ITERM:01495	ribose-5-phosphate isomerase (EC 5.3.1.6)		
2558669441	DRAFT_00109	Locus_type		CDS	
2558669441	DRAFT_00109	Product_name		ribose-5-phosphate isomerase (EC 5.3.1.6)	
2558669441	DRAFT_00109	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669441	DRAFT_00109	Coordinates		85151..85843(+)	
2558669441	DRAFT_00109	DNA_length		693bp	
2558669441	DRAFT_00109	Protein_length		230aa	
2558669441	DRAFT_00109	GC		0.62	
2558669442	DRAFT_00110	COG_category	[C] Energy production and conversion		
2558669442	DRAFT_00110	COG1146	Ferredoxin		3.00E-05

2558669442	DRAFT_00110	Locus_type		CDS	
2558669442	DRAFT_00110	Product_name		Ferredoxin	
2558669442	DRAFT_00110	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669442	DRAFT_00110	Coordinates		85880..86308(+)	
2558669442	DRAFT_00110	DNA_length		429bp	
2558669442	DRAFT_00110	Protein_length		142aa	
2558669442	DRAFT_00110	GC			0.57
2558669443	DRAFT_00111	Locus_type		CDS	
2558669443	DRAFT_00111	Product_name		hypothetical protein	
2558669443	DRAFT_00111	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669443	DRAFT_00111	Coordinates		86532..86909(+)	
2558669443	DRAFT_00111	DNA_length		378bp	
2558669443	DRAFT_00111	Protein_length		125aa	
2558669443	DRAFT_00111	GC			0.59
2558669444	DRAFT_00112	COG_category	[R] General function prediction only		
2558669444	DRAFT_00112	COG2047	Uncharacterized protein (ATP-grasp superfamily)		2.00E-59
2558669444	DRAFT_00112	pfam09754	PAC2		1.80E-45
2558669444	DRAFT_00112	TIGR00162	TIGR00162 family protein		1.90E-67
2558669444	DRAFT_00112	Locus_type		CDS	
2558669444	DRAFT_00112	Product_name		TIGR00162 family protein	
2558669444	DRAFT_00112	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669444	DRAFT_00112	Coordinates		86909..87694(+)	
2558669444	DRAFT_00112	DNA_length		786bp	
2558669444	DRAFT_00112	Protein_length		261aa	
2558669444	DRAFT_00112	GC			0.6
2558669445	DRAFT_00113	Locus_type		CDS	
2558669445	DRAFT_00113	Product_name		hypothetical protein	
2558669445	DRAFT_00113	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669445	DRAFT_00113	Coordinates		88314..88535(+)	
2558669445	DRAFT_00113	DNA_length		222bp	
2558669445	DRAFT_00113	Protein_length		73aa	

2558669445	DRAFT_00113	GC			0.53	
2558669445	DRAFT_00113	Transmembrane		Yes		

2558669446	DRAFT_00114	COG_category	[S] Function unknown			
2558669446	DRAFT_00114	COG1690	Uncharacterized conserved protein			0.00E+00
2558669446	DRAFT_00114	pfam01139	RtcB			0.00E+00
2558669446	DRAFT_00114	EC:6.5.1.3	RNA ligase (ATP).			
2558669446	DRAFT_00114	KO:K14415	tRNA-splicing ligase RtcB [EC:6.5.1.3]			0.00E+00
2558669446	DRAFT_00114	Locus_type		CDS		
2558669446	DRAFT_00114	Product_name		Uncharacterized conserved protein		
2558669446	DRAFT_00114	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669446	DRAFT_00114	Coordinates		88772..90229(-)		
2558669446	DRAFT_00114	DNA_length		1458bp		
2558669446	DRAFT_00114	Protein_length		485aa		
2558669446	DRAFT_00114	GC			0.59	

2558669447	DRAFT_00115	COG_category	[S] Function unknown			
2558669447	DRAFT_00115	COG1371	Uncharacterized conserved protein			1.00E-21
2558669447	DRAFT_00115	pfam01951	Archease			1.60E-30
2558669447	DRAFT_00115	Locus_type		CDS		
2558669447	DRAFT_00115	Product_name		Uncharacterized conserved protein		
2558669447	DRAFT_00115	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669447	DRAFT_00115	Coordinates		90308..90730(-)		
2558669447	DRAFT_00115	DNA_length		423bp		
2558669447	DRAFT_00115	Protein_length		140aa		
2558669447	DRAFT_00115	GC			0.59	

2558669448	DRAFT_00116	Metacyc	PWY-6984: lipoate salvage II			
2558669448	DRAFT_00116	Metacyc	PWY0-522: lipoate salvage I			
2558669448	DRAFT_00116	COG_category	[H] Coenzyme transport and metabolism			
2558669448	DRAFT_00116	COG0095	Lipoate-protein ligase A			1.00E-34
2558669448	DRAFT_00116	pfam03099	BPL_LplA_LipB			1.40E-14
2558669448	DRAFT_00116	EC:2.7.7.63	Lipoate--protein ligase.			
2558669448	DRAFT_00116	KO:K03800	lipoate-protein ligase A [EC:2.7.7.63]			3.20E-26

2558669448	DRAFT_00116	Locus_type		CDS	
2558669448	DRAFT_00116	Product_name		Lipoate-protein ligase A	
2558669448	DRAFT_00116	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669448	DRAFT_00116	Coordinates		90794..91540(+)	
2558669448	DRAFT_00116	DNA_length		747bp	
2558669448	DRAFT_00116	Protein_length		248aa	
2558669448	DRAFT_00116	GC		0.6	
2558669449	DRAFT_00117	Metacyc	THREONINE-DEG2-PWY: threonine degradation II		
2558669449	DRAFT_00117	COG_category	[H] Coenzyme transport and metabolism		
2558669449	DRAFT_00117	COG0156	7-keto-8-aminopelargonate synthetase and related enzymes		2.00E-114
2558669449	DRAFT_00117	pfam00155	Aminotran_1_2		2.10E-61
2558669449	DRAFT_00117	EC:2.3.1.29	Glycine C-acetyltransferase.		
2558669449	DRAFT_00117	TIGR00858	8-amino-7-oxononanoate synthase		8.20E-121
2558669449	DRAFT_00117	TIGR01825	pyridoxal phosphate-dependent acyltransferase, putative		0.00E+00
2558669449	DRAFT_00117	KO:K00639	glycine C-acetyltransferase [EC:2.3.1.29]		0.00E+00
2558669449	DRAFT_00117	Locus_type		CDS	
2558669449	DRAFT_00117	Product_name		7-keto-8-aminopelargonate synthetase and related enzymes	
2558669449	DRAFT_00117	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669449	DRAFT_00117	Coordinates		91526..92740(-)	
2558669449	DRAFT_00117	DNA_length		1215bp	
2558669449	DRAFT_00117	Protein_length		404aa	
2558669449	DRAFT_00117	GC		0.59	
2558669450	DRAFT_00118	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558669450	DRAFT_00118	COG_category	[G] Carbohydrate transport and metabolism		
2558669450	DRAFT_00118	COG0451	Nucleoside-diphosphate-sugar epimerases		2.00E-36
2558669450	DRAFT_00118	pfam01370	Epimerase		1.40E-29
2558669450	DRAFT_00118	Locus_type		CDS	
2558669450	DRAFT_00118	Product_name		Nucleoside-diphosphate-sugar epimerases	
2558669450	DRAFT_00118	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669450	DRAFT_00118	Coordinates		92751..93719(-)	
2558669450	DRAFT_00118	DNA_length		969bp	
2558669450	DRAFT_00118	Protein_length		322aa	

2558669450	DRAFT_00118	GC			0.59	
2558669451	DRAFT_00119	pfam01037	AsnC_trans_reg			1.10E-08
2558669451	DRAFT_00119	Locus_type		CDS		
2558669451	DRAFT_00119	Product_name		Transcriptional regulators		
2558669451	DRAFT_00119	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669451	DRAFT_00119	Coordinates		93765..93995(-)		
2558669451	DRAFT_00119	DNA_length		231bp		
2558669451	DRAFT_00119	Protein_length		76aa		
2558669451	DRAFT_00119	GC			0.52	
2558669452	DRAFT_00120	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2558669452	DRAFT_00120	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2558669452	DRAFT_00120	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558669452	DRAFT_00120	IMG_pathway	493: L-histidine ligation to tRNA(His)			
2558669452	DRAFT_00120	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669452	DRAFT_00120	COG0124	Histidyl-tRNA synthetase			3.00E-77
2558669452	DRAFT_00120	pfam13393	tRNA-synt_His			5.70E-36
2558669452	DRAFT_00120	pfam03129	HGTP_anticodon			4.40E-13
2558669452	DRAFT_00120	EC:6.1.1.21	Histidine--tRNA ligase.			
2558669452	DRAFT_00120	TIGR00442	histidyl-tRNA synthetase			1.80E-95
2558669452	DRAFT_00120	KO:K01892	histidyl-tRNA synthetase [EC:6.1.1.21]			0.00E+00
2558669452	DRAFT_00120	ITERM:00386	histidyl-tRNA synthetase (EC 6.1.1.21)			
2558669452	DRAFT_00120	Locus_type		CDS		
2558669452	DRAFT_00120	Product_name		histidyl-tRNA synthetase (EC 6.1.1.21)		
2558669452	DRAFT_00120	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669452	DRAFT_00120	Coordinates		94060..95271(-)		
2558669452	DRAFT_00120	DNA_length		1212bp		
2558669452	DRAFT_00120	Protein_length		403aa		
2558669452	DRAFT_00120	GC			0.6	
2558669453	DRAFT_00121	pfam13177	DNA_pol3_delta2			4.00E-13
2558669453	DRAFT_00121	pfam08542	Rep_fac_C			2.60E-10
2558669453	DRAFT_00121	KO:K04801	replication factor C small subunit			0.00E+00

2558669453	DRAFT_00121	Locus_type		CDS		
2558669453	DRAFT_00121	Product_name		DNA polymerase III, gamma/tau subunits		
2558669453	DRAFT_00121	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669453	DRAFT_00121	Coordinates		95327..96277(-)		
2558669453	DRAFT_00121	DNA_length		951bp		
2558669453	DRAFT_00121	Protein_length		316aa		
2558669453	DRAFT_00121	GC			0.58	
2558669454	DRAFT_00122	pfam05916	Sld5			7.20E-07
2558669454	DRAFT_00122	Locus_type		CDS		
2558669454	DRAFT_00122	Product_name		GINS complex protein		
2558669454	DRAFT_00122	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669454	DRAFT_00122	Coordinates		96567..97130(+)		
2558669454	DRAFT_00122	DNA_length		564bp		
2558669454	DRAFT_00122	Protein_length		187aa		
2558669454	DRAFT_00122	GC			0.58	
2558669455	DRAFT_00123	IMG_pathway	436: Archaeal replication initiation			
2558669455	DRAFT_00123	COG_category	[L] Replication, recombination and repair			
2558669455	DRAFT_00123	COG1241	Predicted ATPase involved in replication control, Cdc46/Mcm family			0.00E+00
2558669455	DRAFT_00123	pfam14551	MCM_N			5.60E-16
2558669455	DRAFT_00123	pfam00493	MCM			1.60E-114
2558669455	DRAFT_00123	EC:3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; involved in cellular and subc			
2558669455	DRAFT_00123	KO:K10726	replicative DNA helicase Mcm [EC:3.6.4.-]			0.00E+00
2558669455	DRAFT_00123	ITERM:00094	replicative DNA helicase Mcm (EC 3.6.1.-)			
2558669455	DRAFT_00123	Locus_type		CDS		
2558669455	DRAFT_00123	Product_name		replicative DNA helicase Mcm (EC 3.6.1.-)		
2558669455	DRAFT_00123	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669455	DRAFT_00123	Coordinates		97137..99188(+)		
2558669455	DRAFT_00123	DNA_length		2052bp		
2558669455	DRAFT_00123	Protein_length		683aa		
2558669455	DRAFT_00123	GC			0.58	
2558669456	DRAFT_00124	COG_category	[R] General function prediction only			

2558669456	DRAFT_00124	COG1204	Superfamily II helicase			0.00E+00
2558669456	DRAFT_00124	pfam00270	DEAD			1.30E-24
2558669456	DRAFT_00124	pfam00271	Helicase_C			4.00E-07
2558669456	DRAFT_00124	pfam14520	HHH_5			5.40E-12
2558669456	DRAFT_00124	EC:3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; involved in cellular and subc			
2558669456	DRAFT_00124	KO:K03726	helicase [EC:3.6.4.-]			0.00E+00
2558669456	DRAFT_00124	Locus_type		CDS		
2558669456	DRAFT_00124	Product_name		Superfamily II helicase		
2558669456	DRAFT_00124	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669456	DRAFT_00124	Coordinates		99206..101350(+)		
2558669456	DRAFT_00124	DNA_length		2145bp		
2558669456	DRAFT_00124	Protein_length		714aa		
2558669456	DRAFT_00124	GC			0.61	
2558669457	DRAFT_00125	pfam00733	Asn_synthase			9.80E-32
2558669457	DRAFT_00125	Locus_type		CDS		
2558669457	DRAFT_00125	Product_name		Asparagine synthase (glutamine-hydrolyzing)		
2558669457	DRAFT_00125	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669457	DRAFT_00125	Coordinates		101422..102105(+)		
2558669457	DRAFT_00125	DNA_length		684bp		
2558669457	DRAFT_00125	Protein_length		227aa		
2558669457	DRAFT_00125	GC			0.62	
2558669458	DRAFT_00126	Locus_type		CDS		
2558669458	DRAFT_00126	Product_name		hypothetical protein		
2558669458	DRAFT_00126	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669458	DRAFT_00126	Coordinates		102142..102405(+)		
2558669458	DRAFT_00126	DNA_length		264bp		
2558669458	DRAFT_00126	Protein_length		87aa		
2558669458	DRAFT_00126	GC			0.58	
2558669459	DRAFT_00127	pfam13659	Methyltransf_26			2.40E-06
2558669459	DRAFT_00127	Locus_type		CDS		
2558669459	DRAFT_00127	Product_name		Methyltransferase domain		

2558669459	DRAFT_00127	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669459	DRAFT_00127	Coordinates		102402..103028(+)		
2558669459	DRAFT_00127	DNA_length		627bp		
2558669459	DRAFT_00127	Protein_length		208aa		
2558669459	DRAFT_00127	GC			0.58	
2558669460	DRAFT_00128	pfam04967	HTH_10			2.00E-17
2558669460	DRAFT_00128	Locus_type		CDS		
2558669460	DRAFT_00128	Product_name		Predicted DNA binding protein		
2558669460	DRAFT_00128	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669460	DRAFT_00128	Coordinates		103042..103686(+)		
2558669460	DRAFT_00128	DNA_length		645bp		
2558669460	DRAFT_00128	Protein_length		214aa		
2558669460	DRAFT_00128	GC			0.58	
2558669461	DRAFT_00129	Metacyc	TRYPDEG-PWY: tryptophan degradation II (via pyruvate)			
2558669461	DRAFT_00129	COG_category	[E] Amino acid transport and metabolism			
2558669461	DRAFT_00129	COG3033	Tryptophanase			7.00E-129
2558669461	DRAFT_00129	pfam01212	Beta_elim_lyase			3.10E-64
2558669461	DRAFT_00129	EC:4.1.99.1	Tryptophanase.			
2558669461	DRAFT_00129	KO:K01667	tryptophanase [EC:4.1.99.1]			0.00E+00
2558669461	DRAFT_00129	Locus_type		CDS		
2558669461	DRAFT_00129	Product_name		Tryptophanase		
2558669461	DRAFT_00129	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1		
2558669461	DRAFT_00129	Coordinates		103951..105393(+)		
2558669461	DRAFT_00129	DNA_length		1443bp		
2558669461	DRAFT_00129	Protein_length		480aa		
2558669461	DRAFT_00129	GC			0.54	
2558669462	DRAFT_00130	COG_category	[G] Carbohydrate transport and metabolism			
2558669462	DRAFT_00130	COG2814	Arabinose efflux permease			9.00E-11
2558669462	DRAFT_00130	pfam07690	MFS_1			4.00E-23
2558669462	DRAFT_00130	Locus_type		CDS		
2558669462	DRAFT_00130	Product_name		Arabinose efflux permease		

2558669462	DRAFT_00130	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669462	DRAFT_00130	Coordinates		105839..107053(+)	
2558669462	DRAFT_00130	DNA_length		1215bp	
2558669462	DRAFT_00130	Protein_length		404aa	
2558669462	DRAFT_00130	GC		0.58	
2558669462	DRAFT_00130	Transmembrane		Yes	
2558669463	DRAFT_00131	pfam08241	Methyltransf_11		2.40E-20
2558669463	DRAFT_00131	Locus_type		CDS	
2558669463	DRAFT_00131	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	
2558669463	DRAFT_00131	Scaffold		DRAFT_contig_70_5_len_108223_read_count_1902626.1	
2558669463	DRAFT_00131	Coordinates		107311..108111(-)	
2558669463	DRAFT_00131	DNA_length		801bp	
2558669463	DRAFT_00131	Protein_length		266aa	
2558669463	DRAFT_00131	GC		0.58	
2558669464	DRAFT_00132	KEGG_module	M00239: Peptides/nickel transport system		
2558669464	DRAFT_00132	COG_category	[E] Amino acid transport and metabolism		
2558669464	DRAFT_00132	COG_category	[P] Inorganic ion transport and metabolism		
2558669464	DRAFT_00132	COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase com		9.00E-120
2558669464	DRAFT_00132	pfam08352	oligo_HPY		4.70E-21
2558669464	DRAFT_00132	pfam00005	ABC_tran		7.80E-26
2558669464	DRAFT_00132	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termin		1.50E-34
2558669464	DRAFT_00132	KO:K02031	peptide/nickel transport system ATP-binding protein		0.00E+00
2558669464	DRAFT_00132	Locus_type		CDS	
2558669464	DRAFT_00132	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termi	
2558669464	DRAFT_00132	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669464	DRAFT_00132	Coordinates		2..955(-)	
2558669464	DRAFT_00132	DNA_length		954bp	
2558669464	DRAFT_00132	Protein_length		318aa	
2558669464	DRAFT_00132	GC		0.6	
2558669465	DRAFT_00133	KEGG_module	M00239: Peptides/nickel transport system		
2558669465	DRAFT_00133	COG_category	[P] Inorganic ion transport and metabolism		

2558669465	DRAFT_00133	COG_category	[E] Amino acid transport and metabolism		
2558669465	DRAFT_00133	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c		9.00E-62
2558669465	DRAFT_00133	pfam12911	OppC_N		3.30E-06
2558669465	DRAFT_00133	pfam00528	BPD_transp_1		8.80E-25
2558669465	DRAFT_00133	KO:K02034	peptide/nickel transport system permease protein		0.00E+00
2558669465	DRAFT_00133	Locus_type		CDS	
2558669465	DRAFT_00133	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease	
2558669465	DRAFT_00133	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669465	DRAFT_00133	Coordinates		970..2526(-)	
2558669465	DRAFT_00133	DNA_length		1557bp	
2558669465	DRAFT_00133	Protein_length		518aa	
2558669465	DRAFT_00133	GC		0.58	
2558669465	DRAFT_00133	Transmembrane		Yes	

2558669466	DRAFT_00134	KEGG_module	M00239: Peptides/nickel transport system		
2558669466	DRAFT_00134	COG_category	[P] Inorganic ion transport and metabolism		
2558669466	DRAFT_00134	COG_category	[E] Amino acid transport and metabolism		
2558669466	DRAFT_00134	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c		2.00E-60
2558669466	DRAFT_00134	pfam00528	BPD_transp_1		8.30E-38
2558669466	DRAFT_00134	KO:K02033	peptide/nickel transport system permease protein		0.00E+00
2558669466	DRAFT_00134	Locus_type		CDS	
2558669466	DRAFT_00134	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease	
2558669466	DRAFT_00134	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669466	DRAFT_00134	Coordinates		2523..3482(-)	
2558669466	DRAFT_00134	DNA_length		960bp	
2558669466	DRAFT_00134	Protein_length		319aa	
2558669466	DRAFT_00134	GC		0.55	
2558669466	DRAFT_00134	Transmembrane		Yes	

2558669467	DRAFT_00135	pfam00496	SBP_bac_5		2.30E-08
2558669467	DRAFT_00135	pfam00496	SBP_bac_5		2.00E-11
2558669467	DRAFT_00135	Locus_type		CDS	
2558669467	DRAFT_00135	Product_name		Bacterial extracellular solute-binding proteins, family 5 Middle	
2558669467	DRAFT_00135	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	

2558669467	DRAFT_00135	Coordinates		3583..5970(-)	
2558669467	DRAFT_00135	DNA_length		2388bp	
2558669467	DRAFT_00135	Protein_length		795aa	
2558669467	DRAFT_00135	GC		0.56	
2558669467	DRAFT_00135	Signal_peptide		Yes	
2558669467	DRAFT_00135	Transmembrane		Yes	
2558669468	DRAFT_00136	pfam02475	Met_10		3.40E-53
2558669468	DRAFT_00136	EC:2.1.1.228	tRNA (guanine(37)-N(1))-methyltransferase.		
2558669468	DRAFT_00136	KO:K15429	tRNA (guanine37-N1)-methyltransferase [EC:2.1.1.228]		1.20E-40
2558669468	DRAFT_00136	Locus_type		CDS	
2558669468	DRAFT_00136	Product_name		Predicted methyltransferase	
2558669468	DRAFT_00136	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669468	DRAFT_00136	Coordinates		6523..7182(+)	
2558669468	DRAFT_00136	DNA_length		660bp	
2558669468	DRAFT_00136	Protein_length		219aa	
2558669468	DRAFT_00136	GC		0.6	
2558669469	DRAFT_00137	COG_category	[C] Energy production and conversion		
2558669469	DRAFT_00137	COG0277	FAD/FMN-containing dehydrogenases		2.00E-50
2558669469	DRAFT_00137	pfam02913	FAD-oxidase_C		3.10E-41
2558669469	DRAFT_00137	pfam01565	FAD_binding_4		5.20E-23
2558669469	DRAFT_00137	Locus_type		CDS	
2558669469	DRAFT_00137	Product_name		FAD/FMN-containing dehydrogenases	
2558669469	DRAFT_00137	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669469	DRAFT_00137	Coordinates		7207..8787(+)	
2558669469	DRAFT_00137	DNA_length		1581bp	
2558669469	DRAFT_00137	Protein_length		526aa	
2558669469	DRAFT_00137	GC		0.61	
2558669470	DRAFT_00138	COG_category	[S] Function unknown		
2558669470	DRAFT_00138	COG1628	Uncharacterized conserved protein		2.00E-31
2558669470	DRAFT_00138	pfam01949	DUF99		2.10E-52
2558669470	DRAFT_00138	KO:K09120	hypothetical protein		2.80E-45

2558669470	DRAFT_00138	Locus_type		CDS	
2558669470	DRAFT_00138	Product_name		Uncharacterized conserved protein	
2558669470	DRAFT_00138	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669470	DRAFT_00138	Coordinates		8780..9346(-)	
2558669470	DRAFT_00138	DNA_length		567bp	
2558669470	DRAFT_00138	Protein_length		188aa	
2558669470	DRAFT_00138	GC		0.6	

2558669471	DRAFT_00139	COG_category	[R] General function prediction only		
2558669471	DRAFT_00139	COG1661	Predicted DNA-binding protein with PD1-like DNA-binding motif		5.00E-23
2558669471	DRAFT_00139	pfam03479	DUF296		1.60E-24
2558669471	DRAFT_00139	Locus_type		CDS	
2558669471	DRAFT_00139	Product_name		Predicted DNA-binding protein with PD1-like DNA-binding motif	
2558669471	DRAFT_00139	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669471	DRAFT_00139	Coordinates		9393..9815(+)	
2558669471	DRAFT_00139	DNA_length		423bp	
2558669471	DRAFT_00139	Protein_length		140aa	
2558669471	DRAFT_00139	GC		0.56	

2558669472	DRAFT_00140	KEGG_module	M00527: Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine		
2558669472	DRAFT_00140	KEGG_module	M00525: Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine		
2558669472	DRAFT_00140	KEGG_module	M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine		
2558669472	DRAFT_00140	KEGG_module	M00526: Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine		
2558669472	DRAFT_00140	COG_category	[S] Function unknown		
2558669472	DRAFT_00140	COG3804	Uncharacterized conserved protein related to dihydrodipicolinate redu		9.00E-27
2558669472	DRAFT_00140	EC:1.3.1.26	Dihydrodipicolinate reductase.		
2558669472	DRAFT_00140	KO:K00215	dihydrodipicolinate reductase [EC:1.3.1.26]		0.00E+00
2558669472	DRAFT_00140	Locus_type		CDS	
2558669472	DRAFT_00140	Product_name		Uncharacterized conserved protein related to dihydrodipicolinate red	
2558669472	DRAFT_00140	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669472	DRAFT_00140	Coordinates		10150..11085(-)	
2558669472	DRAFT_00140	DNA_length		936bp	
2558669472	DRAFT_00140	Protein_length		311aa	
2558669472	DRAFT_00140	GC		0.61	

2558669473	DRAFT_00141	Locus_type		CDS		
2558669473	DRAFT_00141	Product_name		hypothetical protein		
2558669473	DRAFT_00141	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669473	DRAFT_00141	Coordinates		11145..11333(+)		
2558669473	DRAFT_00141	DNA_length		189bp		
2558669473	DRAFT_00141	Protein_length		62aa		
2558669473	DRAFT_00141	GC			0.5	
2558669474	DRAFT_00142	Locus_type		CDS		
2558669474	DRAFT_00142	Product_name		hypothetical protein		
2558669474	DRAFT_00142	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669474	DRAFT_00142	Coordinates		11273..11545(-)		
2558669474	DRAFT_00142	DNA_length		273bp		
2558669474	DRAFT_00142	Protein_length		90aa		
2558669474	DRAFT_00142	GC			0.55	
2558669475	DRAFT_00143	pfam04471	Mrr_cat			4.40E-06
2558669475	DRAFT_00143	Locus_type		CDS		
2558669475	DRAFT_00143	Product_name		Restriction endonuclease		
2558669475	DRAFT_00143	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669475	DRAFT_00143	Coordinates		11674..12237(-)		
2558669475	DRAFT_00143	DNA_length		564bp		
2558669475	DRAFT_00143	Protein_length		187aa		
2558669475	DRAFT_00143	GC			0.62	
2558669476	DRAFT_00144	Locus_type		CDS		
2558669476	DRAFT_00144	Product_name		hypothetical protein		
2558669476	DRAFT_00144	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669476	DRAFT_00144	Coordinates		12444..12566(+)		
2558669476	DRAFT_00144	DNA_length		123bp		
2558669476	DRAFT_00144	Protein_length		40aa		
2558669476	DRAFT_00144	GC			0.55	

2558669477	DRAFT_00145	pfam00717	Peptidase_S24		1.70E-07
2558669477	DRAFT_00145	TIGR02228	signal peptidase I, archaeal type		1.00E-22
2558669477	DRAFT_00145	Locus_type		CDS	
2558669477	DRAFT_00145	Product_name		signal peptidase I, archaeal type	
2558669477	DRAFT_00145	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669477	DRAFT_00145	Coordinates		12630..13316(+)	
2558669477	DRAFT_00145	DNA_length		687bp	
2558669477	DRAFT_00145	Protein_length		228aa	
2558669477	DRAFT_00145	GC		0.57	
2558669477	DRAFT_00145	Transmembrane		Yes	

2558669478	DRAFT_00146	Locus_type		CDS	
2558669478	DRAFT_00146	Product_name		hypothetical protein	
2558669478	DRAFT_00146	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669478	DRAFT_00146	Coordinates		13696..14010(+)	
2558669478	DRAFT_00146	DNA_length		315bp	
2558669478	DRAFT_00146	Protein_length		104aa	
2558669478	DRAFT_00146	GC		0.56	
2558669478	DRAFT_00146	Transmembrane		Yes	

2558669479	DRAFT_00147	pfam12840	HTH_20		1.10E-07
2558669479	DRAFT_00147	Locus_type		CDS	
2558669479	DRAFT_00147	Product_name		Helix-turn-helix domain	
2558669479	DRAFT_00147	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669479	DRAFT_00147	Coordinates		14007..14372(-)	
2558669479	DRAFT_00147	DNA_length		366bp	
2558669479	DRAFT_00147	Protein_length		121aa	
2558669479	DRAFT_00147	GC		0.53	

2558669480	DRAFT_00148	Locus_type		CDS	
2558669480	DRAFT_00148	Product_name		hypothetical protein	
2558669480	DRAFT_00148	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669480	DRAFT_00148	Coordinates		14413..14541(-)	
2558669480	DRAFT_00148	DNA_length		129bp	

2558669480	DRAFT_00148	Protein_length		42aa		
2558669480	DRAFT_00148	GC			0.54	

2558669481	DRAFT_00149	pfam00339	Arrestin_N			4.10E-05
2558669481	DRAFT_00149	Locus_type		CDS		
2558669481	DRAFT_00149	Product_name		Arrestin (or S-antigen), N-terminal domain		
2558669481	DRAFT_00149	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669481	DRAFT_00149	Coordinates		14578..15156(+)		
2558669481	DRAFT_00149	DNA_length		579bp		
2558669481	DRAFT_00149	Protein_length		192aa		
2558669481	DRAFT_00149	GC			0.54	

2558669482	DRAFT_00150	Locus_type		CDS		
2558669482	DRAFT_00150	Product_name		hypothetical protein		
2558669482	DRAFT_00150	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669482	DRAFT_00150	Coordinates		15533..15745(+)		
2558669482	DRAFT_00150	DNA_length		213bp		
2558669482	DRAFT_00150	Protein_length		70aa		
2558669482	DRAFT_00150	GC			0.46	
2558669482	DRAFT_00150	Transmembrane		Yes		

2558669483	DRAFT_00151	Locus_type		CDS		
2558669483	DRAFT_00151	Product_name		hypothetical protein		
2558669483	DRAFT_00151	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669483	DRAFT_00151	Coordinates		15903..16091(-)		
2558669483	DRAFT_00151	DNA_length		189bp		
2558669483	DRAFT_00151	Protein_length		62aa		
2558669483	DRAFT_00151	GC			0.53	

2558669484	DRAFT_00152	COG_category	[K] Transcription			
2558669484	DRAFT_00152	COG2101	TATA-box binding protein (TBP), component of TFIID and TFIIIB			5.00E-55
2558669484	DRAFT_00152	pfam00352	TBP			3.40E-29
2558669484	DRAFT_00152	pfam00352	TBP			3.60E-31
2558669484	DRAFT_00152	KO:K03120	transcription initiation factor TFIID TATA-box-binding protein			0.00E+00

2558669484	DRAFT_00152	ITERM:01960	TATA binding protein of transcription factor TFIID		
2558669484	DRAFT_00152	Locus_type		CDS	
2558669484	DRAFT_00152	Product_name		TATA binding protein of transcription factor TFIID	
2558669484	DRAFT_00152	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669484	DRAFT_00152	Coordinates		16184..16741(+)	
2558669484	DRAFT_00152	DNA_length		558bp	
2558669484	DRAFT_00152	Protein_length		185aa	
2558669484	DRAFT_00152	GC		0.53	

2558669485	DRAFT_00153	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP		
2558669485	DRAFT_00153	Metacyc	PWY-5686: UMP biosynthesis		
2558669485	DRAFT_00153	IMG_pathway	321: Uridine 5'-monophosphate biosynthesis		
2558669485	DRAFT_00153	COG_category	[F] Nucleotide transport and metabolism		
2558669485	DRAFT_00153	COG0461	Orotate phosphoribosyltransferase		3.00E-33
2558669485	DRAFT_00153	pfam00156	Pribosyltran		5.50E-09
2558669485	DRAFT_00153	EC:2.4.2.10	Orotate phosphoribosyltransferase.		
2558669485	DRAFT_00153	TIGR00336	orotate phosphoribosyltransferase		2.00E-32
2558669485	DRAFT_00153	KO:K00762	orotate phosphoribosyltransferase [EC:2.4.2.10]		9.90E-34
2558669485	DRAFT_00153	ITERM:01392	orotate phosphoribosyltransferase (EC 2.4.2.10)		
2558669485	DRAFT_00153	Locus_type		CDS	
2558669485	DRAFT_00153	Product_name		orotate phosphoribosyltransferase (EC 2.4.2.10)	
2558669485	DRAFT_00153	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669485	DRAFT_00153	Coordinates		16735..17352(-)	
2558669485	DRAFT_00153	DNA_length		618bp	
2558669485	DRAFT_00153	Protein_length		205aa	
2558669485	DRAFT_00153	GC		0.6	

2558669486	DRAFT_00154	Locus_type		CDS	
2558669486	DRAFT_00154	Product_name		hypothetical protein	
2558669486	DRAFT_00154	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669486	DRAFT_00154	Coordinates		17407..18507(+)	
2558669486	DRAFT_00154	DNA_length		1101bp	
2558669486	DRAFT_00154	Protein_length		366aa	
2558669486	DRAFT_00154	GC		0.61	

2558669487	DRAFT_00155	pfam02163	Peptidase_M50			1.80E-07
2558669487	DRAFT_00155	Locus_type		CDS		
2558669487	DRAFT_00155	Product_name		Peptidase family M50		
2558669487	DRAFT_00155	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669487	DRAFT_00155	Coordinates		18499..19647(-)		
2558669487	DRAFT_00155	DNA_length		1149bp		
2558669487	DRAFT_00155	Protein_length		382aa		
2558669487	DRAFT_00155	GC			0.61	
2558669487	DRAFT_00155	Transmembrane		Yes		

2558669488	DRAFT_00156	Locus_type		CDS		
2558669488	DRAFT_00156	Product_name		hypothetical protein		
2558669488	DRAFT_00156	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669488	DRAFT_00156	Coordinates		19964..20167(+)		
2558669488	DRAFT_00156	DNA_length		204bp		
2558669488	DRAFT_00156	Protein_length		67aa		
2558669488	DRAFT_00156	GC			0.49	
2558669488	DRAFT_00156	Transmembrane		Yes		

2558669489	DRAFT_00157	Locus_type		CDS		
2558669489	DRAFT_00157	Product_name		hypothetical protein		
2558669489	DRAFT_00157	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669489	DRAFT_00157	Coordinates		20087..20953(-)		
2558669489	DRAFT_00157	DNA_length		867bp		
2558669489	DRAFT_00157	Protein_length		288aa		
2558669489	DRAFT_00157	GC			0.51	
2558669489	DRAFT_00157	Transmembrane		Yes		

2558669490	DRAFT_00158	Locus_type		CDS		
2558669490	DRAFT_00158	Product_name		hypothetical protein		
2558669490	DRAFT_00158	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669490	DRAFT_00158	Coordinates		20972..21142(-)		
2558669490	DRAFT_00158	DNA_length		171bp		

2558669490	DRAFT_00158	Protein_length		56aa		
2558669490	DRAFT_00158	GC			0.52	
2558669491	DRAFT_00159	COG_category	[L] Replication, recombination and repair			
2558669491	DRAFT_00159	COG3316	Transposase and inactivated derivatives			1.00E-11
2558669491	DRAFT_00159	pfam13610	DDE_Tnp_IS240			9.80E-20
2558669491	DRAFT_00159	pfam04434	SWIM			3.50E-06
2558669491	DRAFT_00159	Locus_type		CDS		
2558669491	DRAFT_00159	Product_name		Transposase and inactivated derivatives		
2558669491	DRAFT_00159	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669491	DRAFT_00159	Coordinates		21211..22365(+)		
2558669491	DRAFT_00159	DNA_length		1155bp		
2558669491	DRAFT_00159	Protein_length		384aa		
2558669491	DRAFT_00159	GC			0.57	
2558669492	DRAFT_00160	COG_category	[R] General function prediction only			
2558669492	DRAFT_00160	COG0456	Acetyltransferases			2.00E-16
2558669492	DRAFT_00160	pfam00583	Acetyltransf_1			4.70E-16
2558669492	DRAFT_00160	EC:2.3.1.128	Ribosomal-protein-alanine N-acetyltransferase.			
2558669492	DRAFT_00160	TIGR01575	ribosomal-protein-alanine acetyltransferase			9.90E-28
2558669492	DRAFT_00160	KO:K03789	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]			0.00E+00
2558669492	DRAFT_00160	Locus_type		CDS		
2558669492	DRAFT_00160	Product_name		Acetyltransferases		
2558669492	DRAFT_00160	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669492	DRAFT_00160	Coordinates		22436..22939(+)		
2558669492	DRAFT_00160	DNA_length		504bp		
2558669492	DRAFT_00160	Protein_length		167aa		
2558669492	DRAFT_00160	GC			0.55	
2558669493	DRAFT_00161	COG_category	[L] Replication, recombination and repair			
2558669493	DRAFT_00161	COG1793	ATP-dependent DNA ligase			3.00E-72
2558669493	DRAFT_00161	pfam01068	DNA_ligase_A_M			6.00E-47
2558669493	DRAFT_00161	pfam04675	DNA_ligase_A_N			3.50E-32
2558669493	DRAFT_00161	pfam04679	DNA_ligase_A_C			2.50E-13

2558669493	DRAFT_00161	EC:6.5.1.1	DNA ligase (ATP).		
2558669493	DRAFT_00161	TIGR00574	DNA ligase I, ATP-dependent (dnl1)		4.40E-106
2558669493	DRAFT_00161	KO:K01971	DNA ligase (ATP) [EC:6.5.1.1]		0.00E+00
2558669493	DRAFT_00161	Locus_type		CDS	
2558669493	DRAFT_00161	Product_name		DNA ligase I, ATP-dependent (dnl1)	
2558669493	DRAFT_00161	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669493	DRAFT_00161	Coordinates		22936..24597(+)	
2558669493	DRAFT_00161	DNA_length		1662bp	
2558669493	DRAFT_00161	Protein_length		553aa	
2558669493	DRAFT_00161	GC		0.59	
2558669494	DRAFT_00162	Locus_type		CDS	
2558669494	DRAFT_00162	Product_name		hypothetical protein	
2558669494	DRAFT_00162	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669494	DRAFT_00162	Coordinates		24649..25254(+)	
2558669494	DRAFT_00162	DNA_length		606bp	
2558669494	DRAFT_00162	Protein_length		201aa	
2558669494	DRAFT_00162	GC		0.58	
2558669494	DRAFT_00162	Transmembrane		Yes	
2558669495	DRAFT_00163	COG_category	[F] Nucleotide transport and metabolism		
2558669495	DRAFT_00163	COG0125	Thymidylate kinase		2.00E-07
2558669495	DRAFT_00163	pfam02223	Thymidylate_kin		7.00E-06
2558669495	DRAFT_00163	Locus_type		CDS	
2558669495	DRAFT_00163	Product_name		Thymidylate kinase	
2558669495	DRAFT_00163	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669495	DRAFT_00163	Coordinates		25298..25885(+)	
2558669495	DRAFT_00163	DNA_length		588bp	
2558669495	DRAFT_00163	Protein_length		195aa	
2558669495	DRAFT_00163	GC		0.53	
2558669496	DRAFT_00164	KEGG_module	M00131: Inositol phosphate metabolism, Ins(1,3,4,5)P4 => Ins(1,3,4)P3 => myo-inositol		
2558669496	DRAFT_00164	Metacyc	PWY-4702: phytate degradation I		
2558669496	DRAFT_00164	Metacyc	PWY-6363: D-<i>myo</i>-inositol (1,4,5)-trisphosphate degradation		

2558669496	DRAFT_00164	Metacyc	PWY-2301: <i>myo</i>-inositol biosynthesis			
2558669496	DRAFT_00164	IMG_pathway	527: Calvin cycle			
2558669496	DRAFT_00164	COG_category	[G] Carbohydrate transport and metabolism			
2558669496	DRAFT_00164	COG0483	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol r			2.00E-40
2558669496	DRAFT_00164	pfam00459	Inositol_P			4.20E-35
2558669496	DRAFT_00164	EC:3.1.3.25	Inositol-phosphate phosphatase.			
2558669496	DRAFT_00164	KO:K01092	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]			2.00E-37
2558669496	DRAFT_00164	ITERM:03309	D-fructose 1,6-bisphosphatase (EC 3.1.3.11)			
2558669496	DRAFT_00164	Locus_type		CDS		
2558669496	DRAFT_00164	Product_name		D-fructose 1,6-bisphosphatase (EC 3.1.3.11)		
2558669496	DRAFT_00164	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669496	DRAFT_00164	Coordinates		25885..26697(+)		
2558669496	DRAFT_00164	DNA_length		813bp		
2558669496	DRAFT_00164	Protein_length		270aa		
2558669496	DRAFT_00164	GC			0.58	
2558669497	DRAFT_00165	COG_category	[R] General function prediction only			
2558669497	DRAFT_00165	COG0546	Predicted phosphatases			9.00E-16
2558669497	DRAFT_00165	pfam13419	HAD_2			1.50E-11
2558669497	DRAFT_00165	Locus_type		CDS		
2558669497	DRAFT_00165	Product_name		Predicted phosphatases		
2558669497	DRAFT_00165	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669497	DRAFT_00165	Coordinates		26675..27304(-)		
2558669497	DRAFT_00165	DNA_length		630bp		
2558669497	DRAFT_00165	Protein_length		209aa		
2558669497	DRAFT_00165	GC			0.57	
2558669498	DRAFT_00166	pfam13535	ATP-grasp_4			1.10E-23
2558669498	DRAFT_00166	Locus_type		CDS		
2558669498	DRAFT_00166	Product_name		Biotin carboxylase		
2558669498	DRAFT_00166	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669498	DRAFT_00166	Coordinates		27283..28377(-)		
2558669498	DRAFT_00166	DNA_length		1095bp		
2558669498	DRAFT_00166	Protein_length		364aa		

2558669498	DRAFT_00166	GC		0.58	
2558669499	DRAFT_00167	Locus_type		CDS	
2558669499	DRAFT_00167	Product_name		hypothetical protein	
2558669499	DRAFT_00167	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669499	DRAFT_00167	Coordinates		28374..29600(-)	
2558669499	DRAFT_00167	DNA_length		1227bp	
2558669499	DRAFT_00167	Protein_length		408aa	
2558669499	DRAFT_00167	GC		0.54	
2558669500	DRAFT_00168	COG_category	[F] Nucleotide transport and metabolism		
2558669500	DRAFT_00168	COG0125	Thymidylate kinase		2.00E-14
2558669500	DRAFT_00168	pfam02223	Thymidylate_kin		2.00E-05
2558669500	DRAFT_00168	Locus_type		CDS	
2558669500	DRAFT_00168	Product_name		Thymidylate kinase	
2558669500	DRAFT_00168	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669500	DRAFT_00168	Coordinates		29597..30544(-)	
2558669500	DRAFT_00168	DNA_length		948bp	
2558669500	DRAFT_00168	Protein_length		315aa	
2558669500	DRAFT_00168	GC		0.52	
2558669500	DRAFT_00168	Transmembrane		Yes	
2558669501	DRAFT_00169	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558669501	DRAFT_00169	COG0463	Glycosyltransferases involved in cell wall biogenesis		5.00E-12
2558669501	DRAFT_00169	pfam00535	Glycos_transf_2		2.80E-13
2558669501	DRAFT_00169	Locus_type		CDS	
2558669501	DRAFT_00169	Product_name		Glycosyltransferases involved in cell wall biogenesis	
2558669501	DRAFT_00169	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669501	DRAFT_00169	Coordinates		30606..31403(-)	
2558669501	DRAFT_00169	DNA_length		798bp	
2558669501	DRAFT_00169	Protein_length		265aa	
2558669501	DRAFT_00169	GC		0.55	
2558669502	DRAFT_00170	pfam00535	Glycos_transf_2		2.90E-11

2558669502	DRAFT_00170	Locus_type		CDS	
2558669502	DRAFT_00170	Product_name		Glycosyltransferases, probably involved in cell wall biogenesis	
2558669502	DRAFT_00170	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669502	DRAFT_00170	Coordinates		31550..32323(-)	
2558669502	DRAFT_00170	DNA_length		774bp	
2558669502	DRAFT_00170	Protein_length		257aa	
2558669502	DRAFT_00170	GC		0.55	
2558669503	DRAFT_00171	Locus_type		CDS	
2558669503	DRAFT_00171	Product_name		hypothetical protein	
2558669503	DRAFT_00171	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669503	DRAFT_00171	Coordinates		32576..33670(+)	
2558669503	DRAFT_00171	DNA_length		1095bp	
2558669503	DRAFT_00171	Protein_length		364aa	
2558669503	DRAFT_00171	GC		0.52	
2558669503	DRAFT_00171	Transmembrane		Yes	
2558669504	DRAFT_00172	pfam13440	Polysacc_synt_3		2.00E-09
2558669504	DRAFT_00172	Locus_type		CDS	
2558669504	DRAFT_00172	Product_name		Polysaccharide biosynthesis protein	
2558669504	DRAFT_00172	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669504	DRAFT_00172	Coordinates		33945..35534(+)	
2558669504	DRAFT_00172	DNA_length		1590bp	
2558669504	DRAFT_00172	Protein_length		529aa	
2558669504	DRAFT_00172	GC		0.58	
2558669504	DRAFT_00172	Transmembrane		Yes	
2558669505	DRAFT_00173	COG_category	[K] Transcription		
2558669505	DRAFT_00173	COG5625	Predicted transcription regulator containing HTH domain		4.00E-05
2558669505	DRAFT_00173	Locus_type		CDS	
2558669505	DRAFT_00173	Product_name		hypothetical protein	
2558669505	DRAFT_00173	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669505	DRAFT_00173	Coordinates		35674..35943(-)	
2558669505	DRAFT_00173	DNA_length		270bp	

2558669505	DRAFT_00173	Protein_length		89aa		
2558669505	DRAFT_00173	GC			0.59	
2558669505	DRAFT_00173	Transmembrane		Yes		
2558669506	DRAFT_00174	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669506	DRAFT_00174	COG5256	Translation elongation factor EF-1alpha (GTPase)			0.00E+00
2558669506	DRAFT_00174	pfam00009	GTP_EFTU			6.20E-49
2558669506	DRAFT_00174	pfam03143	GTP_EFTU_D3			8.60E-29
2558669506	DRAFT_00174	pfam03144	GTP_EFTU_D2			1.30E-16
2558669506	DRAFT_00174	TIGR00483	translation elongation factor EF-1 alpha			0.00E+00
2558669506	DRAFT_00174	TIGR00485	translation elongation factor TU			1.10E-66
2558669506	DRAFT_00174	KO:K03231	elongation factor 1-alpha			0.00E+00
2558669506	DRAFT_00174	Locus_type		CDS		
2558669506	DRAFT_00174	Product_name		translation elongation factor 1A (EF-1A/EF-Tu)		
2558669506	DRAFT_00174	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669506	DRAFT_00174	Coordinates		36451..37776(-)		
2558669506	DRAFT_00174	DNA_length		1326bp		
2558669506	DRAFT_00174	Protein_length		441aa		
2558669506	DRAFT_00174	GC			0.56	
2558669507	DRAFT_00175	Locus_type		CDS		
2558669507	DRAFT_00175	Product_name		hypothetical protein		
2558669507	DRAFT_00175	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669507	DRAFT_00175	Coordinates		38042..38248(-)		
2558669507	DRAFT_00175	DNA_length		207bp		
2558669507	DRAFT_00175	Protein_length		68aa		
2558669507	DRAFT_00175	GC			0.55	
2558669507	DRAFT_00175	Transmembrane		Yes		
2558669508	DRAFT_00176	Locus_type		CDS		
2558669508	DRAFT_00176	Product_name		hypothetical protein		
2558669508	DRAFT_00176	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669508	DRAFT_00176	Coordinates		38329..38502(-)		
2558669508	DRAFT_00176	DNA_length		174bp		

2558669508	DRAFT_00176	Protein_length		57aa		
2558669508	DRAFT_00176	GC			0.55	
2558669508	DRAFT_00176	Transmembrane		Yes		
2558669509	DRAFT_00177	Locus_type		CDS		
2558669509	DRAFT_00177	Product_name		hypothetical protein		
2558669509	DRAFT_00177	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669509	DRAFT_00177	Coordinates		38687..38806(+)		
2558669509	DRAFT_00177	DNA_length		120bp		
2558669509	DRAFT_00177	Protein_length		39aa		
2558669509	DRAFT_00177	GC			0.49	
2558669509	DRAFT_00177	Transmembrane		Yes		
2558669510	DRAFT_00178	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP			
2558669510	DRAFT_00178	Metacyc	PWY-5695: urate biosynthesis/inosine 5'-phosphate degradation			
2558669510	DRAFT_00178	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2558669510	DRAFT_00178	Metacyc	PWY-6596: adenosine nucleotides degradation I			
2558669510	DRAFT_00178	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2558669510	DRAFT_00178	pfam00478	IMPDH			2.70E-96
2558669510	DRAFT_00178	EC:1.1.1.205	IMP dehydrogenase.			
2558669510	DRAFT_00178	KO:K00088	IMP dehydrogenase [EC:1.1.1.205]			0.00E+00
2558669510	DRAFT_00178	Locus_type		CDS		
2558669510	DRAFT_00178	Product_name		IMP dehydrogenase/GMP reductase		
2558669510	DRAFT_00178	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669510	DRAFT_00178	Coordinates		38917..40020(+)		
2558669510	DRAFT_00178	DNA_length		1104bp		
2558669510	DRAFT_00178	Protein_length		367aa		
2558669510	DRAFT_00178	GC			0.6	
2558669511	DRAFT_00179	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP			
2558669511	DRAFT_00179	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2558669511	DRAFT_00179	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2558669511	DRAFT_00179	COG_category	[F] Nucleotide transport and metabolism			
2558669511	DRAFT_00179	COG0519	GMP synthase, PP-ATPase domain/subunit			3.00E-119

2558669511	DRAFT_00179	pfam00958	GMP_synt_C			7.60E-27
2558669511	DRAFT_00179	pfam00733	Asn_synthase			9.20E-06
2558669511	DRAFT_00179	pfam00117	GATase			1.00E-35
2558669511	DRAFT_00179	EC:6.3.5.2	GMP synthase (glutamine-hydrolyzing).			
2558669511	DRAFT_00179	TIGR00884	GMP synthase (glutamine-hydrolyzing), C-terminal domain or B subunit			2.00E-127
2558669511	DRAFT_00179	TIGR00888	GMP synthase (glutamine-hydrolyzing), N-terminal domain or A subuni			3.10E-72
2558669511	DRAFT_00179	KO:K01951	GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]			0.00E+00
2558669511	DRAFT_00179	Locus_type		CDS		
2558669511	DRAFT_00179	Product_name		GMP synthase (glutamine-hydrolyzing), C-terminal domain or B subur		
2558669511	DRAFT_00179	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669511	DRAFT_00179	Coordinates		40022..41569(+)		
2558669511	DRAFT_00179	DNA_length		1548bp		
2558669511	DRAFT_00179	Protein_length		515aa		
2558669511	DRAFT_00179	GC			0.61	
2558669511	DRAFT_00179	Fused_gene		Yes		
2558669512	DRAFT_00180	Metacyc	PWY-6611: adenine and adenosine salvage V			
2558669512	DRAFT_00180	Metacyc	PWY0-1296: purine ribonucleosides degradation			
2558669512	DRAFT_00180	Metacyc	PWY-7179: purine deoxyribonucleosides degradation			
2558669512	DRAFT_00180	Metacyc	PWY-6609: adenine and adenosine salvage III			
2558669512	DRAFT_00180	Metacyc	SALVADEHYPOX-PWY: adenosine nucleotides degradation II			
2558669512	DRAFT_00180	COG_category	[F] Nucleotide transport and metabolism			
2558669512	DRAFT_00180	COG1816	Adenosine deaminase			2.00E-43
2558669512	DRAFT_00180	pfam00962	A_deaminase			6.80E-41
2558669512	DRAFT_00180	EC:3.5.4.4	Adenosine deaminase.			
2558669512	DRAFT_00180	TIGR01430	adenosine deaminase			1.20E-60
2558669512	DRAFT_00180	KO:K01488	adenosine deaminase [EC:3.5.4.4]			0.00E+00
2558669512	DRAFT_00180	Locus_type		CDS		
2558669512	DRAFT_00180	Product_name		Adenosine deaminase		
2558669512	DRAFT_00180	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669512	DRAFT_00180	Coordinates		41575..42558(+)		
2558669512	DRAFT_00180	DNA_length		984bp		
2558669512	DRAFT_00180	Protein_length		327aa		
2558669512	DRAFT_00180	GC			0.57	

2558669513	DRAFT_00181	pfam12697	Abhydrolase_6			1.20E-13
2558669513	DRAFT_00181	Locus_type		CDS		
2558669513	DRAFT_00181	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super		
2558669513	DRAFT_00181	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669513	DRAFT_00181	Coordinates		42629..43228(+)		
2558669513	DRAFT_00181	DNA_length		600bp		
2558669513	DRAFT_00181	Protein_length		199aa		
2558669513	DRAFT_00181	GC			0.61	
2558669514	DRAFT_00182	Locus_type		CDS		
2558669514	DRAFT_00182	Product_name		hypothetical protein		
2558669514	DRAFT_00182	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669514	DRAFT_00182	Coordinates		43225..43344(+)		
2558669514	DRAFT_00182	DNA_length		120bp		
2558669514	DRAFT_00182	Protein_length		39aa		
2558669514	DRAFT_00182	GC			0.57	
2558669515	DRAFT_00183	KEGG_module	M00179: Ribosome, archaea			
2558669515	DRAFT_00183	KEGG_module	M00178: Ribosome, bacteria			
2558669515	DRAFT_00183	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669515	DRAFT_00183	COG0049	Ribosomal protein S7			3.00E-36
2558669515	DRAFT_00183	pfam00177	Ribosomal_S7			5.00E-38
2558669515	DRAFT_00183	TIGR01028	ribosomal protein S7(archaeal)/S5(eukaryotic)			6.40E-76
2558669515	DRAFT_00183	KO:K02992	small subunit ribosomal protein S7			0.00E+00
2558669515	DRAFT_00183	ITERM:01649	SSU ribosomal protein S7P			
2558669515	DRAFT_00183	Locus_type		CDS		
2558669515	DRAFT_00183	Product_name		SSU ribosomal protein S7P		
2558669515	DRAFT_00183	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669515	DRAFT_00183	Coordinates		43337..43948(-)		
2558669515	DRAFT_00183	DNA_length		612bp		
2558669515	DRAFT_00183	Protein_length		203aa		
2558669515	DRAFT_00183	GC			0.56	

2558669516	DRAFT_00184	KEGG_module	M00179: Ribosome, archaea			
2558669516	DRAFT_00184	KEGG_module	M00178: Ribosome, bacteria			
2558669516	DRAFT_00184	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669516	DRAFT_00184	COG0048	Ribosomal protein S12			4.00E-37
2558669516	DRAFT_00184	pfam00164	Ribosom_S12_S23			4.10E-40
2558669516	DRAFT_00184	TIGR00982	ribosomal protein S23 (S12)			3.00E-76
2558669516	DRAFT_00184	KO:K02950	small subunit ribosomal protein S12			0.00E+00
2558669516	DRAFT_00184	Locus_type		CDS		
2558669516	DRAFT_00184	Product_name		SSU ribosomal protein S12P		
2558669516	DRAFT_00184	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669516	DRAFT_00184	Coordinates		43953..44390(-)		
2558669516	DRAFT_00184	DNA_length		438bp		
2558669516	DRAFT_00184	Protein_length		145aa		
2558669516	DRAFT_00184	GC			0.59	

2558669517	DRAFT_00185	pfam07650	KH_2			1.90E-05
2558669517	DRAFT_00185	pfam07650	KH_2			8.00E-14
2558669517	DRAFT_00185	TIGR01952	NusA family KH domain protein, archaeal			6.00E-43
2558669517	DRAFT_00185	KO:K02600	N utilization substance protein A			5.70E-38
2558669517	DRAFT_00185	Locus_type		CDS		
2558669517	DRAFT_00185	Product_name		NusA family KH domain protein, archaeal		
2558669517	DRAFT_00185	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669517	DRAFT_00185	Coordinates		44429..44836(-)		
2558669517	DRAFT_00185	DNA_length		408bp		
2558669517	DRAFT_00185	Protein_length		135aa		
2558669517	DRAFT_00185	GC			0.6	

2558669518	DRAFT_00186	KEGG_module	M00177: Ribosome, eukaryotes			
2558669518	DRAFT_00186	KEGG_module	M00179: Ribosome, archaea			
2558669518	DRAFT_00186	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669518	DRAFT_00186	COG1911	Ribosomal protein L30E			3.00E-09
2558669518	DRAFT_00186	pfam01248	Ribosomal_L7Ae			7.20E-09
2558669518	DRAFT_00186	KO:K02908	large subunit ribosomal protein L30e			2.30E-12
2558669518	DRAFT_00186	Locus_type		CDS		

2558669518	DRAFT_00186	Product_name		Ribosomal protein L30E	
2558669518	DRAFT_00186	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669518	DRAFT_00186	Coordinates		44880..45182(-)	
2558669518	DRAFT_00186	DNA_length		303bp	
2558669518	DRAFT_00186	Protein_length		100aa	
2558669518	DRAFT_00186	GC		0.6	

2558669519	DRAFT_00187	KEGG_module	M00184: RNA polymerase, archaea		
2558669519	DRAFT_00187	COG_category	[K] Transcription		
2558669519	DRAFT_00187	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit		0.00E+00
2558669519	DRAFT_00187	pfam04983	RNA_pol_Rpb1_3		2.50E-34
2558669519	DRAFT_00187	pfam05000	RNA_pol_Rpb1_4		6.20E-24
2558669519	DRAFT_00187	pfam04998	RNA_pol_Rpb1_5		1.00E-86
2558669519	DRAFT_00187	pfam04997	RNA_pol_Rpb1_1		3.20E-84
2558669519	DRAFT_00187	pfam00623	RNA_pol_Rpb1_2		1.40E-66
2558669519	DRAFT_00187	EC:2.7.7.6	DNA-directed RNA polymerase.		
2558669519	DRAFT_00187	TIGR02390	DNA-directed RNA polymerase subunit A'		0.00E+00
2558669519	DRAFT_00187	TIGR02389	DNA-directed RNA polymerase, subunit A''		0.00E+00
2558669519	DRAFT_00187	KO:K03041	DNA-directed RNA polymerase subunit A' [EC:2.7.7.6]		0.00E+00
2558669519	DRAFT_00187	Locus_type		CDS	
2558669519	DRAFT_00187	Product_name		DNA-directed RNA polymerase, subunit A''/DNA-directed RNA polyme	
2558669519	DRAFT_00187	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669519	DRAFT_00187	Coordinates		45188..48976(-)	
2558669519	DRAFT_00187	DNA_length		3789bp	
2558669519	DRAFT_00187	Protein_length		1262aa	
2558669519	DRAFT_00187	GC		0.59	
2558669519	DRAFT_00187	Fused_gene		Yes	

2558669520	DRAFT_00188	KEGG_module	M00184: RNA polymerase, archaea		
2558669520	DRAFT_00188	COG_category	[K] Transcription		
2558669520	DRAFT_00188	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit		0.00E+00
2558669520	DRAFT_00188	pfam04561	RNA_pol_Rpb2_2		3.40E-23
2558669520	DRAFT_00188	pfam04565	RNA_pol_Rpb2_3		2.30E-26
2558669520	DRAFT_00188	pfam00562	RNA_pol_Rpb2_6		1.20E-119

2558669520	DRAFT_00188	pfam04563	RNA_pol_Rpb2_1			2.50E-50
2558669520	DRAFT_00188	pfam04566	RNA_pol_Rpb2_4			1.10E-10
2558669520	DRAFT_00188	pfam04560	RNA_pol_Rpb2_7			2.60E-27
2558669520	DRAFT_00188	pfam04567	RNA_pol_Rpb2_5			2.00E-10
2558669520	DRAFT_00188	EC:2.7.7.6	DNA-directed RNA polymerase.			
2558669520	DRAFT_00188	TIGR03670	DNA-directed RNA polymerase subunit B			0.00E+00
2558669520	DRAFT_00188	KO:K13798	DNA-directed RNA polymerase subunit B [EC:2.7.7.6]			0.00E+00
2558669520	DRAFT_00188	Locus_type		CDS		
2558669520	DRAFT_00188	Product_name		DNA-directed RNA polymerase subunit B		
2558669520	DRAFT_00188	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669520	DRAFT_00188	Coordinates		48981..52337(-)		
2558669520	DRAFT_00188	DNA_length		3357bp		
2558669520	DRAFT_00188	Protein_length		1118aa		
2558669520	DRAFT_00188	GC			0.58	
2558669520	DRAFT_00188	Fused_gene		Yes		
2558669521	DRAFT_00189	KEGG_module	M00184: RNA polymerase, archaea			
2558669521	DRAFT_00189	COG_category	[K] Transcription			
2558669521	DRAFT_00189	COG2012	DNA-directed RNA polymerase, subunit H, RpoH/RPB5			5.00E-18
2558669521	DRAFT_00189	pfam01191	RNA_pol_Rpb5_C			1.30E-27
2558669521	DRAFT_00189	EC:2.7.7.6	DNA-directed RNA polymerase.			
2558669521	DRAFT_00189	KO:K03053	DNA-directed RNA polymerase subunit H [EC:2.7.7.6]			1.20E-17
2558669521	DRAFT_00189	Locus_type		CDS		
2558669521	DRAFT_00189	Product_name		DNA-directed RNA polymerase, subunit H (EC 2.7.7.6)		
2558669521	DRAFT_00189	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669521	DRAFT_00189	Coordinates		52340..52606(-)		
2558669521	DRAFT_00189	DNA_length		267bp		
2558669521	DRAFT_00189	Protein_length		88aa		
2558669521	DRAFT_00189	GC			0.55	
2558669522	DRAFT_00190	Locus_type		CDS		
2558669522	DRAFT_00190	Product_name		hypothetical protein		
2558669522	DRAFT_00190	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669522	DRAFT_00190	Coordinates		52801..53004(-)		

2558669522	DRAFT_00190	DNA_length		204bp	
2558669522	DRAFT_00190	Protein_length		67aa	
2558669522	DRAFT_00190	GC			0.5
2558669523	DRAFT_00191	Locus_type		CDS	
2558669523	DRAFT_00191	Product_name		hypothetical protein	
2558669523	DRAFT_00191	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669523	DRAFT_00191	Coordinates		53200..53397(-)	
2558669523	DRAFT_00191	DNA_length		198bp	
2558669523	DRAFT_00191	Protein_length		65aa	
2558669523	DRAFT_00191	GC			0.57
2558669524	DRAFT_00192	COG_category	[L] Replication, recombination and repair		
2558669524	DRAFT_00192	COG3316	Transposase and inactivated derivatives		8.00E-08
2558669524	DRAFT_00192	pfam04434	SWIM		6.70E-04
2558669524	DRAFT_00192	pfam13610	DDE_Tnp_IS240		1.20E-20
2558669524	DRAFT_00192	Locus_type		CDS	
2558669524	DRAFT_00192	Product_name		Transposase and inactivated derivatives	
2558669524	DRAFT_00192	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669524	DRAFT_00192	Coordinates		53414..54568(-)	
2558669524	DRAFT_00192	DNA_length		1155bp	
2558669524	DRAFT_00192	Protein_length		384aa	
2558669524	DRAFT_00192	GC			0.57
2558669525	DRAFT_00193	Locus_type		CDS	
2558669525	DRAFT_00193	Product_name		hypothetical protein	
2558669525	DRAFT_00193	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669525	DRAFT_00193	Coordinates		54752..54928(+)	
2558669525	DRAFT_00193	DNA_length		177bp	
2558669525	DRAFT_00193	Protein_length		58aa	
2558669525	DRAFT_00193	GC			0.59
2558669526	DRAFT_00194	pfam01420	Methylase_S		1.70E-08
2558669526	DRAFT_00194	Locus_type		CDS	

2558669526	DRAFT_00194	Product_name		Restriction endonuclease S subunits		
2558669526	DRAFT_00194	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669526	DRAFT_00194	Coordinates		54933..55610(-)		
2558669526	DRAFT_00194	DNA_length		678bp		
2558669526	DRAFT_00194	Protein_length		225aa		
2558669526	DRAFT_00194	GC			0.52	
2558669527	DRAFT_00195	COG_category	[V] Defense mechanisms			
2558669527	DRAFT_00195	COG0286	Type I restriction-modification system methyltransferase subunit			1.00E-23
2558669527	DRAFT_00195	pfam02384	N6_Mtase			7.10E-31
2558669527	DRAFT_00195	Locus_type		CDS		
2558669527	DRAFT_00195	Product_name		Type I restriction-modification system methyltransferase subunit		
2558669527	DRAFT_00195	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669527	DRAFT_00195	Coordinates		55634..57610(-)		
2558669527	DRAFT_00195	DNA_length		1977bp		
2558669527	DRAFT_00195	Protein_length		658aa		
2558669527	DRAFT_00195	GC			0.54	
2558669528	DRAFT_00196	pfam01096	TFIIS_C			2.10E-05
2558669528	DRAFT_00196	Locus_type		CDS		
2558669528	DRAFT_00196	Product_name		Transcription factor S-II (TFIIS)		
2558669528	DRAFT_00196	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669528	DRAFT_00196	Coordinates		57914..58048(+)		
2558669528	DRAFT_00196	DNA_length		135bp		
2558669528	DRAFT_00196	Protein_length		44aa		
2558669528	DRAFT_00196	GC			0.53	
2558669529	DRAFT_00197	Locus_type		CDS		
2558669529	DRAFT_00197	Product_name		hypothetical protein		
2558669529	DRAFT_00197	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669529	DRAFT_00197	Coordinates		58206..58502(+)		
2558669529	DRAFT_00197	DNA_length		297bp		
2558669529	DRAFT_00197	Protein_length		98aa		
2558669529	DRAFT_00197	GC			0.55	

2558669530	DRAFT_00198	COG_category	[P] Inorganic ion transport and metabolism			
2558669530	DRAFT_00198	COG2156	K+-transporting ATPase, c chain			3.00E-22
2558669530	DRAFT_00198	pfam02669	KdpC			6.40E-08
2558669530	DRAFT_00198	pfam02669	KdpC			7.30E-14
2558669530	DRAFT_00198	EC:3.6.3.12	Potassium-transporting ATPase.			
2558669530	DRAFT_00198	KO:K01548	K+-transporting ATPase ATPase C chain [EC:3.6.3.12]			5.20E-16
2558669530	DRAFT_00198	Locus_type		CDS		
2558669530	DRAFT_00198	Product_name		K+-transporting ATPase, c chain		
2558669530	DRAFT_00198	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669530	DRAFT_00198	Coordinates		58525..58977(-)		
2558669530	DRAFT_00198	DNA_length		453bp		
2558669530	DRAFT_00198	Protein_length		150aa		
2558669530	DRAFT_00198	GC			0.51	
2558669530	DRAFT_00198	Transmembrane		Yes		
2558669531	DRAFT_00199	COG_category	[P] Inorganic ion transport and metabolism			
2558669531	DRAFT_00199	COG2216	High-affinity K+ transport system, ATPase chain B			0.00E+00
2558669531	DRAFT_00199	pfam00702	Hydrolase			1.20E-27
2558669531	DRAFT_00199	pfam00122	E1-E2_ATPase			2.00E-33
2558669531	DRAFT_00199	EC:3.6.3.12	Potassium-transporting ATPase.			
2558669531	DRAFT_00199	TIGR01494	ATPase, P-type (transporting), HAD superfamily, subfamily IC			4.60E-36
2558669531	DRAFT_00199	KO:K01547	K+-transporting ATPase ATPase B chain [EC:3.6.3.12]			0.00E+00
2558669531	DRAFT_00199	Locus_type		CDS		
2558669531	DRAFT_00199	Product_name		ATPase, P-type (transporting), HAD superfamily, subfamily IC		
2558669531	DRAFT_00199	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669531	DRAFT_00199	Coordinates		58987..61143(-)		
2558669531	DRAFT_00199	DNA_length		2157bp		
2558669531	DRAFT_00199	Protein_length		718aa		
2558669531	DRAFT_00199	GC			0.58	
2558669531	DRAFT_00199	Transmembrane		Yes		
2558669532	DRAFT_00200	COG_category	[P] Inorganic ion transport and metabolism			
2558669532	DRAFT_00200	COG2060	K+-transporting ATPase, A chain			0.00E+00

2558669532	DRAFT_00200	pfam03814	KdpA		0.00E+00
2558669532	DRAFT_00200	EC:3.6.3.12	Potassium-transporting ATPase.		
2558669532	DRAFT_00200	TIGR00680	K+-transporting ATPase, KdpA		0.00E+00
2558669532	DRAFT_00200	KO:K01546	K+-transporting ATPase ATPase A chain [EC:3.6.3.12]		0.00E+00
2558669532	DRAFT_00200	Locus_type		CDS	
2558669532	DRAFT_00200	Product_name		K+-transporting ATPase, KdpA	
2558669532	DRAFT_00200	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669532	DRAFT_00200	Coordinates		61130..62785(-)	
2558669532	DRAFT_00200	DNA_length		1656bp	
2558669532	DRAFT_00200	Protein_length		551aa	
2558669532	DRAFT_00200	GC		0.58	
2558669532	DRAFT_00200	Transmembrane		Yes	
2558669533	DRAFT_00201	pfam01037	AsnC_trans_reg		4.60E-15
2558669533	DRAFT_00201	Locus_type		CDS	
2558669533	DRAFT_00201	Product_name		Transcriptional regulators	
2558669533	DRAFT_00201	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669533	DRAFT_00201	Coordinates		62848..63141(-)	
2558669533	DRAFT_00201	DNA_length		294bp	
2558669533	DRAFT_00201	Protein_length		97aa	
2558669533	DRAFT_00201	GC		0.54	
2558669534	DRAFT_00202	Locus_type		tRNA	
2558669534	DRAFT_00202	Product_name		tRNA_Leu_TAG	
2558669534	DRAFT_00202	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669534	DRAFT_00202	Coordinates		63434..63521(+)	
2558669534	DRAFT_00202	DNA_length		88bp	
2558669534	DRAFT_00202	GC		0.7	
2558669535	DRAFT_00203	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558669535	DRAFT_00203	COG1215	Glycosyltransferases, probably involved in cell wall biogenesis		5.00E-33
2558669535	DRAFT_00203	pfam13641	Glyco_tranf_2_3		5.10E-28
2558669535	DRAFT_00203	Locus_type		CDS	
2558669535	DRAFT_00203	Product_name		Glycosyltransferases, probably involved in cell wall biogenesis	

2558669535	DRAFT_00203	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669535	DRAFT_00203	Coordinates		63588..65114(+)		
2558669535	DRAFT_00203	DNA_length		1527bp		
2558669535	DRAFT_00203	Protein_length		508aa		
2558669535	DRAFT_00203	GC			0.56	
2558669535	DRAFT_00203	Transmembrane		Yes		
2558669536	DRAFT_00204	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2558669536	DRAFT_00204	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2558669536	DRAFT_00204	Metacyc	PWY-6527: stachyose degradation			
2558669536	DRAFT_00204	Metacyc	PWY-3821: galactose degradation III			
2558669536	DRAFT_00204	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2558669536	DRAFT_00204	Metacyc	PWY-6397: mycolyl-arabinogalactan-peptidoglycan complex biosynthesis			
2558669536	DRAFT_00204	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			
2558669536	DRAFT_00204	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558669536	DRAFT_00204	COG_category	[G] Carbohydrate transport and metabolism			
2558669536	DRAFT_00204	COG0451	Nucleoside-diphosphate-sugar epimerases			2.00E-39
2558669536	DRAFT_00204	pfam01370	Epimerase			2.90E-37
2558669536	DRAFT_00204	EC:5.1.3.2	UDP-glucose 4-epimerase.			
2558669536	DRAFT_00204	KO:K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]			0.00E+00
2558669536	DRAFT_00204	Locus_type		CDS		
2558669536	DRAFT_00204	Product_name		Nucleoside-diphosphate-sugar epimerases		
2558669536	DRAFT_00204	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669536	DRAFT_00204	Coordinates		65368..66351(-)		
2558669536	DRAFT_00204	DNA_length		984bp		
2558669536	DRAFT_00204	Protein_length		327aa		
2558669536	DRAFT_00204	GC			0.53	
2558669537	DRAFT_00205	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2558669537	DRAFT_00205	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2558669537	DRAFT_00205	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			
2558669537	DRAFT_00205	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2558669537	DRAFT_00205	Metacyc	PWY-3821: galactose degradation III			
2558669537	DRAFT_00205	Metacyc	PWY-6397: mycolyl-arabinogalactan-peptidoglycan complex biosynthesis			

2558669537	DRAFT_00205	Metacyc	PWY-6527: stachyose degradation			
2558669537	DRAFT_00205	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558669537	DRAFT_00205	COG_category	[G] Carbohydrate transport and metabolism			
2558669537	DRAFT_00205	COG0451	Nucleoside-diphosphate-sugar epimerases			1.00E-48
2558669537	DRAFT_00205	pfam01370	Epimerase			7.50E-41
2558669537	DRAFT_00205	EC:5.1.3.2	UDP-glucose 4-epimerase.			
2558669537	DRAFT_00205	KO:K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]			0.00E+00
2558669537	DRAFT_00205	Locus_type		CDS		
2558669537	DRAFT_00205	Product_name		Nucleoside-diphosphate-sugar epimerases		
2558669537	DRAFT_00205	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669537	DRAFT_00205	Coordinates		66375..67328(-)		
2558669537	DRAFT_00205	DNA_length		954bp		
2558669537	DRAFT_00205	Protein_length		317aa		
2558669537	DRAFT_00205	GC			0.56	
2558669538	DRAFT_00206	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P			
2558669538	DRAFT_00206	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)			
2558669538	DRAFT_00206	Metacyc	PWY-5723: Rubisco shunt			
2558669538	DRAFT_00206	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)			
2558669538	DRAFT_00206	Metacyc	P124-PWY: Bifidobacterium shunt			
2558669538	DRAFT_00206	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)			
2558669538	DRAFT_00206	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2558669538	DRAFT_00206	COG_category	[G] Carbohydrate transport and metabolism			
2558669538	DRAFT_00206	COG0176	Transaldolase			5.00E-37
2558669538	DRAFT_00206	pfam00923	Transaldolase			4.00E-36
2558669538	DRAFT_00206	EC:2.2.1.2	Transaldolase.			
2558669538	DRAFT_00206	TIGR00875	fructose-6-phosphate aldolase, TalC/MipB family			3.80E-54
2558669538	DRAFT_00206	KO:K00616	transaldolase [EC:2.2.1.2]			4.60E-42
2558669538	DRAFT_00206	Locus_type		CDS		
2558669538	DRAFT_00206	Product_name		Transaldolase		
2558669538	DRAFT_00206	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669538	DRAFT_00206	Coordinates		67472..68182(-)		
2558669538	DRAFT_00206	DNA_length		711bp		
2558669538	DRAFT_00206	Protein_length		236aa		

2558669538	DRAFT_00206	GC		0.53	
2558669539	DRAFT_00207	KEGG_module	M00064: ADP-L-glycero-D-manno-heptose biosynthesis		
2558669539	DRAFT_00207	Metacyc	PWY0-1241: ADP-L-<i>glycero</i>-β-D-<i>manno</i>-heptose biosynthesis		
2558669539	DRAFT_00207	Metacyc	PWY-6478: GDP-D-<i>glycero</i>-α-D-<i>manno</i>-heptose biosynthesis		
2558669539	DRAFT_00207	COG_category	[E] Amino acid transport and metabolism		
2558669539	DRAFT_00207	COG0241	Histidinol phosphatase and related phosphatases		4.00E-30
2558669539	DRAFT_00207	pfam13242	Hydrolase_like		1.20E-10
2558669539	DRAFT_00207	EC:3.1.3.83	D-glycero-alpha-D-manno-heptose-1,7-bisphosphate 7-phosphatase.		
2558669539	DRAFT_00207	EC:3.1.3.82	D-glycero-beta-D-manno-heptose 1,7-bisphosphate 7-phosphatase.		
2558669539	DRAFT_00207	TIGR01656	histidinol-phosphate phosphatase family domain		4.90E-34
2558669539	DRAFT_00207	TIGR00213	D,D-heptose 1,7-bisphosphate phosphatase		2.10E-36
2558669539	DRAFT_00207	TIGR01662	HAD-superfamily hydrolase, subfamily IIIA		4.90E-27
2558669539	DRAFT_00207	KO:K03273	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.8		1.00E-32
2558669539	DRAFT_00207	Locus_type		CDS	
2558669539	DRAFT_00207	Product_name		histidinol-phosphate phosphatase family domain/HAD-superfamily hy	
2558669539	DRAFT_00207	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669539	DRAFT_00207	Coordinates		68294..69058(+)	
2558669539	DRAFT_00207	DNA_length		765bp	
2558669539	DRAFT_00207	Protein_length		254aa	
2558669539	DRAFT_00207	GC		0.55	
2558669540	DRAFT_00208	KEGG_module	M00064: ADP-L-glycero-D-manno-heptose biosynthesis		
2558669540	DRAFT_00208	Metacyc	PWY0-1241: ADP-L-<i>glycero</i>-β-D-<i>manno</i>-heptose biosynthesis		
2558669540	DRAFT_00208	Metacyc	PWY-6478: GDP-D-<i>glycero</i>-α-D-<i>manno</i>-heptose biosynthesis		
2558669540	DRAFT_00208	COG_category	[G] Carbohydrate transport and metabolism		
2558669540	DRAFT_00208	COG0279	Phosphoheptose isomerase		5.00E-26
2558669540	DRAFT_00208	pfam13580	SIS_2		5.20E-20
2558669540	DRAFT_00208	EC:5.3.1.28	D-sedoheptulose 7-phosphate isomerase.		
2558669540	DRAFT_00208	KO:K03271	D-sedoheptulose 7-phosphate isomerase [EC:5.3.1.28]		0.00E+00
2558669540	DRAFT_00208	Locus_type		CDS	
2558669540	DRAFT_00208	Product_name		Phosphoheptose isomerase	
2558669540	DRAFT_00208	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669540	DRAFT_00208	Coordinates		69080..69667(-)	

2558669540	DRAFT_00208	DNA_length		588bp		
2558669540	DRAFT_00208	Protein_length		195aa		
2558669540	DRAFT_00208	GC			0.55	
2558669541	DRAFT_00209	Metacyc	PWY-6478: GDP-D-<i>glycero</i>-α-D-<i>manno</i>-heptose biosynthesis			
2558669541	DRAFT_00209	COG_category	[R] General function prediction only			
2558669541	DRAFT_00209	COG2605	Predicted kinase related to galactokinase and mevalonate kinase			7.00E-80
2558669541	DRAFT_00209	pfam00288	GHMP_kinases_N			5.60E-08
2558669541	DRAFT_00209	pfam08544	GHMP_kinases_C			3.20E-10
2558669541	DRAFT_00209	EC:2.7.1.168	D-glycero-alpha-D-manno-heptose-7-phosphate kinase.			
2558669541	DRAFT_00209	KO:K07031	D-glycero-alpha-D-manno-heptose-7-phosphate kinase [EC:2.7.1.168]			0.00E+00
2558669541	DRAFT_00209	Locus_type		CDS		
2558669541	DRAFT_00209	Product_name		Predicted kinase related to galactokinase and mevalonate kinase		
2558669541	DRAFT_00209	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669541	DRAFT_00209	Coordinates		69768..70802(+)		
2558669541	DRAFT_00209	DNA_length		1035bp		
2558669541	DRAFT_00209	Protein_length		344aa		
2558669541	DRAFT_00209	GC			0.55	
2558669542	DRAFT_00210	pfam00483	NTP_transferase			6.10E-17
2558669542	DRAFT_00210	Locus_type		CDS		
2558669542	DRAFT_00210	Product_name		Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopol		
2558669542	DRAFT_00210	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669542	DRAFT_00210	Coordinates		70838..71533(+)		
2558669542	DRAFT_00210	DNA_length		696bp		
2558669542	DRAFT_00210	Protein_length		231aa		
2558669542	DRAFT_00210	GC			0.55	
2558669543	DRAFT_00211	COG_category	[C] Energy production and conversion			
2558669543	DRAFT_00211	COG_category	[G] Carbohydrate transport and metabolism			
2558669543	DRAFT_00211	COG1819	Glycosyl transferases, related to UDP-glucuronosyltransferase			5.00E-28
2558669543	DRAFT_00211	pfam04101	Glyco_tran_28_C			4.40E-11
2558669543	DRAFT_00211	pfam13528	Glyco_trans_1_3			3.50E-12
2558669543	DRAFT_00211	TIGR00661	conserved hypothetical protein			3.40E-15

2558669543	DRAFT_00211	Locus_type		CDS		
2558669543	DRAFT_00211	Product_name		Glycosyl transferases, related to UDP-glucuronosyltransferase		
2558669543	DRAFT_00211	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669543	DRAFT_00211	Coordinates		71581..72753(-)		
2558669543	DRAFT_00211	DNA_length		1173bp		
2558669543	DRAFT_00211	Protein_length		390aa		
2558669543	DRAFT_00211	GC			0.55	
2558669544	DRAFT_00212	pfam12773	DZR			2.30E-09
2558669544	DRAFT_00212	Locus_type		CDS		
2558669544	DRAFT_00212	Product_name		Double zinc ribbon		
2558669544	DRAFT_00212	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669544	DRAFT_00212	Coordinates		72856..74028(+)		
2558669544	DRAFT_00212	DNA_length		1173bp		
2558669544	DRAFT_00212	Protein_length		390aa		
2558669544	DRAFT_00212	GC			0.54	
2558669545	DRAFT_00213	pfam14378	PAP2_3			8.60E-14
2558669545	DRAFT_00213	Locus_type		CDS		
2558669545	DRAFT_00213	Product_name		PAP2 superfamily		
2558669545	DRAFT_00213	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669545	DRAFT_00213	Coordinates		74203..75135(-)		
2558669545	DRAFT_00213	DNA_length		933bp		
2558669545	DRAFT_00213	Protein_length		310aa		
2558669545	DRAFT_00213	GC			0.55	
2558669545	DRAFT_00213	Transmembrane		Yes		
2558669546	DRAFT_00214	KEGG_module	M00368: Ethylene biosynthesis, methionine => ethylene			
2558669546	DRAFT_00214	KEGG_module	M00034: Methionine salvage pathway			
2558669546	DRAFT_00214	KEGG_module	M00035: Methionine degradation			
2558669546	DRAFT_00214	Metacyc	SAM-PWY: S-adenosyl-L-methionine biosynthesis			
2558669546	DRAFT_00214	Metacyc	ETHYL-PWY: ethylene biosynthesis I (plants)			
2558669546	DRAFT_00214	Metacyc	PWY-5041: <i>S</i>-adenosyl-L-methionine cycle II			
2558669546	DRAFT_00214	Metacyc	PWY-5912: 2'-deoxymugineic acid phytosiderophore biosynthesis			

2558669546	DRAFT_00214	Metacyc	METHIONINE-DEG1-PWY: methionine degradation I (to homocysteine)			
2558669546	DRAFT_00214	IMG_pathway	462: S-adenosylmethionine synthesis			
2558669546	DRAFT_00214	COG_category	[H] Coenzyme transport and metabolism			
2558669546	DRAFT_00214	COG0192	S-adenosylmethionine synthetase			0.00E+00
2558669546	DRAFT_00214	pfam00438	S-AdoMet_synt_N			1.00E-39
2558669546	DRAFT_00214	pfam02773	S-AdoMet_synt_C			1.20E-63
2558669546	DRAFT_00214	pfam02772	S-AdoMet_synt_M			6.90E-47
2558669546	DRAFT_00214	EC:2.5.1.6	Methionine adenosyltransferase.			
2558669546	DRAFT_00214	TIGR01034	S-adenosylmethionine synthetase			0.00E+00
2558669546	DRAFT_00214	KO:K00789	S-adenosylmethionine synthetase [EC:2.5.1.6]			0.00E+00
2558669546	DRAFT_00214	ITERM:01673	methionine adenosyltransferase (EC 2.5.1.6)			
2558669546	DRAFT_00214	Locus_type		CDS		
2558669546	DRAFT_00214	Product_name		methionine adenosyltransferase (EC 2.5.1.6)		
2558669546	DRAFT_00214	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669546	DRAFT_00214	Coordinates		75308..76465(-)		
2558669546	DRAFT_00214	DNA_length		1158bp		
2558669546	DRAFT_00214	Protein_length		385aa		
2558669546	DRAFT_00214	GC			0.57	
2558669547	DRAFT_00215	COG_category	[K] Transcription			
2558669547	DRAFT_00215	COG3620	Predicted transcriptional regulator with C-terminal CBS domains			3.00E-33
2558669547	DRAFT_00215	pfam00571	CBS			1.00E-08
2558669547	DRAFT_00215	pfam01381	HTH_3			7.20E-11
2558669547	DRAFT_00215	Locus_type		CDS		
2558669547	DRAFT_00215	Product_name		Predicted transcriptional regulator with C-terminal CBS domains		
2558669547	DRAFT_00215	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669547	DRAFT_00215	Coordinates		76737..77303(+)		
2558669547	DRAFT_00215	DNA_length		567bp		
2558669547	DRAFT_00215	Protein_length		188aa		
2558669547	DRAFT_00215	GC			0.57	
2558669548	DRAFT_00216	COG_category	[S] Function unknown			
2558669548	DRAFT_00216	COG4243	Predicted membrane protein			2.00E-12
2558669548	DRAFT_00216	pfam07884	VKOR			4.10E-18

2558669548	DRAFT_00216	Locus_type		CDS	
2558669548	DRAFT_00216	Product_name		Predicted membrane protein	
2558669548	DRAFT_00216	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669548	DRAFT_00216	Coordinates		77398..77886(-)	
2558669548	DRAFT_00216	DNA_length		489bp	
2558669548	DRAFT_00216	Protein_length		162aa	
2558669548	DRAFT_00216	GC		0.5	
2558669548	DRAFT_00216	Transmembrane		Yes	
2558669549	DRAFT_00217	pfam06053	DUF929		2.20E-27
2558669549	DRAFT_00217	Locus_type		CDS	
2558669549	DRAFT_00217	Product_name		Domain of unknown function (DUF929)	
2558669549	DRAFT_00217	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669549	DRAFT_00217	Coordinates		77887..78759(-)	
2558669549	DRAFT_00217	DNA_length		873bp	
2558669549	DRAFT_00217	Protein_length		290aa	
2558669549	DRAFT_00217	GC		0.53	
2558669549	DRAFT_00217	Transmembrane		Yes	
2558669550	DRAFT_00218	COG_category	[L] Replication, recombination and repair		
2558669550	DRAFT_00218	COG1111	ERCC4-like helicases		0.00E+00
2558669550	DRAFT_00218	pfam00270	DEAD		1.10E-19
2558669550	DRAFT_00218	pfam00271	Helicase_C		5.90E-19
2558669550	DRAFT_00218	Locus_type		CDS	
2558669550	DRAFT_00218	Product_name		ERCC4-like helicases	
2558669550	DRAFT_00218	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669550	DRAFT_00218	Coordinates		78920..80470(+)	
2558669550	DRAFT_00218	DNA_length		1551bp	
2558669550	DRAFT_00218	Protein_length		516aa	
2558669550	DRAFT_00218	GC		0.59	
2558669551	DRAFT_00219	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP		
2558669551	DRAFT_00219	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP		
2558669551	DRAFT_00219	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate		

2558669551	DRAFT_00219	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds		
2558669551	DRAFT_00219	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2558669551	DRAFT_00219	Metacyc	P341-PWY: glycolysis V (Pyrococcus)		
2558669551	DRAFT_00219	Metacyc	PWY-7003: glycerol degradation to butanol		
2558669551	DRAFT_00219	Metacyc	ANARESP1-PWY: respiration (anaerobic)		
2558669551	DRAFT_00219	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)		
2558669551	DRAFT_00219	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis		
2558669551	DRAFT_00219	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)		
2558669551	DRAFT_00219	Metacyc	PWY-5723: Rubisco shunt		
2558669551	DRAFT_00219	Metacyc	PWY-1042: glycolysis IV (plant cytosol)		
2558669551	DRAFT_00219	Metacyc	P122-PWY: heterolactic fermentation		
2558669551	DRAFT_00219	Metacyc	PWY-6901: xylose degradation IV		
2558669551	DRAFT_00219	Metacyc	PWY-5484: glycolysis II (from fructose-6P)		
2558669551	DRAFT_00219	Metacyc	FERMENTATION-PWY: mixed acid fermentation		
2558669551	DRAFT_00219	Metacyc	PWY-2221: Entner-Doudoroff pathway III (semi-phosphorylative)		
2558669551	DRAFT_00219	Metacyc	GLYCOLYSIS: glycolysis I		
2558669551	DRAFT_00219	Metacyc	P124-PWY: Bifidobacterium shunt		
2558669551	DRAFT_00219	IMG_pathway	336: Standard Embden-Meyerhof pathway		
2558669551	DRAFT_00219	IMG_pathway	337: Embden-Meyerhof pathway without bisphosphoglycerate		
2558669551	DRAFT_00219	IMG_pathway	358: Conversion of glyceraldehyde to pyruvate		
2558669551	DRAFT_00219	IMG_pathway	359: Conversion of glyceraldehyde-3-phosphate to pyruvate		
2558669551	DRAFT_00219	COG_category	[G] Carbohydrate transport and metabolism		
2558669551	DRAFT_00219	COG0469	Pyruvate kinase		0.00E+00
2558669551	DRAFT_00219	pfam00224	PK		5.50E-112
2558669551	DRAFT_00219	pfam02887	PK_C		5.30E-29
2558669551	DRAFT_00219	EC:2.7.1.40	Pyruvate kinase.		
2558669551	DRAFT_00219	TIGR01064	pyruvate kinase		0.00E+00
2558669551	DRAFT_00219	KO:K00873	pyruvate kinase [EC:2.7.1.40]		0.00E+00
2558669551	DRAFT_00219	ITERM:01480	pyruvate kinase (EC 2.7.1.40)		
2558669551	DRAFT_00219	Locus_type		CDS	
2558669551	DRAFT_00219	Product_name		pyruvate kinase (EC 2.7.1.40)	
2558669551	DRAFT_00219	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669551	DRAFT_00219	Coordinates		80481..81887(-)	
2558669551	DRAFT_00219	DNA_length		1407bp	

2558669551	DRAFT_00219	Protein_length		468aa		
2558669551	DRAFT_00219	GC			0.62	
2558669552	DRAFT_00220	Locus_type		CDS		
2558669552	DRAFT_00220	Product_name		hypothetical protein		
2558669552	DRAFT_00220	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669552	DRAFT_00220	Coordinates		81899..82069(+)		
2558669552	DRAFT_00220	DNA_length		171bp		
2558669552	DRAFT_00220	Protein_length		56aa		
2558669552	DRAFT_00220	GC			0.51	
2558669552	DRAFT_00220	Transmembrane		Yes		
2558669553	DRAFT_00221	KEGG_module	M00254: ABC-2 type transport system			
2558669553	DRAFT_00221	COG_category	[V] Defense mechanisms			
2558669553	DRAFT_00221	COG1131	ABC-type multidrug transport system, ATPase component			3.00E-61
2558669553	DRAFT_00221	pfam00005	ABC_tran			2.00E-28
2558669553	DRAFT_00221	KO:K01990	ABC-2 type transport system ATP-binding protein			0.00E+00
2558669553	DRAFT_00221	Locus_type		CDS		
2558669553	DRAFT_00221	Product_name		ABC-type multidrug transport system, ATPase component		
2558669553	DRAFT_00221	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669553	DRAFT_00221	Coordinates		82042..82980(+)		
2558669553	DRAFT_00221	DNA_length		939bp		
2558669553	DRAFT_00221	Protein_length		312aa		
2558669553	DRAFT_00221	GC			0.57	
2558669554	DRAFT_00222	KEGG_module	M00254: ABC-2 type transport system			
2558669554	DRAFT_00222	COG_category	[R] General function prediction only			
2558669554	DRAFT_00222	COG1277	ABC-type transport system involved in multi-copper enzyme maturatio			1.00E-08
2558669554	DRAFT_00222	pfam12730	ABC2_membrane_4			2.30E-18
2558669554	DRAFT_00222	KO:K01992	ABC-2 type transport system permease protein			5.60E-45
2558669554	DRAFT_00222	Locus_type		CDS		
2558669554	DRAFT_00222	Product_name		ABC-type transport system involved in multi-copper enzyme maturati		
2558669554	DRAFT_00222	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669554	DRAFT_00222	Coordinates		82986..83855(+)		

2558669554	DRAFT_00222	DNA_length		870bp	
2558669554	DRAFT_00222	Protein_length		289aa	
2558669554	DRAFT_00222	GC		0.53	
2558669554	DRAFT_00222	Transmembrane		Yes	
2558669555	DRAFT_00223	COG_category	[R] General function prediction only		
2558669555	DRAFT_00223	COG2129	Predicted phosphoesterases, related to the Icc protein		2.00E-31
2558669555	DRAFT_00223	Locus_type		CDS	
2558669555	DRAFT_00223	Product_name		Predicted phosphoesterases, related to the Icc protein	
2558669555	DRAFT_00223	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669555	DRAFT_00223	Coordinates		83864..84823(-)	
2558669555	DRAFT_00223	DNA_length		960bp	
2558669555	DRAFT_00223	Protein_length		319aa	
2558669555	DRAFT_00223	GC		0.57	
2558669556	DRAFT_00224	Locus_type		CDS	
2558669556	DRAFT_00224	Product_name		hypothetical protein	
2558669556	DRAFT_00224	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669556	DRAFT_00224	Coordinates		84985..85293(+)	
2558669556	DRAFT_00224	DNA_length		309bp	
2558669556	DRAFT_00224	Protein_length		102aa	
2558669556	DRAFT_00224	GC		0.5	
2558669556	DRAFT_00224	Transmembrane		Yes	
2558669557	DRAFT_00225	Locus_type		CDS	
2558669557	DRAFT_00225	Product_name		hypothetical protein	
2558669557	DRAFT_00225	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669557	DRAFT_00225	Coordinates		85342..85467(+)	
2558669557	DRAFT_00225	DNA_length		126bp	
2558669557	DRAFT_00225	Protein_length		41aa	
2558669557	DRAFT_00225	GC		0.52	
2558669558	DRAFT_00226	Locus_type		CDS	
2558669558	DRAFT_00226	Product_name		hypothetical protein	

2558669558	DRAFT_00226	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669558	DRAFT_00226	Coordinates		85451..85660(+)		
2558669558	DRAFT_00226	DNA_length		210bp		
2558669558	DRAFT_00226	Protein_length		69aa		
2558669558	DRAFT_00226	GC			0.54	
2558669559	DRAFT_00227	COG_category	[R] General function prediction only			
2558669559	DRAFT_00227	COG1694	Predicted pyrophosphatase			3.00E-03
2558669559	DRAFT_00227	Locus_type		CDS		
2558669559	DRAFT_00227	Product_name		Predicted pyrophosphatase		
2558669559	DRAFT_00227	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669559	DRAFT_00227	Coordinates		85657..85983(-)		
2558669559	DRAFT_00227	DNA_length		327bp		
2558669559	DRAFT_00227	Protein_length		108aa		
2558669559	DRAFT_00227	GC			0.56	
2558669560	DRAFT_00228	COG_category	[L] Replication, recombination and repair			
2558669560	DRAFT_00228	COG0177	Predicted EndoIII-related endonuclease			3.00E-65
2558669560	DRAFT_00228	pfam00730	HhH-GPD			3.10E-26
2558669560	DRAFT_00228	EC:4.2.99.18	DNA-(apurinic or apyrimidinic site) lyase.			
2558669560	DRAFT_00228	TIGR01083	endonuclease III			3.10E-61
2558669560	DRAFT_00228	KO:K10773	endonuclease III [EC:4.2.99.18]			0.00E+00
2558669560	DRAFT_00228	Locus_type		CDS		
2558669560	DRAFT_00228	Product_name		Predicted EndoIII-related endonuclease		
2558669560	DRAFT_00228	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669560	DRAFT_00228	Coordinates		86007..86846(-)		
2558669560	DRAFT_00228	DNA_length		840bp		
2558669560	DRAFT_00228	Protein_length		279aa		
2558669560	DRAFT_00228	GC			0.58	
2558669561	DRAFT_00229	COG_category	[R] General function prediction only			
2558669561	DRAFT_00229	COG0517	FOG: CBS domain			2.00E-13
2558669561	DRAFT_00229	pfam00571	CBS			6.00E-09
2558669561	DRAFT_00229	pfam00571	CBS			1.30E-13

2558669561	DRAFT_00229	Locus_type		CDS	
2558669561	DRAFT_00229	Product_name		FOG: CBS domain	
2558669561	DRAFT_00229	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669561	DRAFT_00229	Coordinates		87016..87444(-)	
2558669561	DRAFT_00229	DNA_length		429bp	
2558669561	DRAFT_00229	Protein_length		142aa	
2558669561	DRAFT_00229	GC		0.55	
2558669562	DRAFT_00230	COG_category	[T] Signal transduction mechanisms		
2558669562	DRAFT_00230	COG0589	Universal stress protein UspA and related nucleotide-binding proteins		4.00E-19
2558669562	DRAFT_00230	pfam00582	Usp		1.20E-31
2558669562	DRAFT_00230	Locus_type		CDS	
2558669562	DRAFT_00230	Product_name		Universal stress protein UspA and related nucleotide-binding proteins	
2558669562	DRAFT_00230	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669562	DRAFT_00230	Coordinates		87449..87910(-)	
2558669562	DRAFT_00230	DNA_length		462bp	
2558669562	DRAFT_00230	Protein_length		153aa	
2558669562	DRAFT_00230	GC		0.62	
2558669563	DRAFT_00231	COG_category	[S] Function unknown		
2558669563	DRAFT_00231	COG2210	Uncharacterized conserved protein		7.00E-22
2558669563	DRAFT_00231	pfam13686	DrsE_2		5.70E-41
2558669563	DRAFT_00231	Locus_type		CDS	
2558669563	DRAFT_00231	Product_name		Uncharacterized conserved protein	
2558669563	DRAFT_00231	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669563	DRAFT_00231	Coordinates		88031..88537(+)	
2558669563	DRAFT_00231	DNA_length		507bp	
2558669563	DRAFT_00231	Protein_length		168aa	
2558669563	DRAFT_00231	GC		0.57	
2558669564	DRAFT_00232	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669564	DRAFT_00232	COG0425	Predicted redox protein, regulator of disulfide bond formation		8.00E-12
2558669564	DRAFT_00232	pfam01206	TusA		2.30E-17
2558669564	DRAFT_00232	Locus_type		CDS	

2558669564	DRAFT_00232	Product_name		Predicted redox protein, regulator of disulfide bond formation	
2558669564	DRAFT_00232	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669564	DRAFT_00232	Coordinates		88546..88794(+)	
2558669564	DRAFT_00232	DNA_length		249bp	
2558669564	DRAFT_00232	Protein_length		82aa	
2558669564	DRAFT_00232	GC		0.55	
2558669565	DRAFT_00233	COG_category	[C] Energy production and conversion		
2558669565	DRAFT_00233	COG1252	NADH dehydrogenase, FAD-containing subunit		3.00E-22
2558669565	DRAFT_00233	pfam07992	Pyr_redox_2		5.80E-08
2558669565	DRAFT_00233	Locus_type		CDS	
2558669565	DRAFT_00233	Product_name		NADH dehydrogenase, FAD-containing subunit	
2558669565	DRAFT_00233	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669565	DRAFT_00233	Coordinates		88795..90024(+)	
2558669565	DRAFT_00233	DNA_length		1230bp	
2558669565	DRAFT_00233	Protein_length		409aa	
2558669565	DRAFT_00233	GC		0.59	
2558669566	DRAFT_00234	Locus_type		CDS	
2558669566	DRAFT_00234	Product_name		hypothetical protein	
2558669566	DRAFT_00234	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669566	DRAFT_00234	Coordinates		90090..90452(+)	
2558669566	DRAFT_00234	DNA_length		363bp	
2558669566	DRAFT_00234	Protein_length		120aa	
2558669566	DRAFT_00234	GC		0.55	
2558669567	DRAFT_00235	Locus_type		CDS	
2558669567	DRAFT_00235	Product_name		hypothetical protein	
2558669567	DRAFT_00235	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669567	DRAFT_00235	Coordinates		90516..90788(+)	
2558669567	DRAFT_00235	DNA_length		273bp	
2558669567	DRAFT_00235	Protein_length		90aa	
2558669567	DRAFT_00235	GC		0.54	
2558669567	DRAFT_00235	Transmembrane		Yes	

2558669568	DRAFT_00236	COG_category	[C] Energy production and conversion		
2558669568	DRAFT_00236	COG1042	Acyl-CoA synthetase (NDP forming)		3.00E-125
2558669568	DRAFT_00236	pfam13380	CoA_binding_2		2.40E-22
2558669568	DRAFT_00236	pfam13549	ATP-grasp_5		9.50E-62
2558669568	DRAFT_00236	pfam13607	Succ_CoA_lig		8.80E-53
2558669568	DRAFT_00236	pfam00583	Acetyltransf_1		1.40E-04
2558669568	DRAFT_00236	TIGR02717	acetyl coenzyme A synthetase (ADP forming), alpha domain		0.00E+00
2558669568	DRAFT_00236	Locus_type		CDS	
2558669568	DRAFT_00236	Product_name		Acyl-CoA synthetase (NDP forming)	
2558669568	DRAFT_00236	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669568	DRAFT_00236	Coordinates		91113..93521(+)	
2558669568	DRAFT_00236	DNA_length		2409bp	
2558669568	DRAFT_00236	Protein_length		802aa	
2558669568	DRAFT_00236	GC		0.63	
2558669568	DRAFT_00236	Fused_gene		Yes	

2558669569	DRAFT_00237	KEGG_module	M00357: Methanogenesis, acetate => methane		
2558669569	DRAFT_00237	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)		
2558669569	DRAFT_00237	Metacyc	PWY66-162: ethanol degradation IV		
2558669569	DRAFT_00237	Metacyc	PWY0-1313: acetate conversion to acetyl-CoA		
2558669569	DRAFT_00237	Metacyc	PWY-6672: <i>cis</i>-genanyl-CoA degradation		
2558669569	DRAFT_00237	Metacyc	PWY66-161: oxidative ethanol degradation III		
2558669569	DRAFT_00237	Metacyc	PWY66-21: ethanol degradation II		
2558669569	DRAFT_00237	COG_category	[I] Lipid transport and metabolism		
2558669569	DRAFT_00237	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases		0.00E+00
2558669569	DRAFT_00237	pfam00501	AMP-binding		2.80E-83
2558669569	DRAFT_00237	pfam13193	AMP-binding_C		1.20E-15
2558669569	DRAFT_00237	EC:6.2.1.1	Acetate--CoA ligase.		
2558669569	DRAFT_00237	TIGR02188	acetate--CoA ligase		0.00E+00
2558669569	DRAFT_00237	KO:K01895	acetyl-CoA synthetase [EC:6.2.1.1]		0.00E+00
2558669569	DRAFT_00237	ITERM:05018	acetyl-coenzyme A synthetase (EC 6.2.1.1)		
2558669569	DRAFT_00237	Locus_type		CDS	
2558669569	DRAFT_00237	Product_name		acetyl-coenzyme A synthetase (EC 6.2.1.1)	

2558669569	DRAFT_00237	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669569	DRAFT_00237	Coordinates		93603..95639(+)	
2558669569	DRAFT_00237	DNA_length		2037bp	
2558669569	DRAFT_00237	Protein_length		678aa	
2558669569	DRAFT_00237	GC		0.59	
2558669570	DRAFT_00238	COG_category	[S] Function unknown		
2558669570	DRAFT_00238	COG1584	Predicted membrane protein		3.00E-38
2558669570	DRAFT_00238	pfam01184	Grp1_Fun34_YaaH		4.40E-47
2558669570	DRAFT_00238	Locus_type		CDS	
2558669570	DRAFT_00238	Product_name		Predicted membrane protein	
2558669570	DRAFT_00238	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669570	DRAFT_00238	Coordinates		95660..96277(-)	
2558669570	DRAFT_00238	DNA_length		618bp	
2558669570	DRAFT_00238	Protein_length		205aa	
2558669570	DRAFT_00238	GC		0.58	
2558669570	DRAFT_00238	Transmembrane		Yes	
2558669571	DRAFT_00239	Locus_type		CDS	
2558669571	DRAFT_00239	Product_name		hypothetical protein	
2558669571	DRAFT_00239	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669571	DRAFT_00239	Coordinates		96402..96710(-)	
2558669571	DRAFT_00239	DNA_length		309bp	
2558669571	DRAFT_00239	Protein_length		102aa	
2558669571	DRAFT_00239	GC		0.56	
2558669572	DRAFT_00240	Metacyc	PWY-1341: phenylacetate degradation II (anaerobic)		
2558669572	DRAFT_00240	Metacyc	PWY-6318: phenylalanine degradation IV (mammalian, via side chain)		
2558669572	DRAFT_00240	Metacyc	PWY0-321: phenylacetate degradation I (aerobic)		
2558669572	DRAFT_00240	COG_category	[H] Coenzyme transport and metabolism		
2558669572	DRAFT_00240	COG1541	Coenzyme F390 synthetase		9.00E-122
2558669572	DRAFT_00240	pfam00501	AMP-binding		4.30E-14
2558669572	DRAFT_00240	pfam14535	AMP-binding_C_2		2.60E-11
2558669572	DRAFT_00240	EC:6.2.1.30	Phenylacetate--CoA ligase.		

2558669572	DRAFT_00240	KO:K01912	phenylacetate-CoA ligase [EC:6.2.1.30]		0.00E+00
2558669572	DRAFT_00240	Locus_type		CDS	
2558669572	DRAFT_00240	Product_name		phenylacetate-CoA ligase (EC 6.2.1.30)	
2558669572	DRAFT_00240	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669572	DRAFT_00240	Coordinates		97076..98392(+)	
2558669572	DRAFT_00240	DNA_length		1317bp	
2558669572	DRAFT_00240	Protein_length		438aa	
2558669572	DRAFT_00240	GC		0.55	
2558669573	DRAFT_00241	Locus_type		CDS	
2558669573	DRAFT_00241	Product_name		hypothetical protein	
2558669573	DRAFT_00241	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669573	DRAFT_00241	Coordinates		98535..98960(+)	
2558669573	DRAFT_00241	DNA_length		426bp	
2558669573	DRAFT_00241	Protein_length		141aa	
2558669573	DRAFT_00241	GC		0.57	
2558669573	DRAFT_00241	Transmembrane		Yes	
2558669574	DRAFT_00242	IMG_pathway	667: Ammonium transport via ammonium channel		
2558669574	DRAFT_00242	COG_category	[P] Inorganic ion transport and metabolism		
2558669574	DRAFT_00242	COG0004	Ammonia permease		4.00E-120
2558669574	DRAFT_00242	pfam00909	Ammonium_transp		1.80E-122
2558669574	DRAFT_00242	TIGR00836	ammonium transporter		0.00E+00
2558669574	DRAFT_00242	KO:K03320	ammonium transporter, Amt family		0.00E+00
2558669574	DRAFT_00242	ITERM:05717	ammonium transporter (TC 1.A.11)		
2558669574	DRAFT_00242	Locus_type		CDS	
2558669574	DRAFT_00242	Product_name		ammonium transporter (TC 1.A.11)	
2558669574	DRAFT_00242	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669574	DRAFT_00242	Coordinates		98787..100055(-)	
2558669574	DRAFT_00242	DNA_length		1269bp	
2558669574	DRAFT_00242	Protein_length		422aa	
2558669574	DRAFT_00242	GC		0.57	
2558669574	DRAFT_00242	Transmembrane		Yes	

2558669575	DRAFT_00243	COG_category	[G] Carbohydrate transport and metabolism			
2558669575	DRAFT_00243	COG0647	Predicted sugar phosphatases of the HAD superfamily			2.00E-53
2558669575	DRAFT_00243	pfam13344	Hydrolase_6			1.10E-18
2558669575	DRAFT_00243	pfam13242	Hydrolase_like			1.60E-17
2558669575	DRAFT_00243	EC:3.1.3.41	4-nitrophenylphosphatase.			
2558669575	DRAFT_00243	TIGR01460	Haloacid Dehalogenase Superfamily Class (subfamily) IIA			3.60E-41
2558669575	DRAFT_00243	KO:K01101	4-nitrophenyl phosphatase [EC:3.1.3.41]			5.20E-39
2558669575	DRAFT_00243	Locus_type		CDS		
2558669575	DRAFT_00243	Product_name		Predicted sugar phosphatases of the HAD superfamily		
2558669575	DRAFT_00243	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669575	DRAFT_00243	Coordinates		100169..100951(-)		
2558669575	DRAFT_00243	DNA_length		783bp		
2558669575	DRAFT_00243	Protein_length		260aa		
2558669575	DRAFT_00243	GC			0.57	

2558669576	DRAFT_00244	COG_category	[S] Function unknown			
2558669576	DRAFT_00244	COG1786	Uncharacterized conserved protein			4.00E-16
2558669576	DRAFT_00244	pfam01989	DUF126			3.60E-17
2558669576	DRAFT_00244	KO:K09128	hypothetical protein			1.90E-15
2558669576	DRAFT_00244	ITERM:01401	predicted aconitase subunit 2 (EC 4.2.1.3)			
2558669576	DRAFT_00244	Locus_type		CDS		
2558669576	DRAFT_00244	Product_name		predicted aconitase subunit 2 (EC 4.2.1.3)		
2558669576	DRAFT_00244	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669576	DRAFT_00244	Coordinates		100948..101388(-)		
2558669576	DRAFT_00244	DNA_length		441bp		
2558669576	DRAFT_00244	Protein_length		146aa		
2558669576	DRAFT_00244	GC			0.63	

2558669577	DRAFT_00245	COG_category	[S] Function unknown			
2558669577	DRAFT_00245	COG1679	Uncharacterized conserved protein			3.00E-85
2558669577	DRAFT_00245	pfam04412	DUF521			5.50E-112
2558669577	DRAFT_00245	KO:K09123	hypothetical protein			0.00E+00
2558669577	DRAFT_00245	ITERM:01400	predicted aconitase subunit 1 (EC 4.2.1.3)			
2558669577	DRAFT_00245	Locus_type		CDS		

2558669577	DRAFT_00245	Product_name		predicted aconitase subunit 1 (EC 4.2.1.3)	
2558669577	DRAFT_00245	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669577	DRAFT_00245	Coordinates		101385..102590(-)	
2558669577	DRAFT_00245	DNA_length		1206bp	
2558669577	DRAFT_00245	Protein_length		401aa	
2558669577	DRAFT_00245	GC		0.6	
2558669578	DRAFT_00246	pfam08241	Methyltransf_11		4.80E-13
2558669578	DRAFT_00246	Locus_type		CDS	
2558669578	DRAFT_00246	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	
2558669578	DRAFT_00246	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669578	DRAFT_00246	Coordinates		102982..103800(+)	
2558669578	DRAFT_00246	DNA_length		819bp	
2558669578	DRAFT_00246	Protein_length		272aa	
2558669578	DRAFT_00246	GC		0.53	
2558669579	DRAFT_00247	Locus_type		CDS	
2558669579	DRAFT_00247	Product_name		hypothetical protein	
2558669579	DRAFT_00247	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669579	DRAFT_00247	Coordinates		103837..104163(-)	
2558669579	DRAFT_00247	DNA_length		327bp	
2558669579	DRAFT_00247	Protein_length		108aa	
2558669579	DRAFT_00247	GC		0.52	
2558669579	DRAFT_00247	Transmembrane		Yes	
2558669580	DRAFT_00248	KEGG_module	M00179: Ribosome, archaea		
2558669580	DRAFT_00248	KEGG_module	M00178: Ribosome, bacteria		
2558669580	DRAFT_00248	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669580	DRAFT_00248	COG0051	Ribosomal protein S10		9.00E-24
2558669580	DRAFT_00248	pfam00338	Ribosomal_S10		3.00E-28
2558669580	DRAFT_00248	TIGR01046	ribosomal protein S10(archaeal)/S20(eukaryotic)		1.40E-45
2558669580	DRAFT_00248	KO:K02946	small subunit ribosomal protein S10		2.00E-30
2558669580	DRAFT_00248	ITERM:00293	SSU ribosomal protein S10P		
2558669580	DRAFT_00248	Locus_type		CDS	

2558669580	DRAFT_00248	Product_name		SSU ribosomal protein S10P		
2558669580	DRAFT_00248	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669580	DRAFT_00248	Coordinates		104290..104601(+)		
2558669580	DRAFT_00248	DNA_length		312bp		
2558669580	DRAFT_00248	Protein_length		103aa		
2558669580	DRAFT_00248	GC			0.59	
2558669581	DRAFT_00249	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558669581	DRAFT_00249	COG0677	UDP-N-acetyl-D-mannosaminuronate dehydrogenase			3.00E-108
2558669581	DRAFT_00249	pfam00984	UDPG_MGDP_dh			3.00E-20
2558669581	DRAFT_00249	pfam03720	UDPG_MGDP_dh_C			1.70E-24
2558669581	DRAFT_00249	pfam03721	UDPG_MGDP_dh_N			8.00E-38
2558669581	DRAFT_00249	TIGR03026	nucleotide sugar dehydrogenase			4.90E-113
2558669581	DRAFT_00249	Locus_type		CDS		
2558669581	DRAFT_00249	Product_name		nucleotide sugar dehydrogenase		
2558669581	DRAFT_00249	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2		
2558669581	DRAFT_00249	Coordinates		104787..106151(+)		
2558669581	DRAFT_00249	DNA_length		1365bp		
2558669581	DRAFT_00249	Protein_length		454aa		
2558669581	DRAFT_00249	GC			0.59	
2558669581	DRAFT_00249	Transmembrane		Yes		
2558669582	DRAFT_00250	KEGG_module	M00366: C10-C20 isoprenoid biosynthesis, plants			
2558669582	DRAFT_00250	KEGG_module	M00365: C10-C20 isoprenoid biosynthesis, archaea			
2558669582	DRAFT_00250	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			
2558669582	DRAFT_00250	KEGG_module	M00367: C10-C20 isoprenoid biosynthesis, non-plant eukaryotes			
2558669582	DRAFT_00250	KEGG_module	M00364: C10-C20 isoprenoid biosynthesis, bacteria			
2558669582	DRAFT_00250	KEGG_module	M00096: C5 isoprenoid biosynthesis, non-mevalonate pathway			
2558669582	DRAFT_00250	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis			
2558669582	DRAFT_00250	Metacyc	NONMEVIPP-PWY: methylerythritol phosphate pathway			
2558669582	DRAFT_00250	Metacyc	PWY-6859: <i>all-trans</i>-farnesol biosynthesis			
2558669582	DRAFT_00250	Metacyc	PWY-922: mevalonate pathway I			
2558669582	DRAFT_00250	Metacyc	PWY-5123: <i>trans, trans</i>-farnesyl diphosphate biosynthesis			
2558669582	DRAFT_00250	Metacyc	PWY-6174: mevalonate pathway II (archaea)			

2558669582	DRAFT_00250	Metacyc	PWY-7102: bisabolene biosynthesis		
2558669582	DRAFT_00250	IMG_pathway	365: dimetyhylallyl pyrophosphate biosynthesis via isomerization of isopentenyl diphosphate		
2558669582	DRAFT_00250	COG_category	[I] Lipid transport and metabolism		
2558669582	DRAFT_00250	COG1443	Isopentenyldiphosphate isomerase		2.00E-14
2558669582	DRAFT_00250	pfam00293	NUDIX		3.90E-17
2558669582	DRAFT_00250	EC:5.3.3.2	Isopentenyl-diphosphate Delta-isomerase.		
2558669582	DRAFT_00250	KO:K01823	isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]		9.50E-19
2558669582	DRAFT_00250	ITERM:00469	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)		
2558669582	DRAFT_00250	Locus_type		CDS	
2558669582	DRAFT_00250	Product_name		isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)	
2558669582	DRAFT_00250	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669582	DRAFT_00250	Coordinates		106163..106729(-)	
2558669582	DRAFT_00250	DNA_length		567bp	
2558669582	DRAFT_00250	Protein_length		188aa	
2558669582	DRAFT_00250	GC		0.6	
2558669583	DRAFT_00251	Locus_type		CDS	
2558669583	DRAFT_00251	Product_name		hypothetical protein	
2558669583	DRAFT_00251	Scaffold		DRAFT_contig_70_6_len_107089_read_count_1768889.2	
2558669583	DRAFT_00251	Coordinates		106792..107088(+)	
2558669583	DRAFT_00251	DNA_length		297bp	
2558669583	DRAFT_00251	Protein_length		99aa	
2558669583	DRAFT_00251	GC		0.52	
2558669583	DRAFT_00251	Transmembrane		Yes	
2558669584	DRAFT_00252	Locus_type		CDS	
2558669584	DRAFT_00252	Product_name		hypothetical protein	
2558669584	DRAFT_00252	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669584	DRAFT_00252	Coordinates		2..166(-)	
2558669584	DRAFT_00252	DNA_length		165bp	
2558669584	DRAFT_00252	Protein_length		55aa	
2558669584	DRAFT_00252	GC		0.63	
2558669585	DRAFT_00253	COG_category	[S] Function unknown		

2558669585	DRAFT_00253	COG3410	Uncharacterized conserved protein		1.00E-18
2558669585	DRAFT_00253	pfam09848	DUF2075		8.20E-89
2558669585	DRAFT_00253	KO:K09384	hypothetical protein		0.00E+00
2558669585	DRAFT_00253	Locus_type		CDS	
2558669585	DRAFT_00253	Product_name		Uncharacterized conserved protein	
2558669585	DRAFT_00253	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669585	DRAFT_00253	Coordinates		614..2482(-)	
2558669585	DRAFT_00253	DNA_length		1869bp	
2558669585	DRAFT_00253	Protein_length		622aa	
2558669585	DRAFT_00253	GC		0.57	
2558669586	DRAFT_00254	COG_category	[R] General function prediction only		
2558669586	DRAFT_00254	COG1694	Predicted pyrophosphatase		4.00E-04
2558669586	DRAFT_00254	pfam03819	MazG		1.80E-04
2558669586	DRAFT_00254	Locus_type		CDS	
2558669586	DRAFT_00254	Product_name		Predicted pyrophosphatase	
2558669586	DRAFT_00254	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669586	DRAFT_00254	Coordinates		2479..2811(-)	
2558669586	DRAFT_00254	DNA_length		333bp	
2558669586	DRAFT_00254	Protein_length		110aa	
2558669586	DRAFT_00254	GC		0.5	
2558669587	DRAFT_00255	COG_category	[R] General function prediction only		
2558669587	DRAFT_00255	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa		7.00E-20
2558669587	DRAFT_00255	pfam12697	Abhydrolase_6		6.40E-31
2558669587	DRAFT_00255	Locus_type		CDS	
2558669587	DRAFT_00255	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super	
2558669587	DRAFT_00255	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669587	DRAFT_00255	Coordinates		3805..4533(+)	
2558669587	DRAFT_00255	DNA_length		729bp	
2558669587	DRAFT_00255	Protein_length		242aa	
2558669587	DRAFT_00255	GC		0.59	
2558669588	DRAFT_00256	KEGG_module	M00248: Putative antibiotic transport system		

2558669588	DRAFT_00256	pfam12698	ABC2_membrane_3			6.80E-34
2558669588	DRAFT_00256	KO:K09686	antibiotic transport system permease protein			0.00E+00
2558669588	DRAFT_00256	Locus_type		CDS		
2558669588	DRAFT_00256	Product_name		ABC-type multidrug transport system, permease component		
2558669588	DRAFT_00256	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669588	DRAFT_00256	Coordinates		4514..5605(-)		
2558669588	DRAFT_00256	DNA_length		1092bp		
2558669588	DRAFT_00256	Protein_length		363aa		
2558669588	DRAFT_00256	GC			0.59	
2558669588	DRAFT_00256	Transmembrane		Yes		
2558669589	DRAFT_00257	KEGG_module	M00248: Putative antibiotic transport system			
2558669589	DRAFT_00257	COG_category	[V] Defense mechanisms			
2558669589	DRAFT_00257	COG1131	ABC-type multidrug transport system, ATPase component			2.00E-66
2558669589	DRAFT_00257	pfam00005	ABC_tran			6.20E-24
2558669589	DRAFT_00257	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2558669589	DRAFT_00257	Locus_type		CDS		
2558669589	DRAFT_00257	Product_name		ABC-type multidrug transport system, ATPase component		
2558669589	DRAFT_00257	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669589	DRAFT_00257	Coordinates		5612..6544(-)		
2558669589	DRAFT_00257	DNA_length		933bp		
2558669589	DRAFT_00257	Protein_length		310aa		
2558669589	DRAFT_00257	GC			0.62	
2558669590	DRAFT_00258	Locus_type		CDS		
2558669590	DRAFT_00258	Product_name		hypothetical protein		
2558669590	DRAFT_00258	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669590	DRAFT_00258	Coordinates		6669..7301(+)		
2558669590	DRAFT_00258	DNA_length		633bp		
2558669590	DRAFT_00258	Protein_length		210aa		
2558669590	DRAFT_00258	GC			0.59	
2558669590	DRAFT_00258	Transmembrane		Yes		
2558669591	DRAFT_00259	Locus_type		CDS		

2558669591	DRAFT_00259	Product_name		hypothetical protein		
2558669591	DRAFT_00259	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669591	DRAFT_00259	Coordinates		7175..7429(-)		
2558669591	DRAFT_00259	DNA_length		255bp		
2558669591	DRAFT_00259	Protein_length		84aa		
2558669591	DRAFT_00259	GC			0.6	
2558669592	DRAFT_00260	COG_category	[R] General function prediction only			
2558669592	DRAFT_00260	COG0431	Predicted flavoprotein			6.00E-34
2558669592	DRAFT_00260	pfam03358	FMN_red			5.30E-38
2558669592	DRAFT_00260	Locus_type		CDS		
2558669592	DRAFT_00260	Product_name		Predicted flavoprotein		
2558669592	DRAFT_00260	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669592	DRAFT_00260	Coordinates		7441..8049(-)		
2558669592	DRAFT_00260	DNA_length		609bp		
2558669592	DRAFT_00260	Protein_length		202aa		
2558669592	DRAFT_00260	GC			0.61	
2558669593	DRAFT_00261	pfam13298	LigD_N			1.60E-35
2558669593	DRAFT_00261	EC:6.5.1.1	DNA ligase (ATP).			
2558669593	DRAFT_00261	TIGR02777	DNA ligase D, 3'-phosphoesterase domain			1.80E-49
2558669593	DRAFT_00261	KO:K01971	DNA ligase (ATP) [EC:6.5.1.1]			4.10E-43
2558669593	DRAFT_00261	Locus_type		CDS		
2558669593	DRAFT_00261	Product_name		DNA ligase D, 3'-phosphoesterase domain		
2558669593	DRAFT_00261	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669593	DRAFT_00261	Coordinates		8181..8813(+)		
2558669593	DRAFT_00261	DNA_length		633bp		
2558669593	DRAFT_00261	Protein_length		210aa		
2558669593	DRAFT_00261	GC			0.61	
2558669594	DRAFT_00262	COG_category	[S] Function unknown			
2558669594	DRAFT_00262	COG4805	Uncharacterized protein conserved in bacteria			7.00E-117
2558669594	DRAFT_00262	pfam05960	DUF885			0.00E+00
2558669594	DRAFT_00262	Locus_type		CDS		

2558669594	DRAFT_00262	Product_name		Uncharacterized protein conserved in bacteria	
2558669594	DRAFT_00262	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669594	DRAFT_00262	Coordinates		8835..10544(-)	
2558669594	DRAFT_00262	DNA_length		1710bp	
2558669594	DRAFT_00262	Protein_length		569aa	
2558669594	DRAFT_00262	GC		0.63	
2558669595	DRAFT_00263	COG_category	[R] General function prediction only		
2558669595	DRAFT_00263	COG2406	Protein distantly related to bacterial ferritins		1.00E-19
2558669595	DRAFT_00263	pfam00210	Ferritin		3.10E-23
2558669595	DRAFT_00263	KO:K03594	bacterioferritin		4.20E-31
2558669595	DRAFT_00263	Locus_type		CDS	
2558669595	DRAFT_00263	Product_name		Protein distantly related to bacterial ferritins	
2558669595	DRAFT_00263	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669595	DRAFT_00263	Coordinates		11053..11535(+)	
2558669595	DRAFT_00263	DNA_length		483bp	
2558669595	DRAFT_00263	Protein_length		160aa	
2558669595	DRAFT_00263	GC		0.55	
2558669596	DRAFT_00264	pfam05977	MFS_3		2.00E-30
2558669596	DRAFT_00264	Locus_type		CDS	
2558669596	DRAFT_00264	Product_name		Arabinose efflux permease	
2558669596	DRAFT_00264	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669596	DRAFT_00264	Coordinates		11645..12895(+)	
2558669596	DRAFT_00264	DNA_length		1251bp	
2558669596	DRAFT_00264	Protein_length		416aa	
2558669596	DRAFT_00264	GC		0.58	
2558669596	DRAFT_00264	Transmembrane		Yes	
2558669597	DRAFT_00265	pfam00271	Helicase_C		9.70E-07
2558669597	DRAFT_00265	Locus_type		CDS	
2558669597	DRAFT_00265	Product_name		HrpA-like helicases	
2558669597	DRAFT_00265	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669597	DRAFT_00265	Coordinates		13119..14846(+)	

2558669597	DRAFT_00265	DNA_length		1728bp	
2558669597	DRAFT_00265	Protein_length		575aa	
2558669597	DRAFT_00265	GC		0.48	
2558669598	DRAFT_00266	COG_category	[E] Amino acid transport and metabolism		
2558669598	DRAFT_00266	COG0436	Aspartate/tyrosine/aromatic aminotransferase		5.00E-74
2558669598	DRAFT_00266	pfam00155	Aminotran_1_2		8.10E-62
2558669598	DRAFT_00266	ITERM:00170	L-alanine aminotransferase apoenzyme (EC 2.6.1.2)		
2558669598	DRAFT_00266	Locus_type		CDS	
2558669598	DRAFT_00266	Product_name		L-alanine aminotransferase apoenzyme (EC 2.6.1.2)	
2558669598	DRAFT_00266	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669598	DRAFT_00266	Coordinates		15406..16632(-)	
2558669598	DRAFT_00266	DNA_length		1227bp	
2558669598	DRAFT_00266	Protein_length		408aa	
2558669598	DRAFT_00266	GC		0.5	
2558669599	DRAFT_00267	COG_category	[E] Amino acid transport and metabolism		
2558669599	DRAFT_00267	COG1164	Oligoendopeptidase F		7.00E-60
2558669599	DRAFT_00267	pfam01432	Peptidase_M3		1.70E-37
2558669599	DRAFT_00267	EC:3.4.24.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Metalloendopeptidases.		
2558669599	DRAFT_00267	TIGR02289	oligoendopeptidase, M3 family		0.00E+00
2558669599	DRAFT_00267	KO:K08602	oligoendopeptidase F [EC:3.4.24.-]		0.00E+00
2558669599	DRAFT_00267	Locus_type		CDS	
2558669599	DRAFT_00267	Product_name		oligoendopeptidase, M3 family	
2558669599	DRAFT_00267	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669599	DRAFT_00267	Coordinates		16767..18431(-)	
2558669599	DRAFT_00267	DNA_length		1665bp	
2558669599	DRAFT_00267	Protein_length		554aa	
2558669599	DRAFT_00267	GC		0.55	
2558669600	DRAFT_00268	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2558669600	DRAFT_00268	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis		
2558669600	DRAFT_00268	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II		
2558669600	DRAFT_00268	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I		

2558669600	DRAFT_00268	IMG_pathway	297: 5-amino-1-(5-phospho-D-ribosyl)imidazole synthesis		
2558669600	DRAFT_00268	COG_category	[F] Nucleotide transport and metabolism		
2558669600	DRAFT_00268	COG0150	Phosphoribosylaminoimidazole (AIR) synthetase		1.00E-88
2558669600	DRAFT_00268	pfam00586	AIRS		8.00E-14
2558669600	DRAFT_00268	pfam02769	AIRS_C		4.10E-23
2558669600	DRAFT_00268	EC:6.3.3.1	Phosphoribosylformylglycinamidine cyclo-ligase.		
2558669600	DRAFT_00268	TIGR00878	phosphoribosylaminoimidazole synthetase		1.50E-103
2558669600	DRAFT_00268	KO:K01933	phosphoribosylformylglycinamidine cyclo-ligase [EC:6.3.3.1]		0.00E+00
2558669600	DRAFT_00268	ITERM:01294	phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)		
2558669600	DRAFT_00268	Locus_type		CDS	
2558669600	DRAFT_00268	Product_name		phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	
2558669600	DRAFT_00268	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669600	DRAFT_00268	Coordinates		18645..19562(-)	
2558669600	DRAFT_00268	DNA_length		918bp	
2558669600	DRAFT_00268	Protein_length		305aa	
2558669600	DRAFT_00268	GC		0.59	

2558669601	DRAFT_00269	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2558669601	DRAFT_00269	Metacyc	PWY-6123: inosine-5'-phosphate biosynthesis I		
2558669601	DRAFT_00269	Metacyc	PWY-6124: inosine-5'-phosphate biosynthesis II		
2558669601	DRAFT_00269	IMG_pathway	812: IMP biosynthesis		
2558669601	DRAFT_00269	COG_category	[F] Nucleotide transport and metabolism		
2558669601	DRAFT_00269	COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase		4.00E-51
2558669601	DRAFT_00269	pfam01259	SAICAR_synt		1.80E-59
2558669601	DRAFT_00269	EC:6.3.2.6	Phosphoribosylaminoimidazolesuccinocarboxamide synthase.		
2558669601	DRAFT_00269	TIGR00081	phosphoribosylaminoimidazole-succinocarboxamide synthase		4.10E-64
2558669601	DRAFT_00269	KO:K01923	phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.		0.00E+00
2558669601	DRAFT_00269	ITERM:01292	phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)		
2558669601	DRAFT_00269	Locus_type		CDS	
2558669601	DRAFT_00269	Product_name		phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3	
2558669601	DRAFT_00269	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669601	DRAFT_00269	Coordinates		19701..20543(-)	
2558669601	DRAFT_00269	DNA_length		843bp	
2558669601	DRAFT_00269	Protein_length		280aa	

2558669601	DRAFT_00269	GC			0.57	
2558669602	DRAFT_00270	pfam00731	AIRC			4.50E-35
2558669602	DRAFT_00270	TIGR01162	phosphoribosylaminoimidazole carboxylase, PurE protein			2.10E-40
2558669602	DRAFT_00270	Locus_type		CDS		
2558669602	DRAFT_00270	Product_name		Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase		
2558669602	DRAFT_00270	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669602	DRAFT_00270	Coordinates		20534..20836(-)		
2558669602	DRAFT_00270	DNA_length		303bp		
2558669602	DRAFT_00270	Protein_length		100aa		
2558669602	DRAFT_00270	GC			0.58	
2558669602	DRAFT_00270	Signal_peptide		Yes		
2558669603	DRAFT_00271	Metacyc	PWY-2201: folate transformations I			
2558669603	DRAFT_00271	Metacyc	PWY-3841: folate transformations II			
2558669603	DRAFT_00271	Metacyc	1CMET2-PWY: formylTHF biosynthesis I			
2558669603	DRAFT_00271	COG_category	[H] Coenzyme transport and metabolism			
2558669603	DRAFT_00271	COG0212	5-formyltetrahydrofolate cyclo-ligase			3.00E-35
2558669603	DRAFT_00271	pfam01812	5-FTHF_cyc-lig			9.80E-34
2558669603	DRAFT_00271	EC:6.3.3.2	5-formyltetrahydrofolate cyclo-ligase.			
2558669603	DRAFT_00271	TIGR02727	5,10-methenyltetrahydrofolate synthetase			1.50E-45
2558669603	DRAFT_00271	KO:K01934	5-formyltetrahydrofolate cyclo-ligase [EC:6.3.3.2]			2.80E-29
2558669603	DRAFT_00271	ITERM:05520	5-formyltetrahydrofolate cyclo-ligase			
2558669603	DRAFT_00271	Locus_type		CDS		
2558669603	DRAFT_00271	Product_name		5-formyltetrahydrofolate cyclo-ligase		
2558669603	DRAFT_00271	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669603	DRAFT_00271	Coordinates		20970..21551(-)		
2558669603	DRAFT_00271	DNA_length		582bp		
2558669603	DRAFT_00271	Protein_length		193aa		
2558669603	DRAFT_00271	GC			0.62	
2558669604	DRAFT_00272	KEGG_module	M00140: C1-unit interconversion, prokaryotes			
2558669604	DRAFT_00272	KEGG_module	M00377: Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)			
2558669604	DRAFT_00272	Metacyc	PWY-6613: tetrahydrofolate salvage from 5,10-methenyltetrahydrofolate			

2558669604	DRAFT_00272	Metacyc	1CMET2-PWY: formylTHF biosynthesis I		
2558669604	DRAFT_00272	Metacyc	PWY-2201: folate transformations I		
2558669604	DRAFT_00272	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2558669604	DRAFT_00272	Metacyc	PWY-5030: histidine degradation III		
2558669604	DRAFT_00272	Metacyc	PWY-3841: folate transformations II		
2558669604	DRAFT_00272	Metacyc	P164-PWY: purine nucleobases degradation I (anaerobic)		
2558669604	DRAFT_00272	Metacyc	CODH-PWY: reductive acetyl coenzyme A pathway		
2558669604	DRAFT_00272	Metacyc	PWY-1722: formaldehyde oxidation V (tetrahydrofolate pathway)		
2558669604	DRAFT_00272	COG_category	[H] Coenzyme transport and metabolism		
2558669604	DRAFT_00272	COG0190	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydr		3.00E-102
2558669604	DRAFT_00272	pfam00763	THF_DHG_CYH		4.90E-39
2558669604	DRAFT_00272	pfam02882	THF_DHG_CYH_C		8.00E-64
2558669604	DRAFT_00272	EC:1.5.1.5	Methylenetetrahydrofolate dehydrogenase (NADP(+)).		
2558669604	DRAFT_00272	EC:3.5.4.9	Methenyltetrahydrofolate cyclohydrolase.		
2558669604	DRAFT_00272	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahy		0.00E+00
2558669604	DRAFT_00272	Locus_type		CDS	
2558669604	DRAFT_00272	Product_name		5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahyd	
2558669604	DRAFT_00272	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669604	DRAFT_00272	Coordinates		21548..22426(-)	
2558669604	DRAFT_00272	DNA_length		879bp	
2558669604	DRAFT_00272	Protein_length		292aa	
2558669604	DRAFT_00272	GC		0.58	

2558669605	DRAFT_00273	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	
2558669605	DRAFT_00273	Metacyc	PWY-6613: tetrahydrofolate salvage from 5,10-methenyltetrahydrofolate	
2558669605	DRAFT_00273	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I	
2558669605	DRAFT_00273	IMG_pathway	1031: Tetrahydrofolate salvage from 5,10-methylenetetrahydrofolate	
2558669605	DRAFT_00273	IMG_pathway	297: 5-amino-1-(5-phospho-D-ribosyl)imidazole synthesis	
2558669605	DRAFT_00273	COG_category	[F] Nucleotide transport and metabolism	
2558669605	DRAFT_00273	COG0299	Folate-dependent phosphoribosylglycinamide formyltransferase PurN	5.00E-52
2558669605	DRAFT_00273	pfam00551	Formyl_trans_N	1.40E-40
2558669605	DRAFT_00273	EC:2.1.2.2	Phosphoribosylglycinamide formyltransferase.	
2558669605	DRAFT_00273	TIGR00639	phosphoribosylglycinamide formyltransferase, formyltetrahydrofolate-	1.10E-57
2558669605	DRAFT_00273	KO:K11175	phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]	0.00E+00

2558669605	DRAFT_00273	ITERM:01296	formyltetrahydrofolate-dependent phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)		
2558669605	DRAFT_00273	Locus_type		CDS	
2558669605	DRAFT_00273	Product_name		formyltetrahydrofolate-dependent phosphoribosylglycinamide formy	
2558669605	DRAFT_00273	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669605	DRAFT_00273	Coordinates		22423..22947(-)	
2558669605	DRAFT_00273	DNA_length		525bp	
2558669605	DRAFT_00273	Protein_length		174aa	
2558669605	DRAFT_00273	GC		0.6	
2558669606	DRAFT_00274	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2558669606	DRAFT_00274	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I		
2558669606	DRAFT_00274	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II		
2558669606	DRAFT_00274	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis		
2558669606	DRAFT_00274	IMG_pathway	297: 5-amino-1-(5-phospho-D-ribosyl)imidazole synthesis		
2558669606	DRAFT_00274	COG_category	[F] Nucleotide transport and metabolism		
2558669606	DRAFT_00274	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase		0.00E+00
2558669606	DRAFT_00274	pfam00156	Pribosyltran		3.30E-12
2558669606	DRAFT_00274	pfam13522	GATase_6		3.70E-13
2558669606	DRAFT_00274	EC:2.4.2.14	Amidophosphoribosyltransferase.		
2558669606	DRAFT_00274	TIGR01134	amidophosphoribosyltransferase		4.10E-113
2558669606	DRAFT_00274	KO:K00764	amidophosphoribosyltransferase [EC:2.4.2.14]		0.00E+00
2558669606	DRAFT_00274	ITERM:01274	amidophosphoribosyltransferase (EC 2.4.2.14)		
2558669606	DRAFT_00274	Locus_type		CDS	
2558669606	DRAFT_00274	Product_name		amidophosphoribosyltransferase (EC 2.4.2.14)	
2558669606	DRAFT_00274	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669606	DRAFT_00274	Coordinates		23042..24481(-)	
2558669606	DRAFT_00274	DNA_length		1440bp	
2558669606	DRAFT_00274	Protein_length		479aa	
2558669606	DRAFT_00274	GC		0.6	
2558669607	DRAFT_00275	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2558669607	DRAFT_00275	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I		
2558669607	DRAFT_00275	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II		
2558669607	DRAFT_00275	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis		

2558669607	DRAFT_00275	COG_category	[F] Nucleotide transport and metabolism			
2558669607	DRAFT_00275	COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase dom			0.00E+00
2558669607	DRAFT_00275	pfam00586	AIRS			5.30E-15
2558669607	DRAFT_00275	pfam00586	AIRS			6.30E-23
2558669607	DRAFT_00275	pfam02769	AIRS_C			2.20E-26
2558669607	DRAFT_00275	pfam02769	AIRS_C			6.20E-17
2558669607	DRAFT_00275	EC:6.3.5.3	Phosphoribosylformylglycinamidine synthase.			
2558669607	DRAFT_00275	TIGR01736	phosphoribosylformylglycinamidine synthase II			0.00E+00
2558669607	DRAFT_00275	KO:K01952	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]			0.00E+00
2558669607	DRAFT_00275	Locus_type		CDS		
2558669607	DRAFT_00275	Product_name		phosphoribosylformylglycinamidine synthase II		
2558669607	DRAFT_00275	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669607	DRAFT_00275	Coordinates		24478..26673(-)		
2558669607	DRAFT_00275	DNA_length		2196bp		
2558669607	DRAFT_00275	Protein_length		731aa		
2558669607	DRAFT_00275	GC			0.61	
2558669608	DRAFT_00276	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP			
2558669608	DRAFT_00276	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis			
2558669608	DRAFT_00276	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II			
2558669608	DRAFT_00276	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I			
2558669608	DRAFT_00276	COG_category	[F] Nucleotide transport and metabolism			
2558669608	DRAFT_00276	COG0047	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amid			5.00E-85
2558669608	DRAFT_00276	pfam13507	GATase_5			1.10E-50
2558669608	DRAFT_00276	EC:6.3.5.3	Phosphoribosylformylglycinamidine synthase.			
2558669608	DRAFT_00276	TIGR01737	phosphoribosylformylglycinamidine synthase I			9.60E-100
2558669608	DRAFT_00276	KO:K01952	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]			0.00E+00
2558669608	DRAFT_00276	ITERM:05311	phosphoribosylformylglycinamidine synthase subunit I (EC 6.3.5.3)			
2558669608	DRAFT_00276	Locus_type		CDS		
2558669608	DRAFT_00276	Product_name		phosphoribosylformylglycinamidine synthase subunit I (EC 6.3.5.3)		
2558669608	DRAFT_00276	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669608	DRAFT_00276	Coordinates		26675..27385(-)		
2558669608	DRAFT_00276	DNA_length		711bp		
2558669608	DRAFT_00276	Protein_length		236aa		

2558669608	DRAFT_00276	GC			0.59	
2558669609	DRAFT_00277	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP			
2558669609	DRAFT_00277	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis			
2558669609	DRAFT_00277	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I			
2558669609	DRAFT_00277	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II			
2558669609	DRAFT_00277	COG_category	[F] Nucleotide transport and metabolism			
2558669609	DRAFT_00277	COG1828	Phosphoribosylformylglycinamidine (FGAM) synthase, PurS componen			7.00E-12
2558669609	DRAFT_00277	pfam02700	PurS			3.60E-17
2558669609	DRAFT_00277	EC:6.3.5.3	Phosphoribosylformylglycinamidine synthase.			
2558669609	DRAFT_00277	TIGR00302	phosphoribosylformylglycinamidine synthase, purS protein			1.50E-17
2558669609	DRAFT_00277	KO:K01952	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]			9.70E-15
2558669609	DRAFT_00277	Locus_type		CDS		
2558669609	DRAFT_00277	Product_name		phosphoribosylformylglycinamidine synthase, purS protein		
2558669609	DRAFT_00277	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669609	DRAFT_00277	Coordinates		27382..27642(-)		
2558669609	DRAFT_00277	DNA_length		261bp		
2558669609	DRAFT_00277	Protein_length		86aa		
2558669609	DRAFT_00277	GC			0.56	
2558669610	DRAFT_00278	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP			
2558669610	DRAFT_00278	Metacyc	PWY-6123: inosine-5'-phosphate biosynthesis I			
2558669610	DRAFT_00278	Metacyc	PWY-6124: inosine-5'-phosphate biosynthesis II			
2558669610	DRAFT_00278	COG_category	[F] Nucleotide transport and metabolism			
2558669610	DRAFT_00278	COG0138	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrola			0.00E+00
2558669610	DRAFT_00278	pfam02142	MGS			7.40E-18
2558669610	DRAFT_00278	pfam01808	AICARFT_IMPCHas			1.40E-65
2558669610	DRAFT_00278	EC:2.1.2.3	Phosphoribosylaminoimidazolecarboxamide formyltransferase.			
2558669610	DRAFT_00278	EC:3.5.4.10	IMP cyclohydrolase.			
2558669610	DRAFT_00278	KO:K00602	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP c			0.00E+00
2558669610	DRAFT_00278	Locus_type		CDS		
2558669610	DRAFT_00278	Product_name		AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydro		
2558669610	DRAFT_00278	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669610	DRAFT_00278	Coordinates		27706..29352(+)		

2558669610	DRAFT_00278	DNA_length		1647bp		
2558669610	DRAFT_00278	Protein_length		548aa		
2558669610	DRAFT_00278	GC			0.58	

2558669611	DRAFT_00279	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP			
2558669611	DRAFT_00279	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I			
2558669611	DRAFT_00279	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis			
2558669611	DRAFT_00279	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II			
2558669611	DRAFT_00279	IMG_pathway	297: 5-amino-1-(5-phospho-D-ribosyl)imidazole synthesis			
2558669611	DRAFT_00279	COG_category	[F] Nucleotide transport and metabolism			
2558669611	DRAFT_00279	COG0151	Phosphoribosylamine-glycine ligase			1.00E-45
2558669611	DRAFT_00279	pfam01071	GARS_A			1.40E-22
2558669611	DRAFT_00279	EC:6.3.4.13	Phosphoribosylamine--glycine ligase.			
2558669611	DRAFT_00279	KO:K01945	phosphoribosylamine--glycine ligase [EC:6.3.4.13]			0.00E+00
2558669611	DRAFT_00279	ITERM:01300	phosphoribosylamine--glycine ligase (EC 6.3.4.13)			
2558669611	DRAFT_00279	Locus_type		CDS		
2558669611	DRAFT_00279	Product_name		phosphoribosylamine--glycine ligase (EC 6.3.4.13)		
2558669611	DRAFT_00279	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669611	DRAFT_00279	Coordinates		29349..30743(-)		
2558669611	DRAFT_00279	DNA_length		1395bp		
2558669611	DRAFT_00279	Protein_length		464aa		
2558669611	DRAFT_00279	GC			0.58	

2558669612	DRAFT_00280	Locus_type		CDS		
2558669612	DRAFT_00280	Product_name		hypothetical protein		
2558669612	DRAFT_00280	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669612	DRAFT_00280	Coordinates		31062..31298(-)		
2558669612	DRAFT_00280	DNA_length		237bp		
2558669612	DRAFT_00280	Protein_length		78aa		
2558669612	DRAFT_00280	GC			0.56	

2558669613	DRAFT_00281	Locus_type		CDS		
2558669613	DRAFT_00281	Product_name		hypothetical protein		
2558669613	DRAFT_00281	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		

2558669613	DRAFT_00281	Coordinates		31285..31434(-)	
2558669613	DRAFT_00281	DNA_length		150bp	
2558669613	DRAFT_00281	Protein_length		49aa	
2558669613	DRAFT_00281	GC		0.52	
2558669614	DRAFT_00282	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669614	DRAFT_00282	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal		9.00E-46
2558669614	DRAFT_00282	pfam13365	Trypsin_2		7.60E-18
2558669614	DRAFT_00282	pfam13180	PDZ_2		1.50E-14
2558669614	DRAFT_00282	EC:1.3.1.74	2-alkenal reductase.		
2558669614	DRAFT_00282	KO:K08070	2-alkenal reductase [EC:1.3.1.74]		0.00E+00
2558669614	DRAFT_00282	Locus_type		CDS	
2558669614	DRAFT_00282	Product_name		Trypsin-like serine proteases, typically periplasmic, contain C-termina	
2558669614	DRAFT_00282	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669614	DRAFT_00282	Coordinates		31492..32715(+)	
2558669614	DRAFT_00282	DNA_length		1224bp	
2558669614	DRAFT_00282	Protein_length		407aa	
2558669614	DRAFT_00282	GC		0.55	
2558669614	DRAFT_00282	Transmembrane		Yes	
2558669615	DRAFT_00283	pfam01022	HTH_5		3.00E-09
2558669615	DRAFT_00283	Locus_type		CDS	
2558669615	DRAFT_00283	Product_name		transcriptional regulator, ArsR family	
2558669615	DRAFT_00283	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669615	DRAFT_00283	Coordinates		32839..33147(+)	
2558669615	DRAFT_00283	DNA_length		309bp	
2558669615	DRAFT_00283	Protein_length		102aa	
2558669615	DRAFT_00283	GC		0.56	
2558669616	DRAFT_00284	Locus_type		CDS	
2558669616	DRAFT_00284	Product_name		hypothetical protein	
2558669616	DRAFT_00284	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669616	DRAFT_00284	Coordinates		33144..33620(+)	
2558669616	DRAFT_00284	DNA_length		477bp	

2558669616	DRAFT_00284	Protein_length		158aa		
2558669616	DRAFT_00284	GC			0.55	
2558669616	DRAFT_00284	Transmembrane		Yes		
2558669617	DRAFT_00285	Metacyc	PWY-2301: <i>myo</i>-inositol biosynthesis			
2558669617	DRAFT_00285	Metacyc	PWY-6580: L-1-phosphatidyl-inositol biosynthesis (Mycobacteria)			
2558669617	DRAFT_00285	Metacyc	PWY1G-0: mycothiol biosynthesis			
2558669617	DRAFT_00285	Metacyc	PWY-6372: 1D-<i>myo</i>-inositol hexakisphosphate biosynthesis IV (<i>Dictyostelium</i>)			
2558669617	DRAFT_00285	Metacyc	PWY-6664: di-myo-inositol phosphate biosynthesis			
2558669617	DRAFT_00285	Metacyc	PWY-4661: 1D-<i>myo</i>-inositol hexakisphosphate biosynthesis III (<i>Spirodela polyrrhiza<			
2558669617	DRAFT_00285	COG_category	[I] Lipid transport and metabolism			
2558669617	DRAFT_00285	COG1260	Myo-inositol-1-phosphate synthase			2.00E-64
2558669617	DRAFT_00285	pfam07994	NAD_binding_5			1.60E-27
2558669617	DRAFT_00285	pfam01658	Inos-1-P_synth			4.40E-11
2558669617	DRAFT_00285	EC:5.5.1.4	Inositol-3-phosphate synthase.			
2558669617	DRAFT_00285	KO:K01858	myo-inositol-1-phosphate synthase [EC:5.5.1.4]			0.00E+00
2558669617	DRAFT_00285	Locus_type		CDS		
2558669617	DRAFT_00285	Product_name		Myo-inositol-1-phosphate synthase		
2558669617	DRAFT_00285	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669617	DRAFT_00285	Coordinates		33826..34866(-)		
2558669617	DRAFT_00285	DNA_length		1041bp		
2558669617	DRAFT_00285	Protein_length		346aa		
2558669617	DRAFT_00285	GC			0.57	
2558669618	DRAFT_00286	Locus_type		CDS		
2558669618	DRAFT_00286	Product_name		hypothetical protein		
2558669618	DRAFT_00286	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669618	DRAFT_00286	Coordinates		34872..35075(-)		
2558669618	DRAFT_00286	DNA_length		204bp		
2558669618	DRAFT_00286	Protein_length		67aa		
2558669618	DRAFT_00286	GC			0.54	
2558669618	DRAFT_00286	Transmembrane		Yes		
2558669619	DRAFT_00287	COG_category	[L] Replication, recombination and repair			

2558669619	DRAFT_00287	COG1697	DNA topoisomerase VI, subunit A		2.00E-83
2558669619	DRAFT_00287	pfam04406	TP6A_N		1.00E-16
2558669619	DRAFT_00287	EC:5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).		
2558669619	DRAFT_00287	KO:K03166	DNA topoisomerase VI subunit A [EC:5.99.1.3]		0.00E+00
2558669619	DRAFT_00287	Locus_type		CDS	
2558669619	DRAFT_00287	Product_name		DNA topoisomerase VI, subunit A	
2558669619	DRAFT_00287	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669619	DRAFT_00287	Coordinates		35350..36447(-)	
2558669619	DRAFT_00287	DNA_length		1098bp	
2558669619	DRAFT_00287	Protein_length		365aa	
2558669619	DRAFT_00287	GC		0.56	
2558669620	DRAFT_00288	COG_category	[L] Replication, recombination and repair		
2558669620	DRAFT_00288	COG1389	DNA topoisomerase VI, subunit B		6.00E-127
2558669620	DRAFT_00288	pfam13589	HATPase_c_3		1.90E-07
2558669620	DRAFT_00288	pfam09239	Topo-VIb_trans		1.10E-54
2558669620	DRAFT_00288	EC:5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).		
2558669620	DRAFT_00288	TIGR01052	DNA topoisomerase VI, B subunit		0.00E+00
2558669620	DRAFT_00288	KO:K03167	DNA topoisomerase VI subunit B [EC:5.99.1.3]		0.00E+00
2558669620	DRAFT_00288	Locus_type		CDS	
2558669620	DRAFT_00288	Product_name		DNA topoisomerase VI, B subunit	
2558669620	DRAFT_00288	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669620	DRAFT_00288	Coordinates		36410..37996(-)	
2558669620	DRAFT_00288	DNA_length		1587bp	
2558669620	DRAFT_00288	Protein_length		528aa	
2558669620	DRAFT_00288	GC		0.58	
2558669621	DRAFT_00289	COG_category	[R] General function prediction only		
2558669621	DRAFT_00289	COG1094	Predicted RNA-binding protein (contains KH domains)		1.00E-41
2558669621	DRAFT_00289	pfam00013	KH_1		3.00E-08
2558669621	DRAFT_00289	pfam00013	KH_1		2.00E-04
2558669621	DRAFT_00289	TIGR03665	arCOG04150 universal archaeal KH domain protein		2.30E-59
2558669621	DRAFT_00289	KO:K06961	ribosomal RNA assembly protein		0.00E+00
2558669621	DRAFT_00289	Locus_type		CDS	

2558669621	DRAFT_00289	Product_name		arCOG04150 universal archaeal KH domain protein	
2558669621	DRAFT_00289	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669621	DRAFT_00289	Coordinates		38200..38799(-)	
2558669621	DRAFT_00289	DNA_length		600bp	
2558669621	DRAFT_00289	Protein_length		199aa	
2558669621	DRAFT_00289	GC		0.59	
2558669622	DRAFT_00290	COG_category	[T] Signal transduction mechanisms		
2558669622	DRAFT_00290	COG_category	[D] Cell cycle control, cell division, chromosome partitioning		
2558669622	DRAFT_00290	COG1718	Serine/threonine protein kinase involved in cell cycle control		1.00E-60
2558669622	DRAFT_00290	pfam01163	RIO1		2.40E-49
2558669622	DRAFT_00290	EC:2.7.11.1	Non-specific serine/threonine protein kinase.		
2558669622	DRAFT_00290	KO:K07178	RIO kinase 1 [EC:2.7.11.1]		0.00E+00
2558669622	DRAFT_00290	Locus_type		CDS	
2558669622	DRAFT_00290	Product_name		Serine/threonine protein kinase involved in cell cycle control	
2558669622	DRAFT_00290	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669622	DRAFT_00290	Coordinates		38796..39590(-)	
2558669622	DRAFT_00290	DNA_length		795bp	
2558669622	DRAFT_00290	Protein_length		264aa	
2558669622	DRAFT_00290	GC		0.57	
2558669623	DRAFT_00291	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669623	DRAFT_00291	COG0576	Molecular chaperone GrpE (heat shock protein)		2.00E-27
2558669623	DRAFT_00291	pfam01025	GrpE		2.10E-42
2558669623	DRAFT_00291	KO:K03687	molecular chaperone GrpE		7.40E-28
2558669623	DRAFT_00291	Locus_type		CDS	
2558669623	DRAFT_00291	Product_name		Molecular chaperone GrpE (heat shock protein)	
2558669623	DRAFT_00291	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669623	DRAFT_00291	Coordinates		39808..40437(+)	
2558669623	DRAFT_00291	DNA_length		630bp	
2558669623	DRAFT_00291	Protein_length		209aa	
2558669623	DRAFT_00291	GC		0.57	
2558669624	DRAFT_00292	COG_category	[O] Posttranslational modification, protein turnover, chaperones		

2558669624	DRAFT_00292	COG0443	Molecular chaperone		0.00E+00
2558669624	DRAFT_00292	pfam00012	HSP70		0.00E+00
2558669624	DRAFT_00292	TIGR02350	chaperone protein DnaK		0.00E+00
2558669624	DRAFT_00292	KO:K04043	molecular chaperone DnaK		0.00E+00
2558669624	DRAFT_00292	Locus_type		CDS	
2558669624	DRAFT_00292	Product_name		Molecular chaperone	
2558669624	DRAFT_00292	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669624	DRAFT_00292	Coordinates		40430..42277(+)	
2558669624	DRAFT_00292	DNA_length		1848bp	
2558669624	DRAFT_00292	Protein_length		615aa	
2558669624	DRAFT_00292	GC		0.6	
2558669625	DRAFT_00293	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669625	DRAFT_00293	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain		3.00E-110
2558669625	DRAFT_00293	pfam01556	CTDII		9.20E-22
2558669625	DRAFT_00293	pfam00226	DnaJ		1.10E-28
2558669625	DRAFT_00293	pfam00684	DnaJ_CXXCXGXG		3.10E-14
2558669625	DRAFT_00293	TIGR02349	chaperone protein DnaJ		8.80E-127
2558669625	DRAFT_00293	KO:K03686	molecular chaperone DnaJ		0.00E+00
2558669625	DRAFT_00293	Locus_type		CDS	
2558669625	DRAFT_00293	Product_name		chaperone protein DnaJ	
2558669625	DRAFT_00293	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669625	DRAFT_00293	Coordinates		42290..43363(+)	
2558669625	DRAFT_00293	DNA_length		1074bp	
2558669625	DRAFT_00293	Protein_length		357aa	
2558669625	DRAFT_00293	GC		0.59	
2558669626	DRAFT_00294	COG_category	[S] Function unknown		
2558669626	DRAFT_00294	COG2412	Uncharacterized conserved protein		1.00E-15
2558669626	DRAFT_00294	pfam04242	DUF424		2.40E-20
2558669626	DRAFT_00294	KO:K09148	hypothetical protein		3.50E-19
2558669626	DRAFT_00294	Locus_type		CDS	
2558669626	DRAFT_00294	Product_name		Uncharacterized conserved protein	
2558669626	DRAFT_00294	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	

2558669626	DRAFT_00294	Coordinates		43360..43671(-)	
2558669626	DRAFT_00294	DNA_length		312bp	
2558669626	DRAFT_00294	Protein_length		103aa	
2558669626	DRAFT_00294	GC		0.57	
2558669627	DRAFT_00295	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669627	DRAFT_00295	COG1601	Translation initiation factor 2, beta subunit (eIF-2beta)/eIF-5 N-termina		2.00E-26
2558669627	DRAFT_00295	pfam01873	eIF-5_eIF-2B		1.90E-28
2558669627	DRAFT_00295	TIGR00311	translation initiation factor aIF-2, beta subunit, putative		5.50E-30
2558669627	DRAFT_00295	KO:K03238	translation initiation factor 2 subunit 2		1.40E-36
2558669627	DRAFT_00295	Locus_type		CDS	
2558669627	DRAFT_00295	Product_name		Translation initiation factor 2, beta subunit (eIF-2beta)/eIF-5 N-termir	
2558669627	DRAFT_00295	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669627	DRAFT_00295	Coordinates		43673..44089(-)	
2558669627	DRAFT_00295	DNA_length		417bp	
2558669627	DRAFT_00295	Protein_length		138aa	
2558669627	DRAFT_00295	GC		0.59	
2558669628	DRAFT_00296	Locus_type		CDS	
2558669628	DRAFT_00296	Product_name		hypothetical protein	
2558669628	DRAFT_00296	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669628	DRAFT_00296	Coordinates		44190..44381(+)	
2558669628	DRAFT_00296	DNA_length		192bp	
2558669628	DRAFT_00296	Protein_length		63aa	
2558669628	DRAFT_00296	GC		0.56	
2558669629	DRAFT_00297	KEGG_module	M00034: Methionine salvage pathway		
2558669629	DRAFT_00297	Metacyc	PWY-6756: <i>S</i>-methyl-5'-thioadenosine degradation II		
2558669629	DRAFT_00297	COG_category	[F] Nucleotide transport and metabolism		
2558669629	DRAFT_00297	COG0005	Purine nucleoside phosphorylase		8.00E-68
2558669629	DRAFT_00297	pfam01048	PNP_UDP_1		1.20E-40
2558669629	DRAFT_00297	EC:2.4.2.28	S-methyl-5'-thioadenosine phosphorylase.		
2558669629	DRAFT_00297	TIGR01694	5'-deoxy-5'-methylthioadenosine phosphorylase		2.00E-88
2558669629	DRAFT_00297	KO:K00772	5'-methylthioadenosine phosphorylase [EC:2.4.2.28]		0.00E+00

2558669629	DRAFT_00297	Locus_type		CDS	
2558669629	DRAFT_00297	Product_name		methylthioadenosine phosphorylase (EC 2.4.2.28)	
2558669629	DRAFT_00297	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669629	DRAFT_00297	Coordinates		44384..45283(+)	
2558669629	DRAFT_00297	DNA_length		900bp	
2558669629	DRAFT_00297	Protein_length		299aa	
2558669629	DRAFT_00297	GC		0.59	
2558669630	DRAFT_00298	Metacyc	PWY-6610: adenine and adenosine salvage IV		
2558669630	DRAFT_00298	Metacyc	P121-PWY: adenine and adenosine salvage I		
2558669630	DRAFT_00298	Metacyc	PWY-6605: adenine and adenosine salvage II		
2558669630	DRAFT_00298	IMG_pathway	479: Adenine conversion to AMP		
2558669630	DRAFT_00298	COG_category	[F] Nucleotide transport and metabolism		
2558669630	DRAFT_00298	COG0503	Adenine/guanine phosphoribosyltransferases and related PRPP-bindin		1.00E-41
2558669630	DRAFT_00298	pfam00156	Pribosyltran		7.70E-18
2558669630	DRAFT_00298	EC:2.4.2.7	Adenine phosphoribosyltransferase.		
2558669630	DRAFT_00298	TIGR01090	adenine phosphoribosyltransferase		9.60E-64
2558669630	DRAFT_00298	KO:K00759	adenine phosphoribosyltransferase [EC:2.4.2.7]		0.00E+00
2558669630	DRAFT_00298	ITERM:01830	adenine phosphoribosyltransferase (EC 2.4.2.7)		
2558669630	DRAFT_00298	Locus_type		CDS	
2558669630	DRAFT_00298	Product_name		adenine phosphoribosyltransferase (EC 2.4.2.7)	
2558669630	DRAFT_00298	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669630	DRAFT_00298	Coordinates		45283..45819(+)	
2558669630	DRAFT_00298	DNA_length		537bp	
2558669630	DRAFT_00298	Protein_length		178aa	
2558669630	DRAFT_00298	GC		0.58	
2558669631	DRAFT_00299	KEGG_module	M00035: Methionine degradation		
2558669631	DRAFT_00299	Metacyc	METHIONINE-DEG1-PWY: methionine degradation I (to homocysteine)		
2558669631	DRAFT_00299	Metacyc	PWY-5041: <i>S</i>-adenosyl-L-methionine cycle II		
2558669631	DRAFT_00299	IMG_pathway	398: S-adenosyl-L-homocysteine hydrolysis		
2558669631	DRAFT_00299	COG_category	[H] Coenzyme transport and metabolism		
2558669631	DRAFT_00299	COG0499	S-adenosylhomocysteine hydrolase		0.00E+00
2558669631	DRAFT_00299	pfam00670	AdoHcyase_NAD		4.90E-49

2558669631	DRAFT_00299	pfam05221	AdoHcyase		4.30E-51
2558669631	DRAFT_00299	EC:3.3.1.1	Adenosylhomocysteinase.		
2558669631	DRAFT_00299	TIGR00936	adenosylhomocysteinase		0.00E+00
2558669631	DRAFT_00299	KO:K01251	adenosylhomocysteinase [EC:3.3.1.1]		0.00E+00
2558669631	DRAFT_00299	ITERM:01674	adenosylhomocysteinase (EC 3.3.1.1)		
2558669631	DRAFT_00299	Locus_type		CDS	
2558669631	DRAFT_00299	Product_name		adenosylhomocysteinase (EC 3.3.1.1)	
2558669631	DRAFT_00299	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669631	DRAFT_00299	Coordinates		46079..47311(+)	
2558669631	DRAFT_00299	DNA_length		1233bp	
2558669631	DRAFT_00299	Protein_length		410aa	
2558669631	DRAFT_00299	GC		0.59	
2558669632	DRAFT_00300	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558669632	DRAFT_00300	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558669632	DRAFT_00300	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558669632	DRAFT_00300	IMG_pathway	498: L-methionine ligation to tRNA(Met)		
2558669632	DRAFT_00300	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669632	DRAFT_00300	COG0143	Methionyl-tRNA synthetase		0.00E+00
2558669632	DRAFT_00300	pfam08264	Anticodon_1		9.30E-10
2558669632	DRAFT_00300	pfam09334	tRNA-synt_1g		0.00E+00
2558669632	DRAFT_00300	EC:6.1.1.10	Methionine--tRNA ligase.		
2558669632	DRAFT_00300	TIGR00398	methionyl-tRNA synthetase		0.00E+00
2558669632	DRAFT_00300	KO:K01874	methionyl-tRNA synthetase [EC:6.1.1.10]		0.00E+00
2558669632	DRAFT_00300	ITERM:00402	methionyl-tRNA synthetase (EC 6.1.1.10)		
2558669632	DRAFT_00300	Locus_type		CDS	
2558669632	DRAFT_00300	Product_name		methionyl-tRNA synthetase (EC 6.1.1.10)	
2558669632	DRAFT_00300	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669632	DRAFT_00300	Coordinates		47354..49015(+)	
2558669632	DRAFT_00300	DNA_length		1662bp	
2558669632	DRAFT_00300	Protein_length		553aa	
2558669632	DRAFT_00300	GC		0.56	
2558669633	DRAFT_00301	COG_category	[D] Cell cycle control, cell division, chromosome partitioning		

2558669633	DRAFT_00301	COG0206	Cell division GTPase		2.00E-22
2558669633	DRAFT_00301	pfam00091	Tubulin		2.10E-16
2558669633	DRAFT_00301	Locus_type		CDS	
2558669633	DRAFT_00301	Product_name		Cell division GTPase	
2558669633	DRAFT_00301	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669633	DRAFT_00301	Coordinates		49012..50040(-)	
2558669633	DRAFT_00301	DNA_length		1029bp	
2558669633	DRAFT_00301	Protein_length		342aa	
2558669633	DRAFT_00301	GC		0.6	
2558669633	DRAFT_00301	Transmembrane		Yes	
2558669634	DRAFT_00302	pfam01883	DUF59		6.60E-07
2558669634	DRAFT_00302	Locus_type		CDS	
2558669634	DRAFT_00302	Product_name		Domain of unknown function DUF59	
2558669634	DRAFT_00302	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669634	DRAFT_00302	Coordinates		50151..50465(-)	
2558669634	DRAFT_00302	DNA_length		315bp	
2558669634	DRAFT_00302	Protein_length		104aa	
2558669634	DRAFT_00302	GC		0.58	
2558669635	DRAFT_00303	Metacyc	GLYCLEAV-PWY: glycine cleavage		
2558669635	DRAFT_00303	COG_category	[E] Amino acid transport and metabolism		
2558669635	DRAFT_00303	COG1003	Glycine cleavage system protein P (pyridoxal-binding), C-terminal doma		0.00E+00
2558669635	DRAFT_00303	pfam02347	GDC-P		8.20E-14
2558669635	DRAFT_00303	EC:1.4.4.2	Glycine dehydrogenase (decarboxylating).		
2558669635	DRAFT_00303	KO:K00283	glycine dehydrogenase subunit 2 [EC:1.4.4.2]		0.00E+00
2558669635	DRAFT_00303	Locus_type		CDS	
2558669635	DRAFT_00303	Product_name		glycine dehydrogenase (decarboxylating) beta subunit (EC 1.4.4.2)	
2558669635	DRAFT_00303	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669635	DRAFT_00303	Coordinates		50509..51987(-)	
2558669635	DRAFT_00303	DNA_length		1479bp	
2558669635	DRAFT_00303	Protein_length		492aa	
2558669635	DRAFT_00303	GC		0.6	

2558669636	DRAFT_00304	Metacyc	GLYCLEAV-PWY: glycine cleavage		
2558669636	DRAFT_00304	COG_category	[E] Amino acid transport and metabolism		
2558669636	DRAFT_00304	COG0403	Glycine cleavage system protein P (pyridoxal-binding), N-terminal dom		1.00E-127
2558669636	DRAFT_00304	pfam02347	GDC-P		1.00E-115
2558669636	DRAFT_00304	EC:1.4.4.2	Glycine dehydrogenase (decarboxylating).		
2558669636	DRAFT_00304	KO:K00282	glycine dehydrogenase subunit 1 [EC:1.4.4.2]		0.00E+00
2558669636	DRAFT_00304	Locus_type		CDS	
2558669636	DRAFT_00304	Product_name		Glycine cleavage system protein P (pyridoxal-binding), N-terminal dor	
2558669636	DRAFT_00304	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669636	DRAFT_00304	Coordinates		51989..53314(-)	
2558669636	DRAFT_00304	DNA_length		1326bp	
2558669636	DRAFT_00304	Protein_length		441aa	
2558669636	DRAFT_00304	GC		0.6	
2558669637	DRAFT_00305	Locus_type		CDS	
2558669637	DRAFT_00305	Product_name		hypothetical protein	
2558669637	DRAFT_00305	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669637	DRAFT_00305	Coordinates		53433..55115(+)	
2558669637	DRAFT_00305	DNA_length		1683bp	
2558669637	DRAFT_00305	Protein_length		560aa	
2558669637	DRAFT_00305	GC		0.57	
2558669637	DRAFT_00305	Transmembrane		Yes	
2558669638	DRAFT_00306	Metacyc	THIOREDOX-PWY: thioredoxin pathway		
2558669638	DRAFT_00306	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669638	DRAFT_00306	COG0492	Thioredoxin reductase		3.00E-87
2558669638	DRAFT_00306	pfam07992	Pyr_redox_2		9.10E-28
2558669638	DRAFT_00306	pfam00070	Pyr_redox		1.30E-15
2558669638	DRAFT_00306	EC:1.8.1.9	Thioredoxin-disulfide reductase.		
2558669638	DRAFT_00306	TIGR01292	thioredoxin-disulfide reductase		2.20E-120
2558669638	DRAFT_00306	KO:K00384	thioredoxin reductase (NADPH) [EC:1.8.1.9]		0.00E+00
2558669638	DRAFT_00306	Locus_type		CDS	
2558669638	DRAFT_00306	Product_name		thioredoxin-disulfide reductase	
2558669638	DRAFT_00306	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	

2558669638	DRAFT_00306	Coordinates		55176..56120(+)		
2558669638	DRAFT_00306	DNA_length		945bp		
2558669638	DRAFT_00306	Protein_length		314aa		
2558669638	DRAFT_00306	GC			0.59	
2558669639	DRAFT_00307	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669639	DRAFT_00307	COG1180	Pyruvate-formate lyase-activating enzyme			1.00E-63
2558669639	DRAFT_00307	pfam04055	Radical_SAM			1.40E-08
2558669639	DRAFT_00307	EC:1.97.1.4	[Formate-C-acetyltransferase]-activating enzyme.			
2558669639	DRAFT_00307	TIGR04337	AmmeMemoRadiSam system radical SAM enzyme			1.90E-101
2558669639	DRAFT_00307	KO:K04069	pyruvate formate lyase activating enzyme [EC:1.97.1.4]			0.00E+00
2558669639	DRAFT_00307	Locus_type		CDS		
2558669639	DRAFT_00307	Product_name		AmmeMemoRadiSam system radical SAM enzyme		
2558669639	DRAFT_00307	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669639	DRAFT_00307	Coordinates		56113..57285(-)		
2558669639	DRAFT_00307	DNA_length		1173bp		
2558669639	DRAFT_00307	Protein_length		390aa		
2558669639	DRAFT_00307	GC			0.58	
2558669640	DRAFT_00308	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA			
2558669640	DRAFT_00308	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2558669640	DRAFT_00308	KEGG_module	M00310: Pyruvate:ferredoxin oxidoreductase			
2558669640	DRAFT_00308	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			
2558669640	DRAFT_00308	Metacyc	PWY-6583: pyruvate fermentation to butanol I			
2558669640	DRAFT_00308	Metacyc	PWY-5538: pyruvate fermentation to acetate VI			
2558669640	DRAFT_00308	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)			
2558669640	DRAFT_00308	Metacyc	PWY-5483: pyruvate fermentation to acetate III			
2558669640	DRAFT_00308	Metacyc	PWY-6587: pyruvate fermentation to ethanol III			
2558669640	DRAFT_00308	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)			
2558669640	DRAFT_00308	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2558669640	DRAFT_00308	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)			
2558669640	DRAFT_00308	Metacyc	PWY-7003: glycerol degradation to butanol			
2558669640	DRAFT_00308	Metacyc	PWY-5493: reductive monocarboxylic acid cycle			
2558669640	DRAFT_00308	Metacyc	PWY-6588: pyruvate fermentation to acetone			

2558669640	DRAFT_00308	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate			
2558669640	DRAFT_00308	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)			
2558669640	DRAFT_00308	Metacyc	PWY-6863: pyruvate fermentation to hexanol			
2558669640	DRAFT_00308	Metacyc	PWY-5600: pyruvate fermentation to acetate VII			
2558669640	DRAFT_00308	Metacyc	P142-PWY: pyruvate fermentation to acetate I			
2558669640	DRAFT_00308	Metacyc	P23-PWY: reductive TCA cycle I			
2558669640	DRAFT_00308	Metacyc	PWY-5392: reductive TCA cycle II			
2558669640	DRAFT_00308	Metacyc	PWY-6876: isopropanol biosynthesis			
2558669640	DRAFT_00308	COG_category	[C] Energy production and conversion			
2558669640	DRAFT_00308	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin c			1.00E-71
2558669640	DRAFT_00308	pfam02775	TPP_enzyme_C			5.70E-25
2558669640	DRAFT_00308	EC:1.2.7.1	Pyruvate synthase.			
2558669640	DRAFT_00308	KO:K00170	pyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.1]			0.00E+00
2558669640	DRAFT_00308	Locus_type		CDS		
2558669640	DRAFT_00308	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		
2558669640	DRAFT_00308	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669640	DRAFT_00308	Coordinates		57331..58278(-)		
2558669640	DRAFT_00308	DNA_length		948bp		
2558669640	DRAFT_00308	Protein_length		315aa		
2558669640	DRAFT_00308	GC			0.58	

2558669641	DRAFT_00309	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle
2558669641	DRAFT_00309	KEGG_module	M00310: Pyruvate:ferredoxin oxidoreductase
2558669641	DRAFT_00309	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)
2558669641	DRAFT_00309	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA
2558669641	DRAFT_00309	Metacyc	PWY-5600: pyruvate fermentation to acetate VII
2558669641	DRAFT_00309	Metacyc	PWY-6876: isopropanol biosynthesis
2558669641	DRAFT_00309	Metacyc	PWY-6588: pyruvate fermentation to acetone
2558669641	DRAFT_00309	Metacyc	PWY-5538: pyruvate fermentation to acetate VI
2558669641	DRAFT_00309	Metacyc	PWY-5483: pyruvate fermentation to acetate III
2558669641	DRAFT_00309	Metacyc	PWY-6587: pyruvate fermentation to ethanol III
2558669641	DRAFT_00309	Metacyc	P42-PWY: incomplete reductive TCA cycle
2558669641	DRAFT_00309	Metacyc	PWY-6583: pyruvate fermentation to butanol I
2558669641	DRAFT_00309	Metacyc	P23-PWY: reductive TCA cycle I

2558669641	DRAFT_00309	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)		
2558669641	DRAFT_00309	Metacyc	PWY-5493: reductive monocarboxylic acid cycle		
2558669641	DRAFT_00309	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2558669641	DRAFT_00309	Metacyc	PWY-5392: reductive TCA cycle II		
2558669641	DRAFT_00309	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2558669641	DRAFT_00309	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2558669641	DRAFT_00309	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2558669641	DRAFT_00309	Metacyc	PWY-7003: glycerol degradation to butanol		
2558669641	DRAFT_00309	Metacyc	P142-PWY: pyruvate fermentation to acetate I		
2558669641	DRAFT_00309	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)		
2558669641	DRAFT_00309	COG_category	[C] Energy production and conversion		
2558669641	DRAFT_00309	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		2.00E-76
2558669641	DRAFT_00309	pfam01855	POR_N		1.50E-68
2558669641	DRAFT_00309	EC:1.2.7.1	Pyruvate synthase.		
2558669641	DRAFT_00309	KO:K00169	pyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.1]		0.00E+00
2558669641	DRAFT_00309	Locus_type		CDS	
2558669641	DRAFT_00309	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin	
2558669641	DRAFT_00309	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669641	DRAFT_00309	Coordinates		58279..59463(-)	
2558669641	DRAFT_00309	DNA_length		1185bp	
2558669641	DRAFT_00309	Protein_length		394aa	
2558669641	DRAFT_00309	GC		0.59	
2558669642	DRAFT_00310	KEGG_module	M00310: Pyruvate:ferredoxin oxidoreductase		
2558669642	DRAFT_00310	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2558669642	DRAFT_00310	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA		
2558669642	DRAFT_00310	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2558669642	DRAFT_00310	Metacyc	PWY-6876: isopropanol biosynthesis		
2558669642	DRAFT_00310	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2558669642	DRAFT_00310	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558669642	DRAFT_00310	Metacyc	PWY-6583: pyruvate fermentation to butanol I		
2558669642	DRAFT_00310	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2558669642	DRAFT_00310	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2558669642	DRAFT_00310	Metacyc	PWY-5600: pyruvate fermentation to acetate VII		

2558669642	DRAFT_00310	Metacyc	P142-PWY: pyruvate fermentation to acetate I			
2558669642	DRAFT_00310	Metacyc	PWY-5538: pyruvate fermentation to acetate VI			
2558669642	DRAFT_00310	Metacyc	PWY-5483: pyruvate fermentation to acetate III			
2558669642	DRAFT_00310	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)			
2558669642	DRAFT_00310	Metacyc	PWY-5493: reductive monocarboxylic acid cycle			
2558669642	DRAFT_00310	Metacyc	PWY-6588: pyruvate fermentation to acetone			
2558669642	DRAFT_00310	Metacyc	PWY-6587: pyruvate fermentation to ethanol III			
2558669642	DRAFT_00310	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)			
2558669642	DRAFT_00310	Metacyc	PWY-7003: glycerol degradation to butanol			
2558669642	DRAFT_00310	Metacyc	P23-PWY: reductive TCA cycle I			
2558669642	DRAFT_00310	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)			
2558669642	DRAFT_00310	Metacyc	PWY-5392: reductive TCA cycle II			
2558669642	DRAFT_00310	COG_category	[C] Energy production and conversion			
2558669642	DRAFT_00310	COG1144	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin c			3.00E-20
2558669642	DRAFT_00310	pfam14697	Fer4_21			4.90E-09
2558669642	DRAFT_00310	EC:1.2.7.1	Pyruvate synthase.			
2558669642	DRAFT_00310	TIGR02179	2-oxoacid:acceptor oxidoreductase, delta subunit, pyruvate/2-ketoisov			3.90E-34
2558669642	DRAFT_00310	KO:K00171	pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]			1.90E-21
2558669642	DRAFT_00310	Locus_type		CDS		
2558669642	DRAFT_00310	Product_name		2-oxoacid:acceptor oxidoreductase, delta subunit, pyruvate/2-ketoisc		
2558669642	DRAFT_00310	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669642	DRAFT_00310	Coordinates		59460..59726(-)		
2558669642	DRAFT_00310	DNA_length		267bp		
2558669642	DRAFT_00310	Protein_length		88aa		
2558669642	DRAFT_00310	GC			0.58	
2558669643	DRAFT_00311	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2558669643	DRAFT_00311	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			
2558669643	DRAFT_00311	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA			
2558669643	DRAFT_00311	KEGG_module	M00310: Pyruvate:ferredoxin oxidoreductase			
2558669643	DRAFT_00311	Metacyc	PWY-6583: pyruvate fermentation to butanol I			
2558669643	DRAFT_00311	Metacyc	PWY-5600: pyruvate fermentation to acetate VII			
2558669643	DRAFT_00311	Metacyc	P142-PWY: pyruvate fermentation to acetate I			
2558669643	DRAFT_00311	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)			

2558669643	DRAFT_00311	Metacyc	PWY-5483: pyruvate fermentation to acetate III		
2558669643	DRAFT_00311	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2558669643	DRAFT_00311	Metacyc	PWY-6876: isopropanol biosynthesis		
2558669643	DRAFT_00311	Metacyc	PWY-7003: glycerol degradation to butanol		
2558669643	DRAFT_00311	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2558669643	DRAFT_00311	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2558669643	DRAFT_00311	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2558669643	DRAFT_00311	Metacyc	PWY-5538: pyruvate fermentation to acetate VI		
2558669643	DRAFT_00311	Metacyc	PWY-6587: pyruvate fermentation to ethanol III		
2558669643	DRAFT_00311	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)		
2558669643	DRAFT_00311	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2558669643	DRAFT_00311	Metacyc	P23-PWY: reductive TCA cycle I		
2558669643	DRAFT_00311	Metacyc	PWY-5493: reductive monocarboxylic acid cycle		
2558669643	DRAFT_00311	Metacyc	PWY-5392: reductive TCA cycle II		
2558669643	DRAFT_00311	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558669643	DRAFT_00311	COG_category	[C] Energy production and conversion		
2558669643	DRAFT_00311	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		2.00E-26
2558669643	DRAFT_00311	pfam01558	POR		2.70E-35
2558669643	DRAFT_00311	EC:1.2.7.1	Pyruvate synthase.		
2558669643	DRAFT_00311	TIGR02175	2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-ketois		3.20E-63
2558669643	DRAFT_00311	KO:K00172	pyruvate ferredoxin oxidoreductase, gamma subunit [EC:1.2.7.1]		7.60E-41
2558669643	DRAFT_00311	Locus_type		CDS	
2558669643	DRAFT_00311	Product_name		2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-keto	
2558669643	DRAFT_00311	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3	
2558669643	DRAFT_00311	Coordinates		59723..60280(-)	
2558669643	DRAFT_00311	DNA_length		558bp	
2558669643	DRAFT_00311	Protein_length		185aa	
2558669643	DRAFT_00311	GC		0.63	
2558669644	DRAFT_00312	COG_category	[S] Function unknown		
2558669644	DRAFT_00312	COG5616	Predicted integral membrane protein		1.00E-35
2558669644	DRAFT_00312	pfam00211	Guanylate_cyc		3.30E-26
2558669644	DRAFT_00312	pfam13414	TPR_11		1.50E-09
2558669644	DRAFT_00312	EC:4.6.1.1	Adenylate cyclase.		

2558669644	DRAFT_00312	KO:K01768	adenylate cyclase [EC:4.6.1.1]			0.00E+00
2558669644	DRAFT_00312	Locus_type		CDS		
2558669644	DRAFT_00312	Product_name		Predicted integral membrane protein		
2558669644	DRAFT_00312	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669644	DRAFT_00312	Coordinates		60633..62579(-)		
2558669644	DRAFT_00312	DNA_length		1947bp		
2558669644	DRAFT_00312	Protein_length		648aa		
2558669644	DRAFT_00312	GC			0.57	
2558669644	DRAFT_00312	Fused_gene		Yes		

2558669645	DRAFT_00313	COG_category	[S] Function unknown			
2558669645	DRAFT_00313	COG5616	Predicted integral membrane protein			8.00E-36
2558669645	DRAFT_00313	pfam13414	TPR_11			5.70E-10
2558669645	DRAFT_00313	pfam00211	Guanylate_cyc			1.10E-20
2558669645	DRAFT_00313	EC:4.6.1.1	Adenylate cyclase.			
2558669645	DRAFT_00313	KO:K01768	adenylate cyclase [EC:4.6.1.1]			0.00E+00
2558669645	DRAFT_00313	Locus_type		CDS		
2558669645	DRAFT_00313	Product_name		Predicted integral membrane protein		
2558669645	DRAFT_00313	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669645	DRAFT_00313	Coordinates		62576..64504(-)		
2558669645	DRAFT_00313	DNA_length		1929bp		
2558669645	DRAFT_00313	Protein_length		642aa		
2558669645	DRAFT_00313	GC			0.57	

2558669646	DRAFT_00314	COG_category	[P] Inorganic ion transport and metabolism			
2558669646	DRAFT_00314	COG0798	Arsenite efflux pump ACR3 and related permeases			7.00E-90
2558669646	DRAFT_00314	pfam01758	SBF			4.60E-55
2558669646	DRAFT_00314	TIGR00832	arsenical-resistance protein			3.70E-129
2558669646	DRAFT_00314	KO:K03325	arsenite transporter, ACR3 family			0.00E+00
2558669646	DRAFT_00314	Locus_type		CDS		
2558669646	DRAFT_00314	Product_name		arsenical-resistance protein		
2558669646	DRAFT_00314	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669646	DRAFT_00314	Coordinates		64838..65992(+)		
2558669646	DRAFT_00314	DNA_length		1155bp		

2558669646	DRAFT_00314	Protein_length		384aa		
2558669646	DRAFT_00314	GC			0.58	
2558669646	DRAFT_00314	Transmembrane		Yes		
2558669647	DRAFT_00315	COG_category	[K] Transcription			
2558669647	DRAFT_00315	COG0640	Predicted transcriptional regulators			9.00E-09
2558669647	DRAFT_00315	pfam01022	HTH_5			1.40E-18
2558669647	DRAFT_00315	KO:K03892	ArsR family transcriptional regulator			2.20E-15
2558669647	DRAFT_00315	Locus_type		CDS		
2558669647	DRAFT_00315	Product_name		Predicted transcriptional regulators		
2558669647	DRAFT_00315	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669647	DRAFT_00315	Coordinates		65989..66366(+)		
2558669647	DRAFT_00315	DNA_length		378bp		
2558669647	DRAFT_00315	Protein_length		125aa		
2558669647	DRAFT_00315	GC			0.54	
2558669648	DRAFT_00316	COG_category	[T] Signal transduction mechanisms			
2558669648	DRAFT_00316	COG0394	Protein-tyrosine-phosphatase			2.00E-25
2558669648	DRAFT_00316	pfam01451	LMWPc			5.40E-27
2558669648	DRAFT_00316	Locus_type		CDS		
2558669648	DRAFT_00316	Product_name		Protein-tyrosine-phosphatase		
2558669648	DRAFT_00316	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669648	DRAFT_00316	Coordinates		66376..66783(+)		
2558669648	DRAFT_00316	DNA_length		408bp		
2558669648	DRAFT_00316	Protein_length		135aa		
2558669648	DRAFT_00316	GC			0.57	
2558669649	DRAFT_00317	Locus_type		CDS		
2558669649	DRAFT_00317	Product_name		hypothetical protein		
2558669649	DRAFT_00317	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669649	DRAFT_00317	Coordinates		67017..67325(+)		
2558669649	DRAFT_00317	DNA_length		309bp		
2558669649	DRAFT_00317	Protein_length		102aa		
2558669649	DRAFT_00317	GC			0.54	

2558669649	DRAFT_00317	Transmembrane		Yes		
2558669650	DRAFT_00318	COG_category	[K] Transcription			
2558669650	DRAFT_00318	COG1309	Transcriptional regulator			1.00E-11
2558669650	DRAFT_00318	pfam00440	TetR_N			3.50E-17
2558669650	DRAFT_00318	ITERM:02313	transcriptional regulator, TetR family			
2558669650	DRAFT_00318	Locus_type		CDS		
2558669650	DRAFT_00318	Product_name		transcriptional regulator, TetR family		
2558669650	DRAFT_00318	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669650	DRAFT_00318	Coordinates		67342..67950(+)		
2558669650	DRAFT_00318	DNA_length		609bp		
2558669650	DRAFT_00318	Protein_length		202aa		
2558669650	DRAFT_00318	GC			0.54	
2558669651	DRAFT_00319	Locus_type		CDS		
2558669651	DRAFT_00319	Product_name		hypothetical protein		
2558669651	DRAFT_00319	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669651	DRAFT_00319	Coordinates		68014..68427(+)		
2558669651	DRAFT_00319	DNA_length		414bp		
2558669651	DRAFT_00319	Protein_length		137aa		
2558669651	DRAFT_00319	GC			0.57	
2558669652	DRAFT_00320	pfam13847	Methyltransf_31			7.50E-20
2558669652	DRAFT_00320	Locus_type		CDS		
2558669652	DRAFT_00320	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2558669652	DRAFT_00320	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669652	DRAFT_00320	Coordinates		68424..68936(+)		
2558669652	DRAFT_00320	DNA_length		513bp		
2558669652	DRAFT_00320	Protein_length		170aa		
2558669652	DRAFT_00320	GC			0.58	
2558669653	DRAFT_00321	Locus_type		CDS		
2558669653	DRAFT_00321	Product_name		hypothetical protein		
2558669653	DRAFT_00321	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		

2558669653	DRAFT_00321	Coordinates		68946..69197(+)		
2558669653	DRAFT_00321	DNA_length		252bp		
2558669653	DRAFT_00321	Protein_length		83aa		
2558669653	DRAFT_00321	GC			0.49	
2558669653	DRAFT_00321	Signal_peptide		Yes		
2558669653	DRAFT_00321	Transmembrane		Yes		

2558669654	DRAFT_00322	COG_category	[L] Replication, recombination and repair			
2558669654	DRAFT_00322	COG3316	Transposase and inactivated derivatives			2.00E-15
2558669654	DRAFT_00322	pfam13610	DDE_Tnp_IS240			3.30E-23
2558669654	DRAFT_00322	Locus_type		CDS		
2558669654	DRAFT_00322	Product_name		Transposase and inactivated derivatives		
2558669654	DRAFT_00322	Scaffold		DRAFT_contig_70_22_len_70082_read_count_1249074.3		
2558669654	DRAFT_00322	Coordinates		69160..70080(-)		
2558669654	DRAFT_00322	DNA_length		921bp		
2558669654	DRAFT_00322	Protein_length		306aa		
2558669654	DRAFT_00322	GC			0.54	

2558669655	DRAFT_00323	pfam08494	DEAD_assoc			1.30E-17
2558669655	DRAFT_00323	Locus_type		CDS		
2558669655	DRAFT_00323	Product_name		Lhr-like helicases		
2558669655	DRAFT_00323	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669655	DRAFT_00323	Coordinates		3..884(+)		
2558669655	DRAFT_00323	DNA_length		882bp		
2558669655	DRAFT_00323	Protein_length		293aa		
2558669655	DRAFT_00323	GC			0.59	

2558669656	DRAFT_00324	Locus_type		CDS		
2558669656	DRAFT_00324	Product_name		hypothetical protein		
2558669656	DRAFT_00324	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669656	DRAFT_00324	Coordinates		863..1417(-)		
2558669656	DRAFT_00324	DNA_length		555bp		
2558669656	DRAFT_00324	Protein_length		184aa		
2558669656	DRAFT_00324	GC			0.6	

2558669657	DRAFT_00325	Locus_type		CDS		
2558669657	DRAFT_00325	Product_name		hypothetical protein		
2558669657	DRAFT_00325	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669657	DRAFT_00325	Coordinates		1417..2151(-)		
2558669657	DRAFT_00325	DNA_length		735bp		
2558669657	DRAFT_00325	Protein_length		244aa		
2558669657	DRAFT_00325	GC			0.58	

2558669658	DRAFT_00326	pfam02463	SMC_N			1.30E-34
2558669658	DRAFT_00326	Locus_type		CDS		
2558669658	DRAFT_00326	Product_name		RecF/RecN/SMC N terminal domain		
2558669658	DRAFT_00326	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669658	DRAFT_00326	Coordinates		2177..4183(-)		
2558669658	DRAFT_00326	DNA_length		2007bp		
2558669658	DRAFT_00326	Protein_length		668aa		
2558669658	DRAFT_00326	GC			0.59	

2558669659	DRAFT_00327	COG_category	[R] General function prediction only			
2558669659	DRAFT_00327	COG1201	Lhr-like helicases			0.00E+00
2558669659	DRAFT_00327	pfam00270	DEAD			1.10E-30
2558669659	DRAFT_00327	pfam00271	Helicase_C			1.20E-17
2558669659	DRAFT_00327	pfam08494	DEAD_assoc			7.70E-23
2558669659	DRAFT_00327	EC:3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; involved in cellular and subc			
2558669659	DRAFT_00327	KO:K03724	ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.4.-]			0.00E+00
2558669659	DRAFT_00327	Locus_type		CDS		
2558669659	DRAFT_00327	Product_name		Lhr-like helicases		
2558669659	DRAFT_00327	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669659	DRAFT_00327	Coordinates		4307..7147(+)		
2558669659	DRAFT_00327	DNA_length		2841bp		
2558669659	DRAFT_00327	Protein_length		946aa		
2558669659	DRAFT_00327	GC			0.61	

2558669660	DRAFT_00328	Locus_type		CDS		

2558669660	DRAFT_00328	Product_name		hypothetical protein	
2558669660	DRAFT_00328	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669660	DRAFT_00328	Coordinates		7184..7867(+)	
2558669660	DRAFT_00328	DNA_length		684bp	
2558669660	DRAFT_00328	Protein_length		227aa	
2558669660	DRAFT_00328	GC		0.52	
2558669661	DRAFT_00329	COG_category	[R] General function prediction only		
2558669661	DRAFT_00329	COG1407	Predicted ICC-like phosphoesterases		1.00E-23
2558669661	DRAFT_00329	TIGR00024	putative phosphoesterase, SbcD/Mre11-related		5.00E-24
2558669661	DRAFT_00329	ITERM:01876	putative phosphoesterase		
2558669661	DRAFT_00329	Locus_type		CDS	
2558669661	DRAFT_00329	Product_name		putative phosphoesterase	
2558669661	DRAFT_00329	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669661	DRAFT_00329	Coordinates		7869..8627(+)	
2558669661	DRAFT_00329	DNA_length		759bp	
2558669661	DRAFT_00329	Protein_length		252aa	
2558669661	DRAFT_00329	GC		0.58	
2558669662	DRAFT_00330	IMG_pathway	964: DsbC-DsbD disulfide-isomerizing reductive system		
2558669662	DRAFT_00330	pfam00085	Thioredoxin		1.60E-26
2558669662	DRAFT_00330	TIGR01068	thioredoxin		3.40E-35
2558669662	DRAFT_00330	KO:K03671	thioredoxin 1		2.20E-27
2558669662	DRAFT_00330	ITERM:01894	thioredoxin		
2558669662	DRAFT_00330	Locus_type		CDS	
2558669662	DRAFT_00330	Product_name		thioredoxin	
2558669662	DRAFT_00330	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669662	DRAFT_00330	Coordinates		8634..8969(-)	
2558669662	DRAFT_00330	DNA_length		336bp	
2558669662	DRAFT_00330	Protein_length		111aa	
2558669662	DRAFT_00330	GC		0.58	
2558669663	DRAFT_00331	COG_category	[R] General function prediction only		
2558669663	DRAFT_00331	COG_category	[L] Replication, recombination and repair		

2558669663	DRAFT_00331	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzym			9.00E-09
2558669663	DRAFT_00331	pfam00293	NUDIX			1.50E-20
2558669663	DRAFT_00331	Locus_type		CDS		
2558669663	DRAFT_00331	Product_name		NTP pyrophosphohydrolases including oxidative damage repair enzym		
2558669663	DRAFT_00331	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669663	DRAFT_00331	Coordinates		9078..9620(+)		
2558669663	DRAFT_00331	DNA_length		543bp		
2558669663	DRAFT_00331	Protein_length		180aa		
2558669663	DRAFT_00331	GC			0.58	
2558669664	DRAFT_00332	COG_category	[R] General function prediction only			
2558669664	DRAFT_00332	COG2236	Predicted phosphoribosyltransferases			6.00E-24
2558669664	DRAFT_00332	pfam00156	Pribosyltran			2.60E-29
2558669664	DRAFT_00332	TIGR01203	hypoxanthine phosphoribosyltransferase			6.50E-22
2558669664	DRAFT_00332	Locus_type		CDS		
2558669664	DRAFT_00332	Product_name		Predicted phosphoribosyltransferases		
2558669664	DRAFT_00332	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669664	DRAFT_00332	Coordinates		9936..10430(-)		
2558669664	DRAFT_00332	DNA_length		495bp		
2558669664	DRAFT_00332	Protein_length		164aa		
2558669664	DRAFT_00332	GC			0.56	
2558669665	DRAFT_00333	COG_category	[S] Function unknown			
2558669665	DRAFT_00333	COG1917	Uncharacterized conserved protein, contains double-stranded beta-hel			4.00E-20
2558669665	DRAFT_00333	pfam07883	Cupin_2			1.20E-22
2558669665	DRAFT_00333	Locus_type		CDS		
2558669665	DRAFT_00333	Product_name		Uncharacterized conserved protein, contains double-stranded beta-h		
2558669665	DRAFT_00333	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669665	DRAFT_00333	Coordinates		10601..10978(-)		
2558669665	DRAFT_00333	DNA_length		378bp		
2558669665	DRAFT_00333	Protein_length		125aa		
2558669665	DRAFT_00333	GC			0.51	
2558669666	DRAFT_00334	COG_category	[R] General function prediction only			

2558669666	DRAFT_00334	COG0656	Aldo/keto reductases, related to diketogulonate reductase		3.00E-66
2558669666	DRAFT_00334	pfam00248	Aldo_ket_red		1.30E-61
2558669666	DRAFT_00334	Locus_type		CDS	
2558669666	DRAFT_00334	Product_name		Aldo/keto reductases, related to diketogulonate reductase	
2558669666	DRAFT_00334	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669666	DRAFT_00334	Coordinates		11051..11884(-)	
2558669666	DRAFT_00334	DNA_length		834bp	
2558669666	DRAFT_00334	Protein_length		277aa	
2558669666	DRAFT_00334	GC		0.56	

2558669667	DRAFT_00335	Locus_type		tRNA	
2558669667	DRAFT_00335	Product_name		tRNA_Val_TAC	
2558669667	DRAFT_00335	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669667	DRAFT_00335	Coordinates		12032..12122(-)	
2558669667	DRAFT_00335	DNA_length		91bp	
2558669667	DRAFT_00335	GC		0.67	

2558669668	DRAFT_00336	KEGG_module	M00346: Formaldehyde assimilation, serine pathway
2558669668	DRAFT_00336	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds
2558669668	DRAFT_00336	KEGG_module	M00394: RNA degradosome
2558669668	DRAFT_00336	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate
2558669668	DRAFT_00336	KEGG_module	M00003: Gluconeogenesis, oxaloacetate => fructose-6P
2558669668	DRAFT_00336	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)
2558669668	DRAFT_00336	Metacyc	P122-PWY: heterolactic fermentation
2558669668	DRAFT_00336	Metacyc	PWY-5484: glycolysis II (from fructose-6P)
2558669668	DRAFT_00336	Metacyc	P124-PWY: Bifidobacterium shunt
2558669668	DRAFT_00336	Metacyc	PWY-6901: xylose degradation IV
2558669668	DRAFT_00336	Metacyc	PWY-7124: ethylene biosynthesis V
2558669668	DRAFT_00336	Metacyc	PWY-1042: glycolysis IV (plant cytosol)
2558669668	DRAFT_00336	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)
2558669668	DRAFT_00336	Metacyc	PWY-5723: Rubisco shunt
2558669668	DRAFT_00336	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)
2558669668	DRAFT_00336	Metacyc	P341-PWY: glycolysis V (Pyrococcus)
2558669668	DRAFT_00336	Metacyc	ANARESP1-PWY: respiration (anaerobic)

2558669668	DRAFT_00336	Metacyc	PWY-2221: Entner-Doudoroff pathway III (semi-phosphorylative)		
2558669668	DRAFT_00336	Metacyc	GLUCONEO-PWY: gluconeogenesis I		
2558669668	DRAFT_00336	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis		
2558669668	DRAFT_00336	Metacyc	PWY-7003: glycerol degradation to butanol		
2558669668	DRAFT_00336	Metacyc	GLYCOLYSIS: glycolysis I		
2558669668	DRAFT_00336	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)		
2558669668	DRAFT_00336	IMG_pathway	336: Standard Embden-Meyerhof pathway		
2558669668	DRAFT_00336	IMG_pathway	337: Embden-Meyerhof pathway without bisphosphoglycerate		
2558669668	DRAFT_00336	IMG_pathway	358: Conversion of glyceraldehyde to pyruvate		
2558669668	DRAFT_00336	IMG_pathway	359: Conversion of glyceraldehyde-3-phosphate to pyruvate		
2558669668	DRAFT_00336	IMG_pathway	959: Serine cycle		
2558669668	DRAFT_00336	COG_category	[G] Carbohydrate transport and metabolism		
2558669668	DRAFT_00336	COG0148	Enolase		0.00E+00
2558669668	DRAFT_00336	pfam00113	Enolase_C		2.70E-111
2558669668	DRAFT_00336	pfam03952	Enolase_N		3.80E-56
2558669668	DRAFT_00336	EC:4.2.1.11	Phosphopyruvate hydratase.		
2558669668	DRAFT_00336	TIGR01060	phosphopyruvate hydratase		0.00E+00
2558669668	DRAFT_00336	KO:K01689	enolase [EC:4.2.1.11]		0.00E+00
2558669668	DRAFT_00336	ITERM:01479	enolase (EC 4.2.1.11)		
2558669668	DRAFT_00336	Locus_type		CDS	
2558669668	DRAFT_00336	Product_name		enolase (EC 4.2.1.11)	
2558669668	DRAFT_00336	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669668	DRAFT_00336	Coordinates		12235..13533(+)	
2558669668	DRAFT_00336	DNA_length		1299bp	
2558669668	DRAFT_00336	Protein_length		432aa	
2558669668	DRAFT_00336	GC		0.58	
2558669669	DRAFT_00337	Locus_type		tRNA	
2558669669	DRAFT_00337	Product_name		tRNA_Pseudo_GGT	
2558669669	DRAFT_00337	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669669	DRAFT_00337	Coordinates		13551..13665(-)	
2558669669	DRAFT_00337	DNA_length		88bp	
2558669669	DRAFT_00337	GC		0.64	

2558669670	DRAFT_00338	Locus_type		miscRNA		
2558669670	DRAFT_00338	Product_name		Archaeal signal recognition particle RNA		
2558669670	DRAFT_00338	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669670	DRAFT_00338	Coordinates		13710..14022(-)		
2558669670	DRAFT_00338	DNA_length		313bp		
2558669670	DRAFT_00338	GC			0.66	
2558669671	DRAFT_00339	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2558669671	DRAFT_00339	COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle co			2.00E-43
2558669671	DRAFT_00339	pfam01171	ATP_bind_3			2.80E-17
2558669671	DRAFT_00339	TIGR00269	TIGR00269 family protein			1.40E-24
2558669671	DRAFT_00339	Locus_type		CDS		
2558669671	DRAFT_00339	Product_name		TIGR00269 family protein		
2558669671	DRAFT_00339	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669671	DRAFT_00339	Coordinates		14038..14970(-)		
2558669671	DRAFT_00339	DNA_length		933bp		
2558669671	DRAFT_00339	Protein_length		310aa		
2558669671	DRAFT_00339	GC			0.58	
2558669672	DRAFT_00340	pfam13180	PDZ_2			5.20E-09
2558669672	DRAFT_00340	pfam02163	Peptidase_M50			4.80E-25
2558669672	DRAFT_00340	Locus_type		CDS		
2558669672	DRAFT_00340	Product_name		Trypsin-like serine proteases, typically periplasmic, contain C-termina		
2558669672	DRAFT_00340	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669672	DRAFT_00340	Coordinates		15049..16656(+)		
2558669672	DRAFT_00340	DNA_length		1608bp		
2558669672	DRAFT_00340	Protein_length		535aa		
2558669672	DRAFT_00340	GC			0.58	
2558669672	DRAFT_00340	Transmembrane		Yes		
2558669673	DRAFT_00341	COG_category	[R] General function prediction only			
2558669673	DRAFT_00341	COG1537	Predicted RNA-binding proteins			3.00E-50
2558669673	DRAFT_00341	pfam03464	eRF1_2			2.40E-11
2558669673	DRAFT_00341	pfam03465	eRF1_3			4.50E-11

2558669673	DRAFT_00341	pfam03463	eRF1_1			9.40E-18
2558669673	DRAFT_00341	TIGR00111	mRNA surveillance protein pelota			4.20E-52
2558669673	DRAFT_00341	KO:K06965	protein pelota			0.00E+00
2558669673	DRAFT_00341	Locus_type		CDS		
2558669673	DRAFT_00341	Product_name		Predicted RNA-binding proteins		
2558669673	DRAFT_00341	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669673	DRAFT_00341	Coordinates		16946..18004(-)		
2558669673	DRAFT_00341	DNA_length		1059bp		
2558669673	DRAFT_00341	Protein_length		352aa		
2558669673	DRAFT_00341	GC			0.58	

2558669674	DRAFT_00342	pfam13662	Toprim_4			4.30E-08
2558669674	DRAFT_00342	Locus_type		CDS		
2558669674	DRAFT_00342	Product_name		DNA primase (bacterial type)		
2558669674	DRAFT_00342	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669674	DRAFT_00342	Coordinates		18014..19186(-)		
2558669674	DRAFT_00342	DNA_length		1173bp		
2558669674	DRAFT_00342	Protein_length		390aa		
2558669674	DRAFT_00342	GC			0.57	

2558669675	DRAFT_00343	Locus_type		CDS		
2558669675	DRAFT_00343	Product_name		hypothetical protein		
2558669675	DRAFT_00343	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669675	DRAFT_00343	Coordinates		19394..20035(+)		
2558669675	DRAFT_00343	DNA_length		642bp		
2558669675	DRAFT_00343	Protein_length		213aa		
2558669675	DRAFT_00343	GC			0.51	
2558669675	DRAFT_00343	Transmembrane		Yes		

2558669676	DRAFT_00344	Locus_type		CDS		
2558669676	DRAFT_00344	Product_name		hypothetical protein		
2558669676	DRAFT_00344	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669676	DRAFT_00344	Coordinates		20032..20166(-)		
2558669676	DRAFT_00344	DNA_length		135bp		

2558669676	DRAFT_00344	Protein_length		44aa		
2558669676	DRAFT_00344	GC			0.46	
2558669677	DRAFT_00345	COG_category	[L] Replication, recombination and repair			
2558669677	DRAFT_00345	COG3316	Transposase and inactivated derivatives			1.00E-12
2558669677	DRAFT_00345	pfam04434	SWIM			3.20E-04
2558669677	DRAFT_00345	pfam13610	DDE_Tnp_IS240			2.30E-19
2558669677	DRAFT_00345	Locus_type		CDS		
2558669677	DRAFT_00345	Product_name		Transposase and inactivated derivatives		
2558669677	DRAFT_00345	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669677	DRAFT_00345	Coordinates		20288..21493(+)		
2558669677	DRAFT_00345	DNA_length		1206bp		
2558669677	DRAFT_00345	Protein_length		401aa		
2558669677	DRAFT_00345	GC			0.55	
2558669678	DRAFT_00346	COG_category	[L] Replication, recombination and repair			
2558669678	DRAFT_00346	COG1658	Small primase-like proteins (Toprim domain)			2.00E-07
2558669678	DRAFT_00346	Locus_type		CDS		
2558669678	DRAFT_00346	Product_name		Small primase-like proteins (Toprim domain)		
2558669678	DRAFT_00346	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669678	DRAFT_00346	Coordinates		21871..22266(-)		
2558669678	DRAFT_00346	DNA_length		396bp		
2558669678	DRAFT_00346	Protein_length		131aa		
2558669678	DRAFT_00346	GC			0.57	
2558669679	DRAFT_00347	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2558669679	DRAFT_00347	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2558669679	DRAFT_00347	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558669679	DRAFT_00347	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669679	DRAFT_00347	COG0072	Phenylalanyl-tRNA synthetase beta subunit			3.00E-79
2558669679	DRAFT_00347	pfam03484	B5			2.70E-10
2558669679	DRAFT_00347	pfam03483	B3_4			1.10E-10
2558669679	DRAFT_00347	EC:6.1.1.20	Phenylalanine--tRNA ligase.			
2558669679	DRAFT_00347	TIGR00471	phenylalanyl-tRNA synthetase, beta subunit			0.00E+00

2558669679	DRAFT_00347	KO:K01890	phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]		0.00E+00
2558669679	DRAFT_00347	ITERM:00403	phenylalanyl-tRNA synthetase beta subunit (EC 6.1.1.20)		
2558669679	DRAFT_00347	Locus_type		CDS	
2558669679	DRAFT_00347	Product_name		phenylalanyl-tRNA synthetase beta subunit (EC 6.1.1.20)	
2558669679	DRAFT_00347	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669679	DRAFT_00347	Coordinates		22486..24120(-)	
2558669679	DRAFT_00347	DNA_length		1635bp	
2558669679	DRAFT_00347	Protein_length		544aa	
2558669679	DRAFT_00347	GC		0.6	
2558669680	DRAFT_00348	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558669680	DRAFT_00348	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558669680	DRAFT_00348	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558669680	DRAFT_00348	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669680	DRAFT_00348	COG0016	Phenylalanyl-tRNA synthetase alpha subunit		2.00E-80
2558669680	DRAFT_00348	pfam01409	tRNA-synt_2d		1.50E-81
2558669680	DRAFT_00348	EC:6.1.1.20	Phenylalanine--tRNA ligase.		
2558669680	DRAFT_00348	TIGR00468	phenylalanyl-tRNA synthetase, alpha subunit		2.00E-110
2558669680	DRAFT_00348	KO:K01889	phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]		0.00E+00
2558669680	DRAFT_00348	ITERM:01968	phenylalanyl-tRNA synthetase, alpha subunit (EC 6.1.1.20)		
2558669680	DRAFT_00348	Locus_type		CDS	
2558669680	DRAFT_00348	Product_name		phenylalanyl-tRNA synthetase, alpha subunit (EC 6.1.1.20)	
2558669680	DRAFT_00348	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669680	DRAFT_00348	Coordinates		24107..25591(-)	
2558669680	DRAFT_00348	DNA_length		1485bp	
2558669680	DRAFT_00348	Protein_length		494aa	
2558669680	DRAFT_00348	GC		0.58	
2558669681	DRAFT_00349	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558669681	DRAFT_00349	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558669681	DRAFT_00349	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558669681	DRAFT_00349	IMG_pathway	506: L-tryptophan ligation to tRNA(Trp)		
2558669681	DRAFT_00349	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669681	DRAFT_00349	COG0180	Tryptophanyl-tRNA synthetase		6.00E-63

2558669681	DRAFT_00349	pfam00579	tRNA-synt_1b			6.00E-32
2558669681	DRAFT_00349	EC:6.1.1.2	Tryptophan--tRNA ligase.			
2558669681	DRAFT_00349	TIGR00233	tryptophanyl-tRNA synthetase			1.60E-72
2558669681	DRAFT_00349	KO:K01867	tryptophanyl-tRNA synthetase [EC:6.1.1.2]			0.00E+00
2558669681	DRAFT_00349	ITERM:00401	tryptophanyl-tRNA synthetase (EC 6.1.1.2)			
2558669681	DRAFT_00349	Locus_type		CDS		
2558669681	DRAFT_00349	Product_name		tryptophanyl-tRNA synthetase (EC 6.1.1.2)		
2558669681	DRAFT_00349	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669681	DRAFT_00349	Coordinates		25597..26727(-)		
2558669681	DRAFT_00349	DNA_length		1131bp		
2558669681	DRAFT_00349	Protein_length		376aa		
2558669681	DRAFT_00349	GC			0.57	
2558669682	DRAFT_00350	KEGG_module	M00120: Coenzyme A biosynthesis, pantothenate => CoA			
2558669682	DRAFT_00350	Metacyc	COA-PWY: coenzyme A biosynthesis			
2558669682	DRAFT_00350	COG_category	[R] General function prediction only			
2558669682	DRAFT_00350	COG1019	Predicted nucleotidyltransferase			2.00E-40
2558669682	DRAFT_00350	pfam01467	CTP_transf_2			1.40E-11
2558669682	DRAFT_00350	EC:2.7.7.3	Pantetheine-phosphate adenylyltransferase.			
2558669682	DRAFT_00350	TIGR00125	cytidyltransferase-like domain			1.20E-15
2558669682	DRAFT_00350	KO:K02201	pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]			1.10E-32
2558669682	DRAFT_00350	Locus_type		CDS		
2558669682	DRAFT_00350	Product_name		cytidyltransferase-like domain		
2558669682	DRAFT_00350	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669682	DRAFT_00350	Coordinates		26777..27256(-)		
2558669682	DRAFT_00350	DNA_length		480bp		
2558669682	DRAFT_00350	Protein_length		159aa		
2558669682	DRAFT_00350	GC			0.58	
2558669683	DRAFT_00351	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669683	DRAFT_00351	COG0024	Methionine aminopeptidase			3.00E-37
2558669683	DRAFT_00351	pfam00557	Peptidase_M24			5.20E-30
2558669683	DRAFT_00351	EC:3.4.11.18	Methionyl aminopeptidase.			
2558669683	DRAFT_00351	TIGR00501	methionine aminopeptidase, type II			1.50E-72

2558669683	DRAFT_00351	KO:K01265	methionyl aminopeptidase [EC:3.4.11.18]		0.00E+00
2558669683	DRAFT_00351	Locus_type		CDS	
2558669683	DRAFT_00351	Product_name		methionine aminopeptidase, type II	
2558669683	DRAFT_00351	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669683	DRAFT_00351	Coordinates		27427..28233(+)	
2558669683	DRAFT_00351	DNA_length		807bp	
2558669683	DRAFT_00351	Protein_length		268aa	
2558669683	DRAFT_00351	GC		0.59	
2558669684	DRAFT_00352	Locus_type		CDS	
2558669684	DRAFT_00352	Product_name		hypothetical protein	
2558669684	DRAFT_00352	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669684	DRAFT_00352	Coordinates		28225..28428(-)	
2558669684	DRAFT_00352	DNA_length		204bp	
2558669684	DRAFT_00352	Protein_length		67aa	
2558669684	DRAFT_00352	GC		0.53	
2558669685	DRAFT_00353	COG_category	[S] Function unknown		
2558669685	DRAFT_00353	COG4046	Uncharacterized protein conserved in archaea		1.00E-79
2558669685	DRAFT_00353	pfam07431	DUF1512		7.30E-101
2558669685	DRAFT_00353	Locus_type		CDS	
2558669685	DRAFT_00353	Product_name		Uncharacterized protein conserved in archaea	
2558669685	DRAFT_00353	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669685	DRAFT_00353	Coordinates		28425..29546(-)	
2558669685	DRAFT_00353	DNA_length		1122bp	
2558669685	DRAFT_00353	Protein_length		373aa	
2558669685	DRAFT_00353	GC		0.55	
2558669685	DRAFT_00353	Transmembrane		Yes	
2558669686	DRAFT_00354	Locus_type		rRNA	
2558669686	DRAFT_00354	Gene_symbol		5S	
2558669686	DRAFT_00354	Product_name		5S rRNA. Archaeal TSU	
2558669686	DRAFT_00354	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669686	DRAFT_00354	Coordinates		29633..29752(-)	

2558669686	DRAFT_00354	DNA_length		120bp		
2558669686	DRAFT_00354	GC			0.62	
2558669687	DRAFT_00355	COG_category	[S] Function unknown			
2558669687	DRAFT_00355	COG2835	Uncharacterized conserved protein			2.00E-10
2558669687	DRAFT_00355	pfam03966	Trm112p			2.30E-10
2558669687	DRAFT_00355	Locus_type		CDS		
2558669687	DRAFT_00355	Product_name		Uncharacterized conserved protein		
2558669687	DRAFT_00355	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669687	DRAFT_00355	Coordinates		29812..30102(+)		
2558669687	DRAFT_00355	DNA_length		291bp		
2558669687	DRAFT_00355	Protein_length		96aa		
2558669687	DRAFT_00355	GC			0.54	
2558669688	DRAFT_00356	COG_category	[R] General function prediction only			
2558669688	DRAFT_00356	COG2403	Predicted GTPase			2.00E-122
2558669688	DRAFT_00356	pfam02492	cobW			4.10E-05
2558669688	DRAFT_00356	Locus_type		CDS		
2558669688	DRAFT_00356	Product_name		Predicted GTPase		
2558669688	DRAFT_00356	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669688	DRAFT_00356	Coordinates		30191..31507(+)		
2558669688	DRAFT_00356	DNA_length		1317bp		
2558669688	DRAFT_00356	Protein_length		438aa		
2558669688	DRAFT_00356	GC			0.56	
2558669689	DRAFT_00357	Locus_type		tRNA		
2558669689	DRAFT_00357	Product_name		tRNA_Thr_GGT		
2558669689	DRAFT_00357	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669689	DRAFT_00357	Coordinates		31553..31722(+)		
2558669689	DRAFT_00357	DNA_length		76bp		
2558669689	DRAFT_00357	GC			0.61	
2558669690	DRAFT_00358	COG_category	[S] Function unknown			
2558669690	DRAFT_00358	COG1379	Uncharacterized conserved protein			4.00E-81

2558669690	DRAFT_00358	TIGR00375	TIGR00375 family protein		9.10E-70
2558669690	DRAFT_00358	Locus_type		CDS	
2558669690	DRAFT_00358	Product_name		Uncharacterized conserved protein	
2558669690	DRAFT_00358	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669690	DRAFT_00358	Coordinates		31858..33066(-)	
2558669690	DRAFT_00358	DNA_length		1209bp	
2558669690	DRAFT_00358	Protein_length		402aa	
2558669690	DRAFT_00358	GC		0.57	
2558669691	DRAFT_00359	pfam02245	Pur_DNA_glyco		8.90E-18
2558669691	DRAFT_00359	Locus_type		CDS	
2558669691	DRAFT_00359	Product_name		3-methyladenine DNA glycosylase	
2558669691	DRAFT_00359	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669691	DRAFT_00359	Coordinates		33325..33474(+)	
2558669691	DRAFT_00359	DNA_length		150bp	
2558669691	DRAFT_00359	Protein_length		49aa	
2558669691	DRAFT_00359	GC		0.57	
2558669692	DRAFT_00360	pfam02245	Pur_DNA_glyco		7.60E-13
2558669692	DRAFT_00360	Locus_type		CDS	
2558669692	DRAFT_00360	Product_name		3-methyladenine DNA glycosylase	
2558669692	DRAFT_00360	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669692	DRAFT_00360	Coordinates		33507..33824(+)	
2558669692	DRAFT_00360	DNA_length		318bp	
2558669692	DRAFT_00360	Protein_length		105aa	
2558669692	DRAFT_00360	GC		0.51	
2558669693	DRAFT_00361	Locus_type		tRNA	
2558669693	DRAFT_00361	Product_name		tRNA_Pro_TGG	
2558669693	DRAFT_00361	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669693	DRAFT_00361	Coordinates		33849..33927(+)	
2558669693	DRAFT_00361	DNA_length		79bp	
2558669693	DRAFT_00361	GC		0.63	

2558669694	DRAFT_00362	KEGG_module	M00179: Ribosome, archaea		
2558669694	DRAFT_00362	KEGG_module	M00177: Ribosome, eukaryotes		
2558669694	DRAFT_00362	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669694	DRAFT_00362	COG4352	Ribosomal protein L13E		2.00E-03
2558669694	DRAFT_00362	KO:K02873	large subunit ribosomal protein L13e		2.70E-07
2558669694	DRAFT_00362	Locus_type		CDS	
2558669694	DRAFT_00362	Product_name		Ribosomal protein L13E	
2558669694	DRAFT_00362	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669694	DRAFT_00362	Coordinates		34036..34506(+)	
2558669694	DRAFT_00362	DNA_length		471bp	
2558669694	DRAFT_00362	Protein_length		156aa	
2558669694	DRAFT_00362	GC		0.59	
2558669695	DRAFT_00363	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP		
2558669695	DRAFT_00363	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis		
2558669695	DRAFT_00363	Metacyc	PWY-7187: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis II		
2558669695	DRAFT_00363	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis		
2558669695	DRAFT_00363	Metacyc	PWY0-166: superpathway of pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis (E.		
2558669695	DRAFT_00363	COG_category	[F] Nucleotide transport and metabolism		
2558669695	DRAFT_00363	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase		2.00E-27
2558669695	DRAFT_00363	pfam03477	ATP-cone		1.10E-04
2558669695	DRAFT_00363	pfam13597	NRDD		4.10E-13
2558669695	DRAFT_00363	EC:1.17.4.2	Ribonucleoside-triphosphate reductase.		
2558669695	DRAFT_00363	KO:K00527	ribonucleoside-triphosphate reductase [EC:1.17.4.2]		0.00E+00
2558669695	DRAFT_00363	Locus_type		CDS	
2558669695	DRAFT_00363	Product_name		Oxygen-sensitive ribonucleoside-triphosphate reductase	
2558669695	DRAFT_00363	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669695	DRAFT_00363	Coordinates		34958..37045(+)	
2558669695	DRAFT_00363	DNA_length		2088bp	
2558669695	DRAFT_00363	Protein_length		695aa	
2558669695	DRAFT_00363	GC		0.58	
2558669696	DRAFT_00364	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP		
2558669696	DRAFT_00364	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis		

2558669696	DRAFT_00364	Metacyc	PWY0-166: superpathway of pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis (E.			
2558669696	DRAFT_00364	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2558669696	DRAFT_00364	Metacyc	PWY-7184: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis I			
2558669696	DRAFT_00364	Metacyc	PWY-7198: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis IV			
2558669696	DRAFT_00364	Metacyc	PWY-6545: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis III			
2558669696	DRAFT_00364	Metacyc	PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP			
2558669696	DRAFT_00364	COG_category	[F] Nucleotide transport and metabolism			
2558669696	DRAFT_00364	COG0209	Ribonucleotide reductase, alpha subunit			1.00E-95
2558669696	DRAFT_00364	pfam12637	TSCPD			9.00E-22
2558669696	DRAFT_00364	pfam02867	Ribonuc_red_lgC			1.20E-122
2558669696	DRAFT_00364	pfam00317	Ribonuc_red_lgN			4.90E-13
2558669696	DRAFT_00364	EC:1.17.4.1	Ribonucleoside-diphosphate reductase.			
2558669696	DRAFT_00364	TIGR02504	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent			0.00E+00
2558669696	DRAFT_00364	KO:K00525	ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]			0.00E+00
2558669696	DRAFT_00364	ITERM:00726	ribonucleoside-diphosphate reductase class II (EC 1.17.4.-)			
2558669696	DRAFT_00364	Locus_type		CDS		
2558669696	DRAFT_00364	Product_name		ribonucleoside-diphosphate reductase class II (EC 1.17.4.-)		
2558669696	DRAFT_00364	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669696	DRAFT_00364	Coordinates		37092..39506(+)		
2558669696	DRAFT_00364	DNA_length		2415bp		
2558669696	DRAFT_00364	Protein_length		804aa		
2558669696	DRAFT_00364	GC			0.57	

2558669697	DRAFT_00365	Locus_type		CDS		
2558669697	DRAFT_00365	Product_name		hypothetical protein		
2558669697	DRAFT_00365	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669697	DRAFT_00365	Coordinates		39571..39810(+)		
2558669697	DRAFT_00365	DNA_length		240bp		
2558669697	DRAFT_00365	Protein_length		79aa		
2558669697	DRAFT_00365	GC			0.57	
2558669697	DRAFT_00365	Transmembrane		Yes		

2558669698	DRAFT_00366	Locus_type		CDS		
2558669698	DRAFT_00366	Product_name		hypothetical protein		

2558669698	DRAFT_00366	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669698	DRAFT_00366	Coordinates		39800..39937(-)	
2558669698	DRAFT_00366	DNA_length		138bp	
2558669698	DRAFT_00366	Protein_length		45aa	
2558669698	DRAFT_00366	GC		0.58	
2558669699	DRAFT_00367	KEGG_module	M00159: V-type ATPase, prokaryotes		
2558669699	DRAFT_00367	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis		
2558669699	DRAFT_00367	COG_category	[C] Energy production and conversion		
2558669699	DRAFT_00367	COG1394	Archaeal/vacuolar-type H+-ATPase subunit D		1.00E-37
2558669699	DRAFT_00367	pfam01813	ATP-synt_D		3.40E-53
2558669699	DRAFT_00367	EC:3.6.3.14	H(+)-transporting two-sector ATPase.		
2558669699	DRAFT_00367	TIGR00309	H(+)-transporting ATP synthase, vacuolar type, subunit D		7.60E-43
2558669699	DRAFT_00367	KO:K02120	V-type H+-transporting ATPase subunit D [EC:3.6.3.14]		0.00E+00
2558669699	DRAFT_00367	Locus_type		CDS	
2558669699	DRAFT_00367	Product_name		H(+)-transporting ATP synthase, vacuolar type, subunit D	
2558669699	DRAFT_00367	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669699	DRAFT_00367	Coordinates		39934..40575(-)	
2558669699	DRAFT_00367	DNA_length		642bp	
2558669699	DRAFT_00367	Protein_length		213aa	
2558669699	DRAFT_00367	GC		0.59	
2558669700	DRAFT_00368	KEGG_module	M00159: V-type ATPase, prokaryotes		
2558669700	DRAFT_00368	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis		
2558669700	DRAFT_00368	COG_category	[C] Energy production and conversion		
2558669700	DRAFT_00368	COG1156	Archaeal/vacuolar-type H+-ATPase subunit B		0.00E+00
2558669700	DRAFT_00368	pfam00306	ATP-synt_ab_C		4.90E-12
2558669700	DRAFT_00368	pfam00006	ATP-synt_ab		2.20E-56
2558669700	DRAFT_00368	pfam02874	ATP-synt_ab_N		4.10E-09
2558669700	DRAFT_00368	EC:3.6.3.14	H(+)-transporting two-sector ATPase.		
2558669700	DRAFT_00368	KO:K02118	V-type H+-transporting ATPase subunit B [EC:3.6.3.14]		0.00E+00
2558669700	DRAFT_00368	Locus_type		CDS	
2558669700	DRAFT_00368	Product_name		Archaeal/vacuolar-type H+-ATPase subunit B	
2558669700	DRAFT_00368	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	

2558669700	DRAFT_00368	Coordinates		40578..41990(-)		
2558669700	DRAFT_00368	DNA_length		1413bp		
2558669700	DRAFT_00368	Protein_length		470aa		
2558669700	DRAFT_00368	GC			0.6	
2558669701	DRAFT_00369	KEGG_module	M00159: V-type ATPase, prokaryotes			
2558669701	DRAFT_00369	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558669701	DRAFT_00369	COG_category	[C] Energy production and conversion			
2558669701	DRAFT_00369	COG1155	Archaeal/vacuolar-type H+-ATPase subunit A			0.00E+00
2558669701	DRAFT_00369	pfam00306	ATP-synt_ab_C			1.20E-15
2558669701	DRAFT_00369	pfam00006	ATP-synt_ab			2.90E-89
2558669701	DRAFT_00369	pfam02874	ATP-synt_ab_N			1.00E-10
2558669701	DRAFT_00369	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2558669701	DRAFT_00369	KO:K02117	V-type H+-transporting ATPase subunit A [EC:3.6.3.14]			0.00E+00
2558669701	DRAFT_00369	Locus_type		CDS		
2558669701	DRAFT_00369	Product_name		Archaeal/vacuolar-type H+-ATPase subunit A		
2558669701	DRAFT_00369	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669701	DRAFT_00369	Coordinates		41987..43774(-)		
2558669701	DRAFT_00369	DNA_length		1788bp		
2558669701	DRAFT_00369	Protein_length		595aa		
2558669701	DRAFT_00369	GC			0.6	
2558669702	DRAFT_00370	KEGG_module	M00159: V-type ATPase, prokaryotes			
2558669702	DRAFT_00370	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558669702	DRAFT_00370	COG_category	[C] Energy production and conversion			
2558669702	DRAFT_00370	COG1390	Archaeal/vacuolar-type H+-ATPase subunit E			3.00E-13
2558669702	DRAFT_00370	pfam01991	vATP-synt_E			3.00E-26
2558669702	DRAFT_00370	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2558669702	DRAFT_00370	KO:K02121	V-type H+-transporting ATPase subunit E [EC:3.6.3.14]			5.10E-27
2558669702	DRAFT_00370	Locus_type		CDS		
2558669702	DRAFT_00370	Product_name		Archaeal/vacuolar-type H+-ATPase subunit E		
2558669702	DRAFT_00370	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669702	DRAFT_00370	Coordinates		43991..44587(-)		
2558669702	DRAFT_00370	DNA_length		597bp		

2558669702	DRAFT_00370	Protein_length		198aa		
2558669702	DRAFT_00370	GC			0.59	
2558669703	DRAFT_00371	KEGG_module	M00159: V-type ATPase, prokaryotes			
2558669703	DRAFT_00371	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558669703	DRAFT_00371	COG_category	[C] Energy production and conversion			
2558669703	DRAFT_00371	COG1436	Archaeal/vacuolar-type H+-ATPase subunit F			1.00E-10
2558669703	DRAFT_00371	pfam01990	ATP-synt_F			3.70E-16
2558669703	DRAFT_00371	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2558669703	DRAFT_00371	KO:K02122	V-type H+-transporting ATPase subunit F [EC:3.6.3.14]			4.90E-23
2558669703	DRAFT_00371	Locus_type		CDS		
2558669703	DRAFT_00371	Product_name		Archaeal/vacuolar-type H+-ATPase subunit F		
2558669703	DRAFT_00371	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669703	DRAFT_00371	Coordinates		44593..44889(-)		
2558669703	DRAFT_00371	DNA_length		297bp		
2558669703	DRAFT_00371	Protein_length		98aa		
2558669703	DRAFT_00371	GC			0.62	
2558669704	DRAFT_00372	KEGG_module	M00159: V-type ATPase, prokaryotes			
2558669704	DRAFT_00372	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558669704	DRAFT_00372	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2558669704	DRAFT_00372	KO:K02121	V-type H+-transporting ATPase subunit E [EC:3.6.3.14]			2.30E-06
2558669704	DRAFT_00372	Locus_type		CDS		
2558669704	DRAFT_00372	Product_name		hypothetical protein		
2558669704	DRAFT_00372	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669704	DRAFT_00372	Coordinates		44886..45245(-)		
2558669704	DRAFT_00372	DNA_length		360bp		
2558669704	DRAFT_00372	Protein_length		119aa		
2558669704	DRAFT_00372	GC			0.53	
2558669705	DRAFT_00373	Locus_type		CDS		
2558669705	DRAFT_00373	Product_name		hypothetical protein		
2558669705	DRAFT_00373	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669705	DRAFT_00373	Coordinates		45253..45378(-)		

2558669705	DRAFT_00373	DNA_length		126bp		
2558669705	DRAFT_00373	Protein_length		41aa		
2558669705	DRAFT_00373	GC			0.53	
2558669706	DRAFT_00374	Metacyc	PWY-6087: 4-chlorocatechol degradation			
2558669706	DRAFT_00374	Metacyc	PWY-6089: 3-chlorocatechol degradation I (<i>ortho</i>)			
2558669706	DRAFT_00374	Metacyc	PWY-6193: 3-chlorocatechol degradation II (<i>ortho</i>)			
2558669706	DRAFT_00374	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2558669706	DRAFT_00374	COG0412	Dienelactone hydrolase and related enzymes			1.00E-39
2558669706	DRAFT_00374	pfam01738	DLH			3.20E-52
2558669706	DRAFT_00374	EC:3.1.1.45	Carboxymethylenebutenolidase.			
2558669706	DRAFT_00374	KO:K01061	carboxymethylenebutenolidase [EC:3.1.1.45]			0.00E+00
2558669706	DRAFT_00374	Locus_type		CDS		
2558669706	DRAFT_00374	Product_name		Dienelactone hydrolase and related enzymes		
2558669706	DRAFT_00374	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669706	DRAFT_00374	Coordinates		45398..46216(-)		
2558669706	DRAFT_00374	DNA_length		819bp		
2558669706	DRAFT_00374	Protein_length		272aa		
2558669706	DRAFT_00374	GC			0.56	
2558669707	DRAFT_00375	Locus_type		CDS		
2558669707	DRAFT_00375	Product_name		hypothetical protein		
2558669707	DRAFT_00375	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669707	DRAFT_00375	Coordinates		46306..46440(+)		
2558669707	DRAFT_00375	DNA_length		135bp		
2558669707	DRAFT_00375	Protein_length		44aa		
2558669707	DRAFT_00375	GC			0.56	
2558669708	DRAFT_00376	KEGG_module	M00029: Urea cycle			
2558669708	DRAFT_00376	Metacyc	ARGSYN-PWY: arginine biosynthesis I			
2558669708	DRAFT_00376	Metacyc	PWY-4981: proline biosynthesis II (from arginine)			
2558669708	DRAFT_00376	Metacyc	CITRULBIO-PWY: citrulline biosynthesis			
2558669708	DRAFT_00376	Metacyc	PWY-4984: urea cycle			
2558669708	DRAFT_00376	Metacyc	ARGSYNBSUB-PWY: arginine biosynthesis II (acetyl cycle)			

2558669708	DRAFT_00376	Metacyc	ARGININE-SYN4-PWY: arginine biosynthesis IV		
2558669708	DRAFT_00376	Metacyc	CITRULLINE-DEG-PWY: citrulline degradation		
2558669708	DRAFT_00376	COG_category	[E] Amino acid transport and metabolism		
2558669708	DRAFT_00376	COG0078	Ornithine carbamoyltransferase		6.00E-127
2558669708	DRAFT_00376	pfam02729	OTCace_N		6.10E-47
2558669708	DRAFT_00376	pfam00185	OTCace		4.60E-50
2558669708	DRAFT_00376	EC:2.1.3.3	Ornithine carbamoyltransferase.		
2558669708	DRAFT_00376	TIGR00658	ornithine carbamoyltransferase		2.20E-124
2558669708	DRAFT_00376	KO:K00611	ornithine carbamoyltransferase [EC:2.1.3.3]		0.00E+00
2558669708	DRAFT_00376	Locus_type		CDS	
2558669708	DRAFT_00376	Product_name		ornithine carbamoyltransferase (EC 2.1.3.3)	
2558669708	DRAFT_00376	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669708	DRAFT_00376	Coordinates		46403..47353(-)	
2558669708	DRAFT_00376	DNA_length		951bp	
2558669708	DRAFT_00376	Protein_length		316aa	
2558669708	DRAFT_00376	GC		0.59	
2558669709	DRAFT_00377	COG_category	[K] Transcription		
2558669709	DRAFT_00377	COG1308	Transcription factor homologous to NACalpha-BTF3		3.00E-18
2558669709	DRAFT_00377	pfam01849	NAC		7.50E-18
2558669709	DRAFT_00377	TIGR00264	alpha-NAC-related protein		4.80E-30
2558669709	DRAFT_00377	KO:K03626	nascent polypeptide-associated complex subunit alpha		1.90E-23
2558669709	DRAFT_00377	ITERM:02070	Nascent polypeptide associated complex NAC		
2558669709	DRAFT_00377	Locus_type		CDS	
2558669709	DRAFT_00377	Product_name		Nascent polypeptide associated complex NAC	
2558669709	DRAFT_00377	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669709	DRAFT_00377	Coordinates		47448..47777(-)	
2558669709	DRAFT_00377	DNA_length		330bp	
2558669709	DRAFT_00377	Protein_length		109aa	
2558669709	DRAFT_00377	GC		0.56	
2558669710	DRAFT_00378	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669710	DRAFT_00378	COG1370	Prefoldin, molecular chaperone implicated in de novo protein folding,		2.00E-26
2558669710	DRAFT_00378	pfam01472	PUA		5.40E-12

2558669710	DRAFT_00378	pfam14810	TGT_C2			3.20E-13
2558669710	DRAFT_00378	TIGR00451	uncharacterized domain 2			9.80E-12
2558669710	DRAFT_00378	KO:K07398	conserved protein with predicted RNA binding PUA domain			1.20E-26
2558669710	DRAFT_00378	Locus_type		CDS		
2558669710	DRAFT_00378	Product_name		Prefoldin, molecular chaperone implicated in de novo protein folding,		
2558669710	DRAFT_00378	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669710	DRAFT_00378	Coordinates		47774..48241(-)		
2558669710	DRAFT_00378	DNA_length		468bp		
2558669710	DRAFT_00378	Protein_length		155aa		
2558669710	DRAFT_00378	GC			0.6	
2558669711	DRAFT_00379	COG_category	[R] General function prediction only			
2558669711	DRAFT_00379	COG2262	GTPases			3.00E-87
2558669711	DRAFT_00379	pfam13167	GTP-bdg_N			4.00E-12
2558669711	DRAFT_00379	pfam01926	MMR_HSR1			2.60E-16
2558669711	DRAFT_00379	TIGR03156	GTP-binding protein HflX			3.00E-93
2558669711	DRAFT_00379	KO:K03665	GTP-binding protein HflX			0.00E+00
2558669711	DRAFT_00379	Locus_type		CDS		
2558669711	DRAFT_00379	Product_name		GTP-binding protein HflX		
2558669711	DRAFT_00379	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669711	DRAFT_00379	Coordinates		48276..49469(+)		
2558669711	DRAFT_00379	DNA_length		1194bp		
2558669711	DRAFT_00379	Protein_length		397aa		
2558669711	DRAFT_00379	GC			0.6	
2558669712	DRAFT_00380	COG_category	[S] Function unknown			
2558669712	DRAFT_00380	COG1303	Uncharacterized protein conserved in archaea			1.00E-47
2558669712	DRAFT_00380	pfam01994	Trm56			1.40E-41
2558669712	DRAFT_00380	EC:2.1.1.206	tRNA (cytidine(56)-2'-O)-methyltransferase.			
2558669712	DRAFT_00380	KO:K07254	tRNA (cytidine56-2'-O)-methyltransferase [EC:2.1.1.206]			1.30E-42
2558669712	DRAFT_00380	Locus_type		CDS		
2558669712	DRAFT_00380	Product_name		Uncharacterized protein conserved in archaea		
2558669712	DRAFT_00380	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669712	DRAFT_00380	Coordinates		49466..49993(+)		

2558669712	DRAFT_00380	DNA_length		528bp	
2558669712	DRAFT_00380	Protein_length		175aa	
2558669712	DRAFT_00380	GC		0.58	
2558669713	DRAFT_00381	COG_category	[K] Transcription		
2558669713	DRAFT_00381	COG1675	Transcription initiation factor IIE, alpha subunit		5.00E-26
2558669713	DRAFT_00381	pfam02002	TFIIE_alpha		4.10E-17
2558669713	DRAFT_00381	TIGR00373	transcription factor E		4.00E-37
2558669713	DRAFT_00381	KO:K03136	transcription initiation factor TFIIE subunit alpha		0.00E+00
2558669713	DRAFT_00381	Locus_type		CDS	
2558669713	DRAFT_00381	Product_name		Transcription factor E (TFE)	
2558669713	DRAFT_00381	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669713	DRAFT_00381	Coordinates		49990..50499(+)	
2558669713	DRAFT_00381	DNA_length		510bp	
2558669713	DRAFT_00381	Protein_length		169aa	
2558669713	DRAFT_00381	GC		0.57	
2558669714	DRAFT_00382	pfam01966	HD		7.40E-12
2558669714	DRAFT_00382	TIGR00277	uncharacterized domain HDIG		1.10E-17
2558669714	DRAFT_00382	TIGR00295	TIGR00295 family protein		4.40E-46
2558669714	DRAFT_00382	KO:K06950	uncharacterized protein		6.20E-27
2558669714	DRAFT_00382	Locus_type		CDS	
2558669714	DRAFT_00382	Product_name		uncharacterized domain HDIG	
2558669714	DRAFT_00382	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4	
2558669714	DRAFT_00382	Coordinates		50496..51047(+)	
2558669714	DRAFT_00382	DNA_length		552bp	
2558669714	DRAFT_00382	Protein_length		183aa	
2558669714	DRAFT_00382	GC		0.58	
2558669715	DRAFT_00383	KEGG_module	M00338: Cysteine biosynthesis, homocysteine + serine => cysteine		
2558669715	DRAFT_00383	Metacyc	LCYSDEG-PWY: L-cysteine degradation II		
2558669715	DRAFT_00383	Metacyc	PWY-801: homocysteine and cysteine interconversion		
2558669715	DRAFT_00383	Metacyc	HOMOCYSDEGR-PWY: cysteine biosynthesis/homocysteine degradation		
2558669715	DRAFT_00383	COG_category	[E] Amino acid transport and metabolism		

2558669715	DRAFT_00383	COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases			0.00E+00
2558669715	DRAFT_00383	pfam01053	Cys_Met_Meta_PP			0.00E+00
2558669715	DRAFT_00383	EC:4.4.1.1	Cystathionine gamma-lyase.			
2558669715	DRAFT_00383	KO:K01758	cystathionine gamma-lyase [EC:4.4.1.1]			0.00E+00
2558669715	DRAFT_00383	Locus_type		CDS		
2558669715	DRAFT_00383	Product_name		Cystathionine beta-lyases/cystathionine gamma-synthases		
2558669715	DRAFT_00383	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669715	DRAFT_00383	Coordinates		51485..52735(+)		
2558669715	DRAFT_00383	DNA_length		1251bp		
2558669715	DRAFT_00383	Protein_length		416aa		
2558669715	DRAFT_00383	GC			0.59	
2558669716	DRAFT_00384	COG_category	[R] General function prediction only			
2558669716	DRAFT_00384	COG1571	Predicted DNA-binding protein containing a Zn-ribbon domain			2.00E-71
2558669716	DRAFT_00384	pfam01336	tRNA_anti-codon			5.00E-05
2558669716	DRAFT_00384	pfam08489	DUF1743			5.50E-33
2558669716	DRAFT_00384	Locus_type		CDS		
2558669716	DRAFT_00384	Product_name		Predicted DNA-binding protein containing a Zn-ribbon domain		
2558669716	DRAFT_00384	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669716	DRAFT_00384	Coordinates		52713..53918(-)		
2558669716	DRAFT_00384	DNA_length		1206bp		
2558669716	DRAFT_00384	Protein_length		401aa		
2558669716	DRAFT_00384	GC			0.63	
2558669717	DRAFT_00385	pfam01037	AsnC_trans_reg			4.90E-12
2558669717	DRAFT_00385	Locus_type		CDS		
2558669717	DRAFT_00385	Product_name		transcriptional regulator, AsnC family		
2558669717	DRAFT_00385	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669717	DRAFT_00385	Coordinates		53965..54198(-)		
2558669717	DRAFT_00385	DNA_length		234bp		
2558669717	DRAFT_00385	Protein_length		77aa		
2558669717	DRAFT_00385	GC			0.57	
2558669718	DRAFT_00386	COG_category	[S] Function unknown			

2558669718	DRAFT_00386	COG2042	Uncharacterized conserved protein			5.00E-46
2558669718	DRAFT_00386	pfam04034	DUF367			7.10E-41
2558669718	DRAFT_00386	KO:K09140	pre-rRNA-processing protein TSR3			1.80E-36
2558669718	DRAFT_00386	Locus_type		CDS		
2558669718	DRAFT_00386	Product_name		Uncharacterized conserved protein		
2558669718	DRAFT_00386	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669718	DRAFT_00386	Coordinates		54347..54856(+)		
2558669718	DRAFT_00386	DNA_length		510bp		
2558669718	DRAFT_00386	Protein_length		169aa		
2558669718	DRAFT_00386	GC			0.6	
2558669719	DRAFT_00387	Locus_type		miscRNA		
2558669719	DRAFT_00387	Product_name		Archaeal RNase P		
2558669719	DRAFT_00387	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669719	DRAFT_00387	Coordinates		54899..55186(+)		
2558669719	DRAFT_00387	DNA_length		288bp		
2558669719	DRAFT_00387	GC			0.66	
2558669720	DRAFT_00388	pfam00171	Aldedh			1.10E-83
2558669720	DRAFT_00388	Locus_type		CDS		
2558669720	DRAFT_00388	Product_name		NAD-dependent aldehyde dehydrogenases		
2558669720	DRAFT_00388	Scaffold		DRAFT_contig_70_37_len_56021_read_count_1021764.4		
2558669720	DRAFT_00388	Coordinates		55280..56020(-)		
2558669720	DRAFT_00388	DNA_length		741bp		
2558669720	DRAFT_00388	Protein_length		246aa		
2558669720	DRAFT_00388	GC			0.55	
2558669721	DRAFT_00389	COG_category	[R] General function prediction only			
2558669721	DRAFT_00389	COG1310	Predicted metal-dependent protease of the PAD1/JAB1 superfamily			4.00E-06
2558669721	DRAFT_00389	pfam14464	Prok-JAB			3.20E-12
2558669721	DRAFT_00389	Locus_type		CDS		
2558669721	DRAFT_00389	Product_name		Predicted metal-dependent protease of the PAD1/JAB1 superfamily		
2558669721	DRAFT_00389	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669721	DRAFT_00389	Coordinates		274..660(-)		

2558669721	DRAFT_00389	DNA_length		387bp		
2558669721	DRAFT_00389	Protein_length		128aa		
2558669721	DRAFT_00389	GC			0.56	
2558669722	DRAFT_00390	Locus_type		CDS		
2558669722	DRAFT_00390	Product_name		hypothetical protein		
2558669722	DRAFT_00390	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669722	DRAFT_00390	Coordinates		670..825(-)		
2558669722	DRAFT_00390	DNA_length		156bp		
2558669722	DRAFT_00390	Protein_length		51aa		
2558669722	DRAFT_00390	GC			0.55	
2558669723	DRAFT_00391	KEGG_module	M00343: Archaeal proteasome			
2558669723	DRAFT_00391	KEGG_module	M00342: Bacterial proteasome			
2558669723	DRAFT_00391	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669723	DRAFT_00391	COG0638	20S proteasome, alpha and beta subunits			1.00E-50
2558669723	DRAFT_00391	pfam10584	Proteasome_A_N			3.40E-14
2558669723	DRAFT_00391	pfam00227	Proteasome			1.40E-54
2558669723	DRAFT_00391	EC:3.4.25.1	Proteasome endopeptidase complex.			
2558669723	DRAFT_00391	TIGR03633	proteasome endopeptidase complex, archaeal, alpha subunit			1.60E-91
2558669723	DRAFT_00391	KO:K03432	proteasome alpha subunit [EC:3.4.25.1]			0.00E+00
2558669723	DRAFT_00391	Locus_type		CDS		
2558669723	DRAFT_00391	Product_name		proteasome endopeptidase complex, archaeal, alpha subunit		
2558669723	DRAFT_00391	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669723	DRAFT_00391	Coordinates		997..1746(+)		
2558669723	DRAFT_00391	DNA_length		750bp		
2558669723	DRAFT_00391	Protein_length		249aa		
2558669723	DRAFT_00391	GC			0.57	
2558669724	DRAFT_00392	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669724	DRAFT_00392	COG1500	Predicted exosome subunit			5.00E-58
2558669724	DRAFT_00392	pfam09377	SBDS_C			2.80E-17
2558669724	DRAFT_00392	pfam01172	SBDS			3.00E-21
2558669724	DRAFT_00392	TIGR00291	rRNA metabolism protein, SBDS family			8.20E-68

2558669724	DRAFT_00392	KO:K14574	ribosome maturation protein SDO1			0.00E+00
2558669724	DRAFT_00392	Locus_type		CDS		
2558669724	DRAFT_00392	Product_name		rRNA metabolism protein, SBDS family		
2558669724	DRAFT_00392	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669724	DRAFT_00392	Coordinates		1763..2503(+)		
2558669724	DRAFT_00392	DNA_length		741bp		
2558669724	DRAFT_00392	Protein_length		246aa		
2558669724	DRAFT_00392	GC			0.58	
2558669725	DRAFT_00393	KEGG_module	M00391: Exosome, eukaryotes			
2558669725	DRAFT_00393	KEGG_module	M00390: Exosome, archaea			
2558669725	DRAFT_00393	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669725	DRAFT_00393	COG1097	RNA-binding protein Rrp4 and related proteins (contain S1 domain and			4.00E-46
2558669725	DRAFT_00393	pfam00575	S1			1.10E-06
2558669725	DRAFT_00393	pfam00013	KH_1			2.60E-12
2558669725	DRAFT_00393	KO:K03679	exosome complex component RRP4			0.00E+00
2558669725	DRAFT_00393	Locus_type		CDS		
2558669725	DRAFT_00393	Product_name		RNA-binding protein Rrp4 and related proteins (contain S1 domain an		
2558669725	DRAFT_00393	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669725	DRAFT_00393	Coordinates		2514..3191(+)		
2558669725	DRAFT_00393	DNA_length		678bp		
2558669725	DRAFT_00393	Protein_length		225aa		
2558669725	DRAFT_00393	GC			0.56	
2558669726	DRAFT_00394	KEGG_module	M00390: Exosome, archaea			
2558669726	DRAFT_00394	KEGG_module	M00391: Exosome, eukaryotes			
2558669726	DRAFT_00394	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669726	DRAFT_00394	COG0689	RNase PH			4.00E-68
2558669726	DRAFT_00394	pfam01138	RNase_PH			6.70E-34
2558669726	DRAFT_00394	pfam03725	RNase_PH_C			7.00E-13
2558669726	DRAFT_00394	TIGR02065	archaeal exosome-like complex exonuclease 1			3.70E-114
2558669726	DRAFT_00394	KO:K11600	exosome complex component RRP41			0.00E+00
2558669726	DRAFT_00394	Locus_type		CDS		
2558669726	DRAFT_00394	Product_name		ribosomal RNA-processing protein RRP41/SKI6 (EC 3.1.13.-)		

2558669726	DRAFT_00394	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669726	DRAFT_00394	Coordinates		3166..3933(+)		
2558669726	DRAFT_00394	DNA_length		768bp		
2558669726	DRAFT_00394	Protein_length		255aa		
2558669726	DRAFT_00394	GC			0.59	
2558669727	DRAFT_00395	KEGG_module	M00390: Exosome, archaea			
2558669727	DRAFT_00395	KEGG_module	M00391: Exosome, eukaryotes			
2558669727	DRAFT_00395	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669727	DRAFT_00395	COG2123	RNase PH-related exoribonuclease			4.00E-73
2558669727	DRAFT_00395	pfam01138	RNase_PH			7.90E-25
2558669727	DRAFT_00395	pfam03725	RNase_PH_C			2.20E-09
2558669727	DRAFT_00395	KO:K12589	exosome complex component RRP42			0.00E+00
2558669727	DRAFT_00395	ITERM:02704	ribosomal RNA-processing protein RRP42 (EC 3.1.13.-)			
2558669727	DRAFT_00395	Locus_type		CDS		
2558669727	DRAFT_00395	Product_name		ribosomal RNA-processing protein RRP42 (EC 3.1.13.-)		
2558669727	DRAFT_00395	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669727	DRAFT_00395	Coordinates		3944..4750(+)		
2558669727	DRAFT_00395	DNA_length		807bp		
2558669727	DRAFT_00395	Protein_length		268aa		
2558669727	DRAFT_00395	GC			0.57	
2558669728	DRAFT_00396	KEGG_module	M00177: Ribosome, eukaryotes			
2558669728	DRAFT_00396	KEGG_module	M00179: Ribosome, archaea			
2558669728	DRAFT_00396	pfam01780	Ribosomal_L37ae			2.50E-18
2558669728	DRAFT_00396	KO:K02921	large subunit ribosomal protein L37Ae			1.10E-14
2558669728	DRAFT_00396	Locus_type		CDS		
2558669728	DRAFT_00396	Product_name		Ribosomal L37ae protein family		
2558669728	DRAFT_00396	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669728	DRAFT_00396	Coordinates		4750..4974(+)		
2558669728	DRAFT_00396	DNA_length		225bp		
2558669728	DRAFT_00396	Protein_length		74aa		
2558669728	DRAFT_00396	GC			0.59	

2558669729	DRAFT_00397	Locus_type		CDS	
2558669729	DRAFT_00397	Product_name		hypothetical protein	
2558669729	DRAFT_00397	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669729	DRAFT_00397	Coordinates		4946..5185(+)	
2558669729	DRAFT_00397	DNA_length		240bp	
2558669729	DRAFT_00397	Protein_length		79aa	
2558669729	DRAFT_00397	GC		0.55	
2558669730	DRAFT_00398	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669730	DRAFT_00398	COG1382	Prefoldin, chaperonin cofactor		2.00E-13
2558669730	DRAFT_00398	pfam01920	Prefoldin_2		8.20E-15
2558669730	DRAFT_00398	TIGR02338	prefoldin, beta subunit, archaeal		1.20E-34
2558669730	DRAFT_00398	KO:K04798	prefoldin beta subunit		8.80E-33
2558669730	DRAFT_00398	Locus_type		CDS	
2558669730	DRAFT_00398	Product_name		prefoldin, beta subunit, archaeal	
2558669730	DRAFT_00398	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669730	DRAFT_00398	Coordinates		5210..5590(+)	
2558669730	DRAFT_00398	DNA_length		381bp	
2558669730	DRAFT_00398	Protein_length		126aa	
2558669730	DRAFT_00398	GC		0.56	
2558669731	DRAFT_00399	COG_category	[R] General function prediction only		
2558669731	DRAFT_00399	COG0618	Exopolyphosphatase-related proteins		1.00E-28
2558669731	DRAFT_00399	pfam01368	DHH		8.10E-12
2558669731	DRAFT_00399	pfam02272	DHHA1		2.00E-10
2558669731	DRAFT_00399	KO:K06881	phosphoesterase RecJ domain-containing protein		4.30E-34
2558669731	DRAFT_00399	Locus_type		CDS	
2558669731	DRAFT_00399	Product_name		Exopolyphosphatase-related proteins	
2558669731	DRAFT_00399	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669731	DRAFT_00399	Coordinates		5605..6612(+)	
2558669731	DRAFT_00399	DNA_length		1008bp	
2558669731	DRAFT_00399	Protein_length		335aa	
2558669731	DRAFT_00399	GC		0.6	

2558669732	DRAFT_00400	KEGG_module	M00096: C5 isoprenoid biosynthesis, non-mevalonate pathway			
2558669732	DRAFT_00400	KEGG_module	M00365: C10-C20 isoprenoid biosynthesis, archaea			
2558669732	DRAFT_00400	KEGG_module	M00364: C10-C20 isoprenoid biosynthesis, bacteria			
2558669732	DRAFT_00400	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			
2558669732	DRAFT_00400	KEGG_module	M00366: C10-C20 isoprenoid biosynthesis, plants			
2558669732	DRAFT_00400	KEGG_module	M00367: C10-C20 isoprenoid biosynthesis, non-plant eukaryotes			
2558669732	DRAFT_00400	Metacyc	PWY-6174: mevalonate pathway II (archaea)			
2558669732	DRAFT_00400	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis			
2558669732	DRAFT_00400	Metacyc	PWY-5123: <i>trans, trans</i>-farnesyl diphosphate biosynthesis			
2558669732	DRAFT_00400	Metacyc	PWY-7102: bisabolene biosynthesis			
2558669732	DRAFT_00400	Metacyc	PWY-922: mevalonate pathway I			
2558669732	DRAFT_00400	Metacyc	NONMEVIPP-PWY: methylerythritol phosphate pathway			
2558669732	DRAFT_00400	Metacyc	PWY-6859: <i>all-trans</i>-farnesol biosynthesis			
2558669732	DRAFT_00400	IMG_pathway	365: dimetyhylallyl pyrophosphate biosynthesis via isomerization of isopentenyl diphosphate			
2558669732	DRAFT_00400	COG_category	[I] Lipid transport and metabolism			
2558669732	DRAFT_00400	COG1443	Isopentenyldiphosphate isomerase			7.00E-30
2558669732	DRAFT_00400	pfam00293	NUDIX			2.30E-12
2558669732	DRAFT_00400	EC:5.3.3.2	Isopentenyl-diphosphate Delta-isomerase.			
2558669732	DRAFT_00400	TIGR02150	isopentenyl-diphosphate delta-isomerase, type 1			1.80E-35
2558669732	DRAFT_00400	KO:K01823	isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]			6.50E-29
2558669732	DRAFT_00400	ITERM:00469	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)			
2558669732	DRAFT_00400	Locus_type		CDS		
2558669732	DRAFT_00400	Product_name		isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)		
2558669732	DRAFT_00400	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669732	DRAFT_00400	Coordinates		6622..7164(-)		
2558669732	DRAFT_00400	DNA_length		543bp		
2558669732	DRAFT_00400	Protein_length		180aa		
2558669732	DRAFT_00400	GC			0.58	
2558669733	DRAFT_00401	Metacyc	PWY-6167: flavin biosynthesis II (archaea)			
2558669733	DRAFT_00401	COG_category	[K] Transcription			
2558669733	DRAFT_00401	COG_category	[H] Coenzyme transport and metabolism			
2558669733	DRAFT_00401	COG1339	Transcriptional regulator of a riboflavin/FAD biosynthetic operon			3.00E-44
2558669733	DRAFT_00401	pfam12802	MarR_2			1.60E-10

2558669733	DRAFT_00401	pfam01982	CTP-dep_RFKase		3.90E-39
2558669733	DRAFT_00401	EC:2.7.1.161	CTP-dependent riboflavin kinase.		
2558669733	DRAFT_00401	KO:K07732	riboflavin kinase, archaea type [EC:2.7.1.161]		0.00E+00
2558669733	DRAFT_00401	Locus_type		CDS	
2558669733	DRAFT_00401	Product_name		Transcriptional regulator of a riboflavin/FAD biosynthetic operon	
2558669733	DRAFT_00401	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669733	DRAFT_00401	Coordinates		7206..7901(-)	
2558669733	DRAFT_00401	DNA_length		696bp	
2558669733	DRAFT_00401	Protein_length		231aa	
2558669733	DRAFT_00401	GC		0.56	
2558669734	DRAFT_00402	Locus_type		CDS	
2558669734	DRAFT_00402	Product_name		Predicted membrane protein	
2558669734	DRAFT_00402	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669734	DRAFT_00402	Coordinates		7963..8544(+)	
2558669734	DRAFT_00402	DNA_length		582bp	
2558669734	DRAFT_00402	Protein_length		193aa	
2558669734	DRAFT_00402	GC		0.55	
2558669734	DRAFT_00402	Transmembrane		Yes	
2558669735	DRAFT_00403	Metacyc	PWYG-321: mycolate biosynthesis		
2558669735	DRAFT_00403	Metacyc	PWY-6972: oleandomycin activation/inactivation		
2558669735	DRAFT_00403	COG_category	[P] Inorganic ion transport and metabolism		
2558669735	DRAFT_00403	COG1122	ABC-type cobalt transport system, ATPase component		2.00E-63
2558669735	DRAFT_00403	pfam00005	ABC_tran		3.20E-28
2558669735	DRAFT_00403	EC:3.6.3.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; catalyzing transmembrane n		
2558669735	DRAFT_00403	KO:K16786	energy-coupling factor transport system ATP-binding protein [EC:3.6.3.		0.00E+00
2558669735	DRAFT_00403	Locus_type		CDS	
2558669735	DRAFT_00403	Product_name		ABC-type cobalt transport system, ATPase component	
2558669735	DRAFT_00403	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669735	DRAFT_00403	Coordinates		8600..9445(+)	
2558669735	DRAFT_00403	DNA_length		846bp	
2558669735	DRAFT_00403	Protein_length		281aa	
2558669735	DRAFT_00403	GC		0.59	

2558669736	DRAFT_00404	Metacyc	PWY-6972: oleandomycin activation/inactivation			
2558669736	DRAFT_00404	Metacyc	PWYG-321: mycolate biosynthesis			
2558669736	DRAFT_00404	COG_category	[P] Inorganic ion transport and metabolism			
2558669736	DRAFT_00404	COG1122	ABC-type cobalt transport system, ATPase component			9.00E-60
2558669736	DRAFT_00404	pfam00005	ABC_tran			6.20E-29
2558669736	DRAFT_00404	EC:3.6.3.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; catalyzing transmembrane			
2558669736	DRAFT_00404	KO:K16787	energy-coupling factor transport system ATP-binding protein [EC:3.6.3.			0.00E+00
2558669736	DRAFT_00404	Locus_type		CDS		
2558669736	DRAFT_00404	Product_name		ABC-type cobalt transport system, ATPase component		
2558669736	DRAFT_00404	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669736	DRAFT_00404	Coordinates		9442..10251(+)		
2558669736	DRAFT_00404	DNA_length		810bp		
2558669736	DRAFT_00404	Protein_length		269aa		
2558669736	DRAFT_00404	GC			0.61	
2558669737	DRAFT_00405	KEGG_module	M00245: Cobalt transport system			
2558669737	DRAFT_00405	KEGG_module	M00246: Nickel transport system			
2558669737	DRAFT_00405	COG_category	[P] Inorganic ion transport and metabolism			
2558669737	DRAFT_00405	COG0619	ABC-type cobalt transport system, permease component CbiQ and rela			2.00E-18
2558669737	DRAFT_00405	pfam02361	CbiQ			2.30E-29
2558669737	DRAFT_00405	KO:K02008	cobalt/nickel transport system permease protein			1.60E-30
2558669737	DRAFT_00405	Locus_type		CDS		
2558669737	DRAFT_00405	Product_name		ABC-type cobalt transport system, permease component CbiQ and re		
2558669737	DRAFT_00405	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669737	DRAFT_00405	Coordinates		10253..10999(+)		
2558669737	DRAFT_00405	DNA_length		747bp		
2558669737	DRAFT_00405	Protein_length		248aa		
2558669737	DRAFT_00405	GC			0.58	
2558669737	DRAFT_00405	Transmembrane		Yes		
2558669738	DRAFT_00406	Metacyc	PWY-1921: indole-3-acetate activation II			
2558669738	DRAFT_00406	COG_category	[L] Replication, recombination and repair			
2558669738	DRAFT_00406	COG1948	ERCC4-type nuclease			7.00E-44

2558669738	DRAFT_00406	pfam02732	ERCC4		7.60E-24
2558669738	DRAFT_00406	EC:3.1.-	Hydrolases. Acting on ester bonds.		
2558669738	DRAFT_00406	KO:K10848	DNA excision repair protein ERCC-4 [EC:3.1.-.-]		5.10E-39
2558669738	DRAFT_00406	Locus_type		CDS	
2558669738	DRAFT_00406	Product_name		ERCC4-type nuclease	
2558669738	DRAFT_00406	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669738	DRAFT_00406	Coordinates		10996..11682(+)	
2558669738	DRAFT_00406	DNA_length		687bp	
2558669738	DRAFT_00406	Protein_length		228aa	
2558669738	DRAFT_00406	GC		0.6	
2558669739	DRAFT_00407	COG_category	[R] General function prediction only		
2558669739	DRAFT_00407	COG2085	Predicted dinucleotide-binding enzymes		1.00E-31
2558669739	DRAFT_00407	pfam03807	F420_oxidored		2.90E-19
2558669739	DRAFT_00407	TIGR01915	NADPH-dependent F420 reductase		1.60E-48
2558669739	DRAFT_00407	Locus_type		CDS	
2558669739	DRAFT_00407	Product_name		NADPH-dependent F420 reductase	
2558669739	DRAFT_00407	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669739	DRAFT_00407	Coordinates		11679..12305(+)	
2558669739	DRAFT_00407	DNA_length		627bp	
2558669739	DRAFT_00407	Protein_length		208aa	
2558669739	DRAFT_00407	GC		0.6	
2558669740	DRAFT_00408	COG_category	[E] Amino acid transport and metabolism		
2558669740	DRAFT_00408	COG0308	Aminopeptidase N		1.00E-126
2558669740	DRAFT_00408	pfam11838	ERAP1_C		8.70E-30
2558669740	DRAFT_00408	pfam01433	Peptidase_M1		4.90E-103
2558669740	DRAFT_00408	EC:3.4.11.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Aminopeptidases.		
2558669740	DRAFT_00408	KO:K13722	tricorn protease interacting factor F2/3 [EC:3.4.11.-]		0.00E+00
2558669740	DRAFT_00408	Locus_type		CDS	
2558669740	DRAFT_00408	Product_name		Aminopeptidase N	
2558669740	DRAFT_00408	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669740	DRAFT_00408	Coordinates		12372..14777(-)	
2558669740	DRAFT_00408	DNA_length		2406bp	

2558669740	DRAFT_00408	Protein_length		801aa	
2558669740	DRAFT_00408	GC		0.6	
2558669741	DRAFT_00409	Locus_type		CDS	
2558669741	DRAFT_00409	Product_name		hypothetical protein	
2558669741	DRAFT_00409	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669741	DRAFT_00409	Coordinates		14922..15377(-)	
2558669741	DRAFT_00409	DNA_length		456bp	
2558669741	DRAFT_00409	Protein_length		151aa	
2558669741	DRAFT_00409	GC		0.52	
2558669742	DRAFT_00410	Locus_type		CDS	
2558669742	DRAFT_00410	Product_name		hypothetical protein	
2558669742	DRAFT_00410	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669742	DRAFT_00410	Coordinates		16110..16511(-)	
2558669742	DRAFT_00410	DNA_length		402bp	
2558669742	DRAFT_00410	Protein_length		133aa	
2558669742	DRAFT_00410	GC		0.57	
2558669742	DRAFT_00410	Signal_peptide		Yes	
2558669742	DRAFT_00410	Transmembrane		Yes	
2558669743	DRAFT_00411	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669743	DRAFT_00411	COG0480	Translation elongation factors (GTPases)		0.00E+00
2558669743	DRAFT_00411	pfam03764	EFG_IV		2.80E-21
2558669743	DRAFT_00411	pfam00679	EFG_C		2.30E-18
2558669743	DRAFT_00411	pfam00009	GTP_EFTU		1.40E-56
2558669743	DRAFT_00411	pfam03144	GTP_EFTU_D2		9.40E-11
2558669743	DRAFT_00411	pfam14492	EFG_II		2.90E-18
2558669743	DRAFT_00411	TIGR00231	small GTP-binding protein domain		2.20E-22
2558669743	DRAFT_00411	TIGR00490	translation elongation factor aEF-2		0.00E+00
2558669743	DRAFT_00411	KO:K03234	elongation factor 2		0.00E+00
2558669743	DRAFT_00411	Locus_type		CDS	
2558669743	DRAFT_00411	Product_name		translation elongation factor aEF-2	
2558669743	DRAFT_00411	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	

2558669743	DRAFT_00411	Coordinates		16679..18871(-)		
2558669743	DRAFT_00411	DNA_length		2193bp		
2558669743	DRAFT_00411	Protein_length		730aa		
2558669743	DRAFT_00411	GC			0.58	
2558669744	DRAFT_00412	pfam09594	DUF2029			1.40E-06
2558669744	DRAFT_00412	Locus_type		CDS		
2558669744	DRAFT_00412	Product_name		Protein of unknown function (DUF2029)		
2558669744	DRAFT_00412	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669744	DRAFT_00412	Coordinates		18926..19882(-)		
2558669744	DRAFT_00412	DNA_length		957bp		
2558669744	DRAFT_00412	Protein_length		318aa		
2558669744	DRAFT_00412	GC			0.57	
2558669744	DRAFT_00412	Transmembrane		Yes		
2558669745	DRAFT_00413	Locus_type		CDS		
2558669745	DRAFT_00413	Product_name		hypothetical protein		
2558669745	DRAFT_00413	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669745	DRAFT_00413	Coordinates		20030..20251(+)		
2558669745	DRAFT_00413	DNA_length		222bp		
2558669745	DRAFT_00413	Protein_length		73aa		
2558669745	DRAFT_00413	GC			0.56	
2558669745	DRAFT_00413	Transmembrane		Yes		
2558669746	DRAFT_00414	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669746	DRAFT_00414	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal			1.00E-52
2558669746	DRAFT_00414	pfam13180	PDZ_2			1.20E-10
2558669746	DRAFT_00414	pfam13365	Trypsin_2			2.90E-20
2558669746	DRAFT_00414	Locus_type		CDS		
2558669746	DRAFT_00414	Product_name		Trypsin-like serine proteases, typically periplasmic, contain C-termina		
2558669746	DRAFT_00414	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669746	DRAFT_00414	Coordinates		20426..21400(-)		
2558669746	DRAFT_00414	DNA_length		975bp		
2558669746	DRAFT_00414	Protein_length		324aa		

2558669746	DRAFT_00414	GC			0.62	
2558669747	DRAFT_00415	COG_category	[K] Transcription			
2558669747	DRAFT_00415	COG1733	Predicted transcriptional regulators			1.00E-18
2558669747	DRAFT_00415	pfam01638	HxlR			3.60E-23
2558669747	DRAFT_00415	ITERM:02284	transcriptional regulator, HxlR family			
2558669747	DRAFT_00415	Locus_type		CDS		
2558669747	DRAFT_00415	Product_name		transcriptional regulator, HxlR family		
2558669747	DRAFT_00415	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669747	DRAFT_00415	Coordinates		21599..21973(+)		
2558669747	DRAFT_00415	DNA_length		375bp		
2558669747	DRAFT_00415	Protein_length		124aa		
2558669747	DRAFT_00415	GC			0.57	
2558669748	DRAFT_00416	Locus_type		CDS		
2558669748	DRAFT_00416	Product_name		hypothetical protein		
2558669748	DRAFT_00416	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669748	DRAFT_00416	Coordinates		21980..22378(-)		
2558669748	DRAFT_00416	DNA_length		399bp		
2558669748	DRAFT_00416	Protein_length		132aa		
2558669748	DRAFT_00416	GC			0.55	
2558669748	DRAFT_00416	Transmembrane		Yes		
2558669749	DRAFT_00417	Locus_type		CDS		
2558669749	DRAFT_00417	Product_name		hypothetical protein		
2558669749	DRAFT_00417	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669749	DRAFT_00417	Coordinates		22419..22853(-)		
2558669749	DRAFT_00417	DNA_length		435bp		
2558669749	DRAFT_00417	Protein_length		144aa		
2558669749	DRAFT_00417	GC			0.58	
2558669749	DRAFT_00417	Transmembrane		Yes		
2558669750	DRAFT_00418	Locus_type		CDS		
2558669750	DRAFT_00418	Product_name		hypothetical protein		

2558669750	DRAFT_00418	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669750	DRAFT_00418	Coordinates		22910..23077(+)	
2558669750	DRAFT_00418	DNA_length		168bp	
2558669750	DRAFT_00418	Protein_length		55aa	
2558669750	DRAFT_00418	GC		0.55	
2558669750	DRAFT_00418	Transmembrane		Yes	
2558669751	DRAFT_00419	COG_category	[R] General function prediction only		
2558669751	DRAFT_00419	COG1832	Predicted CoA-binding protein		3.00E-32
2558669751	DRAFT_00419	pfam13380	CoA_binding_2		3.60E-29
2558669751	DRAFT_00419	Locus_type		CDS	
2558669751	DRAFT_00419	Product_name		Predicted CoA-binding protein	
2558669751	DRAFT_00419	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669751	DRAFT_00419	Coordinates		23305..23712(+)	
2558669751	DRAFT_00419	DNA_length		408bp	
2558669751	DRAFT_00419	Protein_length		135aa	
2558669751	DRAFT_00419	GC		0.56	
2558669752	DRAFT_00420	Locus_type		CDS	
2558669752	DRAFT_00420	Product_name		hypothetical protein	
2558669752	DRAFT_00420	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669752	DRAFT_00420	Coordinates		23712..23903(+)	
2558669752	DRAFT_00420	DNA_length		192bp	
2558669752	DRAFT_00420	Protein_length		63aa	
2558669752	DRAFT_00420	GC		0.59	
2558669753	DRAFT_00421	pfam14907	NTP_transf_5		8.60E-07
2558669753	DRAFT_00421	Locus_type		CDS	
2558669753	DRAFT_00421	Product_name		Uncharacterised nucleotidyltransferase	
2558669753	DRAFT_00421	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669753	DRAFT_00421	Coordinates		24092..24853(+)	
2558669753	DRAFT_00421	DNA_length		762bp	
2558669753	DRAFT_00421	Protein_length		253aa	
2558669753	DRAFT_00421	GC		0.54	

2558669754	DRAFT_00422	Locus_type		CDS	
2558669754	DRAFT_00422	Product_name		hypothetical protein	
2558669754	DRAFT_00422	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669754	DRAFT_00422	Coordinates		24850..25215(-)	
2558669754	DRAFT_00422	DNA_length		366bp	
2558669754	DRAFT_00422	Protein_length		121aa	
2558669754	DRAFT_00422	GC		0.57	
2558669755	DRAFT_00423	Locus_type		CDS	
2558669755	DRAFT_00423	Product_name		hypothetical protein	
2558669755	DRAFT_00423	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669755	DRAFT_00423	Coordinates		25190..25480(-)	
2558669755	DRAFT_00423	DNA_length		291bp	
2558669755	DRAFT_00423	Protein_length		96aa	
2558669755	DRAFT_00423	GC		0.53	
2558669756	DRAFT_00424	Locus_type		CDS	
2558669756	DRAFT_00424	Product_name		hypothetical protein	
2558669756	DRAFT_00424	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669756	DRAFT_00424	Coordinates		25572..25946(-)	
2558669756	DRAFT_00424	DNA_length		375bp	
2558669756	DRAFT_00424	Protein_length		124aa	
2558669756	DRAFT_00424	GC		0.56	
2558669757	DRAFT_00425	pfam13683	rve_3		7.00E-07
2558669757	DRAFT_00425	Locus_type		CDS	
2558669757	DRAFT_00425	Product_name		Integrase core domain	
2558669757	DRAFT_00425	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669757	DRAFT_00425	Coordinates		25960..26259(+)	
2558669757	DRAFT_00425	DNA_length		300bp	
2558669757	DRAFT_00425	Protein_length		99aa	
2558669757	DRAFT_00425	GC		0.53	

2558669758	DRAFT_00426	Locus_type		CDS	
2558669758	DRAFT_00426	Product_name		hypothetical protein	
2558669758	DRAFT_00426	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669758	DRAFT_00426	Coordinates		26715..27236(-)	
2558669758	DRAFT_00426	DNA_length		522bp	
2558669758	DRAFT_00426	Protein_length		173aa	
2558669758	DRAFT_00426	GC			0.41

2558669759	DRAFT_00427	Locus_type		CDS	
2558669759	DRAFT_00427	Product_name		hypothetical protein	
2558669759	DRAFT_00427	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669759	DRAFT_00427	Coordinates		27646..28116(-)	
2558669759	DRAFT_00427	DNA_length		471bp	
2558669759	DRAFT_00427	Protein_length		156aa	
2558669759	DRAFT_00427	GC			0.48

2558669760	DRAFT_00428	Locus_type		CDS	
2558669760	DRAFT_00428	Product_name		hypothetical protein	
2558669760	DRAFT_00428	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669760	DRAFT_00428	Coordinates		28100..28285(-)	
2558669760	DRAFT_00428	DNA_length		186bp	
2558669760	DRAFT_00428	Protein_length		61aa	
2558669760	DRAFT_00428	GC			0.48

2558669761	DRAFT_00429	COG_category	[L] Replication, recombination and repair		
2558669761	DRAFT_00429	COG3316	Transposase and inactivated derivatives		2.00E-11
2558669761	DRAFT_00429	pfam13610	DDE_Tnp_IS240		1.90E-19
2558669761	DRAFT_00429	Locus_type		CDS	
2558669761	DRAFT_00429	Product_name		Transposase and inactivated derivatives	
2558669761	DRAFT_00429	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669761	DRAFT_00429	Coordinates		28412..29611(+)	
2558669761	DRAFT_00429	DNA_length		1200bp	
2558669761	DRAFT_00429	Protein_length		399aa	
2558669761	DRAFT_00429	GC			0.56

2558669762	DRAFT_00430	Locus_type		CDS	
2558669762	DRAFT_00430	Product_name		hypothetical protein	
2558669762	DRAFT_00430	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669762	DRAFT_00430	Coordinates		29608..30135(+)	
2558669762	DRAFT_00430	DNA_length		528bp	
2558669762	DRAFT_00430	Protein_length		175aa	
2558669762	DRAFT_00430	GC		0.47	
2558669762	DRAFT_00430	Transmembrane		Yes	
2558669763	DRAFT_00431	Locus_type		CDS	
2558669763	DRAFT_00431	Product_name		hypothetical protein	
2558669763	DRAFT_00431	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669763	DRAFT_00431	Coordinates		30316..30843(+)	
2558669763	DRAFT_00431	DNA_length		528bp	
2558669763	DRAFT_00431	Protein_length		175aa	
2558669763	DRAFT_00431	GC		0.49	
2558669764	DRAFT_00432	Locus_type		CDS	
2558669764	DRAFT_00432	Product_name		hypothetical protein	
2558669764	DRAFT_00432	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669764	DRAFT_00432	Coordinates		31013..31249(-)	
2558669764	DRAFT_00432	DNA_length		237bp	
2558669764	DRAFT_00432	Protein_length		78aa	
2558669764	DRAFT_00432	GC		0.52	
2558669764	DRAFT_00432	Transmembrane		Yes	
2558669765	DRAFT_00433	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669765	DRAFT_00433	COG0459	Chaperonin GroEL (HSP60 family)		0.00E+00
2558669765	DRAFT_00433	pfam00118	Cpn60_TCP1		0.00E+00
2558669765	DRAFT_00433	TIGR02339	thermosome, various subunits, archaeal		0.00E+00
2558669765	DRAFT_00433	TIGR02343	T-complex protein 1, epsilon subunit		0.00E+00
2558669765	DRAFT_00433	Locus_type		CDS	
2558669765	DRAFT_00433	Product_name		thermosome, various subunits, archaeal	

2558669765	DRAFT_00433	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669765	DRAFT_00433	Coordinates		31507..33150(+)	
2558669765	DRAFT_00433	DNA_length		1644bp	
2558669765	DRAFT_00433	Protein_length		547aa	
2558669765	DRAFT_00433	GC			0.59
2558669766	DRAFT_00434	Locus_type		CDS	
2558669766	DRAFT_00434	Product_name		hypothetical protein	
2558669766	DRAFT_00434	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669766	DRAFT_00434	Coordinates		33304..34965(-)	
2558669766	DRAFT_00434	DNA_length		1662bp	
2558669766	DRAFT_00434	Protein_length		553aa	
2558669766	DRAFT_00434	GC			0.58
2558669767	DRAFT_00435	pfam00589	Phage_integrase		4.10E-06
2558669767	DRAFT_00435	Locus_type		CDS	
2558669767	DRAFT_00435	Product_name		Phage integrase family	
2558669767	DRAFT_00435	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669767	DRAFT_00435	Coordinates		35006..36211(+)	
2558669767	DRAFT_00435	DNA_length		1206bp	
2558669767	DRAFT_00435	Protein_length		401aa	
2558669767	DRAFT_00435	GC			0.59
2558669768	DRAFT_00436	Locus_type		CDS	
2558669768	DRAFT_00436	Product_name		hypothetical protein	
2558669768	DRAFT_00436	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669768	DRAFT_00436	Coordinates		36241..36885(-)	
2558669768	DRAFT_00436	DNA_length		645bp	
2558669768	DRAFT_00436	Protein_length		214aa	
2558669768	DRAFT_00436	GC			0.6
2558669769	DRAFT_00437	Locus_type		CDS	
2558669769	DRAFT_00437	Product_name		hypothetical protein	
2558669769	DRAFT_00437	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	

2558669769	DRAFT_00437	Coordinates		36882..38678(-)	
2558669769	DRAFT_00437	DNA_length		1797bp	
2558669769	DRAFT_00437	Protein_length		598aa	
2558669769	DRAFT_00437	GC		0.6	
2558669770	DRAFT_00438	Locus_type		CDS	
2558669770	DRAFT_00438	Product_name		hypothetical protein	
2558669770	DRAFT_00438	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669770	DRAFT_00438	Coordinates		38861..39712(+)	
2558669770	DRAFT_00438	DNA_length		852bp	
2558669770	DRAFT_00438	Protein_length		283aa	
2558669770	DRAFT_00438	GC		0.51	
2558669771	DRAFT_00439	Locus_type		CDS	
2558669771	DRAFT_00439	Product_name		hypothetical protein	
2558669771	DRAFT_00439	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669771	DRAFT_00439	Coordinates		39959..40396(+)	
2558669771	DRAFT_00439	DNA_length		438bp	
2558669771	DRAFT_00439	Protein_length		145aa	
2558669771	DRAFT_00439	GC		0.55	
2558669772	DRAFT_00440	COG_category	[S] Function unknown		
2558669772	DRAFT_00440	COG1520	FOG: WD40-like repeat		4.00E-18
2558669772	DRAFT_00440	pfam01011	PQQ		3.70E-06
2558669772	DRAFT_00440	pfam13360	PQQ_2		9.20E-22
2558669772	DRAFT_00440	pfam05048	NosD		3.20E-14
2558669772	DRAFT_00440	TIGR03804	parallel beta-helix repeat (two copies)		3.00E-14
2558669772	DRAFT_00440	Locus_type		CDS	
2558669772	DRAFT_00440	Product_name		parallel beta-helix repeat (two copies)	
2558669772	DRAFT_00440	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669772	DRAFT_00440	Coordinates		40977..42755(+)	
2558669772	DRAFT_00440	DNA_length		1779bp	
2558669772	DRAFT_00440	Protein_length		592aa	
2558669772	DRAFT_00440	GC		0.52	

2558669773	DRAFT_00441	Locus_type		CDS	
2558669773	DRAFT_00441	Product_name		hypothetical protein	
2558669773	DRAFT_00441	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669773	DRAFT_00441	Coordinates		42823..44565(-)	
2558669773	DRAFT_00441	DNA_length		1743bp	
2558669773	DRAFT_00441	Protein_length		580aa	
2558669773	DRAFT_00441	GC		0.52	
2558669773	DRAFT_00441	Transmembrane		Yes	

2558669774	DRAFT_00442	Locus_type		CDS	
2558669774	DRAFT_00442	Product_name		hypothetical protein	
2558669774	DRAFT_00442	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669774	DRAFT_00442	Coordinates		44516..45133(-)	
2558669774	DRAFT_00442	DNA_length		618bp	
2558669774	DRAFT_00442	Protein_length		205aa	
2558669774	DRAFT_00442	GC		0.53	
2558669774	DRAFT_00442	Transmembrane		Yes	

2558669775	DRAFT_00443	Locus_type		CDS	
2558669775	DRAFT_00443	Product_name		hypothetical protein	
2558669775	DRAFT_00443	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669775	DRAFT_00443	Coordinates		45272..45448(-)	
2558669775	DRAFT_00443	DNA_length		177bp	
2558669775	DRAFT_00443	Protein_length		58aa	
2558669775	DRAFT_00443	GC		0.5	

2558669776	DRAFT_00444	pfam05048	NosD		3.00E-08
2558669776	DRAFT_00444	TIGR03804	parallel beta-helix repeat (two copies)		5.60E-10
2558669776	DRAFT_00444	Locus_type		CDS	
2558669776	DRAFT_00444	Product_name		parallel beta-helix repeat (two copies)	
2558669776	DRAFT_00444	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669776	DRAFT_00444	Coordinates		45610..46002(-)	
2558669776	DRAFT_00444	DNA_length		393bp	

2558669776	DRAFT_00444	Protein_length		130aa		
2558669776	DRAFT_00444	GC			0.54	

2558669777	DRAFT_00445	pfam13229	Beta_helix			5.30E-26
2558669777	DRAFT_00445	TIGR03804	parallel beta-helix repeat (two copies)			3.00E-08
2558669777	DRAFT_00445	Locus_type		CDS		
2558669777	DRAFT_00445	Product_name		parallel beta-helix repeat (two copies)		
2558669777	DRAFT_00445	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669777	DRAFT_00445	Coordinates		46095..47885(+)		
2558669777	DRAFT_00445	DNA_length		1791bp		
2558669777	DRAFT_00445	Protein_length		596aa		
2558669777	DRAFT_00445	GC			0.55	
2558669777	DRAFT_00445	Transmembrane		Yes		

2558669778	DRAFT_00446	pfam05048	NosD			2.20E-17
2558669778	DRAFT_00446	pfam13229	Beta_helix			3.00E-07
2558669778	DRAFT_00446	pfam05048	NosD			9.60E-16
2558669778	DRAFT_00446	TIGR03804	parallel beta-helix repeat (two copies)			3.30E-12
2558669778	DRAFT_00446	Locus_type		CDS		
2558669778	DRAFT_00446	Product_name		parallel beta-helix repeat (two copies)		
2558669778	DRAFT_00446	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669778	DRAFT_00446	Coordinates		48174..49832(+)		
2558669778	DRAFT_00446	DNA_length		1659bp		
2558669778	DRAFT_00446	Protein_length		552aa		
2558669778	DRAFT_00446	GC			0.52	
2558669778	DRAFT_00446	Signal_peptide		Yes		
2558669778	DRAFT_00446	Transmembrane		Yes		

2558669779	DRAFT_00447	Locus_type		CDS		
2558669779	DRAFT_00447	Product_name		hypothetical protein		
2558669779	DRAFT_00447	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5		
2558669779	DRAFT_00447	Coordinates		49858..51030(-)		
2558669779	DRAFT_00447	DNA_length		1173bp		
2558669779	DRAFT_00447	Protein_length		390aa		

2558669779	DRAFT_00447	GC			0.52
2558669779	DRAFT_00447	Transmembrane		Yes	
2558669780	DRAFT_00448	Locus_type		CDS	
2558669780	DRAFT_00448	Product_name		hypothetical protein	
2558669780	DRAFT_00448	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669780	DRAFT_00448	Coordinates		51434..52984(-)	
2558669780	DRAFT_00448	DNA_length		1551bp	
2558669780	DRAFT_00448	Protein_length		516aa	
2558669780	DRAFT_00448	GC			0.53
2558669780	DRAFT_00448	Transmembrane		Yes	
2558669781	DRAFT_00449	pfam02661	Fic		4.80E-22
2558669781	DRAFT_00449	Locus_type		CDS	
2558669781	DRAFT_00449	Product_name		Uncharacterized conserved protein	
2558669781	DRAFT_00449	Scaffold		DRAFT_contig_70_39_len_54107_read_count_943702.5	
2558669781	DRAFT_00449	Coordinates		53138..54028(-)	
2558669781	DRAFT_00449	DNA_length		891bp	
2558669781	DRAFT_00449	Protein_length		296aa	
2558669781	DRAFT_00449	GC			0.44
2558669782	DRAFT_00450	Locus_type		CDS	
2558669782	DRAFT_00450	Product_name		hypothetical protein	
2558669782	DRAFT_00450	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669782	DRAFT_00450	Coordinates		3..2792(+)	
2558669782	DRAFT_00450	DNA_length		2790bp	
2558669782	DRAFT_00450	Protein_length		929aa	
2558669782	DRAFT_00450	GC			0.57
2558669782	DRAFT_00450	Transmembrane		Yes	
2558669783	DRAFT_00451	Metacyc	PWY-2301: <i>myo</i>-inositol biosynthesis		
2558669783	DRAFT_00451	Metacyc	PWY-6372: 1D-<i>myo</i>-inositol hexakisphosphate biosynthesis IV (<i>Dictyostelium</i>)		
2558669783	DRAFT_00451	Metacyc	PWY-6580: L-1-phosphatidyl-inositol biosynthesis (Mycobacteria)		
2558669783	DRAFT_00451	Metacyc	PWY-6664: di-myo-inositol phosphate biosynthesis		

2558669783	DRAFT_00451	Metacyc	PWY-4661: 1D-<i>myo</i>-inositol hexakisphosphate biosynthesis III (<i>Spirodela polyrrhiza<		
2558669783	DRAFT_00451	Metacyc	PWY1G-0: mycothiol biosynthesis		
2558669783	DRAFT_00451	COG_category	[I] Lipid transport and metabolism		
2558669783	DRAFT_00451	COG1260	Myo-inositol-1-phosphate synthase		4.00E-112
2558669783	DRAFT_00451	pfam07994	NAD_binding_5		5.60E-47
2558669783	DRAFT_00451	pfam01658	Inos-1-P_synth		2.00E-25
2558669783	DRAFT_00451	EC:5.5.1.4	Inositol-3-phosphate synthase.		
2558669783	DRAFT_00451	KO:K01858	myo-inositol-1-phosphate synthase [EC:5.5.1.4]		0.00E+00
2558669783	DRAFT_00451	Locus_type		CDS	
2558669783	DRAFT_00451	Product_name		Myo-inositol-1-phosphate synthase	
2558669783	DRAFT_00451	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669783	DRAFT_00451	Coordinates		2767..3828(-)	
2558669783	DRAFT_00451	DNA_length		1062bp	
2558669783	DRAFT_00451	Protein_length		353aa	
2558669783	DRAFT_00451	GC		0.59	
2558669784	DRAFT_00452	Locus_type		CDS	
2558669784	DRAFT_00452	Product_name		hypothetical protein	
2558669784	DRAFT_00452	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669784	DRAFT_00452	Coordinates		4151..4858(+)	
2558669784	DRAFT_00452	DNA_length		708bp	
2558669784	DRAFT_00452	Protein_length		235aa	
2558669784	DRAFT_00452	GC		0.51	
2558669785	DRAFT_00453	Locus_type		CDS	
2558669785	DRAFT_00453	Product_name		hypothetical protein	
2558669785	DRAFT_00453	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669785	DRAFT_00453	Coordinates		4853..4987(-)	
2558669785	DRAFT_00453	DNA_length		135bp	
2558669785	DRAFT_00453	Protein_length		44aa	
2558669785	DRAFT_00453	GC		0.51	
2558669786	DRAFT_00454	COG_category	[L] Replication, recombination and repair		
2558669786	DRAFT_00454	COG3316	Transposase and inactivated derivatives		5.00E-12

2558669786	DRAFT_00454	pfam13610	DDE_Tnp_IS240		3.20E-22
2558669786	DRAFT_00454	pfam04434	SWIM		5.60E-08
2558669786	DRAFT_00454	Locus_type		CDS	
2558669786	DRAFT_00454	Product_name		Transposase and inactivated derivatives	
2558669786	DRAFT_00454	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669786	DRAFT_00454	Coordinates		5038..6282(+)	
2558669786	DRAFT_00454	DNA_length		1245bp	
2558669786	DRAFT_00454	Protein_length		414aa	
2558669786	DRAFT_00454	GC		0.55	
2558669787	DRAFT_00455	Locus_type		CDS	
2558669787	DRAFT_00455	Product_name		hypothetical protein	
2558669787	DRAFT_00455	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669787	DRAFT_00455	Coordinates		6279..6761(+)	
2558669787	DRAFT_00455	DNA_length		483bp	
2558669787	DRAFT_00455	Protein_length		160aa	
2558669787	DRAFT_00455	GC		0.48	
2558669788	DRAFT_00456	Locus_type		CDS	
2558669788	DRAFT_00456	Product_name		hypothetical protein	
2558669788	DRAFT_00456	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669788	DRAFT_00456	Coordinates		6893..7297(+)	
2558669788	DRAFT_00456	DNA_length		405bp	
2558669788	DRAFT_00456	Protein_length		134aa	
2558669788	DRAFT_00456	GC		0.47	
2558669788	DRAFT_00456	Transmembrane		Yes	
2558669789	DRAFT_00457	Locus_type		CDS	
2558669789	DRAFT_00457	Product_name		hypothetical protein	
2558669789	DRAFT_00457	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669789	DRAFT_00457	Coordinates		7294..7437(-)	
2558669789	DRAFT_00457	DNA_length		144bp	
2558669789	DRAFT_00457	Protein_length		47aa	
2558669789	DRAFT_00457	GC		0.45	

2558669790	DRAFT_00458	COG_category	[L] Replication, recombination and repair		
2558669790	DRAFT_00458	COG_category	[R] General function prediction only		
2558669790	DRAFT_00458	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzyme		2.00E-06
2558669790	DRAFT_00458	pfam00293	NUDIX		5.80E-14
2558669790	DRAFT_00458	Locus_type		CDS	
2558669790	DRAFT_00458	Product_name		NTP pyrophosphohydrolases including oxidative damage repair enzym	
2558669790	DRAFT_00458	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669790	DRAFT_00458	Coordinates		7533..7973(+)	
2558669790	DRAFT_00458	DNA_length		441bp	
2558669790	DRAFT_00458	Protein_length		146aa	
2558669790	DRAFT_00458	GC		0.57	
2558669791	DRAFT_00459	Locus_type		CDS	
2558669791	DRAFT_00459	Product_name		hypothetical protein	
2558669791	DRAFT_00459	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669791	DRAFT_00459	Coordinates		7964..8728(-)	
2558669791	DRAFT_00459	DNA_length		765bp	
2558669791	DRAFT_00459	Protein_length		254aa	
2558669791	DRAFT_00459	GC		0.54	
2558669792	DRAFT_00460	Locus_type		CDS	
2558669792	DRAFT_00460	Product_name		hypothetical protein	
2558669792	DRAFT_00460	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669792	DRAFT_00460	Coordinates		8766..9134(+)	
2558669792	DRAFT_00460	DNA_length		369bp	
2558669792	DRAFT_00460	Protein_length		122aa	
2558669792	DRAFT_00460	GC		0.56	
2558669793	DRAFT_00461	Locus_type		CDS	
2558669793	DRAFT_00461	Product_name		hypothetical protein	
2558669793	DRAFT_00461	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669793	DRAFT_00461	Coordinates		9097..9567(-)	
2558669793	DRAFT_00461	DNA_length		471bp	

2558669793	DRAFT_00461	Protein_length		156aa		
2558669793	DRAFT_00461	GC			0.55	
2558669794	DRAFT_00462	COG_category	[I] Lipid transport and metabolism			
2558669794	DRAFT_00462	COG0020	Undecaprenyl pyrophosphate synthase			1.00E-72
2558669794	DRAFT_00462	pfam01255	Prenyltransf			2.60E-77
2558669794	DRAFT_00462	EC:2.5.1.89	Tritrans,polycis-undecaprenyl-diphosphate synthase (geranylgeranyl- diphosphate specific).			
2558669794	DRAFT_00462	TIGR00055	undecaprenyl diphosphate synthase			5.80E-75
2558669794	DRAFT_00462	KO:K15888	tritrans,polycis-undecaprenyl-diphosphate synthase [geranylgeranyl-di			0.00E+00
2558669794	DRAFT_00462	Locus_type		CDS		
2558669794	DRAFT_00462	Product_name		Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)		
2558669794	DRAFT_00462	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669794	DRAFT_00462	Coordinates		9609..10391(-)		
2558669794	DRAFT_00462	DNA_length		783bp		
2558669794	DRAFT_00462	Protein_length		260aa		
2558669794	DRAFT_00462	GC			0.57	
2558669795	DRAFT_00463	COG_category	[S] Function unknown			
2558669795	DRAFT_00463	COG2237	Predicted membrane protein			1.00E-56
2558669795	DRAFT_00463	pfam04123	DUF373			1.50E-91
2558669795	DRAFT_00463	KO:K08975	putative membrane protein			0.00E+00
2558669795	DRAFT_00463	Locus_type		CDS		
2558669795	DRAFT_00463	Product_name		Predicted membrane protein		
2558669795	DRAFT_00463	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669795	DRAFT_00463	Coordinates		10395..11489(-)		
2558669795	DRAFT_00463	DNA_length		1095bp		
2558669795	DRAFT_00463	Protein_length		364aa		
2558669795	DRAFT_00463	GC			0.58	
2558669795	DRAFT_00463	Transmembrane		Yes		
2558669796	DRAFT_00464	KEGG_module	M00373: Ethylmalonyl pathway			
2558669796	DRAFT_00464	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle			
2558669796	DRAFT_00464	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone			
2558669796	DRAFT_00464	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			

2558669796	DRAFT_00464	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway		
2558669796	DRAFT_00464	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis		
2558669796	DRAFT_00464	Metacyc	PWY-5741: ethylmalonyl pathway		
2558669796	DRAFT_00464	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2558669796	DRAFT_00464	Metacyc	PWY-6583: pyruvate fermentation to butanol I		
2558669796	DRAFT_00464	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II		
2558669796	DRAFT_00464	Metacyc	PWY66-367: ketogenesis		
2558669796	DRAFT_00464	Metacyc	PWY-6883: pyruvate fermentation to butanol II		
2558669796	DRAFT_00464	Metacyc	PWY-6876: isopropanol biosynthesis		
2558669796	DRAFT_00464	Metacyc	PWY-7003: glycerol degradation to butanol		
2558669796	DRAFT_00464	Metacyc	PWY-922: mevalonate pathway I		
2558669796	DRAFT_00464	Metacyc	PWY-6174: mevalonate pathway II (archaea)		
2558669796	DRAFT_00464	Metacyc	PWY66-368: ketolysis		
2558669796	DRAFT_00464	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2558669796	DRAFT_00464	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate		
2558669796	DRAFT_00464	Metacyc	PWY-5177: glutaryl-CoA degradation		
2558669796	DRAFT_00464	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis		
2558669796	DRAFT_00464	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2558669796	DRAFT_00464	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)		
2558669796	DRAFT_00464	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2558669796	DRAFT_00464	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2558669796	DRAFT_00464	COG_category	[I] Lipid transport and metabolism		
2558669796	DRAFT_00464	COG0183	Acetyl-CoA acetyltransferase		3.00E-85
2558669796	DRAFT_00464	pfam02803	Thiolase_C		1.40E-43
2558669796	DRAFT_00464	pfam00108	Thiolase_N		4.10E-94
2558669796	DRAFT_00464	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.		
2558669796	DRAFT_00464	TIGR01930	acetyl-CoA acetyltransferases		0.00E+00
2558669796	DRAFT_00464	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]		0.00E+00
2558669796	DRAFT_00464	Locus_type		CDS	
2558669796	DRAFT_00464	Product_name		acetyl-CoA acetyltransferase (EC 2.3.1.9)	
2558669796	DRAFT_00464	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669796	DRAFT_00464	Coordinates		11705..12883(-)	
2558669796	DRAFT_00464	DNA_length		1179bp	
2558669796	DRAFT_00464	Protein_length		392aa	

2558669796	DRAFT_00464	GC		0.6	
2558669797	DRAFT_00465	KEGG_module	M00119: Pantothenate biosynthesis, valine/L-aspartate => pantothenate		
2558669797	DRAFT_00465	KEGG_module	M00570: Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine		
2558669797	DRAFT_00465	KEGG_module	M00019: Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine		
2558669797	DRAFT_00465	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA		
2558669797	DRAFT_00465	Metacyc	PWY-5108: isoleucine biosynthesis V		
2558669797	DRAFT_00465	Metacyc	VALDEG-PWY: valine degradation I		
2558669797	DRAFT_00465	Metacyc	LEU-DEG2-PWY: leucine degradation I		
2558669797	DRAFT_00465	Metacyc	PWY-5078: isoleucine degradation II		
2558669797	DRAFT_00465	Metacyc	ALANINE-VALINESYN-PWY: alanine biosynthesis I		
2558669797	DRAFT_00465	Metacyc	PWY-5104: isoleucine biosynthesis IV		
2558669797	DRAFT_00465	Metacyc	LEUSYN-PWY: leucine biosynthesis		
2558669797	DRAFT_00465	Metacyc	PWY-5076: leucine degradation III		
2558669797	DRAFT_00465	Metacyc	PWY-5101: isoleucine biosynthesis II		
2558669797	DRAFT_00465	Metacyc	VALSYN-PWY: valine biosynthesis		
2558669797	DRAFT_00465	Metacyc	PWY-5057: valine degradation II		
2558669797	DRAFT_00465	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2558669797	DRAFT_00465	Metacyc	PWY-5103: isoleucine biosynthesis III		
2558669797	DRAFT_00465	Metacyc	ILEUSYN-PWY: isoleucine biosynthesis I (from threonine)		
2558669797	DRAFT_00465	COG_category	[E] Amino acid transport and metabolism		
2558669797	DRAFT_00465	COG_category	[H] Coenzyme transport and metabolism		
2558669797	DRAFT_00465	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorism		8.00E-67
2558669797	DRAFT_00465	pfam01063	Aminotran_4		4.70E-43
2558669797	DRAFT_00465	EC:2.6.1.42	Branched-chain-amino-acid transaminase.		
2558669797	DRAFT_00465	TIGR01122	branched-chain amino acid aminotransferase, group I		4.30E-122
2558669797	DRAFT_00465	KO:K00826	branched-chain amino acid aminotransferase [EC:2.6.1.42]		0.00E+00
2558669797	DRAFT_00465	Locus_type		CDS	
2558669797	DRAFT_00465	Product_name		branched-chain amino acid aminotransferase, group I	
2558669797	DRAFT_00465	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669797	DRAFT_00465	Coordinates		12953..13897(+)	
2558669797	DRAFT_00465	DNA_length		945bp	
2558669797	DRAFT_00465	Protein_length		314aa	
2558669797	DRAFT_00465	GC		0.56	

2558669798	DRAFT_00466	COG_category	[R] General function prediction only		
2558669798	DRAFT_00466	COG1545	Predicted nucleic-acid-binding protein containing a Zn-ribbon		3.00E-18
2558669798	DRAFT_00466	Locus_type		CDS	
2558669798	DRAFT_00466	Product_name		Predicted nucleic-acid-binding protein containing a Zn-ribbon	
2558669798	DRAFT_00466	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669798	DRAFT_00466	Coordinates		13899..14360(-)	
2558669798	DRAFT_00466	DNA_length		462bp	
2558669798	DRAFT_00466	Protein_length		153aa	
2558669798	DRAFT_00466	GC		0.6	
2558669799	DRAFT_00467	COG_category	[R] General function prediction only		
2558669799	DRAFT_00467	COG1545	Predicted nucleic-acid-binding protein containing a Zn-ribbon		1.00E-27
2558669799	DRAFT_00467	pfam01796	DUF35		8.50E-11
2558669799	DRAFT_00467	pfam12172	DUF35_N		1.20E-05
2558669799	DRAFT_00467	Locus_type		CDS	
2558669799	DRAFT_00467	Product_name		Predicted nucleic-acid-binding protein containing a Zn-ribbon	
2558669799	DRAFT_00467	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669799	DRAFT_00467	Coordinates		14363..14872(-)	
2558669799	DRAFT_00467	DNA_length		510bp	
2558669799	DRAFT_00467	Protein_length		169aa	
2558669799	DRAFT_00467	GC		0.57	
2558669800	DRAFT_00468	COG_category	[I] Lipid transport and metabolism		
2558669800	DRAFT_00468	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases		4.00E-120
2558669800	DRAFT_00468	pfam00501	AMP-binding		6.60E-54
2558669800	DRAFT_00468	pfam13193	AMP-binding_C		2.70E-06
2558669800	DRAFT_00468	EC:6.2.1.16	Acetoacetate--CoA ligase.		
2558669800	DRAFT_00468	TIGR01217	acetoacetyl-CoA synthase		0.00E+00
2558669800	DRAFT_00468	KO:K01907	acetoacetyl-CoA synthetase [EC:6.2.1.16]		0.00E+00
2558669800	DRAFT_00468	Locus_type		CDS	
2558669800	DRAFT_00468	Product_name		acetoacetyl-CoA synthase	
2558669800	DRAFT_00468	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669800	DRAFT_00468	Coordinates		14904..16883(-)	

2558669800	DRAFT_00468	DNA_length		1980bp	
2558669800	DRAFT_00468	Protein_length		659aa	
2558669800	DRAFT_00468	GC			0.62

2558669801	DRAFT_00469	KEGG_module	M00373: Ethylmalonyl pathway		
2558669801	DRAFT_00469	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle		
2558669801	DRAFT_00469	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2558669801	DRAFT_00469	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone		
2558669801	DRAFT_00469	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway		
2558669801	DRAFT_00469	Metacyc	PWY-922: mevalonate pathway I		
2558669801	DRAFT_00469	Metacyc	PWY-5741: ethylmalonyl pathway		
2558669801	DRAFT_00469	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis		
2558669801	DRAFT_00469	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis		
2558669801	DRAFT_00469	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate		
2558669801	DRAFT_00469	Metacyc	PWY-7003: glycerol degradation to butanol		
2558669801	DRAFT_00469	Metacyc	PWY-6883: pyruvate fermentation to butanol II		
2558669801	DRAFT_00469	Metacyc	PWY-6583: pyruvate fermentation to butanol I		
2558669801	DRAFT_00469	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2558669801	DRAFT_00469	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)		
2558669801	DRAFT_00469	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II		
2558669801	DRAFT_00469	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2558669801	DRAFT_00469	Metacyc	PWY66-368: ketolysis		
2558669801	DRAFT_00469	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2558669801	DRAFT_00469	Metacyc	PWY66-367: ketogenesis		
2558669801	DRAFT_00469	Metacyc	PWY-6174: mevalonate pathway II (archaea)		
2558669801	DRAFT_00469	Metacyc	PWY-6876: isopropanol biosynthesis		
2558669801	DRAFT_00469	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2558669801	DRAFT_00469	Metacyc	PWY-5177: glutaryl-CoA degradation		
2558669801	DRAFT_00469	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2558669801	DRAFT_00469	COG_category	[I] Lipid transport and metabolism		
2558669801	DRAFT_00469	COG0183	Acetyl-CoA acetyltransferase		5.00E-72
2558669801	DRAFT_00469	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.		
2558669801	DRAFT_00469	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]		0.00E+00
2558669801	DRAFT_00469	Locus_type		CDS	

2558669801	DRAFT_00469	Product_name	Acetyl-CoA acetyltransferase
2558669801	DRAFT_00469	Scaffold	DRAFT_contig_70_41_len_53364_read_count_885993.6
2558669801	DRAFT_00469	Coordinates	16891..18048(-)
2558669801	DRAFT_00469	DNA_length	1158bp
2558669801	DRAFT_00469	Protein_length	385aa
2558669801	DRAFT_00469	GC	0.59

2558669802	DRAFT_00470	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle	
2558669802	DRAFT_00470	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway	
2558669802	DRAFT_00470	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle	
2558669802	DRAFT_00470	KEGG_module	M00373: Ethylmalonyl pathway	
2558669802	DRAFT_00470	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone	
2558669802	DRAFT_00470	Metacyc	PWY-6863: pyruvate fermentation to hexanol	
2558669802	DRAFT_00470	Metacyc	PWY-6876: isopropanol biosynthesis	
2558669802	DRAFT_00470	Metacyc	PWY-7003: glycerol degradation to butanol	
2558669802	DRAFT_00470	Metacyc	PWY-6174: mevalonate pathway II (archaea)	
2558669802	DRAFT_00470	Metacyc	PWY-6588: pyruvate fermentation to acetone	
2558669802	DRAFT_00470	Metacyc	PWY66-368: ketolysis	
2558669802	DRAFT_00470	Metacyc	PWY66-367: ketogenesis	
2558669802	DRAFT_00470	Metacyc	PWY-5741: ethylmalonyl pathway	
2558669802	DRAFT_00470	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate	
2558669802	DRAFT_00470	Metacyc	ILEUDEG-PWY: isoleucine degradation I	
2558669802	DRAFT_00470	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis	
2558669802	DRAFT_00470	Metacyc	PWY-6583: pyruvate fermentation to butanol I	
2558669802	DRAFT_00470	Metacyc	PWY-5177: glutaryl-CoA degradation	
2558669802	DRAFT_00470	Metacyc	PWY-922: mevalonate pathway I	
2558669802	DRAFT_00470	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate	
2558669802	DRAFT_00470	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle	
2558669802	DRAFT_00470	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis	
2558669802	DRAFT_00470	Metacyc	PWY-6883: pyruvate fermentation to butanol II	
2558669802	DRAFT_00470	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II	
2558669802	DRAFT_00470	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)	
2558669802	DRAFT_00470	COG_category	[I] Lipid transport and metabolism	
2558669802	DRAFT_00470	COG0183	Acetyl-CoA acetyltransferase	4.00E-21

2558669802	DRAFT_00470	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.			
2558669802	DRAFT_00470	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]			0.00E+00
2558669802	DRAFT_00470	Locus_type		CDS		
2558669802	DRAFT_00470	Product_name		Acetyl-CoA acetyltransferase		
2558669802	DRAFT_00470	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669802	DRAFT_00470	Coordinates		18053..19186(-)		
2558669802	DRAFT_00470	DNA_length		1134bp		
2558669802	DRAFT_00470	Protein_length		377aa		
2558669802	DRAFT_00470	GC			0.61	
2558669803	DRAFT_00471	COG_category	[I] Lipid transport and metabolism			
2558669803	DRAFT_00471	COG1960	Acyl-CoA dehydrogenases			4.00E-83
2558669803	DRAFT_00471	pfam02771	Acyl-CoA_dh_N			1.80E-16
2558669803	DRAFT_00471	pfam02770	Acyl-CoA_dh_M			2.10E-20
2558669803	DRAFT_00471	pfam00441	Acyl-CoA_dh_1			1.40E-40
2558669803	DRAFT_00471	Locus_type		CDS		
2558669803	DRAFT_00471	Product_name		Acyl-CoA dehydrogenases		
2558669803	DRAFT_00471	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669803	DRAFT_00471	Coordinates		19307..20512(+)		
2558669803	DRAFT_00471	DNA_length		1206bp		
2558669803	DRAFT_00471	Protein_length		401aa		
2558669803	DRAFT_00471	GC			0.58	
2558669804	DRAFT_00472	COG_category	[C] Energy production and conversion			
2558669804	DRAFT_00472	COG2086	Electron transfer flavoprotein, beta subunit			1.00E-52
2558669804	DRAFT_00472	pfam01012	ETF			7.30E-33
2558669804	DRAFT_00472	KO:K03521	electron transfer flavoprotein beta subunit			0.00E+00
2558669804	DRAFT_00472	ITERM:01639	electron transfer flavoprotein beta subunit			
2558669804	DRAFT_00472	Locus_type		CDS		
2558669804	DRAFT_00472	Product_name		electron transfer flavoprotein beta subunit		
2558669804	DRAFT_00472	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669804	DRAFT_00472	Coordinates		20509..21276(+)		
2558669804	DRAFT_00472	DNA_length		768bp		
2558669804	DRAFT_00472	Protein_length		255aa		

2558669804	DRAFT_00472	GC			0.62	
2558669805	DRAFT_00473	COG_category	[C] Energy production and conversion			
2558669805	DRAFT_00473	COG2025	Electron transfer flavoprotein, alpha subunit			3.00E-55
2558669805	DRAFT_00473	pfam01012	ETF			1.40E-13
2558669805	DRAFT_00473	pfam00766	ETF_alpha			2.70E-30
2558669805	DRAFT_00473	KO:K03522	electron transfer flavoprotein alpha subunit			0.00E+00
2558669805	DRAFT_00473	ITERM:01638	electron transfer flavoprotein alpha subunit apoprotein			
2558669805	DRAFT_00473	Locus_type		CDS		
2558669805	DRAFT_00473	Product_name		electron transfer flavoprotein alpha subunit apoprotein		
2558669805	DRAFT_00473	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669805	DRAFT_00473	Coordinates		21273..22205(+)		
2558669805	DRAFT_00473	DNA_length		933bp		
2558669805	DRAFT_00473	Protein_length		310aa		
2558669805	DRAFT_00473	GC			0.63	
2558669806	DRAFT_00474	COG_category	[C] Energy production and conversion			
2558669806	DRAFT_00474	COG0247	Fe-S oxidoreductase			9.00E-73
2558669806	DRAFT_00474	pfam02754	CCG			4.20E-15
2558669806	DRAFT_00474	pfam02754	CCG			6.90E-16
2558669806	DRAFT_00474	pfam13183	Fer4_8			1.20E-12
2558669806	DRAFT_00474	Locus_type		CDS		
2558669806	DRAFT_00474	Product_name		Fe-S oxidoreductase		
2558669806	DRAFT_00474	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669806	DRAFT_00474	Coordinates		22292..24367(-)		
2558669806	DRAFT_00474	DNA_length		2076bp		
2558669806	DRAFT_00474	Protein_length		691aa		
2558669806	DRAFT_00474	GC			0.61	
2558669806	DRAFT_00474	Transmembrane		Yes		
2558669806	DRAFT_00474	Fused_gene		Yes		
2558669807	DRAFT_00475	COG_category	[K] Transcription			
2558669807	DRAFT_00475	COG1293	Predicted RNA-binding protein homologous to eukaryotic snRNP			8.00E-58
2558669807	DRAFT_00475	pfam05670	DUF814			7.30E-17

2558669807	DRAFT_00475	pfam05833	FbpA		4.70E-30
2558669807	DRAFT_00475	Locus_type		CDS	
2558669807	DRAFT_00475	Product_name		Predicted RNA-binding protein homologous to eukaryotic snRNP	
2558669807	DRAFT_00475	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669807	DRAFT_00475	Coordinates		24395..26236(-)	
2558669807	DRAFT_00475	DNA_length		1842bp	
2558669807	DRAFT_00475	Protein_length		613aa	
2558669807	DRAFT_00475	GC		0.61	
2558669808	DRAFT_00476	Locus_type		CDS	
2558669808	DRAFT_00476	Product_name		hypothetical protein	
2558669808	DRAFT_00476	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669808	DRAFT_00476	Coordinates		26244..26522(+)	
2558669808	DRAFT_00476	DNA_length		279bp	
2558669808	DRAFT_00476	Protein_length		92aa	
2558669808	DRAFT_00476	GC		0.53	
2558669808	DRAFT_00476	Transmembrane		Yes	
2558669809	DRAFT_00477	Locus_type		CDS	
2558669809	DRAFT_00477	Product_name		hypothetical protein	
2558669809	DRAFT_00477	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669809	DRAFT_00477	Coordinates		26503..26835(-)	
2558669809	DRAFT_00477	DNA_length		333bp	
2558669809	DRAFT_00477	Protein_length		110aa	
2558669809	DRAFT_00477	GC		0.56	
2558669810	DRAFT_00478	pfam12680	SnoaL_2		8.90E-10
2558669810	DRAFT_00478	Locus_type		CDS	
2558669810	DRAFT_00478	Product_name		SnoaL-like domain	
2558669810	DRAFT_00478	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669810	DRAFT_00478	Coordinates		26961..27311(-)	
2558669810	DRAFT_00478	DNA_length		351bp	
2558669810	DRAFT_00478	Protein_length		116aa	
2558669810	DRAFT_00478	GC		0.43	

2558669811	DRAFT_00479	COG_category	[L] Replication, recombination and repair		
2558669811	DRAFT_00479	COG0468	RecA/RadA recombinase		9.00E-29
2558669811	DRAFT_00479	pfam08423	Rad51		1.40E-31
2558669811	DRAFT_00479	KO:K04483	DNA repair protein RadA		1.00E-26
2558669811	DRAFT_00479	Locus_type		CDS	
2558669811	DRAFT_00479	Product_name		RecA/RadA recombinase	
2558669811	DRAFT_00479	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669811	DRAFT_00479	Coordinates		27445..28149(-)	
2558669811	DRAFT_00479	DNA_length		705bp	
2558669811	DRAFT_00479	Protein_length		234aa	
2558669811	DRAFT_00479	GC		0.59	
2558669812	DRAFT_00480	COG_category	[K] Transcription		
2558669812	DRAFT_00480	COG1958	Small nuclear ribonucleoprotein (snRNP) homolog		9.00E-10
2558669812	DRAFT_00480	pfam01423	LSM		2.20E-17
2558669812	DRAFT_00480	KO:K04796	small nuclear ribonucleoprotein		1.60E-22
2558669812	DRAFT_00480	Locus_type		CDS	
2558669812	DRAFT_00480	Product_name		Small nuclear ribonucleoprotein (snRNP) homolog	
2558669812	DRAFT_00480	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669812	DRAFT_00480	Coordinates		28234..28485(+)	
2558669812	DRAFT_00480	DNA_length		252bp	
2558669812	DRAFT_00480	Protein_length		83aa	
2558669812	DRAFT_00480	GC		0.54	
2558669813	DRAFT_00481	COG_category	[T] Signal transduction mechanisms		
2558669813	DRAFT_00481	COG0478	RIO-like serine/threonine protein kinase fused to N-terminal HTH doma		5.00E-55
2558669813	DRAFT_00481	pfam01163	RIO1		4.70E-38
2558669813	DRAFT_00481	pfam09202	Rio2_N		3.60E-08
2558669813	DRAFT_00481	EC:2.7.11.1	Non-specific serine/threonine protein kinase.		
2558669813	DRAFT_00481	KO:K07179	RIO kinase 2 [EC:2.7.11.1]		0.00E+00
2558669813	DRAFT_00481	Locus_type		CDS	
2558669813	DRAFT_00481	Product_name		RIO-like serine/threonine protein kinase fused to N-terminal HTH don	
2558669813	DRAFT_00481	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	

2558669813	DRAFT_00481	Coordinates		28677..29564(-)	
2558669813	DRAFT_00481	DNA_length		888bp	
2558669813	DRAFT_00481	Protein_length		295aa	
2558669813	DRAFT_00481	GC			0.62
2558669814	DRAFT_00482	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669814	DRAFT_00482	COG0309	Hydrogenase maturation factor		3.00E-58
2558669814	DRAFT_00482	pfam00586	AIRS		1.40E-06
2558669814	DRAFT_00482	pfam02769	AIRS_C		6.00E-19
2558669814	DRAFT_00482	Locus_type		CDS	
2558669814	DRAFT_00482	Product_name		Hydrogenase maturation factor	
2558669814	DRAFT_00482	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669814	DRAFT_00482	Coordinates		29746..30786(-)	
2558669814	DRAFT_00482	DNA_length		1041bp	
2558669814	DRAFT_00482	Protein_length		346aa	
2558669814	DRAFT_00482	GC			0.6
2558669815	DRAFT_00483	pfam07155	ECF-ribofla_trS		3.40E-06
2558669815	DRAFT_00483	Locus_type		CDS	
2558669815	DRAFT_00483	Product_name		ECF-type riboflavin transporter, S component	
2558669815	DRAFT_00483	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669815	DRAFT_00483	Coordinates		30808..31341(-)	
2558669815	DRAFT_00483	DNA_length		534bp	
2558669815	DRAFT_00483	Protein_length		177aa	
2558669815	DRAFT_00483	GC			0.61
2558669815	DRAFT_00483	Transmembrane		Yes	
2558669816	DRAFT_00484	COG_category	[S] Function unknown		
2558669816	DRAFT_00484	COG1992	Uncharacterized conserved protein		1.00E-33
2558669816	DRAFT_00484	pfam10120	Aldolase_2		4.70E-40
2558669816	DRAFT_00484	Locus_type		CDS	
2558669816	DRAFT_00484	Product_name		Uncharacterized conserved protein	
2558669816	DRAFT_00484	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669816	DRAFT_00484	Coordinates		31445..32380(+)	

2558669816	DRAFT_00484	DNA_length		936bp		
2558669816	DRAFT_00484	Protein_length		311aa		
2558669816	DRAFT_00484	GC			0.61	
2558669817	DRAFT_00485	KEGG_module	M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP			
2558669817	DRAFT_00485	Metacyc	PWY-7176: UTP and CTP <i>de novo</i> biosynthesis			
2558669817	DRAFT_00485	Metacyc	PWY-7185: UTP and CTP dephosphorylation I			
2558669817	DRAFT_00485	Metacyc	PWY-7177: UTP and CTP dephosphorylation II			
2558669817	DRAFT_00485	IMG_pathway	324: CTP synthesis			
2558669817	DRAFT_00485	COG_category	[F] Nucleotide transport and metabolism			
2558669817	DRAFT_00485	COG0504	CTP synthase (UTP-ammonia lyase)			0.00E+00
2558669817	DRAFT_00485	pfam06418	CTP_synth_N			5.00E-119
2558669817	DRAFT_00485	pfam00117	GATase			8.80E-43
2558669817	DRAFT_00485	EC:6.3.4.2	CTP synthase.			
2558669817	DRAFT_00485	TIGR00337	CTP synthase			0.00E+00
2558669817	DRAFT_00485	KO:K01937	CTP synthase [EC:6.3.4.2]			0.00E+00
2558669817	DRAFT_00485	ITERM:01398	CTP synthase (EC 6.3.4.2)			
2558669817	DRAFT_00485	Locus_type		CDS		
2558669817	DRAFT_00485	Product_name		CTP synthase (EC 6.3.4.2)		
2558669817	DRAFT_00485	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669817	DRAFT_00485	Coordinates		32369..34012(-)		
2558669817	DRAFT_00485	DNA_length		1644bp		
2558669817	DRAFT_00485	Protein_length		547aa		
2558669817	DRAFT_00485	GC			0.58	
2558669818	DRAFT_00486	COG_category	[P] Inorganic ion transport and metabolism			
2558669818	DRAFT_00486	COG0704	Phosphate uptake regulator			3.00E-18
2558669818	DRAFT_00486	pfam01895	PhoU			2.80E-10
2558669818	DRAFT_00486	pfam04014	Antitoxin-MazE			4.00E-06
2558669818	DRAFT_00486	Locus_type		CDS		
2558669818	DRAFT_00486	Product_name		Phosphate uptake regulator		
2558669818	DRAFT_00486	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669818	DRAFT_00486	Coordinates		34108..35097(-)		
2558669818	DRAFT_00486	DNA_length		990bp		

2558669818	DRAFT_00486	Protein_length		329aa		
2558669818	DRAFT_00486	GC			0.57	
2558669819	DRAFT_00487	Locus_type		CDS		
2558669819	DRAFT_00487	Product_name		hypothetical protein		
2558669819	DRAFT_00487	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669819	DRAFT_00487	Coordinates		35297..35482(-)		
2558669819	DRAFT_00487	DNA_length		186bp		
2558669819	DRAFT_00487	Protein_length		61aa		
2558669819	DRAFT_00487	GC			0.56	
2558669820	DRAFT_00488	COG_category	[C] Energy production and conversion			
2558669820	DRAFT_00488	COG1254	Acylphosphatases			2.00E-10
2558669820	DRAFT_00488	pfam00708	Acylphosphatase			3.70E-17
2558669820	DRAFT_00488	EC:3.6.1.7	Acylphosphatase.			
2558669820	DRAFT_00488	KO:K01512	acylphosphatase [EC:3.6.1.7]			1.50E-13
2558669820	DRAFT_00488	Locus_type		CDS		
2558669820	DRAFT_00488	Product_name		Acylphosphatases		
2558669820	DRAFT_00488	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669820	DRAFT_00488	Coordinates		35674..35883(+)		
2558669820	DRAFT_00488	DNA_length		210bp		
2558669820	DRAFT_00488	Protein_length		69aa		
2558669820	DRAFT_00488	GC			0.62	
2558669821	DRAFT_00489	Locus_type		CDS		
2558669821	DRAFT_00489	Product_name		hypothetical protein		
2558669821	DRAFT_00489	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669821	DRAFT_00489	Coordinates		36140..36670(+)		
2558669821	DRAFT_00489	DNA_length		531bp		
2558669821	DRAFT_00489	Protein_length		176aa		
2558669821	DRAFT_00489	GC			0.57	
2558669822	DRAFT_00490	COG_category	[G] Carbohydrate transport and metabolism			
2558669822	DRAFT_00490	COG0524	Sugar kinases, ribokinase family			2.00E-14

2558669822	DRAFT_00490	pfam00294	PfkB		3.30E-09
2558669822	DRAFT_00490	Locus_type		CDS	
2558669822	DRAFT_00490	Product_name		Sugar kinases, ribokinase family	
2558669822	DRAFT_00490	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669822	DRAFT_00490	Coordinates		36671..37633(-)	
2558669822	DRAFT_00490	DNA_length		963bp	
2558669822	DRAFT_00490	Protein_length		320aa	
2558669822	DRAFT_00490	GC		0.59	
2558669823	DRAFT_00491	COG_category	[R] General function prediction only		
2558669823	DRAFT_00491	COG0312	Predicted Zn-dependent proteases and their inactivated homologs		2.00E-68
2558669823	DRAFT_00491	pfam01523	PmbA_TldD		2.60E-53
2558669823	DRAFT_00491	KO:K03592	PmbA protein		0.00E+00
2558669823	DRAFT_00491	Locus_type		CDS	
2558669823	DRAFT_00491	Product_name		Predicted Zn-dependent proteases and their inactivated homologs	
2558669823	DRAFT_00491	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669823	DRAFT_00491	Coordinates		37782..39113(-)	
2558669823	DRAFT_00491	DNA_length		1332bp	
2558669823	DRAFT_00491	Protein_length		443aa	
2558669823	DRAFT_00491	GC		0.59	
2558669824	DRAFT_00492	COG_category	[R] General function prediction only		
2558669824	DRAFT_00492	COG0312	Predicted Zn-dependent proteases and their inactivated homologs		8.00E-76
2558669824	DRAFT_00492	pfam01523	PmbA_TldD		8.40E-54
2558669824	DRAFT_00492	KO:K03568	TldD protein		0.00E+00
2558669824	DRAFT_00492	Locus_type		CDS	
2558669824	DRAFT_00492	Product_name		Predicted Zn-dependent proteases and their inactivated homologs	
2558669824	DRAFT_00492	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669824	DRAFT_00492	Coordinates		39119..40564(-)	
2558669824	DRAFT_00492	DNA_length		1446bp	
2558669824	DRAFT_00492	Protein_length		481aa	
2558669824	DRAFT_00492	GC		0.58	
2558669825	DRAFT_00493	COG_category	[R] General function prediction only		

2558669825	DRAFT_00493	COG0595	Predicted hydrolase of the metallo-beta-lactamase superfamily		2.00E-42
2558669825	DRAFT_00493	pfam07521	RMMBL		8.30E-06
2558669825	DRAFT_00493	pfam12706	Lactamase_B_2		5.20E-14
2558669825	DRAFT_00493	Locus_type		CDS	
2558669825	DRAFT_00493	Product_name		Predicted hydrolase of the metallo-beta-lactamase superfamily	
2558669825	DRAFT_00493	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669825	DRAFT_00493	Coordinates		40663..42033(-)	
2558669825	DRAFT_00493	DNA_length		1371bp	
2558669825	DRAFT_00493	Protein_length		456aa	
2558669825	DRAFT_00493	GC		0.59	
2558669826	DRAFT_00494	Locus_type		CDS	
2558669826	DRAFT_00494	Product_name		hypothetical protein	
2558669826	DRAFT_00494	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669826	DRAFT_00494	Coordinates		42144..42269(+)	
2558669826	DRAFT_00494	DNA_length		126bp	
2558669826	DRAFT_00494	Protein_length		41aa	
2558669826	DRAFT_00494	GC		0.52	
2558669826	DRAFT_00494	Transmembrane		Yes	
2558669827	DRAFT_00495	KEGG_module	M00532: Photorespiration		
2558669827	DRAFT_00495	Metacyc	PWY-181: photorespiration		
2558669827	DRAFT_00495	COG_category	[R] General function prediction only		
2558669827	DRAFT_00495	COG0546	Predicted phosphatases		8.00E-31
2558669827	DRAFT_00495	pfam13419	HAD_2		2.00E-30
2558669827	DRAFT_00495	EC:3.1.3.18	Phosphoglycolate phosphatase.		
2558669827	DRAFT_00495	TIGR01549	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m		8.40E-14
2558669827	DRAFT_00495	TIGR01428	2-haloalkanoic acid dehalogenase, type II		4.80E-24
2558669827	DRAFT_00495	TIGR01509	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third m		3.10E-12
2558669827	DRAFT_00495	TIGR01493	Haloacid dehalogenase superfamily, subfamily IA, variant 2 with 3rd m		1.10E-09
2558669827	DRAFT_00495	KO:K01091	phosphoglycolate phosphatase [EC:3.1.3.18]		4.20E-21
2558669827	DRAFT_00495	Locus_type		CDS	
2558669827	DRAFT_00495	Product_name		haloacid dehalogenase superfamily, subfamily IA, variant 3 with third	
2558669827	DRAFT_00495	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	

2558669827	DRAFT_00495	Coordinates		42273..42938(+)		
2558669827	DRAFT_00495	DNA_length		666bp		
2558669827	DRAFT_00495	Protein_length		221aa		
2558669827	DRAFT_00495	GC			0.59	

2558669828	DRAFT_00496	Locus_type		CDS		
2558669828	DRAFT_00496	Product_name		hypothetical protein		
2558669828	DRAFT_00496	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669828	DRAFT_00496	Coordinates		43127..43489(+)		
2558669828	DRAFT_00496	DNA_length		363bp		
2558669828	DRAFT_00496	Protein_length		120aa		
2558669828	DRAFT_00496	GC			0.57	

2558669829	DRAFT_00497	Metacyc	PWY-7112: 4-hydroxy-2-nonenal detoxification			
2558669829	DRAFT_00497	Metacyc	PWY-6842: glutathione-mediated detoxification II			
2558669829	DRAFT_00497	Metacyc	PWY-4061: glutathione-mediated detoxification I			
2558669829	DRAFT_00497	COG_category	[E] Amino acid transport and metabolism			
2558669829	DRAFT_00497	COG0308	Aminopeptidase N			5.00E-87
2558669829	DRAFT_00497	pfam13646	HEAT_2			1.20E-10
2558669829	DRAFT_00497	pfam01433	Peptidase_M1			5.70E-68
2558669829	DRAFT_00497	EC:3.4.11.2	Membrane alanyl aminopeptidase.			
2558669829	DRAFT_00497	KO:K01256	aminopeptidase N [EC:3.4.11.2]			0.00E+00
2558669829	DRAFT_00497	Locus_type		CDS		
2558669829	DRAFT_00497	Product_name		Aminopeptidase N		
2558669829	DRAFT_00497	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669829	DRAFT_00497	Coordinates		43518..46001(-)		
2558669829	DRAFT_00497	DNA_length		2484bp		
2558669829	DRAFT_00497	Protein_length		827aa		
2558669829	DRAFT_00497	GC			0.57	

2558669830	DRAFT_00498	Locus_type		CDS		
2558669830	DRAFT_00498	Product_name		hypothetical protein		
2558669830	DRAFT_00498	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669830	DRAFT_00498	Coordinates		46081..46254(+)		

2558669830	DRAFT_00498	DNA_length		174bp	
2558669830	DRAFT_00498	Protein_length		57aa	
2558669830	DRAFT_00498	GC		0.64	
2558669831	DRAFT_00499	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2558669831	DRAFT_00499	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I		
2558669831	DRAFT_00499	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis		
2558669831	DRAFT_00499	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II		
2558669831	DRAFT_00499	COG_category	[F] Nucleotide transport and metabolism		
2558669831	DRAFT_00499	COG0151	Phosphoribosylamine-glycine ligase		7.00E-27
2558669831	DRAFT_00499	pfam01071	GARS_A		9.40E-09
2558669831	DRAFT_00499	pfam02843	GARS_C		9.20E-11
2558669831	DRAFT_00499	EC:6.3.4.13	Phosphoribosylamine--glycine ligase.		
2558669831	DRAFT_00499	KO:K01945	phosphoribosylamine--glycine ligase [EC:6.3.4.13]		0.00E+00
2558669831	DRAFT_00499	Locus_type		CDS	
2558669831	DRAFT_00499	Product_name		Phosphoribosylamine-glycine ligase	
2558669831	DRAFT_00499	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669831	DRAFT_00499	Coordinates		46251..47579(-)	
2558669831	DRAFT_00499	DNA_length		1329bp	
2558669831	DRAFT_00499	Protein_length		442aa	
2558669831	DRAFT_00499	GC		0.55	
2558669832	DRAFT_00500	Locus_type		CDS	
2558669832	DRAFT_00500	Product_name		hypothetical protein	
2558669832	DRAFT_00500	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669832	DRAFT_00500	Coordinates		47994..48248(+)	
2558669832	DRAFT_00500	DNA_length		255bp	
2558669832	DRAFT_00500	Protein_length		84aa	
2558669832	DRAFT_00500	GC		0.54	
2558669832	DRAFT_00500	Transmembrane		Yes	
2558669833	DRAFT_00501	pfam08448	PAS_4		4.80E-07
2558669833	DRAFT_00501	Locus_type		CDS	
2558669833	DRAFT_00501	Product_name		Uncharacterized conserved protein	

2558669833	DRAFT_00501	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669833	DRAFT_00501	Coordinates		48362..48712(-)	
2558669833	DRAFT_00501	DNA_length		351bp	
2558669833	DRAFT_00501	Protein_length		116aa	
2558669833	DRAFT_00501	GC		0.53	

2558669834	DRAFT_00502	Locus_type		CDS	
2558669834	DRAFT_00502	Product_name		hypothetical protein	
2558669834	DRAFT_00502	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669834	DRAFT_00502	Coordinates		48997..49263(+)	
2558669834	DRAFT_00502	DNA_length		267bp	
2558669834	DRAFT_00502	Protein_length		88aa	
2558669834	DRAFT_00502	GC		0.51	
2558669834	DRAFT_00502	Transmembrane		Yes	

2558669835	DRAFT_00503	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558669835	DRAFT_00503	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558669835	DRAFT_00503	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558669835	DRAFT_00503	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669835	DRAFT_00503	COG0018	Arginyl-tRNA synthetase		4.00E-92
2558669835	DRAFT_00503	pfam05746	DALR_1		8.10E-23
2558669835	DRAFT_00503	pfam00750	tRNA-synt_1d		8.00E-23
2558669835	DRAFT_00503	pfam03485	Arg_tRNA_synt_N		6.50E-09
2558669835	DRAFT_00503	EC:6.1.1.19	Arginine--tRNA ligase.		
2558669835	DRAFT_00503	KO:K01887	arginyl-tRNA synthetase [EC:6.1.1.19]		0.00E+00
2558669835	DRAFT_00503	Locus_type		CDS	
2558669835	DRAFT_00503	Product_name		Arginyl-tRNA synthetase	
2558669835	DRAFT_00503	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669835	DRAFT_00503	Coordinates		49365..51266(+)	
2558669835	DRAFT_00503	DNA_length		1902bp	
2558669835	DRAFT_00503	Protein_length		633aa	
2558669835	DRAFT_00503	GC		0.59	

2558669836	DRAFT_00504	KEGG_module	M00020: Serine biosynthesis, glycerate-3P => serine		

2558669836	DRAFT_00504	Metacyc	SERSYN-PWY: serine biosynthesis		
2558669836	DRAFT_00504	COG_category	[E] Amino acid transport and metabolism		
2558669836	DRAFT_00504	COG0560	Phosphoserine phosphatase		4.00E-23
2558669836	DRAFT_00504	pfam12710	HAD		4.20E-14
2558669836	DRAFT_00504	EC:3.1.3.3	Phosphoserine phosphatase.		
2558669836	DRAFT_00504	TIGR01488	Haloacid Dehalogenase superfamily, subfamily IB, phosphoserine phos		1.10E-29
2558669836	DRAFT_00504	TIGR01491	HAD-superfamily, subfamily-IB PSPase-like hydrolase, archaeal		5.80E-48
2558669836	DRAFT_00504	KO:K01079	phosphoserine phosphatase [EC:3.1.3.3]		1.10E-24
2558669836	DRAFT_00504	Locus_type		CDS	
2558669836	DRAFT_00504	Product_name		Haloacid Dehalogenase superfamily, subfamily IB, phosphoserine pho	
2558669836	DRAFT_00504	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669836	DRAFT_00504	Coordinates		51429..52067(+)	
2558669836	DRAFT_00504	DNA_length		639bp	
2558669836	DRAFT_00504	Protein_length		212aa	
2558669836	DRAFT_00504	GC		0.57	

2558669837	DRAFT_00505	KEGG_module	M00532: Photorespiration		
2558669837	DRAFT_00505	KEGG_module	M00346: Formaldehyde assimilation, serine pathway		
2558669837	DRAFT_00505	Metacyc	PWY-181: photorespiration		
2558669837	DRAFT_00505	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)		
2558669837	DRAFT_00505	Metacyc	GLYSYN-ALA-PWY: glycine biosynthesis III		
2558669837	DRAFT_00505	COG_category	[E] Amino acid transport and metabolism		
2558669837	DRAFT_00505	COG0075	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferas		9.00E-90
2558669837	DRAFT_00505	pfam00266	Aminotran_5		5.10E-32
2558669837	DRAFT_00505	EC:2.6.1.51	Serine--pyruvate transaminase.		
2558669837	DRAFT_00505	EC:2.6.1.44	Alanine--glyoxylate transaminase.		
2558669837	DRAFT_00505	EC:2.6.1.45	Serine--glyoxylate transaminase.		
2558669837	DRAFT_00505	KO:K00830	alanine-glyoxylate transaminase / serine-glyoxylate transaminase / seri		0.00E+00
2558669837	DRAFT_00505	Locus_type		CDS	
2558669837	DRAFT_00505	Product_name		Serine-pyruvate aminotransferase/archaeal aspartate aminotransfera	
2558669837	DRAFT_00505	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6	
2558669837	DRAFT_00505	Coordinates		52114..53241(+)	
2558669837	DRAFT_00505	DNA_length		1128bp	
2558669837	DRAFT_00505	Protein_length		375aa	

2558669837	DRAFT_00505	GC			0.59	
2558669838	DRAFT_00506	Locus_type		tRNA		
2558669838	DRAFT_00506	Product_name		tRNA_Gln_CTG		
2558669838	DRAFT_00506	Scaffold		DRAFT_contig_70_41_len_53364_read_count_885993.6		
2558669838	DRAFT_00506	Coordinates		53291..53363(+)		
2558669838	DRAFT_00506	DNA_length		73bp		
2558669838	DRAFT_00506	GC			0.62	
2558669839	DRAFT_00507	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2558669839	DRAFT_00507	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558669839	DRAFT_00507	Metacyc	PWY-6692: Fe(II) oxidation			
2558669839	DRAFT_00507	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558669839	DRAFT_00507	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558669839	DRAFT_00507	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558669839	DRAFT_00507	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558669839	DRAFT_00507	COG_category	[C] Energy production and conversion			
2558669839	DRAFT_00507	COG0852	NADH:ubiquinone oxidoreductase 27 kD subunit			1.00E-14
2558669839	DRAFT_00507	pfam00329	Complex1_30kDa			1.70E-20
2558669839	DRAFT_00507	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558669839	DRAFT_00507	KO:K00332	NADH-quinone oxidoreductase subunit C [EC:1.6.5.3]			5.10E-16
2558669839	DRAFT_00507	ITERM:05529	NADH dehydrogenase subunit C (EC 1.6.5.3)			
2558669839	DRAFT_00507	Locus_type		CDS		
2558669839	DRAFT_00507	Product_name		NADH dehydrogenase subunit C (EC 1.6.5.3)		
2558669839	DRAFT_00507	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669839	DRAFT_00507	Coordinates		82..525(+)		
2558669839	DRAFT_00507	DNA_length		444bp		
2558669839	DRAFT_00507	Protein_length		147aa		
2558669839	DRAFT_00507	GC			0.59	
2558669840	DRAFT_00508	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558669840	DRAFT_00508	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558669840	DRAFT_00508	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558669840	DRAFT_00508	Metacyc	PWY-6692: Fe(II) oxidation			

2558669840	DRAFT_00508	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558669840	DRAFT_00508	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558669840	DRAFT_00508	COG_category	[C] Energy production and conversion			
2558669840	DRAFT_00508	COG3261	Ni,Fe-hydrogenase III large subunit			8.00E-98
2558669840	DRAFT_00508	pfam00346	Complex1_49kDa			1.80E-31
2558669840	DRAFT_00508	pfam00374	NiFeSe_Hases			3.10E-09
2558669840	DRAFT_00508	pfam00346	Complex1_49kDa			3.90E-12
2558669840	DRAFT_00508	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558669840	DRAFT_00508	KO:K00329	NADH dehydrogenase [EC:1.6.5.3]			0.00E+00
2558669840	DRAFT_00508	Locus_type		CDS		
2558669840	DRAFT_00508	Product_name		Ni,Fe-hydrogenase III large subunit		
2558669840	DRAFT_00508	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669840	DRAFT_00508	Coordinates		518..1756(+)		
2558669840	DRAFT_00508	DNA_length		1239bp		
2558669840	DRAFT_00508	Protein_length		412aa		
2558669840	DRAFT_00508	GC			0.58	

2558669841	DRAFT_00509	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2558669841	DRAFT_00509	Metacyc	PWY-6692: Fe(II) oxidation			
2558669841	DRAFT_00509	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558669841	DRAFT_00509	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558669841	DRAFT_00509	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558669841	DRAFT_00509	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558669841	DRAFT_00509	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558669841	DRAFT_00509	COG_category	[C] Energy production and conversion			
2558669841	DRAFT_00509	COG1005	NADH:ubiquinone oxidoreductase subunit 1 (chain H)			9.00E-49
2558669841	DRAFT_00509	pfam00146	NADHdh			2.70E-59
2558669841	DRAFT_00509	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558669841	DRAFT_00509	KO:K00337	NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]			0.00E+00
2558669841	DRAFT_00509	ITERM:05535	NADH dehydrogenase subunit H (EC 1.6.5.3)			
2558669841	DRAFT_00509	Locus_type		CDS		
2558669841	DRAFT_00509	Product_name		NADH dehydrogenase subunit H (EC 1.6.5.3)		
2558669841	DRAFT_00509	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669841	DRAFT_00509	Coordinates		1762..2727(+)		

2558669841	DRAFT_00509	DNA_length		966bp	
2558669841	DRAFT_00509	Protein_length		321aa	
2558669841	DRAFT_00509	GC		0.58	
2558669841	DRAFT_00509	Transmembrane		Yes	

2558669842	DRAFT_00510	pfam12838	Fer4_7		3.80E-12
2558669842	DRAFT_00510	Locus_type		CDS	
2558669842	DRAFT_00510	Product_name		Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase	
2558669842	DRAFT_00510	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669842	DRAFT_00510	Coordinates		2769..3128(+)	
2558669842	DRAFT_00510	DNA_length		360bp	
2558669842	DRAFT_00510	Protein_length		119aa	
2558669842	DRAFT_00510	GC		0.52	

2558669843	DRAFT_00511	pfam00499	Oxidored_q3		2.50E-07
2558669843	DRAFT_00511	Locus_type		CDS	
2558669843	DRAFT_00511	Product_name		NADH-ubiquinone/plastoquinone oxidoreductase chain 6	
2558669843	DRAFT_00511	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669843	DRAFT_00511	Coordinates		3118..3600(+)	
2558669843	DRAFT_00511	DNA_length		483bp	
2558669843	DRAFT_00511	Protein_length		160aa	
2558669843	DRAFT_00511	GC		0.55	
2558669843	DRAFT_00511	Transmembrane		Yes	

2558669844	DRAFT_00512	COG_category	[C] Energy production and conversion		
2558669844	DRAFT_00512	COG0713	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)		4.00E-06
2558669844	DRAFT_00512	pfam00420	Oxidored_q2		3.40E-16
2558669844	DRAFT_00512	KO:K05567	multicomponent Na+:H+ antiporter subunit C		1.40E-10
2558669844	DRAFT_00512	Locus_type		CDS	
2558669844	DRAFT_00512	Product_name		NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)	
2558669844	DRAFT_00512	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669844	DRAFT_00512	Coordinates		3601..3927(+)	
2558669844	DRAFT_00512	DNA_length		327bp	
2558669844	DRAFT_00512	Protein_length		108aa	

2558669844	DRAFT_00512	GC			0.57	
2558669844	DRAFT_00512	Transmembrane		Yes		
2558669845	DRAFT_00513	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2558669845	DRAFT_00513	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558669845	DRAFT_00513	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558669845	DRAFT_00513	Metacyc	PWY-6692: Fe(II) oxidation			
2558669845	DRAFT_00513	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558669845	DRAFT_00513	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558669845	DRAFT_00513	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558669845	DRAFT_00513	COG_category	[C] Energy production and conversion			
2558669845	DRAFT_00513	COG_category	[P] Inorganic ion transport and metabolism			
2558669845	DRAFT_00513	COG1009	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+			6.00E-99
2558669845	DRAFT_00513	pfam00361	Oxidored_q1			2.60E-77
2558669845	DRAFT_00513	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558669845	DRAFT_00513	TIGR01974	proton-translocating NADH-quinone oxidoreductase, chain L			0.00E+00
2558669845	DRAFT_00513	KO:K00341	NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]			0.00E+00
2558669845	DRAFT_00513	Locus_type		CDS		
2558669845	DRAFT_00513	Product_name		proton-translocating NADH-quinone oxidoreductase, chain L		
2558669845	DRAFT_00513	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669845	DRAFT_00513	Coordinates		3927..5708(+)		
2558669845	DRAFT_00513	DNA_length		1782bp		
2558669845	DRAFT_00513	Protein_length		593aa		
2558669845	DRAFT_00513	GC			0.6	
2558669845	DRAFT_00513	Transmembrane		Yes		
2558669846	DRAFT_00514	COG_category	[C] Energy production and conversion			
2558669846	DRAFT_00514	COG1007	NADH:ubiquinone oxidoreductase subunit 2 (chain N)			5.00E-47
2558669846	DRAFT_00514	pfam00361	Oxidored_q1			4.90E-46
2558669846	DRAFT_00514	TIGR01770	proton-translocating NADH-quinone oxidoreductase, chain N			2.80E-66
2558669846	DRAFT_00514	KO:K05568	multicomponent Na+:H+ antiporter subunit D			0.00E+00
2558669846	DRAFT_00514	Locus_type		CDS		
2558669846	DRAFT_00514	Product_name		NADH:ubiquinone oxidoreductase subunit 2 (chain N)		
2558669846	DRAFT_00514	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		

2558669846	DRAFT_00514	Coordinates		5712..7160(+)		
2558669846	DRAFT_00514	DNA_length		1449bp		
2558669846	DRAFT_00514	Protein_length		482aa		
2558669846	DRAFT_00514	GC			0.59	
2558669846	DRAFT_00514	Transmembrane		Yes		
2558669847	DRAFT_00515	Locus_type		CDS		
2558669847	DRAFT_00515	Product_name		hypothetical protein		
2558669847	DRAFT_00515	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669847	DRAFT_00515	Coordinates		7211..7528(+)		
2558669847	DRAFT_00515	DNA_length		318bp		
2558669847	DRAFT_00515	Protein_length		105aa		
2558669847	DRAFT_00515	GC			0.58	
2558669848	DRAFT_00516	Locus_type		CDS		
2558669848	DRAFT_00516	Product_name		hypothetical protein		
2558669848	DRAFT_00516	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669848	DRAFT_00516	Coordinates		7537..8307(-)		
2558669848	DRAFT_00516	DNA_length		771bp		
2558669848	DRAFT_00516	Protein_length		256aa		
2558669848	DRAFT_00516	GC			0.58	
2558669849	DRAFT_00517	pfam01455	HupF_HypC			5.90E-07
2558669849	DRAFT_00517	Locus_type		CDS		
2558669849	DRAFT_00517	Product_name		HupF/HypC family		
2558669849	DRAFT_00517	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669849	DRAFT_00517	Coordinates		8304..8561(-)		
2558669849	DRAFT_00517	DNA_length		258bp		
2558669849	DRAFT_00517	Protein_length		85aa		
2558669849	DRAFT_00517	GC			0.61	
2558669850	DRAFT_00518	COG_category	[G] Carbohydrate transport and metabolism			
2558669850	DRAFT_00518	COG2814	Arabinose efflux permease			6.00E-23
2558669850	DRAFT_00518	pfam07690	MFS_1			8.60E-44

2558669850	DRAFT_00518	Locus_type		CDS	
2558669850	DRAFT_00518	Product_name		Arabinose efflux permease	
2558669850	DRAFT_00518	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669850	DRAFT_00518	Coordinates		8617..9849(-)	
2558669850	DRAFT_00518	DNA_length		1233bp	
2558669850	DRAFT_00518	Protein_length		410aa	
2558669850	DRAFT_00518	GC		0.6	
2558669850	DRAFT_00518	Transmembrane		Yes	

2558669851	DRAFT_00519	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558669851	DRAFT_00519	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558669851	DRAFT_00519	Metacyc	PWY-5392: reductive TCA cycle II		
2558669851	DRAFT_00519	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558669851	DRAFT_00519	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558669851	DRAFT_00519	Metacyc	P23-PWY: reductive TCA cycle I		
2558669851	DRAFT_00519	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558669851	DRAFT_00519	COG_category	[C] Energy production and conversion		
2558669851	DRAFT_00519	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		2.00E-16
2558669851	DRAFT_00519	pfam01558	POR		1.40E-25
2558669851	DRAFT_00519	EC:1.2.7.3	2-oxoglutarate synthase.		
2558669851	DRAFT_00519	KO:K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]		8.40E-32
2558669851	DRAFT_00519	Locus_type		CDS	
2558669851	DRAFT_00519	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin	
2558669851	DRAFT_00519	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669851	DRAFT_00519	Coordinates		9875..10495(-)	
2558669851	DRAFT_00519	DNA_length		621bp	
2558669851	DRAFT_00519	Protein_length		206aa	
2558669851	DRAFT_00519	GC		0.59	

2558669852	DRAFT_00520	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558669852	DRAFT_00520	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558669852	DRAFT_00520	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558669852	DRAFT_00520	Metacyc	PWY-5392: reductive TCA cycle II		
2558669852	DRAFT_00520	Metacyc	P23-PWY: reductive TCA cycle I		

2558669852	DRAFT_00520	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558669852	DRAFT_00520	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558669852	DRAFT_00520	pfam02775	TPP_enzyme_C		6.50E-21
2558669852	DRAFT_00520	EC:1.2.7.3	2-oxoglutarate synthase.		
2558669852	DRAFT_00520	KO:K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]		0.00E+00
2558669852	DRAFT_00520	Locus_type		CDS	
2558669852	DRAFT_00520	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin	
2558669852	DRAFT_00520	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669852	DRAFT_00520	Coordinates		10492..11304(-)	
2558669852	DRAFT_00520	DNA_length		813bp	
2558669852	DRAFT_00520	Protein_length		270aa	
2558669852	DRAFT_00520	GC		0.6	
2558669853	DRAFT_00521	KEGG_module	M00312: 2-oxoisovalerate:ferredoxin oxidoreductase		
2558669853	DRAFT_00521	COG_category	[C] Energy production and conversion		
2558669853	DRAFT_00521	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		4.00E-51
2558669853	DRAFT_00521	pfam01855	POR_N		4.70E-48
2558669853	DRAFT_00521	pfam02780	Transketolase_C		1.80E-06
2558669853	DRAFT_00521	EC:1.2.7.7	3-methyl-2-oxobutanoate dehydrogenase (ferredoxin).		
2558669853	DRAFT_00521	KO:K00186	2-oxoisovalerate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.7]		0.00E+00
2558669853	DRAFT_00521	ITERM:00694	ketoisovalerate ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.7)		
2558669853	DRAFT_00521	Locus_type		CDS	
2558669853	DRAFT_00521	Product_name		ketoisovalerate ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.7)	
2558669853	DRAFT_00521	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669853	DRAFT_00521	Coordinates		11301..12368(-)	
2558669853	DRAFT_00521	DNA_length		1068bp	
2558669853	DRAFT_00521	Protein_length		355aa	
2558669853	DRAFT_00521	GC		0.58	
2558669854	DRAFT_00522	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558669854	DRAFT_00522	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558669854	DRAFT_00522	Metacyc	P23-PWY: reductive TCA cycle I		
2558669854	DRAFT_00522	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558669854	DRAFT_00522	Metacyc	P42-PWY: incomplete reductive TCA cycle		

2558669854	DRAFT_00522	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558669854	DRAFT_00522	Metacyc	PWY-5392: reductive TCA cycle II		
2558669854	DRAFT_00522	pfam12838	Fer4_7		6.50E-09
2558669854	DRAFT_00522	EC:1.2.7.3	2-oxoglutarate synthase.		
2558669854	DRAFT_00522	KO:K00176	2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7.3]		1.60E-13
2558669854	DRAFT_00522	Locus_type		CDS	
2558669854	DRAFT_00522	Product_name		Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits	
2558669854	DRAFT_00522	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669854	DRAFT_00522	Coordinates		12365..12616(-)	
2558669854	DRAFT_00522	DNA_length		252bp	
2558669854	DRAFT_00522	Protein_length		83aa	
2558669854	DRAFT_00522	GC		0.56	
2558669855	DRAFT_00523	KEGG_module	M00169: CAM (Crassulacean acid metabolism), light		
2558669855	DRAFT_00523	KEGG_module	M00171: C4-dicarboxylic acid cycle, NAD+ -malic enzyme type		
2558669855	DRAFT_00523	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2558669855	DRAFT_00523	KEGG_module	M00172: C4-dicarboxylic acid cycle, NADP+ -malic enzyme type		
2558669855	DRAFT_00523	Metacyc	PWY-6549: glutamine biosynthesis III		
2558669855	DRAFT_00523	Metacyc	PWY-7117: C4 photosynthetic carbon assimilation cycle, PEPCK type		
2558669855	DRAFT_00523	Metacyc	PWY-241: C4 photosynthetic carbon assimilation cycle, NADP-ME type		
2558669855	DRAFT_00523	Metacyc	PWY-7115: C4 photosynthetic carbon assimilation cycle, NAD-ME type		
2558669855	DRAFT_00523	IMG_pathway	289: Oxaloacetate synthesis via phosphoenolpyruvate		
2558669855	DRAFT_00523	COG_category	[G] Carbohydrate transport and metabolism		
2558669855	DRAFT_00523	COG0574	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase		0.00E+00
2558669855	DRAFT_00523	pfam00391	PEP-utilizers		4.00E-21
2558669855	DRAFT_00523	pfam02896	PEP-utilizers_C		1.40E-100
2558669855	DRAFT_00523	pfam01326	PPDK_N		7.40E-64
2558669855	DRAFT_00523	EC:2.7.9.1	Pyruvate, phosphate dikinase.		
2558669855	DRAFT_00523	TIGR01828	pyruvate, phosphate dikinase		0.00E+00
2558669855	DRAFT_00523	KO:K01006	pyruvate,orthophosphate dikinase [EC:2.7.9.1]		0.00E+00
2558669855	DRAFT_00523	ITERM:00813	pyruvate phosphate dikinase (EC 2.7.9.1)		
2558669855	DRAFT_00523	Locus_type		CDS	
2558669855	DRAFT_00523	Product_name		pyruvate phosphate dikinase (EC 2.7.9.1)	
2558669855	DRAFT_00523	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	

2558669855	DRAFT_00523	Coordinates		12707..15355(-)	
2558669855	DRAFT_00523	DNA_length		2649bp	
2558669855	DRAFT_00523	Protein_length		882aa	
2558669855	DRAFT_00523	GC		0.59	
2558669856	DRAFT_00524	pfam00583	Acetyltransf_1		1.40E-18
2558669856	DRAFT_00524	Locus_type		CDS	
2558669856	DRAFT_00524	Product_name		Predicted acetyltransferase	
2558669856	DRAFT_00524	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669856	DRAFT_00524	Coordinates		15402..15953(-)	
2558669856	DRAFT_00524	DNA_length		552bp	
2558669856	DRAFT_00524	Protein_length		183aa	
2558669856	DRAFT_00524	GC		0.57	
2558669857	DRAFT_00525	COG_category	[E] Amino acid transport and metabolism		
2558669857	DRAFT_00525	COG1748	Saccharopine dehydrogenase and related proteins		3.00E-56
2558669857	DRAFT_00525	pfam03435	Saccharop_dh		7.30E-53
2558669857	DRAFT_00525	Locus_type		CDS	
2558669857	DRAFT_00525	Product_name		Saccharopine dehydrogenase and related proteins	
2558669857	DRAFT_00525	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669857	DRAFT_00525	Coordinates		16115..17266(-)	
2558669857	DRAFT_00525	DNA_length		1152bp	
2558669857	DRAFT_00525	Protein_length		383aa	
2558669857	DRAFT_00525	GC		0.61	
2558669858	DRAFT_00526	pfam00571	CBS		1.00E-10
2558669858	DRAFT_00526	pfam00571	CBS		1.80E-07
2558669858	DRAFT_00526	pfam13894	zf-C2H2_4		9.80E-05
2558669858	DRAFT_00526	Locus_type		CDS	
2558669858	DRAFT_00526	Product_name		Predicted signal-transduction protein containing cAMP-binding and C	
2558669858	DRAFT_00526	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669858	DRAFT_00526	Coordinates		17347..17892(+)	
2558669858	DRAFT_00526	DNA_length		546bp	
2558669858	DRAFT_00526	Protein_length		181aa	

2558669858	DRAFT_00526	GC		0.62	
2558669859	DRAFT_00527	COG_category	[E] Amino acid transport and metabolism		
2558669859	DRAFT_00527	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase a		3.00E-51
2558669859	DRAFT_00527	pfam01546	Peptidase_M20		5.00E-31
2558669859	DRAFT_00527	pfam07687	M20_dimer		9.20E-19
2558669859	DRAFT_00527	Locus_type		CDS	
2558669859	DRAFT_00527	Product_name		Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase	
2558669859	DRAFT_00527	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669859	DRAFT_00527	Coordinates		17894..19252(-)	
2558669859	DRAFT_00527	DNA_length		1359bp	
2558669859	DRAFT_00527	Protein_length		452aa	
2558669859	DRAFT_00527	GC		0.6	
2558669860	DRAFT_00528	COG_category	[P] Inorganic ion transport and metabolism		
2558669860	DRAFT_00528	COG2217	Cation transport ATPase		0.00E+00
2558669860	DRAFT_00528	pfam00702	Hydrolase		2.90E-55
2558669860	DRAFT_00528	pfam00122	E1-E2_ATPase		3.40E-61
2558669860	DRAFT_00528	pfam04945	YHS		2.40E-06
2558669860	DRAFT_00528	EC:3.6.3.4	Copper-exporting ATPase.		
2558669860	DRAFT_00528	TIGR01494	ATPase, P-type (transporting), HAD superfamily, subfamily IC		1.70E-100
2558669860	DRAFT_00528	TIGR01511	copper-(or silver)-translocating P-type ATPase		0.00E+00
2558669860	DRAFT_00528	TIGR01525	heavy metal translocating P-type ATPase		0.00E+00
2558669860	DRAFT_00528	KO:K01533	Cu2+-exporting ATPase [EC:3.6.3.4]		0.00E+00
2558669860	DRAFT_00528	Locus_type		CDS	
2558669860	DRAFT_00528	Product_name		copper-(or silver)-translocating P-type ATPase	
2558669860	DRAFT_00528	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669860	DRAFT_00528	Coordinates		19331..21385(-)	
2558669860	DRAFT_00528	DNA_length		2055bp	
2558669860	DRAFT_00528	Protein_length		684aa	
2558669860	DRAFT_00528	GC		0.6	
2558669860	DRAFT_00528	Transmembrane		Yes	
2558669861	DRAFT_00529	COG_category	[S] Function unknown		

2558669861	DRAFT_00529	COG3350	Uncharacterized conserved protein			1.00E-06
2558669861	DRAFT_00529	pfam04945	YHS			4.10E-11
2558669861	DRAFT_00529	Locus_type		CDS		
2558669861	DRAFT_00529	Product_name		Uncharacterized conserved protein		
2558669861	DRAFT_00529	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669861	DRAFT_00529	Coordinates		21458..21616(+)		
2558669861	DRAFT_00529	DNA_length		159bp		
2558669861	DRAFT_00529	Protein_length		52aa		
2558669861	DRAFT_00529	GC			0.55	

2558669862	DRAFT_00530	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2558669862	DRAFT_00530	Metacyc	PWY-7118: chitin degradation to ethanol			
2558669862	DRAFT_00530	COG_category	[C] Energy production and conversion			
2558669862	DRAFT_00530	COG0281	Malic enzyme			0.00E+00
2558669862	DRAFT_00530	pfam03949	Malic_M			5.90E-60
2558669862	DRAFT_00530	pfam00390	malic			9.40E-25
2558669862	DRAFT_00530	EC:1.1.1.38	Malate dehydrogenase (oxaloacetate-decarboxylating).			
2558669862	DRAFT_00530	KO:K00027	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]			0.00E+00
2558669862	DRAFT_00530	Locus_type		CDS		
2558669862	DRAFT_00530	Product_name		Malic enzyme		
2558669862	DRAFT_00530	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669862	DRAFT_00530	Coordinates		21726..23108(+)		
2558669862	DRAFT_00530	DNA_length		1383bp		
2558669862	DRAFT_00530	Protein_length		460aa		
2558669862	DRAFT_00530	GC			0.55	

2558669863	DRAFT_00531	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669863	DRAFT_00531	COG1225	Peroxiredoxin			2.00E-56
2558669863	DRAFT_00531	pfam00578	AhpC-TSA			1.70E-37
2558669863	DRAFT_00531	EC:1.11.1.15	Peroxiredoxin.			
2558669863	DRAFT_00531	KO:K03564	peroxiredoxin Q/BCP [EC:1.11.1.15]			0.00E+00
2558669863	DRAFT_00531	Locus_type		CDS		
2558669863	DRAFT_00531	Product_name		Peroxiredoxin		
2558669863	DRAFT_00531	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		

2558669863	DRAFT_00531	Coordinates		23372..23848(-)		
2558669863	DRAFT_00531	DNA_length		477bp		
2558669863	DRAFT_00531	Protein_length		158aa		
2558669863	DRAFT_00531	GC			0.56	

2558669864	DRAFT_00532	COG_category	[E] Amino acid transport and metabolism			
2558669864	DRAFT_00532	COG2309	Leucyl aminopeptidase (aminopeptidase T)			2.00E-05
2558669864	DRAFT_00532	pfam02073	Peptidase_M29			5.10E-12
2558669864	DRAFT_00532	Locus_type		CDS		
2558669864	DRAFT_00532	Product_name		Leucyl aminopeptidase (aminopeptidase T)		
2558669864	DRAFT_00532	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669864	DRAFT_00532	Coordinates		24026..25075(-)		
2558669864	DRAFT_00532	DNA_length		1050bp		
2558669864	DRAFT_00532	Protein_length		349aa		
2558669864	DRAFT_00532	GC			0.59	

2558669865	DRAFT_00533	Locus_type		CDS		
2558669865	DRAFT_00533	Product_name		hypothetical protein		
2558669865	DRAFT_00533	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669865	DRAFT_00533	Coordinates		25138..25458(-)		
2558669865	DRAFT_00533	DNA_length		321bp		
2558669865	DRAFT_00533	Protein_length		106aa		
2558669865	DRAFT_00533	GC			0.57	

2558669866	DRAFT_00534	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2558669866	DRAFT_00534	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2558669866	DRAFT_00534	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558669866	DRAFT_00534	IMG_pathway	488: L-cysteine ligation to tRNA(Cys)			
2558669866	DRAFT_00534	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669866	DRAFT_00534	COG0215	Cysteinyl-tRNA synthetase			1.00E-117
2558669866	DRAFT_00534	pfam01406	tRNA-synt_1e			1.30E-89
2558669866	DRAFT_00534	pfam09190	DALR_2			3.30E-07
2558669866	DRAFT_00534	EC:6.1.1.16	Cysteine--tRNA ligase.			
2558669866	DRAFT_00534	TIGR00435	cysteinyl-tRNA synthetase			1.90E-111

2558669866	DRAFT_00534	KO:K01883	cysteinyl-tRNA synthetase [EC:6.1.1.16]			0.00E+00
2558669866	DRAFT_00534	ITERM:00404	cysteinyl-tRNA synthetase (EC 6.1.1.16)			
2558669866	DRAFT_00534	Locus_type		CDS		
2558669866	DRAFT_00534	Product_name		cysteinyl-tRNA synthetase (EC 6.1.1.16)		
2558669866	DRAFT_00534	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669866	DRAFT_00534	Coordinates		25500..26699(+)		
2558669866	DRAFT_00534	DNA_length		1200bp		
2558669866	DRAFT_00534	Protein_length		399aa		
2558669866	DRAFT_00534	GC			0.6	
2558669867	DRAFT_00535	pfam13508	Acetyltransf_7			2.20E-07
2558669867	DRAFT_00535	Locus_type		CDS		
2558669867	DRAFT_00535	Product_name		Acetyltransferase (GNAT) domain		
2558669867	DRAFT_00535	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669867	DRAFT_00535	Coordinates		26692..27462(+)		
2558669867	DRAFT_00535	DNA_length		771bp		
2558669867	DRAFT_00535	Protein_length		256aa		
2558669867	DRAFT_00535	GC			0.57	
2558669868	DRAFT_00536	Locus_type		CDS		
2558669868	DRAFT_00536	Product_name		hypothetical protein		
2558669868	DRAFT_00536	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669868	DRAFT_00536	Coordinates		27470..27952(+)		
2558669868	DRAFT_00536	DNA_length		483bp		
2558669868	DRAFT_00536	Protein_length		160aa		
2558669868	DRAFT_00536	GC			0.57	
2558669869	DRAFT_00537	Locus_type		CDS		
2558669869	DRAFT_00537	Product_name		hypothetical protein		
2558669869	DRAFT_00537	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669869	DRAFT_00537	Coordinates		28100..28504(-)		
2558669869	DRAFT_00537	DNA_length		405bp		
2558669869	DRAFT_00537	Protein_length		134aa		
2558669869	DRAFT_00537	GC			0.6	

2558669870	DRAFT_00538	pfam09969	DUF2203			9.70E-24
2558669870	DRAFT_00538	Locus_type		CDS		
2558669870	DRAFT_00538	Product_name		Uncharacterized conserved protein (DUF2203)		
2558669870	DRAFT_00538	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669870	DRAFT_00538	Coordinates		28589..28876(-)		
2558669870	DRAFT_00538	DNA_length		288bp		
2558669870	DRAFT_00538	Protein_length		95aa		
2558669870	DRAFT_00538	GC			0.57	

2558669871	DRAFT_00539	COG_category	[S] Function unknown			
2558669871	DRAFT_00539	COG5616	Predicted integral membrane protein			4.00E-36
2558669871	DRAFT_00539	pfam00211	Guanylate_cyc			1.40E-24
2558669871	DRAFT_00539	pfam13414	TPR_11			9.90E-09
2558669871	DRAFT_00539	pfam13414	TPR_11			1.20E-06
2558669871	DRAFT_00539	EC:4.6.1.1	Adenylate cyclase.			
2558669871	DRAFT_00539	KO:K01768	adenylate cyclase [EC:4.6.1.1]			0.00E+00
2558669871	DRAFT_00539	Locus_type		CDS		
2558669871	DRAFT_00539	Product_name		Predicted integral membrane protein		
2558669871	DRAFT_00539	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669871	DRAFT_00539	Coordinates		29353..31323(-)		
2558669871	DRAFT_00539	DNA_length		1971bp		
2558669871	DRAFT_00539	Protein_length		656aa		
2558669871	DRAFT_00539	GC			0.55	

2558669872	DRAFT_00540	pfam05048	NosD			5.40E-16
2558669872	DRAFT_00540	TIGR03804	parallel beta-helix repeat (two copies)			2.10E-08
2558669872	DRAFT_00540	Locus_type		CDS		
2558669872	DRAFT_00540	Product_name		parallel beta-helix repeat (two copies)		
2558669872	DRAFT_00540	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669872	DRAFT_00540	Coordinates		31585..34266(+)		
2558669872	DRAFT_00540	DNA_length		2682bp		
2558669872	DRAFT_00540	Protein_length		893aa		
2558669872	DRAFT_00540	GC			0.57	

2558669872	DRAFT_00540	Transmembrane		Yes	
2558669873	DRAFT_00541	COG_category	[S] Function unknown		
2558669873	DRAFT_00541	COG2096	Uncharacterized conserved protein		2.00E-46
2558669873	DRAFT_00541	pfam01923	Cob_adeno_trans		2.50E-51
2558669873	DRAFT_00541	TIGR00636	ATP:cob(I)alamin adenosyltransferase		4.20E-57
2558669873	DRAFT_00541	Locus_type		CDS	
2558669873	DRAFT_00541	Product_name		ATP:cob(I)alamin adenosyltransferase	
2558669873	DRAFT_00541	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669873	DRAFT_00541	Coordinates		34603..35136(+)	
2558669873	DRAFT_00541	DNA_length		534bp	
2558669873	DRAFT_00541	Protein_length		177aa	
2558669873	DRAFT_00541	GC		0.58	
2558669874	DRAFT_00542	Metacyc	PWY0-321: phenylacetate degradation I (aerobic)		
2558669874	DRAFT_00542	COG_category	[I] Lipid transport and metabolism		
2558669874	DRAFT_00542	COG1024	Enoyl-CoA hydratase/carnithine racemase		1.00E-44
2558669874	DRAFT_00542	pfam00378	ECH		4.70E-47
2558669874	DRAFT_00542	EC:5.3.3.18	2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase.		
2558669874	DRAFT_00542	KO:K15866	2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase [EC:5.3.3.18]		0.00E+00
2558669874	DRAFT_00542	Locus_type		CDS	
2558669874	DRAFT_00542	Product_name		Enoyl-CoA hydratase/carnithine racemase	
2558669874	DRAFT_00542	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669874	DRAFT_00542	Coordinates		35147..35890(-)	
2558669874	DRAFT_00542	DNA_length		744bp	
2558669874	DRAFT_00542	Protein_length		247aa	
2558669874	DRAFT_00542	GC		0.6	
2558669875	DRAFT_00543	KEGG_module	M00013: Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA		
2558669875	DRAFT_00543	KEGG_module	M00087: beta-Oxidation		
2558669875	DRAFT_00543	KEGG_module	M00032: Lysine degradation, lysine => saccharopine => acetoacetyl-CoA		
2558669875	DRAFT_00543	Metacyc	PWY-6435: 4-hydroxybenzoate biosynthesis V		
2558669875	DRAFT_00543	Metacyc	PWY-7046: 4-coumarate degradation (anaerobic)		
2558669875	DRAFT_00543	Metacyc	PWY-5138: unsaturated, even numbered fatty acid β-oxidation		

2558669875	DRAFT_00543	Metacyc	PWY-5136: fatty acid β-oxidation II (peroxisome)		
2558669875	DRAFT_00543	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2558669875	DRAFT_00543	Metacyc	PWY-7007: methyl ketone biosynthesis		
2558669875	DRAFT_00543	Metacyc	FAO-PWY: fatty acid β-oxidation I		
2558669875	DRAFT_00543	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis		
2558669875	DRAFT_00543	Metacyc	VALDEG-PWY: valine degradation I		
2558669875	DRAFT_00543	Metacyc	PWY66-391: fatty acid β-oxidation VI (peroxisome)		
2558669875	DRAFT_00543	Metacyc	PWY-735: jasmonic acid biosynthesis		
2558669875	DRAFT_00543	Metacyc	PWY-7094: fatty acid salvage		
2558669875	DRAFT_00543	Metacyc	PWY0-321: phenylacetate degradation I (aerobic)		
2558669875	DRAFT_00543	IMG_pathway	222: L-isoleucine degradation to propionyl-CoA and acetyl-CoA		
2558669875	DRAFT_00543	IMG_pathway	227: L-valine degradation to propionyl-CoA		
2558669875	DRAFT_00543	COG_category	[I] Lipid transport and metabolism		
2558669875	DRAFT_00543	COG1024	Enoyl-CoA hydratase/carnithine racemase		4.00E-62
2558669875	DRAFT_00543	pfam00378	ECH		4.90E-72
2558669875	DRAFT_00543	EC:4.2.1.17	Enoyl-CoA hydratase.		
2558669875	DRAFT_00543	KO:K01692	enoyl-CoA hydratase [EC:4.2.1.17]		0.00E+00
2558669875	DRAFT_00543	ITERM:00575	short chain enoyl-CoA hydratase (EC 4.2.1.17)		
2558669875	DRAFT_00543	Locus_type		CDS	
2558669875	DRAFT_00543	Product_name		short chain enoyl-CoA hydratase (EC 4.2.1.17)	
2558669875	DRAFT_00543	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669875	DRAFT_00543	Coordinates		35891..36667(-)	
2558669875	DRAFT_00543	DNA_length		777bp	
2558669875	DRAFT_00543	Protein_length		258aa	
2558669875	DRAFT_00543	GC		0.58	

2558669876	DRAFT_00544	Locus_type		CDS
2558669876	DRAFT_00544	Product_name		hypothetical protein
2558669876	DRAFT_00544	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7
2558669876	DRAFT_00544	Coordinates		36915..37106(+)
2558669876	DRAFT_00544	DNA_length		192bp
2558669876	DRAFT_00544	Protein_length		63aa
2558669876	DRAFT_00544	GC		0.54

2558669877	DRAFT_00545	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone		
2558669877	DRAFT_00545	Metacyc	PWY66-367: ketogenesis		
2558669877	DRAFT_00545	Metacyc	PWY66-368: ketolysis		
2558669877	DRAFT_00545	COG_category	[R] General function prediction only		
2558669877	DRAFT_00545	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism		
2558669877	DRAFT_00545	COG_category	[I] Lipid transport and metabolism		
2558669877	DRAFT_00545	COG1028	Dehydrogenases with different specificities (related to short-chain alco		5.00E-43
2558669877	DRAFT_00545	pfam00106	adh_short		3.10E-30
2558669877	DRAFT_00545	EC:1.1.1.30	3-hydroxybutyrate dehydrogenase.		
2558669877	DRAFT_00545	TIGR01963	3-hydroxybutyrate dehydrogenase		4.40E-98
2558669877	DRAFT_00545	KO:K00019	3-hydroxybutyrate dehydrogenase [EC:1.1.1.30]		0.00E+00
2558669877	DRAFT_00545	Locus_type		CDS	
2558669877	DRAFT_00545	Product_name		3-hydroxybutyrate dehydrogenase	
2558669877	DRAFT_00545	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669877	DRAFT_00545	Coordinates		37031..37831(-)	
2558669877	DRAFT_00545	DNA_length		801bp	
2558669877	DRAFT_00545	Protein_length		266aa	
2558669877	DRAFT_00545	GC		0.53	

2558669878	DRAFT_00546	Metacyc	PWY-5958: acridone alkaloid biosynthesis
2558669878	DRAFT_00546	Metacyc	PWY-6948: sitosterol degradation to androstenedione
2558669878	DRAFT_00546	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle
2558669878	DRAFT_00546	Metacyc	PWY-6593: sulfoacetate degradation
2558669878	DRAFT_00546	Metacyc	PWY-6733: sporopollenin precursor biosynthesis
2558669878	DRAFT_00546	Metacyc	CARNMET-PWY: carnitine degradation I
2558669878	DRAFT_00546	Metacyc	PWY-6457: <i>trans</i>-cinnamoyl-CoA biosynthesis
2558669878	DRAFT_00546	Metacyc	PWY-735: jasmonic acid biosynthesis
2558669878	DRAFT_00546	Metacyc	PWY-5140: cannabinoid biosynthesis
2558669878	DRAFT_00546	Metacyc	PWYG-321: mycolate biosynthesis
2558669878	DRAFT_00546	Metacyc	PWY-6799: fatty acid biosynthesis (plant mitochondria)
2558669878	DRAFT_00546	Metacyc	PWY66-388: fatty acid α-oxidation III
2558669878	DRAFT_00546	Metacyc	PWY-6048: methylthiopropionate degradation I (cleavage)
2558669878	DRAFT_00546	Metacyc	PWY-7064: 3-amino-3-phenylpropanoyl-CoA formation (Taxol 13C-side chain biosynthesis)
2558669878	DRAFT_00546	Metacyc	PWY-6670: citronellol degradation

2558669878	DRAFT_00546	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2558669878	DRAFT_00546	COG_category	[I] Lipid transport and metabolism			
2558669878	DRAFT_00546	COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II			3.00E-98
2558669878	DRAFT_00546	pfam00501	AMP-binding			7.40E-69
2558669878	DRAFT_00546	pfam13193	AMP-binding_C			1.30E-15
2558669878	DRAFT_00546	EC:6.2.1.-	Ligases. Forming carbon-sulfur bonds. Acid--thiol ligases.			
2558669878	DRAFT_00546	KO:K00666	fatty-acyl-CoA synthase [EC:6.2.1.-]			0.00E+00
2558669878	DRAFT_00546	Locus_type		CDS		
2558669878	DRAFT_00546	Product_name		Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II		
2558669878	DRAFT_00546	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669878	DRAFT_00546	Coordinates		38020..39453(+)		
2558669878	DRAFT_00546	DNA_length		1434bp		
2558669878	DRAFT_00546	Protein_length		477aa		
2558669878	DRAFT_00546	GC			0.48	

2558669879	DRAFT_00547	KEGG_module	M00082: Fatty acid biosynthesis, initiation			
2558669879	DRAFT_00547	KEGG_module	M00083: Fatty acid biosynthesis, elongation			
2558669879	DRAFT_00547	Metacyc	PWY-6519: 7-keto-8-aminopelargonate biosynthesis I			
2558669879	DRAFT_00547	Metacyc	PWY-4381: fatty acid biosynthesis initiation I			
2558669879	DRAFT_00547	COG_category	[I] Lipid transport and metabolism			
2558669879	DRAFT_00547	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III			5.00E-25
2558669879	DRAFT_00547	pfam08545	ACP_syn_III			2.00E-06
2558669879	DRAFT_00547	pfam08541	ACP_syn_III_C			8.90E-15
2558669879	DRAFT_00547	EC:2.3.1.180	Beta-ketoacyl-[acyl-carrier-protein] synthase III.			
2558669879	DRAFT_00547	KO:K00648	3-oxoacyl-[acyl-carrier-protein] synthase III [EC:2.3.1.180]			0.00E+00
2558669879	DRAFT_00547	Locus_type		CDS		
2558669879	DRAFT_00547	Product_name		3-oxoacyl-[acyl-carrier-protein] synthase III		
2558669879	DRAFT_00547	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669879	DRAFT_00547	Coordinates		39434..40435(+)		
2558669879	DRAFT_00547	DNA_length		1002bp		
2558669879	DRAFT_00547	Protein_length		333aa		
2558669879	DRAFT_00547	GC			0.49	
2558669879	DRAFT_00547	Transmembrane		Yes		

2558669880	DRAFT_00548	COG_category	[R] General function prediction only		
2558669880	DRAFT_00548	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa		1.00E-30
2558669880	DRAFT_00548	pfam12697	Abhydrolase_6		4.10E-34
2558669880	DRAFT_00548	Locus_type		CDS	
2558669880	DRAFT_00548	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super	
2558669880	DRAFT_00548	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669880	DRAFT_00548	Coordinates		40435..41280(+)	
2558669880	DRAFT_00548	DNA_length		846bp	
2558669880	DRAFT_00548	Protein_length		281aa	
2558669880	DRAFT_00548	GC		0.5	
2558669881	DRAFT_00549	KEGG_module	M00237: Branched-chain amino acid transport system		
2558669881	DRAFT_00549	COG_category	[E] Amino acid transport and metabolism		
2558669881	DRAFT_00549	COG0410	ABC-type branched-chain amino acid transport systems, ATPase compo		2.00E-69
2558669881	DRAFT_00549	pfam00005	ABC_tran		3.50E-27
2558669881	DRAFT_00549	KO:K01996	branched-chain amino acid transport system ATP-binding protein		0.00E+00
2558669881	DRAFT_00549	ITERM:06079	amino acid/amide ABC transporter ATP-binding protein 2, HAAT family (TC 3.A.1.4.-)		
2558669881	DRAFT_00549	Locus_type		CDS	
2558669881	DRAFT_00549	Product_name		amino acid/amide ABC transporter ATP-binding protein 2, HAAT famil	
2558669881	DRAFT_00549	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669881	DRAFT_00549	Coordinates		41368..42078(-)	
2558669881	DRAFT_00549	DNA_length		711bp	
2558669881	DRAFT_00549	Protein_length		236aa	
2558669881	DRAFT_00549	GC		0.56	
2558669882	DRAFT_00550	KEGG_module	M00237: Branched-chain amino acid transport system		
2558669882	DRAFT_00550	COG_category	[E] Amino acid transport and metabolism		
2558669882	DRAFT_00550	COG0411	ABC-type branched-chain amino acid transport systems, ATPase compo		2.00E-71
2558669882	DRAFT_00550	pfam00005	ABC_tran		2.00E-25
2558669882	DRAFT_00550	pfam12399	BCA_ABC_TP_C		2.60E-08
2558669882	DRAFT_00550	KO:K01995	branched-chain amino acid transport system ATP-binding protein		0.00E+00
2558669882	DRAFT_00550	ITERM:06078	amino acid/amide ABC transporter ATP-binding protein 1, HAAT family (TC 3.A.1.4.-)		
2558669882	DRAFT_00550	Locus_type		CDS	
2558669882	DRAFT_00550	Product_name		amino acid/amide ABC transporter ATP-binding protein 1, HAAT famil	

2558669882	DRAFT_00550	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669882	DRAFT_00550	Coordinates		42075..42848(-)	
2558669882	DRAFT_00550	DNA_length		774bp	
2558669882	DRAFT_00550	Protein_length		257aa	
2558669882	DRAFT_00550	GC		0.6	
2558669883	DRAFT_00551	COG_category	[E] Amino acid transport and metabolism		
2558669883	DRAFT_00551	COG4177	ABC-type branched-chain amino acid transport system, permease com		3.00E-18
2558669883	DRAFT_00551	pfam02653	BPD_transp_2		1.40E-28
2558669883	DRAFT_00551	Locus_type		CDS	
2558669883	DRAFT_00551	Product_name		ABC-type branched-chain amino acid transport system, permease cor	
2558669883	DRAFT_00551	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669883	DRAFT_00551	Coordinates		42849..44063(-)	
2558669883	DRAFT_00551	DNA_length		1215bp	
2558669883	DRAFT_00551	Protein_length		404aa	
2558669883	DRAFT_00551	GC		0.58	
2558669883	DRAFT_00551	Transmembrane		Yes	
2558669884	DRAFT_00552	KEGG_module	M00237: Branched-chain amino acid transport system		
2558669884	DRAFT_00552	COG_category	[E] Amino acid transport and metabolism		
2558669884	DRAFT_00552	COG0559	Branched-chain amino acid ABC-type transport system, permease com		4.00E-33
2558669884	DRAFT_00552	pfam02653	BPD_transp_2		1.40E-31
2558669884	DRAFT_00552	KO:K01997	branched-chain amino acid transport system permease protein		0.00E+00
2558669884	DRAFT_00552	Locus_type		CDS	
2558669884	DRAFT_00552	Product_name		Branched-chain amino acid ABC-type transport system, permease cor	
2558669884	DRAFT_00552	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669884	DRAFT_00552	Coordinates		44065..44934(-)	
2558669884	DRAFT_00552	DNA_length		870bp	
2558669884	DRAFT_00552	Protein_length		289aa	
2558669884	DRAFT_00552	GC		0.58	
2558669884	DRAFT_00552	Transmembrane		Yes	
2558669885	DRAFT_00553	COG_category	[E] Amino acid transport and metabolism		
2558669885	DRAFT_00553	COG0683	ABC-type branched-chain amino acid transport systems, periplasmic co		2.00E-27

2558669885	DRAFT_00553	pfam13458	Peripla_BP_6			9.60E-41
2558669885	DRAFT_00553	Locus_type		CDS		
2558669885	DRAFT_00553	Product_name		ABC-type branched-chain amino acid transport systems, periplasmic c		
2558669885	DRAFT_00553	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669885	DRAFT_00553	Coordinates		44986..46941(-)		
2558669885	DRAFT_00553	DNA_length		1956bp		
2558669885	DRAFT_00553	Protein_length		651aa		
2558669885	DRAFT_00553	GC			0.55	
2558669885	DRAFT_00553	Transmembrane		Yes		
2558669886	DRAFT_00554	COG_category	[R] General function prediction only			
2558669886	DRAFT_00554	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa			4.00E-25
2558669886	DRAFT_00554	pfam12697	Abhydrolase_6			1.10E-40
2558669886	DRAFT_00554	Locus_type		CDS		
2558669886	DRAFT_00554	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super		
2558669886	DRAFT_00554	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669886	DRAFT_00554	Coordinates		47169..47924(+)		
2558669886	DRAFT_00554	DNA_length		756bp		
2558669886	DRAFT_00554	Protein_length		251aa		
2558669886	DRAFT_00554	GC			0.6	
2558669887	DRAFT_00555	COG_category	[I] Lipid transport and metabolism			
2558669887	DRAFT_00555	COG2030	Acyl dehydratase			2.00E-33
2558669887	DRAFT_00555	pfam01575	MaoC_dehydratas			3.50E-32
2558669887	DRAFT_00555	Locus_type		CDS		
2558669887	DRAFT_00555	Product_name		Acyl dehydratase		
2558669887	DRAFT_00555	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669887	DRAFT_00555	Coordinates		47939..48367(+)		
2558669887	DRAFT_00555	DNA_length		429bp		
2558669887	DRAFT_00555	Protein_length		142aa		
2558669887	DRAFT_00555	GC			0.57	
2558669888	DRAFT_00556	IMG_pathway	1014: Dicarboxylate/4-hydroxybutyrate cycle			
2558669888	DRAFT_00556	IMG_pathway	222: L-isoleucine degradation to propionyl-CoA and acetyl-CoA			

2558669888	DRAFT_00556	IMG_pathway	369: Pyruvate conversion to butyrate		
2558669888	DRAFT_00556	IMG_pathway	389: Crotonyl-CoA conversion to acetate		
2558669888	DRAFT_00556	IMG_pathway	596: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2558669888	DRAFT_00556	IMG_pathway	962: Glyoxylate from acetyl-CoA via ethylmalonyl-CoA pathway		
2558669888	DRAFT_00556	COG_category	[I] Lipid transport and metabolism		
2558669888	DRAFT_00556	COG1250	3-hydroxyacyl-CoA dehydrogenase		2.00E-91
2558669888	DRAFT_00556	pfam00725	3HCDH		2.00E-36
2558669888	DRAFT_00556	pfam02737	3HCDH_N		7.80E-59
2558669888	DRAFT_00556	EC:1.1.1.157	3-hydroxybutyryl-CoA dehydrogenase.		
2558669888	DRAFT_00556	KO:K00074	3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]		0.00E+00
2558669888	DRAFT_00556	ITERM:00577	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)		
2558669888	DRAFT_00556	Locus_type		CDS	
2558669888	DRAFT_00556	Product_name		3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	
2558669888	DRAFT_00556	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669888	DRAFT_00556	Coordinates		48457..49350(-)	
2558669888	DRAFT_00556	DNA_length		894bp	
2558669888	DRAFT_00556	Protein_length		297aa	
2558669888	DRAFT_00556	GC		0.57	
2558669889	DRAFT_00557	pfam00583	Acetyltransf_1		7.70E-10
2558669889	DRAFT_00557	Locus_type		CDS	
2558669889	DRAFT_00557	Product_name		Predicted acetyltransferase	
2558669889	DRAFT_00557	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669889	DRAFT_00557	Coordinates		49376..50233(-)	
2558669889	DRAFT_00557	DNA_length		858bp	
2558669889	DRAFT_00557	Protein_length		285aa	
2558669889	DRAFT_00557	GC		0.57	
2558669890	DRAFT_00558	Locus_type		tRNA	
2558669890	DRAFT_00558	Product_name		tRNA_Ser_TGA	
2558669890	DRAFT_00558	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7	
2558669890	DRAFT_00558	Coordinates		50372..50466(+)	
2558669890	DRAFT_00558	DNA_length		85bp	
2558669890	DRAFT_00558	GC		0.67	

2558669891	DRAFT_00559	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669891	DRAFT_00559	COG0425	Predicted redox protein, regulator of disulfide bond formation			2.00E-07
2558669891	DRAFT_00559	pfam01206	TusA			2.70E-10
2558669891	DRAFT_00559	Locus_type		CDS		
2558669891	DRAFT_00559	Product_name		Predicted redox protein, regulator of disulfide bond formation		
2558669891	DRAFT_00559	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669891	DRAFT_00559	Coordinates		50668..51309(+)		
2558669891	DRAFT_00559	DNA_length		642bp		
2558669891	DRAFT_00559	Protein_length		213aa		
2558669891	DRAFT_00559	GC			0.6	
2558669892	DRAFT_00560	KEGG_module	M00373: Ethylmalonyl pathway			
2558669892	DRAFT_00560	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			
2558669892	DRAFT_00560	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle			
2558669892	DRAFT_00560	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			
2558669892	DRAFT_00560	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone			
2558669892	DRAFT_00560	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis			
2558669892	DRAFT_00560	Metacyc	PWY-6883: pyruvate fermentation to butanol II			
2558669892	DRAFT_00560	Metacyc	PWY-6863: pyruvate fermentation to hexanol			
2558669892	DRAFT_00560	Metacyc	PWY-5177: glutaryl-CoA degradation			
2558669892	DRAFT_00560	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate			
2558669892	DRAFT_00560	Metacyc	PWY-6876: isopropanol biosynthesis			
2558669892	DRAFT_00560	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II			
2558669892	DRAFT_00560	Metacyc	PWY-6174: mevalonate pathway II (archaea)			
2558669892	DRAFT_00560	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate			
2558669892	DRAFT_00560	Metacyc	ILEUDEG-PWY: isoleucine degradation I			
2558669892	DRAFT_00560	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)			
2558669892	DRAFT_00560	Metacyc	PWY-922: mevalonate pathway I			
2558669892	DRAFT_00560	Metacyc	PWY-7003: glycerol degradation to butanol			
2558669892	DRAFT_00560	Metacyc	PWY-5741: ethylmalonyl pathway			
2558669892	DRAFT_00560	Metacyc	PWY-6583: pyruvate fermentation to butanol I			
2558669892	DRAFT_00560	Metacyc	PWY66-368: ketolysis			
2558669892	DRAFT_00560	Metacyc	PWY66-367: ketogenesis			

2558669892	DRAFT_00560	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			
2558669892	DRAFT_00560	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis			
2558669892	DRAFT_00560	Metacyc	PWY-6588: pyruvate fermentation to acetone			
2558669892	DRAFT_00560	COG_category	[I] Lipid transport and metabolism			
2558669892	DRAFT_00560	COG0183	Acetyl-CoA acetyltransferase			5.00E-86
2558669892	DRAFT_00560	pfam02803	Thiolase_C			2.50E-43
2558669892	DRAFT_00560	pfam00108	Thiolase_N			4.40E-84
2558669892	DRAFT_00560	pfam00108	Thiolase_N			3.80E-08
2558669892	DRAFT_00560	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.			
2558669892	DRAFT_00560	TIGR01930	acetyl-CoA acetyltransferases			1.30E-129
2558669892	DRAFT_00560	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]			0.00E+00
2558669892	DRAFT_00560	Locus_type		CDS		
2558669892	DRAFT_00560	Product_name		acetyl-CoA acetyltransferase (EC 2.3.1.9)		
2558669892	DRAFT_00560	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669892	DRAFT_00560	Coordinates		51398..52690(+)		
2558669892	DRAFT_00560	DNA_length		1293bp		
2558669892	DRAFT_00560	Protein_length		430aa		
2558669892	DRAFT_00560	GC			0.54	

2558669893	DRAFT_00561	pfam00696	AA_kinase			1.10E-18
2558669893	DRAFT_00561	TIGR00746	carbamate kinase			3.00E-63
2558669893	DRAFT_00561	Locus_type		CDS		
2558669893	DRAFT_00561	Product_name		Carbamate kinase		
2558669893	DRAFT_00561	Scaffold		DRAFT_contig_70_42_len_53196_read_count_896652.7		
2558669893	DRAFT_00561	Coordinates		52709..53194(-)		
2558669893	DRAFT_00561	DNA_length		486bp		
2558669893	DRAFT_00561	Protein_length		161aa		
2558669893	DRAFT_00561	GC			0.61	

2558669894	DRAFT_00562	Locus_type		tRNA		
2558669894	DRAFT_00562	Product_name		tRNA_Undet_???		
2558669894	DRAFT_00562	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669894	DRAFT_00562	Coordinates		49..176(-)		
2558669894	DRAFT_00562	DNA_length		128bp		

2558669894	DRAFT_00562	GC			0.64	
2558669895	DRAFT_00563	pfam02511	Thy1			2.20E-04
2558669895	DRAFT_00563	Locus_type		CDS		
2558669895	DRAFT_00563	Product_name		Thymidylate synthase complementing protein		
2558669895	DRAFT_00563	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669895	DRAFT_00563	Coordinates		329..811(+)		
2558669895	DRAFT_00563	DNA_length		483bp		
2558669895	DRAFT_00563	Protein_length		160aa		
2558669895	DRAFT_00563	GC			0.52	
2558669896	DRAFT_00564	Metacyc	PWY-6545: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis III			
2558669896	DRAFT_00564	pfam02511	Thy1			2.60E-48
2558669896	DRAFT_00564	EC:2.1.1.148	Thymidylate synthase (FAD).			
2558669896	DRAFT_00564	TIGR02170	thymidylate synthase, flavin-dependent			1.80E-43
2558669896	DRAFT_00564	KO:K03465	thymidylate synthase (FAD) [EC:2.1.1.148]			1.10E-33
2558669896	DRAFT_00564	Locus_type		CDS		
2558669896	DRAFT_00564	Product_name		thymidylate synthase, flavin-dependent		
2558669896	DRAFT_00564	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669896	DRAFT_00564	Coordinates		801..1331(+)		
2558669896	DRAFT_00564	DNA_length		531bp		
2558669896	DRAFT_00564	Protein_length		176aa		
2558669896	DRAFT_00564	GC			0.54	
2558669897	DRAFT_00565	COG_category	[G] Carbohydrate transport and metabolism			
2558669897	DRAFT_00565	COG1109	Phosphomannomutase			8.00E-80
2558669897	DRAFT_00565	pfam02879	PGM_PMM_II			1.70E-19
2558669897	DRAFT_00565	pfam02880	PGM_PMM_III			5.60E-05
2558669897	DRAFT_00565	pfam02878	PGM_PMM_I			4.50E-29
2558669897	DRAFT_00565	pfam00408	PGM_PMM_IV			1.40E-11
2558669897	DRAFT_00565	Locus_type		CDS		
2558669897	DRAFT_00565	Product_name		Phosphomannomutase		
2558669897	DRAFT_00565	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669897	DRAFT_00565	Coordinates		1335..2660(+)		

2558669897	DRAFT_00565	DNA_length		1326bp		
2558669897	DRAFT_00565	Protein_length		441aa		
2558669897	DRAFT_00565	GC			0.59	

2558669898	DRAFT_00566	KEGG_module	M00264: DNA polymerase II complex, archaea			
2558669898	DRAFT_00566	COG_category	[L] Replication, recombination and repair			
2558669898	DRAFT_00566	COG1311	Archaeal DNA polymerase II, small subunit/DNA polymerase delta, sub			6.00E-96
2558669898	DRAFT_00566	pfam04042	DNA_pol_E_B			1.60E-17
2558669898	DRAFT_00566	EC:2.7.7.7	DNA-directed DNA polymerase.			
2558669898	DRAFT_00566	KO:K02323	DNA polymerase II small subunit [EC:2.7.7.7]			0.00E+00
2558669898	DRAFT_00566	Locus_type		CDS		
2558669898	DRAFT_00566	Product_name		Archaeal DNA polymerase II, small subunit/DNA polymerase delta, su		
2558669898	DRAFT_00566	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669898	DRAFT_00566	Coordinates		2682..4193(+)		
2558669898	DRAFT_00566	DNA_length		1512bp		
2558669898	DRAFT_00566	Protein_length		503aa		
2558669898	DRAFT_00566	GC			0.55	

2558669899	DRAFT_00567	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669899	DRAFT_00567	COG_category	[L] Replication, recombination and repair			
2558669899	DRAFT_00567	COG1474	Cdc6-related protein, AAA superfamily ATPase			1.00E-82
2558669899	DRAFT_00567	pfam13401	AAA_22			1.90E-09
2558669899	DRAFT_00567	pfam09079	Cdc6_C			2.20E-19
2558669899	DRAFT_00567	TIGR02928	orc1/cdc6 family replication initiation protein			3.90E-117
2558669899	DRAFT_00567	KO:K10725	archaeal cell division control protein 6			0.00E+00
2558669899	DRAFT_00567	Locus_type		CDS		
2558669899	DRAFT_00567	Product_name		orc1/cdc6 family replication initiation protein		
2558669899	DRAFT_00567	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669899	DRAFT_00567	Coordinates		4190..5383(-)		
2558669899	DRAFT_00567	DNA_length		1194bp		
2558669899	DRAFT_00567	Protein_length		397aa		
2558669899	DRAFT_00567	GC			0.54	

2558669900	DRAFT_00568	pfam03965	Penicillinase_R			9.00E-07

2558669900	DRAFT_00568	Locus_type		CDS
2558669900	DRAFT_00568	Product_name		Penicillinase repressor
2558669900	DRAFT_00568	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8
2558669900	DRAFT_00568	Coordinates		5901..6299(+)
2558669900	DRAFT_00568	DNA_length		399bp
2558669900	DRAFT_00568	Protein_length		132aa
2558669900	DRAFT_00568	GC		0.51
2558669901	DRAFT_00569	Locus_type		CDS
2558669901	DRAFT_00569	Product_name		hypothetical protein
2558669901	DRAFT_00569	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8
2558669901	DRAFT_00569	Coordinates		6281..6829(-)
2558669901	DRAFT_00569	DNA_length		549bp
2558669901	DRAFT_00569	Protein_length		182aa
2558669901	DRAFT_00569	GC		0.47
2558669901	DRAFT_00569	Transmembrane		Yes
2558669902	DRAFT_00570	Locus_type		CDS
2558669902	DRAFT_00570	Product_name		hypothetical protein
2558669902	DRAFT_00570	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8
2558669902	DRAFT_00570	Coordinates		6878..7234(-)
2558669902	DRAFT_00570	DNA_length		357bp
2558669902	DRAFT_00570	Protein_length		118aa
2558669902	DRAFT_00570	GC		0.43
2558669903	DRAFT_00571	Locus_type		CDS
2558669903	DRAFT_00571	Product_name		hypothetical protein
2558669903	DRAFT_00571	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8
2558669903	DRAFT_00571	Coordinates		7504..7680(+)
2558669903	DRAFT_00571	DNA_length		177bp
2558669903	DRAFT_00571	Protein_length		58aa
2558669903	DRAFT_00571	GC		0.49
2558669904	DRAFT_00572	Metacyc	PWY-6834: spermidine biosynthesis III	

2558669904	DRAFT_00572	Metacyc	PWY-5135: xanthohumol biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-7169: hyperxanthone E biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5132: humulone biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-6403: carrageenan biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5365: linear furanocoumarin biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5027: phylloquinol biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-6262: demethylmenaquinol-8 biosynthesis II		
2558669904	DRAFT_00572	Metacyc	PWY-702: methionine biosynthesis II		
2558669904	DRAFT_00572	Metacyc	PWY-5133: cohumulone biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-6681: neurosporaxanthin biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5808: hyperforin and adhyperforin biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5817: dodecaprenyl diphosphate biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-2681: <i>trans</i>-zeatin biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5802: alizarin biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5064: chlorophyll <i>a</i> biosynthesis II		
2558669904	DRAFT_00572	Metacyc	PWY-4681: kievitone biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5068: chlorophyll cycle		
2558669904	DRAFT_00572	Metacyc	PWY-5893: tridecaprenyl diphosphate biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5770: phenazine-1-carboxylate biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-4502: wighteone and luteone biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-6936: seleno-amino acid biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-5816: all <i>trans</i> undecaprenyl diphosphate biosynthesis		
2558669904	DRAFT_00572	Metacyc	PWY-6793: demethylmenaquinol-8 biosynthesis III		
2558669904	DRAFT_00572	COG_category	[R] General function prediction only		
2558669904	DRAFT_00572	COG1646	Predicted phosphate-binding enzymes, TIM-barrel fold		1.00E-56
2558669904	DRAFT_00572	pfam01884	PcrB		1.10E-63
2558669904	DRAFT_00572	EC:2.5.1.-	Transferases. Transferring alkyl or aryl groups, other than methyl groups. Transferring alkyl or		
2558669904	DRAFT_00572	TIGR01769	phosphoglycerol geranylgeranyltransferase		9.90E-71
2558669904	DRAFT_00572	TIGR01768	geranylgeranylglyceryl phosphate synthase family protein		3.00E-63
2558669904	DRAFT_00572	KO:K07094	putative glycerol-1-phosphate prenyltransferase [EC:2.5.1.-]		0.00E+00
2558669904	DRAFT_00572	Locus_type		CDS	
2558669904	DRAFT_00572	Product_name		phosphoglycerol geranylgeranyltransferase	
2558669904	DRAFT_00572	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669904	DRAFT_00572	Coordinates		7682..8518(+)	

2558669904	DRAFT_00572	DNA_length		837bp	
2558669904	DRAFT_00572	Protein_length		278aa	
2558669904	DRAFT_00572	GC		0.52	
2558669905	DRAFT_00573	KEGG_module	M00264: DNA polymerase II complex, archaea		
2558669905	DRAFT_00573	COG_category	[L] Replication, recombination and repair		
2558669905	DRAFT_00573	COG1933	Archaeal DNA polymerase II, large subunit		5.00E-68
2558669905	DRAFT_00573	pfam03833	PolC_DP2		0.00E+00
2558669905	DRAFT_00573	EC:2.7.7.7	DNA-directed DNA polymerase.		
2558669905	DRAFT_00573	TIGR00354	DNA polymerase, archaeal type II, large subunit		0.00E+00
2558669905	DRAFT_00573	KO:K02322	DNA polymerase II large subunit [EC:2.7.7.7]		0.00E+00
2558669905	DRAFT_00573	ITERM:00108	DNA polymerase II large subunit (EC 2.7.7.7)		
2558669905	DRAFT_00573	Locus_type		CDS	
2558669905	DRAFT_00573	Product_name		DNA polymerase II large subunit (EC 2.7.7.7)	
2558669905	DRAFT_00573	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669905	DRAFT_00573	Coordinates		8577..12077(+)	
2558669905	DRAFT_00573	DNA_length		3501bp	
2558669905	DRAFT_00573	Protein_length		1166aa	
2558669905	DRAFT_00573	GC		0.58	
2558669906	DRAFT_00574	KEGG_module	M00346: Formaldehyde assimilation, serine pathway		
2558669906	DRAFT_00574	KEGG_module	M00140: C1-unit interconversion, prokaryotes		
2558669906	DRAFT_00574	KEGG_module	M00141: C1-unit interconversion, eukaryotes		
2558669906	DRAFT_00574	KEGG_module	M00532: Photorespiration		
2558669906	DRAFT_00574	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2558669906	DRAFT_00574	Metacyc	PWY-2161: folate polyglutamylation		
2558669906	DRAFT_00574	Metacyc	PWY-3841: folate transformations II		
2558669906	DRAFT_00574	Metacyc	PWY-2201: folate transformations I		
2558669906	DRAFT_00574	Metacyc	GLYSYN-PWY: glycine biosynthesis I		
2558669906	DRAFT_00574	Metacyc	PWY-3661: glycine betaine degradation		
2558669906	DRAFT_00574	Metacyc	1CMET2-PWY: formylTHF biosynthesis I		
2558669906	DRAFT_00574	Metacyc	PWY-181: photorespiration		
2558669906	DRAFT_00574	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)		
2558669906	DRAFT_00574	COG_category	[E] Amino acid transport and metabolism		

2558669906	DRAFT_00574	COG0112	Glycine/serine hydroxymethyltransferase			5.00E-117
2558669906	DRAFT_00574	pfam00464	SHMT			1.30E-72
2558669906	DRAFT_00574	EC:2.1.2.1	Glycine hydroxymethyltransferase.			
2558669906	DRAFT_00574	KO:K00600	glycine hydroxymethyltransferase [EC:2.1.2.1]			0.00E+00
2558669906	DRAFT_00574	Locus_type		CDS		
2558669906	DRAFT_00574	Product_name		Glycine/serine hydroxymethyltransferase		
2558669906	DRAFT_00574	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669906	DRAFT_00574	Coordinates		12054..13343(-)		
2558669906	DRAFT_00574	DNA_length		1290bp		
2558669906	DRAFT_00574	Protein_length		429aa		
2558669906	DRAFT_00574	GC			0.57	
2558669907	DRAFT_00575	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2558669907	DRAFT_00575	COG4023	Preprotein translocase subunit Sec61beta			3.00E-03
2558669907	DRAFT_00575	pfam03911	Sec61_beta			9.00E-13
2558669907	DRAFT_00575	Locus_type		CDS		
2558669907	DRAFT_00575	Product_name		Preprotein translocase subunit Sec61beta		
2558669907	DRAFT_00575	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669907	DRAFT_00575	Coordinates		13453..13626(+)		
2558669907	DRAFT_00575	DNA_length		174bp		
2558669907	DRAFT_00575	Protein_length		57aa		
2558669907	DRAFT_00575	GC			0.51	
2558669907	DRAFT_00575	Transmembrane		Yes		
2558669908	DRAFT_00576	COG_category	[S] Function unknown			
2558669908	DRAFT_00576	COG3356	Predicted membrane protein			1.00E-42
2558669908	DRAFT_00576	pfam09843	DUF2070			2.00E-28
2558669908	DRAFT_00576	Locus_type		CDS		
2558669908	DRAFT_00576	Product_name		Predicted membrane protein		
2558669908	DRAFT_00576	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669908	DRAFT_00576	Coordinates		13601..15391(+)		
2558669908	DRAFT_00576	DNA_length		1791bp		
2558669908	DRAFT_00576	Protein_length		596aa		
2558669908	DRAFT_00576	GC			0.57	

2558669908	DRAFT_00576	Transmembrane		Yes		
2558669909	DRAFT_00577	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP			
2558669909	DRAFT_00577	COG_category	[F] Nucleotide transport and metabolism			
2558669909	DRAFT_00577	COG0125	Thymidylate kinase			2.00E-28
2558669909	DRAFT_00577	pfam02223	Thymidylate_kin			4.80E-31
2558669909	DRAFT_00577	EC:2.7.4.9	dTMP kinase.			
2558669909	DRAFT_00577	TIGR00041	thymidylate kinase			7.10E-29
2558669909	DRAFT_00577	KO:K00943	dTMP kinase [EC:2.7.4.9]			7.90E-39
2558669909	DRAFT_00577	Locus_type		CDS		
2558669909	DRAFT_00577	Product_name		thymidylate kinase		
2558669909	DRAFT_00577	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669909	DRAFT_00577	Coordinates		15428..16045(+)		
2558669909	DRAFT_00577	DNA_length		618bp		
2558669909	DRAFT_00577	Protein_length		205aa		
2558669909	DRAFT_00577	GC			0.55	
2558669910	DRAFT_00578	COG_category	[R] General function prediction only			
2558669910	DRAFT_00578	COG1078	HD superfamily phosphohydrolases			7.00E-70
2558669910	DRAFT_00578	pfam01966	HD			1.60E-11
2558669910	DRAFT_00578	Locus_type		CDS		
2558669910	DRAFT_00578	Product_name		HD superfamily phosphohydrolases		
2558669910	DRAFT_00578	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669910	DRAFT_00578	Coordinates		16073..17368(+)		
2558669910	DRAFT_00578	DNA_length		1296bp		
2558669910	DRAFT_00578	Protein_length		431aa		
2558669910	DRAFT_00578	GC			0.58	
2558669911	DRAFT_00579	Locus_type		CDS		
2558669911	DRAFT_00579	Product_name		hypothetical protein		
2558669911	DRAFT_00579	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669911	DRAFT_00579	Coordinates		17608..18267(-)		
2558669911	DRAFT_00579	DNA_length		660bp		
2558669911	DRAFT_00579	Protein_length		219aa		

2558669911	DRAFT_00579	GC			0.58
2558669912	DRAFT_00580	Locus_type		CDS	
2558669912	DRAFT_00580	Product_name		hypothetical protein	
2558669912	DRAFT_00580	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669912	DRAFT_00580	Coordinates		18270..18872(+)	
2558669912	DRAFT_00580	DNA_length		603bp	
2558669912	DRAFT_00580	Protein_length		200aa	
2558669912	DRAFT_00580	GC			0.55
2558669913	DRAFT_00581	Locus_type		CDS	
2558669913	DRAFT_00581	Product_name		hypothetical protein	
2558669913	DRAFT_00581	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669913	DRAFT_00581	Coordinates		18865..19263(-)	
2558669913	DRAFT_00581	DNA_length		399bp	
2558669913	DRAFT_00581	Protein_length		132aa	
2558669913	DRAFT_00581	GC			0.55
2558669913	DRAFT_00581	Transmembrane		Yes	
2558669914	DRAFT_00582	Locus_type		CDS	
2558669914	DRAFT_00582	Product_name		hypothetical protein	
2558669914	DRAFT_00582	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669914	DRAFT_00582	Coordinates		19265..19471(-)	
2558669914	DRAFT_00582	DNA_length		207bp	
2558669914	DRAFT_00582	Protein_length		68aa	
2558669914	DRAFT_00582	GC			0.48
2558669915	DRAFT_00583	COG_category	[L] Replication, recombination and repair		
2558669915	DRAFT_00583	COG0550	Topoisomerase IA		1.00E-122
2558669915	DRAFT_00583	pfam01131	Topoisom_bac		2.60E-95
2558669915	DRAFT_00583	pfam01751	Toprim		9.00E-09
2558669915	DRAFT_00583	pfam01396	zf-C4_Topoisom		6.90E-07
2558669915	DRAFT_00583	EC:5.99.1.2	DNA topoisomerase.		
2558669915	DRAFT_00583	TIGR01057	DNA topoisomerase I, archaeal		0.00E+00

2558669915	DRAFT_00583	KO:K03168	DNA topoisomerase I [EC:5.99.1.2]			0.00E+00
2558669915	DRAFT_00583	ITERM:00090	DNA topoisomerase I (EC 5.99.1.2)			
2558669915	DRAFT_00583	Locus_type		CDS		
2558669915	DRAFT_00583	Product_name		DNA topoisomerase I (EC 5.99.1.2)		
2558669915	DRAFT_00583	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669915	DRAFT_00583	Coordinates		19468..21558(-)		
2558669915	DRAFT_00583	DNA_length		2091bp		
2558669915	DRAFT_00583	Protein_length		696aa		
2558669915	DRAFT_00583	GC			0.57	
2558669916	DRAFT_00584	Locus_type		CDS		
2558669916	DRAFT_00584	Product_name		hypothetical protein		
2558669916	DRAFT_00584	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669916	DRAFT_00584	Coordinates		21589..21765(-)		
2558669916	DRAFT_00584	DNA_length		177bp		
2558669916	DRAFT_00584	Protein_length		58aa		
2558669916	DRAFT_00584	GC			0.52	
2558669917	DRAFT_00585	pfam01522	Polysacc_deac_1			3.30E-13
2558669917	DRAFT_00585	Locus_type		CDS		
2558669917	DRAFT_00585	Product_name		Predicted xylanase/chitin deacetylase		
2558669917	DRAFT_00585	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669917	DRAFT_00585	Coordinates		22042..22986(+)		
2558669917	DRAFT_00585	DNA_length		945bp		
2558669917	DRAFT_00585	Protein_length		314aa		
2558669917	DRAFT_00585	GC			0.53	
2558669918	DRAFT_00586	pfam00132	Hexapep			1.00E-08
2558669918	DRAFT_00586	Locus_type		CDS		
2558669918	DRAFT_00586	Product_name		Bacterial transferase hexapeptide (six repeats)		
2558669918	DRAFT_00586	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669918	DRAFT_00586	Coordinates		22978..23442(-)		
2558669918	DRAFT_00586	DNA_length		465bp		
2558669918	DRAFT_00586	Protein_length		154aa		

2558669918	DRAFT_00586	GC			0.59	
2558669918	DRAFT_00586	Transmembrane		Yes		
2558669919	DRAFT_00587	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2558669919	DRAFT_00587	COG3882	Predicted enzyme involved in methoxymalonyl-ACP biosynthesis			0.00E+00
2558669919	DRAFT_00587	pfam13673	Acetyltransf_10			1.30E-08
2558669919	DRAFT_00587	TIGR01681	HAD-superfamily phosphatase, subfamily IIIC			2.00E-19
2558669919	DRAFT_00587	TIGR01686	FkbH-like domain			2.40E-95
2558669919	DRAFT_00587	Locus_type		CDS		
2558669919	DRAFT_00587	Product_name		HAD-superfamily phosphatase, subfamily IIIC/FkbH-like domain		
2558669919	DRAFT_00587	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669919	DRAFT_00587	Coordinates		23526..25379(+)		
2558669919	DRAFT_00587	DNA_length		1854bp		
2558669919	DRAFT_00587	Protein_length		617aa		
2558669919	DRAFT_00587	GC			0.54	
2558669920	DRAFT_00588	KO:K02078	acyl carrier protein			1.20E-10
2558669920	DRAFT_00588	Locus_type		CDS		
2558669920	DRAFT_00588	Product_name		hypothetical protein		
2558669920	DRAFT_00588	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669920	DRAFT_00588	Coordinates		25385..25606(+)		
2558669920	DRAFT_00588	DNA_length		222bp		
2558669920	DRAFT_00588	Protein_length		73aa		
2558669920	DRAFT_00588	GC			0.48	
2558669921	DRAFT_00589	COG_category	[I] Lipid transport and metabolism			
2558669921	DRAFT_00589	COG2030	Acyl dehydratase			1.00E-12
2558669921	DRAFT_00589	pfam01575	MaoC_dehydratas			5.20E-17
2558669921	DRAFT_00589	Locus_type		CDS		
2558669921	DRAFT_00589	Product_name		Acyl dehydratase		
2558669921	DRAFT_00589	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669921	DRAFT_00589	Coordinates		25603..26022(+)		
2558669921	DRAFT_00589	DNA_length		420bp		
2558669921	DRAFT_00589	Protein_length		139aa		

2558669921	DRAFT_00589	GC			0.53	

2558669922	DRAFT_00590	Metacyc	PWY-6012: acyl carrier protein metabolism			
2558669922	DRAFT_00590	COG_category	[I] Lipid transport and metabolism			
2558669922	DRAFT_00590	COG0736	Phosphopantetheinyl transferase (holo-ACP synthase)			2.00E-16
2558669922	DRAFT_00590	pfam01648	ACPS			3.00E-16
2558669922	DRAFT_00590	EC:2.7.8.7	Holo-[acyl-carrier-protein] synthase.			
2558669922	DRAFT_00590	TIGR00516	holo-[acyl-carrier-protein] synthase			2.00E-19
2558669922	DRAFT_00590	TIGR00556	phosphopantetheine--protein transferase domain			2.20E-25
2558669922	DRAFT_00590	KO:K00997	holo-[acyl-carrier protein] synthase [EC:2.7.8.7]			1.20E-13
2558669922	DRAFT_00590	Locus_type		CDS		
2558669922	DRAFT_00590	Product_name		phosphopantetheine--protein transferase domain		
2558669922	DRAFT_00590	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669922	DRAFT_00590	Coordinates		26028..26411(-)		
2558669922	DRAFT_00590	DNA_length		384bp		
2558669922	DRAFT_00590	Protein_length		127aa		
2558669922	DRAFT_00590	GC			0.5	

2558669923	DRAFT_00591	Metacyc	GLYCLEAV-PWY: glycine cleavage			
2558669923	DRAFT_00591	COG_category	[E] Amino acid transport and metabolism			
2558669923	DRAFT_00591	COG0404	Glycine cleavage system T protein (aminomethyltransferase)			3.00E-93
2558669923	DRAFT_00591	pfam01571	GCV_T			5.30E-67
2558669923	DRAFT_00591	pfam08669	GCV_T_C			2.00E-15
2558669923	DRAFT_00591	EC:2.1.2.10	Aminomethyltransferase.			
2558669923	DRAFT_00591	TIGR00528	glycine cleavage system T protein			2.00E-98
2558669923	DRAFT_00591	KO:K00605	aminomethyltransferase [EC:2.1.2.10]			0.00E+00
2558669923	DRAFT_00591	Locus_type		CDS		
2558669923	DRAFT_00591	Product_name		glycine cleavage system T protein		
2558669923	DRAFT_00591	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669923	DRAFT_00591	Coordinates		26564..27679(+)		
2558669923	DRAFT_00591	DNA_length		1116bp		
2558669923	DRAFT_00591	Protein_length		371aa		
2558669923	DRAFT_00591	GC			0.58	

2558669924	DRAFT_00592	KEGG_module	M00532: Photorespiration		
2558669924	DRAFT_00592	COG_category	[E] Amino acid transport and metabolism		
2558669924	DRAFT_00592	COG0509	Glycine cleavage system H protein (lipoate-binding)		6.00E-34
2558669924	DRAFT_00592	pfam01597	GCV_H		5.90E-37
2558669924	DRAFT_00592	TIGR00527	glycine cleavage system H protein		1.00E-43
2558669924	DRAFT_00592	KO:K02437	glycine cleavage system H protein		5.30E-30
2558669924	DRAFT_00592	Locus_type		CDS	
2558669924	DRAFT_00592	Product_name		glycine cleavage system H protein	
2558669924	DRAFT_00592	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669924	DRAFT_00592	Coordinates		27704..28123(+)	
2558669924	DRAFT_00592	DNA_length		420bp	
2558669924	DRAFT_00592	Protein_length		139aa	
2558669924	DRAFT_00592	GC		0.55	
2558669925	DRAFT_00593	KEGG_module	M00072: Oligosaccharyltransferase		
2558669925	DRAFT_00593	COG_category	[R] General function prediction only		
2558669925	DRAFT_00593	COG1287	Uncharacterized membrane protein, required for N-linked glycosylatio		6.00E-30
2558669925	DRAFT_00593	pfam02516	STT3		7.30E-24
2558669925	DRAFT_00593	EC:2.4.99.18	Dolichyl-diphosphooligosaccharide--protein glycotransferase.		
2558669925	DRAFT_00593	KO:K07151	dolichyl-diphosphooligosaccharide--protein glycosyltransferase [EC:2.4		0.00E+00
2558669925	DRAFT_00593	Locus_type		CDS	
2558669925	DRAFT_00593	Product_name		Uncharacterized membrane protein, required for N-linked glycosylati	
2558669925	DRAFT_00593	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669925	DRAFT_00593	Coordinates		28080..30503(+)	
2558669925	DRAFT_00593	DNA_length		2424bp	
2558669925	DRAFT_00593	Protein_length		807aa	
2558669925	DRAFT_00593	GC		0.57	
2558669925	DRAFT_00593	Transmembrane		Yes	
2558669926	DRAFT_00594	KEGG_module	M00425: H/ACA ribonucleoprotein complex		
2558669926	DRAFT_00594	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669926	DRAFT_00594	COG2260	Predicted Zn-ribbon RNA-binding protein		2.00E-12
2558669926	DRAFT_00594	pfam04135	Nop10p		1.90E-22
2558669926	DRAFT_00594	KO:K11130	H/ACA ribonucleoprotein complex subunit 3		8.40E-11

2558669926	DRAFT_00594	Locus_type		CDS		
2558669926	DRAFT_00594	Product_name		Predicted Zn-ribbon RNA-binding protein		
2558669926	DRAFT_00594	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669926	DRAFT_00594	Coordinates		30500..30652(-)		
2558669926	DRAFT_00594	DNA_length		153bp		
2558669926	DRAFT_00594	Protein_length		50aa		
2558669926	DRAFT_00594	GC			0.56	

2558669927	DRAFT_00595	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669927	DRAFT_00595	COG1093	Translation initiation factor 2, alpha subunit (eIF-2alpha)			8.00E-58
2558669927	DRAFT_00595	pfam00575	S1			3.00E-13
2558669927	DRAFT_00595	pfam07541	EIF_2_alpha			2.00E-25
2558669927	DRAFT_00595	KO:K03237	translation initiation factor 2 subunit 1			0.00E+00
2558669927	DRAFT_00595	ITERM:01963	translation initiation factor 2 subunit alpha (aeIF-2a)			
2558669927	DRAFT_00595	Locus_type		CDS		
2558669927	DRAFT_00595	Product_name		translation initiation factor 2 subunit alpha (aeIF-2a)		
2558669927	DRAFT_00595	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669927	DRAFT_00595	Coordinates		30661..31461(-)		
2558669927	DRAFT_00595	DNA_length		801bp		
2558669927	DRAFT_00595	Protein_length		266aa		
2558669927	DRAFT_00595	GC			0.57	

2558669928	DRAFT_00596	KEGG_module	M00179: Ribosome, archaea			
2558669928	DRAFT_00596	KEGG_module	M00177: Ribosome, eukaryotes			
2558669928	DRAFT_00596	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669928	DRAFT_00596	COG2051	Ribosomal protein S27E			6.00E-11
2558669928	DRAFT_00596	pfam01667	Ribosomal_S27e			2.90E-16
2558669928	DRAFT_00596	KO:K02978	small subunit ribosomal protein S27e			1.40E-10
2558669928	DRAFT_00596	Locus_type		CDS		
2558669928	DRAFT_00596	Product_name		SSU ribosomal protein S27E		
2558669928	DRAFT_00596	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669928	DRAFT_00596	Coordinates		31557..31754(-)		
2558669928	DRAFT_00596	DNA_length		198bp		
2558669928	DRAFT_00596	Protein_length		65aa		

2558669928	DRAFT_00596	GC			0.56	
2558669929	DRAFT_00597	KEGG_module	M00179: Ribosome, archaea			
2558669929	DRAFT_00597	KEGG_module	M00177: Ribosome, eukaryotes			
2558669929	DRAFT_00597	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669929	DRAFT_00597	COG1631	Ribosomal protein L44E			2.00E-15
2558669929	DRAFT_00597	pfam00935	Ribosomal_L44			2.40E-25
2558669929	DRAFT_00597	KO:K02929	large subunit ribosomal protein L44e			4.30E-29
2558669929	DRAFT_00597	Locus_type		CDS		
2558669929	DRAFT_00597	Product_name		Ribosomal protein L44E		
2558669929	DRAFT_00597	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669929	DRAFT_00597	Coordinates		31751..32029(-)		
2558669929	DRAFT_00597	DNA_length		279bp		
2558669929	DRAFT_00597	Protein_length		92aa		
2558669929	DRAFT_00597	GC			0.52	
2558669930	DRAFT_00598	KEGG_module	M00295: BRCA1-associated genome surveillance complex (BASC)			
2558669930	DRAFT_00598	pfam00705	PCNA_N			1.00E-15
2558669930	DRAFT_00598	pfam02747	PCNA_C			4.70E-16
2558669930	DRAFT_00598	TIGR00590	proliferating cell nuclear antigen (pcna)			1.60E-43
2558669930	DRAFT_00598	KO:K04802	proliferating cell nuclear antigen			0.00E+00
2558669930	DRAFT_00598	Locus_type		CDS		
2558669930	DRAFT_00598	Product_name		proliferating cell nuclear antigen (pcna)		
2558669930	DRAFT_00598	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669930	DRAFT_00598	Coordinates		32371..33123(+)		
2558669930	DRAFT_00598	DNA_length		753bp		
2558669930	DRAFT_00598	Protein_length		250aa		
2558669930	DRAFT_00598	GC			0.56	
2558669931	DRAFT_00599	Locus_type		CDS		
2558669931	DRAFT_00599	Product_name		hypothetical protein		
2558669931	DRAFT_00599	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669931	DRAFT_00599	Coordinates		33162..33305(-)		
2558669931	DRAFT_00599	DNA_length		144bp		

2558669931	DRAFT_00599	Protein_length		47aa		
2558669931	DRAFT_00599	GC			0.58	
2558669932	DRAFT_00600	Metacyc	PWY-6749: CMP-legionaminate biosynthesis I			
2558669932	DRAFT_00600	Metacyc	PWY-6679: jadomycin biosynthesis			
2558669932	DRAFT_00600	Metacyc	PWY-7127: CDP-D-mannitol biosynthesis			
2558669932	DRAFT_00600	Metacyc	PWY-6998: CDP-D-arabitol biosynthesis			
2558669932	DRAFT_00600	Metacyc	PWY4FS-4: phosphatidylcholine biosynthesis IV			
2558669932	DRAFT_00600	Metacyc	PWY-6626: CDP-2-glycerol biosynthesis			
2558669932	DRAFT_00600	COG_category	[L] Replication, recombination and repair			
2558669932	DRAFT_00600	COG1467	Eukaryotic-type DNA primase, catalytic (small) subunit			2.00E-47
2558669932	DRAFT_00600	pfam01896	DNA_primase_S			7.00E-16
2558669932	DRAFT_00600	EC:2.7.7.-	Transferases. Transferring phosphorous-containing groups. Nucleotidyltransferases.			
2558669932	DRAFT_00600	KO:K02683	DNA primase [EC:2.7.7.-]			0.00E+00
2558669932	DRAFT_00600	Locus_type		CDS		
2558669932	DRAFT_00600	Product_name		Eukaryotic-type DNA primase, catalytic (small) subunit		
2558669932	DRAFT_00600	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669932	DRAFT_00600	Coordinates		33484..34572(+)		
2558669932	DRAFT_00600	DNA_length		1089bp		
2558669932	DRAFT_00600	Protein_length		362aa		
2558669932	DRAFT_00600	GC			0.59	
2558669933	DRAFT_00601	Locus_type		CDS		
2558669933	DRAFT_00601	Product_name		hypothetical protein		
2558669933	DRAFT_00601	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669933	DRAFT_00601	Coordinates		34573..35130(+)		
2558669933	DRAFT_00601	DNA_length		558bp		
2558669933	DRAFT_00601	Protein_length		185aa		
2558669933	DRAFT_00601	GC			0.55	
2558669934	DRAFT_00602	COG_category	[K] Transcription			
2558669934	DRAFT_00602	COG1594	DNA-directed RNA polymerase, subunit M/Transcription elongation fac			1.00E-19
2558669934	DRAFT_00602	pfam01096	TFIIS_C			2.00E-20
2558669934	DRAFT_00602	TIGR01384	transcription factor S, archaeal			2.30E-26

2558669934	DRAFT_00602	KO:K03057	transcription elongation factor			2.90E-21
2558669934	DRAFT_00602	Locus_type		CDS		
2558669934	DRAFT_00602	Product_name		DNA-directed RNA polymerase, subunit M (EC 2.7.7.6)		
2558669934	DRAFT_00602	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669934	DRAFT_00602	Coordinates		35127..35441(-)		
2558669934	DRAFT_00602	DNA_length		315bp		
2558669934	DRAFT_00602	Protein_length		104aa		
2558669934	DRAFT_00602	GC			0.53	
2558669935	DRAFT_00603	KEGG_module	M00180: RNA polymerase II, eukaryotes			
2558669935	DRAFT_00603	COG_category	[K] Transcription			
2558669935	DRAFT_00603	COG1761	DNA-directed RNA polymerase, subunit L			3.00E-08
2558669935	DRAFT_00603	pfam13656	RNA_pol_L_2			2.10E-16
2558669935	DRAFT_00603	KO:K03008	DNA-directed RNA polymerase II subunit RPB11			4.70E-06
2558669935	DRAFT_00603	Locus_type		CDS		
2558669935	DRAFT_00603	Product_name		DNA-directed RNA polymerase, subunit L		
2558669935	DRAFT_00603	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669935	DRAFT_00603	Coordinates		35468..35755(-)		
2558669935	DRAFT_00603	DNA_length		288bp		
2558669935	DRAFT_00603	Protein_length		95aa		
2558669935	DRAFT_00603	GC			0.55	
2558669936	DRAFT_00604	KEGG_module	M00390: Exosome, archaea			
2558669936	DRAFT_00604	KEGG_module	M00391: Exosome, eukaryotes			
2558669936	DRAFT_00604	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669936	DRAFT_00604	COG1096	Predicted RNA-binding protein (consists of S1 domain and a Zn-ribbon			4.00E-26
2558669936	DRAFT_00604	KO:K07573	exosome complex component CSL4			3.90E-24
2558669936	DRAFT_00604	Locus_type		CDS		
2558669936	DRAFT_00604	Product_name		Predicted RNA-binding protein (consists of S1 domain and a Zn-ribbor		
2558669936	DRAFT_00604	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669936	DRAFT_00604	Coordinates		35791..36363(-)		
2558669936	DRAFT_00604	DNA_length		573bp		
2558669936	DRAFT_00604	Protein_length		190aa		
2558669936	DRAFT_00604	GC			0.59	

2558669937	DRAFT_00605	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669937	DRAFT_00605	COG1736	Diphthamide synthase subunit DPH2			4.00E-51
2558669937	DRAFT_00605	pfam01866	Diphthamide_syn			4.10E-69
2558669937	DRAFT_00605	TIGR03682	diphthamide biosynthesis enzyme Dph2			1.50E-69
2558669937	DRAFT_00605	TIGR00322	diphthamide biosynthesis enzyme Dph1/Dph2 domain			7.70E-64
2558669937	DRAFT_00605	KO:K07561	diphthamide synthase subunit DPH2			0.00E+00
2558669937	DRAFT_00605	Locus_type		CDS		
2558669937	DRAFT_00605	Product_name		diphthamide biosynthesis enzyme Dph2		
2558669937	DRAFT_00605	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669937	DRAFT_00605	Coordinates		36360..37391(-)		
2558669937	DRAFT_00605	DNA_length		1032bp		
2558669937	DRAFT_00605	Protein_length		343aa		
2558669937	DRAFT_00605	GC			0.58	

2558669938	DRAFT_00606	KEGG_module	M00179: Ribosome, archaea			
2558669938	DRAFT_00606	KEGG_module	M00177: Ribosome, eukaryotes			
2558669938	DRAFT_00606	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669938	DRAFT_00606	COG0197	Ribosomal protein L16/L10E			1.00E-21
2558669938	DRAFT_00606	pfam00252	Ribosomal_L16			2.40E-25
2558669938	DRAFT_00606	TIGR00279	ribosomal protein L10.e			9.60E-54
2558669938	DRAFT_00606	KO:K02866	large subunit ribosomal protein L10e			1.30E-42
2558669938	DRAFT_00606	Locus_type		CDS		
2558669938	DRAFT_00606	Product_name		LSU ribosomal protein L10AE		
2558669938	DRAFT_00606	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669938	DRAFT_00606	Coordinates		37388..37897(-)		
2558669938	DRAFT_00606	DNA_length		510bp		
2558669938	DRAFT_00606	Protein_length		169aa		
2558669938	DRAFT_00606	GC			0.55	

2558669939	DRAFT_00607	pfam13659	Methyltransf_26			1.00E-17
2558669939	DRAFT_00607	Locus_type		CDS		
2558669939	DRAFT_00607	Product_name		Methyltransferase domain		
2558669939	DRAFT_00607	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		

2558669939	DRAFT_00607	Coordinates		37983..39164(+)
2558669939	DRAFT_00607	DNA_length		1182bp
2558669939	DRAFT_00607	Protein_length		393aa
2558669939	DRAFT_00607	GC		0.61
2558669940	DRAFT_00608	Metacyc	PWY-6739: pinitol biosynthesis II	
2558669940	DRAFT_00608	Metacyc	PWY-7076: 3,5-dimethoxytoluene biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-7025: gentamicin biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-7045: mithramycin biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-6286: spheroidene and spheroidenone biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-5305: bixin biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-6973: dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycarose biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-6650: juvenile hormone III biosynthesis II	
2558669940	DRAFT_00608	Metacyc	PWY-702: methionine biosynthesis II	
2558669940	DRAFT_00608	Metacyc	PWY-6151: <i>S</i>-adenosyl-L-methionine cycle I	
2558669940	DRAFT_00608	Metacyc	PWY-5135: xanthohumol biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-7151: polymethylated quercetin glucoside biosynthesis II - quercetagetin series (Chryso	
2558669940	DRAFT_00608	Metacyc	PWY-7149: superpathway polymethylated quercetin/quercetagetin glucoside biosynthesis (Ch	
2558669940	DRAFT_00608	Metacyc	PWY-5391: syringetin biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-5729: vestitol and sativan biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-3542: choline biosynthesis II	
2558669940	DRAFT_00608	Metacyc	PWY-1422: vitamin E biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-5975: furaneol biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-6682: dehydrophos biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-5882: epoxypseudoisoeugenol-2-methylbutyrate biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-7161: polymethylated quercetin biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-5867: <i>t</i>-anethole biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-7135: emetine biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-5287: sanguinarine and macarpine biosynthesis	
2558669940	DRAFT_00608	Metacyc	PWY-6154: autoinducer AI-2 biosynthesis II (<i>Vibrio</i>)	
2558669940	DRAFT_00608	Metacyc	METH-ACETATE-PWY: methanogenesis from acetate	
2558669940	DRAFT_00608	Metacyc	PWY-6339: syringate degradation	
2558669940	DRAFT_00608	Metacyc	PWY-6045: methylthiopropionate degradation II (demethylation)	
2558669940	DRAFT_00608	Metacyc	PWY-6736: sulfur volatiles biosynthesis	

2558669940	DRAFT_00608	Metacyc	PWY-6303: methyl indole-3-acetate interconversion
2558669940	DRAFT_00608	Metacyc	PWY-6666: pyocyanin biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5987: sorgoleone biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5876: magnoflorine biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5846: colchicine biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-6581: spirilloxanthin and 2,2'-diketo-spirilloxanthin biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5773: gossypol biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-6424: sitosterol biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5765: 1,3,5-trimethoxybenzene biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5665: vanilla biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-7150: polymethylated quercetin glucoside biosynthesis I - quercetin series (Chrysospleniu
2558669940	DRAFT_00608	Metacyc	PWY-7055: daphnetin modification
2558669940	DRAFT_00608	Metacyc	PWY-4942: cyclopropane and cyclopropene fatty acid biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5507: adenosylcobalamin biosynthesis I (early cobalt insertion)
2558669940	DRAFT_00608	Metacyc	PWY-1581: plastoquinol-9 biosynthesis I
2558669940	DRAFT_00608	Metacyc	PWY-7104: dTDP-L-megosamine biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-7163: polymethylated kaempferol biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-6631: <i>O</i> -methylation of tricetin
2558669940	DRAFT_00608	Metacyc	PWY-6427: rot-2'-enonate biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-7186: superpathway of scopolin and esculin biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-6442: spermidine hydroxycinnamic acid conjugates biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5748: γ-coniciene and coniine biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-5467: gramine biosynthesis
2558669940	DRAFT_00608	Metacyc	METHIONINE-DEG1-PWY: methionine degradation I (to homocysteine)
2558669940	DRAFT_00608	Metacyc	PWY-6477: gibberellin inactivation II (methylation)
2558669940	DRAFT_00608	Metacyc	PWY-1061: homogalacturonan biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-6976: dTDP-L-mycarose biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-6575: juvenile hormone III biosynthesis I
2558669940	DRAFT_00608	Metacyc	PWY-5041: <i>S</i>-adenosyl-L-methionine cycle II
2558669940	DRAFT_00608	Metacyc	PWY-6955: lincomycin biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-7160: polymethylated myricetin biosynthesis (tomato)
2558669940	DRAFT_00608	Metacyc	PWY-7079: geodin biosynthesis
2558669940	DRAFT_00608	Metacyc	PWY-6933: seleno-amino acid detoxification and volatilization III
2558669940	DRAFT_00608	Metacyc	PWY-6153: autoinducer AI-2 biosynthesis I

2558669940	DRAFT_00608	Metacyc	PWY-6978: plastoquinol-9 biosynthesis II		
2558669940	DRAFT_00608	Metacyc	PWY-4021: β-alanine betaine biosynthesis		
2558669940	DRAFT_00608	Metacyc	PWY-6835: 6-gingerol biosynthesis		
2558669940	DRAFT_00608	Metacyc	PWY-7157: eupatolitin 3-<i>O</i>-glucoside biosynthesis		
2558669940	DRAFT_00608	Metacyc	PWY-7058: esculetin modification		
2558669940	DRAFT_00608	Metacyc	PWY-5479: podophyllotoxin and 6-methoxypodophyllotoxin biosynthesis		
2558669940	DRAFT_00608	Metacyc	PWY-7138: noscapine biosynthesis		
2558669940	DRAFT_00608	Metacyc	PWY-5290: secologanin and strictosidine biosynthesis		
2558669940	DRAFT_00608	Metacyc	PWYG-321: mycolate biosynthesis		
2558669940	DRAFT_00608	Metacyc	PWY-5209: methyl-coenzyme M oxidation to CO₂		
2558669940	DRAFT_00608	Metacyc	PWY-7097: vanillin and vanillate degradation I		
2558669940	DRAFT_00608	Metacyc	PWY-6052: dimethylsulfoniopropionate degradation III (demethylation)		
2558669940	DRAFT_00608	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558669940	DRAFT_00608	COG0565	rRNA methylase		9.00E-38
2558669940	DRAFT_00608	pfam00588	SpoU_methylase		3.60E-24
2558669940	DRAFT_00608	EC:2.1.1.-	Transferases. Transferring one-carbon groups. Methyltransferases.		
2558669940	DRAFT_00608	TIGR00050	RNA methyltransferase, TrmH family, group 1		2.10E-46
2558669940	DRAFT_00608	KO:K02533	tRNA/rRNA methyltransferase [EC:2.1.1.-]		9.70E-33
2558669940	DRAFT_00608	Locus_type		CDS	
2558669940	DRAFT_00608	Product_name		rRNA methylase	
2558669940	DRAFT_00608	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669940	DRAFT_00608	Coordinates		39140..39853(-)	
2558669940	DRAFT_00608	DNA_length		714bp	
2558669940	DRAFT_00608	Protein_length		237aa	
2558669940	DRAFT_00608	GC		0.56	

2558669941	DRAFT_00609	Locus_type		CDS
2558669941	DRAFT_00609	Product_name		hypothetical protein
2558669941	DRAFT_00609	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8
2558669941	DRAFT_00609	Coordinates		39995..40219(+)
2558669941	DRAFT_00609	DNA_length		225bp
2558669941	DRAFT_00609	Protein_length		74aa
2558669941	DRAFT_00609	GC		0.57

2558669942	DRAFT_00610	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669942	DRAFT_00610	COG0030	Dimethyladenosine transferase (rRNA methylation)			6.00E-36
2558669942	DRAFT_00610	pfam00398	RrnaAD			6.50E-33
2558669942	DRAFT_00610	EC:2.1.1.182	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase.			
2558669942	DRAFT_00610	KO:K02528	16S rRNA (adenine1518-N6/adenine1519-N6)-dimethyltransferase [EC:			4.50E-41
2558669942	DRAFT_00610	Locus_type		CDS		
2558669942	DRAFT_00610	Product_name		Dimethyladenosine transferase (rRNA methylation)		
2558669942	DRAFT_00610	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669942	DRAFT_00610	Coordinates		40143..40886(-)		
2558669942	DRAFT_00610	DNA_length		744bp		
2558669942	DRAFT_00610	Protein_length		247aa		
2558669942	DRAFT_00610	GC			0.58	
2558669943	DRAFT_00611	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669943	DRAFT_00611	COG1491	Predicted RNA-binding protein			5.00E-42
2558669943	DRAFT_00611	pfam04919	DUF655			9.10E-52
2558669943	DRAFT_00611	KO:K07572	putative nucleotide binding protein			0.00E+00
2558669943	DRAFT_00611	Locus_type		CDS		
2558669943	DRAFT_00611	Product_name		Predicted RNA-binding protein		
2558669943	DRAFT_00611	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669943	DRAFT_00611	Coordinates		40883..41440(-)		
2558669943	DRAFT_00611	DNA_length		558bp		
2558669943	DRAFT_00611	Protein_length		185aa		
2558669943	DRAFT_00611	GC			0.56	
2558669944	DRAFT_00612	KEGG_module	M00184: RNA polymerase, archaea			
2558669944	DRAFT_00612	COG_category	[S] Function unknown			
2558669944	DRAFT_00612	COG1460	Uncharacterized protein conserved in archaea			9.00E-10
2558669944	DRAFT_00612	pfam03874	RNA_pol_Rpb4			3.10E-14
2558669944	DRAFT_00612	EC:2.7.7.6	DNA-directed RNA polymerase.			
2558669944	DRAFT_00612	KO:K03051	DNA-directed RNA polymerase subunit F [EC:2.7.7.6]			2.80E-24
2558669944	DRAFT_00612	ITERM:01967	DNA-directed RNA polymerase, subunit F (EC 2.7.7.6)			
2558669944	DRAFT_00612	Locus_type		CDS		
2558669944	DRAFT_00612	Product_name		DNA-directed RNA polymerase, subunit F (EC 2.7.7.6)		

2558669944	DRAFT_00612	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669944	DRAFT_00612	Coordinates		41587..41907(-)		
2558669944	DRAFT_00612	DNA_length		321bp		
2558669944	DRAFT_00612	Protein_length		106aa		
2558669944	DRAFT_00612	GC			0.52	

2558669945	DRAFT_00613	KEGG_module	M00177: Ribosome, eukaryotes			
2558669945	DRAFT_00613	KEGG_module	M00179: Ribosome, archaea			
2558669945	DRAFT_00613	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669945	DRAFT_00613	COG2139	Ribosomal protein L21E			2.00E-17
2558669945	DRAFT_00613	pfam01157	Ribosomal_L21e			3.80E-15
2558669945	DRAFT_00613	KO:K02889	large subunit ribosomal protein L21e			3.70E-23
2558669945	DRAFT_00613	Locus_type		CDS		
2558669945	DRAFT_00613	Product_name		Ribosomal protein L21E		
2558669945	DRAFT_00613	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669945	DRAFT_00613	Coordinates		41904..42191(-)		
2558669945	DRAFT_00613	DNA_length		288bp		
2558669945	DRAFT_00613	Protein_length		95aa		
2558669945	DRAFT_00613	GC			0.54	

2558669946	DRAFT_00614	Metacyc	RIBOKIN-PWY: ribose degradation			
2558669946	DRAFT_00614	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669946	DRAFT_00614	COG1258	Predicted pseudouridylate synthase			1.00E-33
2558669946	DRAFT_00614	pfam02926	THUMP			2.20E-04
2558669946	DRAFT_00614	EC:5.4.99.-	Isomerases. Intramolecular transferases (mutases). Transferring other groups.			
2558669946	DRAFT_00614	TIGR01213	tRNA pseudouridine(54/55) synthase			1.30E-39
2558669946	DRAFT_00614	KO:K07583	tRNA pseudouridine synthase 10 [EC:5.4.99.-]			0.00E+00
2558669946	DRAFT_00614	Locus_type		CDS		
2558669946	DRAFT_00614	Product_name		Predicted pseudouridylate synthase		
2558669946	DRAFT_00614	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669946	DRAFT_00614	Coordinates		42157..43275(-)		
2558669946	DRAFT_00614	DNA_length		1119bp		
2558669946	DRAFT_00614	Protein_length		372aa		
2558669946	DRAFT_00614	GC			0.61	

2558669947	DRAFT_00615	KEGG_module	M00335: Sec (secretion) system			
2558669947	DRAFT_00615	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2558669947	DRAFT_00615	COG0541	Signal recognition particle GTPase			0.00E+00
2558669947	DRAFT_00615	pfam02978	SRP_SPB			4.40E-30
2558669947	DRAFT_00615	pfam00448	SRP54			6.70E-68
2558669947	DRAFT_00615	pfam02881	SRP54_N			9.20E-16
2558669947	DRAFT_00615	KO:K03106	signal recognition particle subunit SRP54			0.00E+00
2558669947	DRAFT_00615	ITERM:01969	signal recognition particle subunit FFH/SRP54 (srp54)			
2558669947	DRAFT_00615	Locus_type		CDS		
2558669947	DRAFT_00615	Product_name		signal recognition particle subunit FFH/SRP54 (srp54)		
2558669947	DRAFT_00615	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669947	DRAFT_00615	Coordinates		43286..44608(-)		
2558669947	DRAFT_00615	DNA_length		1323bp		
2558669947	DRAFT_00615	Protein_length		440aa		
2558669947	DRAFT_00615	GC			0.6	
2558669948	DRAFT_00616	COG_category	[R] General function prediction only			
2558669948	DRAFT_00616	COG2102	Predicted ATPases of PP-loop superfamily			2.00E-68
2558669948	DRAFT_00616	pfam01902	ATP_bind_4			1.40E-65
2558669948	DRAFT_00616	TIGR00289	TIGR00289 family protein			2.20E-73
2558669948	DRAFT_00616	TIGR03679	arCOG00187 universal archaeal metal-binding-domain/4Fe-4S-binding-			2.10E-83
2558669948	DRAFT_00616	TIGR00290	MJ0570-related uncharacterized domain			5.60E-68
2558669948	DRAFT_00616	Locus_type		CDS		
2558669948	DRAFT_00616	Product_name		arCOG00187 universal archaeal metal-binding-domain/4Fe-4S-binding		
2558669948	DRAFT_00616	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669948	DRAFT_00616	Coordinates		44689..45378(+)		
2558669948	DRAFT_00616	DNA_length		690bp		
2558669948	DRAFT_00616	Protein_length		229aa		
2558669948	DRAFT_00616	GC			0.63	
2558669949	DRAFT_00617	COG_category	[R] General function prediction only			
2558669949	DRAFT_00617	COG2262	GTPases			2.00E-73
2558669949	DRAFT_00617	pfam13167	GTP-bdg_N			2.10E-10

2558669949	DRAFT_00617	pfam01926	MMR_HSR1			4.30E-17
2558669949	DRAFT_00617	TIGR03156	GTP-binding protein HflX			9.60E-86
2558669949	DRAFT_00617	KO:K03665	GTP-binding protein HflX			0.00E+00
2558669949	DRAFT_00617	Locus_type		CDS		
2558669949	DRAFT_00617	Product_name		GTP-binding protein HflX		
2558669949	DRAFT_00617	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669949	DRAFT_00617	Coordinates		45418..46446(-)		
2558669949	DRAFT_00617	DNA_length		1029bp		
2558669949	DRAFT_00617	Protein_length		342aa		
2558669949	DRAFT_00617	GC			0.59	
2558669950	DRAFT_00618	IMG_pathway	854: Hypusine synthesis			
2558669950	DRAFT_00618	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558669950	DRAFT_00618	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (e			4.00E-25
2558669950	DRAFT_00618	pfam08207	EFP_N			4.00E-06
2558669950	DRAFT_00618	pfam01287	eIF-5a			3.60E-12
2558669950	DRAFT_00618	TIGR00037	translation elongation factor IF5A			2.10E-41
2558669950	DRAFT_00618	KO:K03263	translation initiation factor 5A			3.00E-34
2558669950	DRAFT_00618	ITERM:01965	translation initiation factor 5A precursor (eIF-5A)			
2558669950	DRAFT_00618	Locus_type		CDS		
2558669950	DRAFT_00618	Product_name		translation initiation factor 5A precursor (eIF-5A)		
2558669950	DRAFT_00618	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669950	DRAFT_00618	Coordinates		47428..47838(-)		
2558669950	DRAFT_00618	DNA_length		411bp		
2558669950	DRAFT_00618	Protein_length		136aa		
2558669950	DRAFT_00618	GC			0.58	
2558669951	DRAFT_00619	Locus_type		CDS		
2558669951	DRAFT_00619	Product_name		hypothetical protein		
2558669951	DRAFT_00619	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669951	DRAFT_00619	Coordinates		47978..48613(-)		
2558669951	DRAFT_00619	DNA_length		636bp		
2558669951	DRAFT_00619	Protein_length		211aa		
2558669951	DRAFT_00619	GC			0.54	

2558669951	DRAFT_00619	Transmembrane		Yes	
2558669952	DRAFT_00620	COG_category	[R] General function prediction only		
2558669952	DRAFT_00620	COG1439	Predicted nucleic acid-binding protein, consists of a PIN domain and a		9.00E-32
2558669952	DRAFT_00620	KO:K07060	UPF0271 protein		1.10E-22
2558669952	DRAFT_00620	Locus_type		CDS	
2558669952	DRAFT_00620	Product_name		Predicted nucleic acid-binding protein, consists of a PIN domain and a	
2558669952	DRAFT_00620	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669952	DRAFT_00620	Coordinates		48980..49474(+)	
2558669952	DRAFT_00620	DNA_length		495bp	
2558669952	DRAFT_00620	Protein_length		164aa	
2558669952	DRAFT_00620	GC		0.59	
2558669953	DRAFT_00621	COG_category	[K] Transcription		
2558669953	DRAFT_00621	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiati		1.00E-70
2558669953	DRAFT_00621	pfam08271	TF_Zn_Ribbon		2.80E-13
2558669953	DRAFT_00621	pfam00382	TFIIB		5.50E-15
2558669953	DRAFT_00621	pfam00382	TFIIB		9.30E-17
2558669953	DRAFT_00621	KO:K03124	transcription initiation factor TFIIB		0.00E+00
2558669953	DRAFT_00621	ITERM:01912	Transcription initiation factor IIB (TFIIB)		
2558669953	DRAFT_00621	Locus_type		CDS	
2558669953	DRAFT_00621	Product_name		Transcription initiation factor IIB (TFIIB)	
2558669953	DRAFT_00621	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669953	DRAFT_00621	Coordinates		49600..50562(+)	
2558669953	DRAFT_00621	DNA_length		963bp	
2558669953	DRAFT_00621	Protein_length		320aa	
2558669953	DRAFT_00621	GC		0.61	
2558669954	DRAFT_00622	Locus_type		tRNA	
2558669954	DRAFT_00622	Product_name		tRNA_Ala_CGC	
2558669954	DRAFT_00622	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669954	DRAFT_00622	Coordinates		50570..50660(-)	
2558669954	DRAFT_00622	DNA_length		91bp	
2558669954	DRAFT_00622	GC		0.69	

2558669955	DRAFT_00623	Metacyc	PYRIDNUCSAL-PWY: NAD salvage pathway I		
2558669955	DRAFT_00623	Metacyc	PWY-5381: pyridine nucleotide cycling (plants)		
2558669955	DRAFT_00623	COG_category	[H] Coenzyme transport and metabolism		
2558669955	DRAFT_00623	COG1488	Nicotinic acid phosphoribosyltransferase		1.00E-67
2558669955	DRAFT_00623	pfam01729	QRPTase_C		2.80E-17
2558669955	DRAFT_00623	EC:2.4.2.11	Nicotinate phosphoribosyltransferase.		
2558669955	DRAFT_00623	TIGR01513	putative nicotinate phosphoribosyltransferase		1.90E-45
2558669955	DRAFT_00623	KO:K00763	nicotinate phosphoribosyltransferase [EC:2.4.2.11]		0.00E+00
2558669955	DRAFT_00623	Locus_type		CDS	
2558669955	DRAFT_00623	Product_name		Nicotinic acid phosphoribosyltransferase	
2558669955	DRAFT_00623	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8	
2558669955	DRAFT_00623	Coordinates		50767..51987(+)	
2558669955	DRAFT_00623	DNA_length		1221bp	
2558669955	DRAFT_00623	Protein_length		406aa	
2558669955	DRAFT_00623	GC		0.62	

2558669956	DRAFT_00624	Metacyc	PWY-5846: colchicine biosynthesis		
2558669956	DRAFT_00624	Metacyc	PWY-6984: lipoate salvage II		
2558669956	DRAFT_00624	Metacyc	PWY-5381: pyridine nucleotide cycling (plants)		
2558669956	DRAFT_00624	Metacyc	PYRIDNUCSAL-PWY: NAD salvage pathway I		
2558669956	DRAFT_00624	Metacyc	LYSDEGII-PWY: lysine degradation III		
2558669956	DRAFT_00624	Metacyc	P621-PWY: nylon-6 oligomer degradation		
2558669956	DRAFT_00624	Metacyc	PWY-5665: vanilla biosynthesis		
2558669956	DRAFT_00624	Metacyc	PWY-6899: base-degraded thiamin salvage		
2558669956	DRAFT_00624	Metacyc	PWY-6431: 4-hydroxybenzoate biosynthesis IV		
2558669956	DRAFT_00624	Metacyc	PWY-6855: chitin degradation I (archaea)		
2558669956	DRAFT_00624	Metacyc	PWY-1822: indole-3-acetate activation I		
2558669956	DRAFT_00624	Metacyc	PWY-7018: paromomycin biosynthesis		
2558669956	DRAFT_00624	Metacyc	P345-PWY: aldoxime degradation		
2558669956	DRAFT_00624	Metacyc	PWY-5784: IAA conjugate biosynthesis II		
2558669956	DRAFT_00624	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism		
2558669956	DRAFT_00624	COG1335	Amidases related to nicotinamidase		5.00E-34
2558669956	DRAFT_00624	pfam00857	Isochorismatase		5.30E-36

2558669956	DRAFT_00624	EC:3.5.1.19	Nicotinamidase.			
2558669956	DRAFT_00624	EC:3.5.1.-	Hydrolases. Acting on carbon-nitrogen bonds, other than peptide bonds. In linear amides.			
2558669956	DRAFT_00624	KO:K08281	nicotinamidase/pyrazinamidase [EC:3.5.1.19 3.5.1.-]			0.00E+00
2558669956	DRAFT_00624	Locus_type		CDS		
2558669956	DRAFT_00624	Product_name		Amidases related to nicotinamidase		
2558669956	DRAFT_00624	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669956	DRAFT_00624	Coordinates		52012..52617(+)		
2558669956	DRAFT_00624	DNA_length		606bp		
2558669956	DRAFT_00624	Protein_length		201aa		
2558669956	DRAFT_00624	GC			0.61	
2558669957	DRAFT_00625	TIGR03804	parallel beta-helix repeat (two copies)			2.00E-09
2558669957	DRAFT_00625	Locus_type		CDS		
2558669957	DRAFT_00625	Product_name		parallel beta-helix repeat (two copies)		
2558669957	DRAFT_00625	Scaffold		DRAFT_contig_70_43_len_52827_read_count_999642.8		
2558669957	DRAFT_00625	Coordinates		52636..52824(+)		
2558669957	DRAFT_00625	DNA_length		189bp		
2558669957	DRAFT_00625	Protein_length		63aa		
2558669957	DRAFT_00625	GC			0.6	
2558669958	DRAFT_00626	Locus_type		CDS		
2558669958	DRAFT_00626	Product_name		hypothetical protein		
2558669958	DRAFT_00626	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669958	DRAFT_00626	Coordinates		103..375(+)		
2558669958	DRAFT_00626	DNA_length		273bp		
2558669958	DRAFT_00626	Protein_length		90aa		
2558669958	DRAFT_00626	GC			0.49	
2558669959	DRAFT_00627	Locus_type		CDS		
2558669959	DRAFT_00627	Product_name		hypothetical protein		
2558669959	DRAFT_00627	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669959	DRAFT_00627	Coordinates		668..994(+)		
2558669959	DRAFT_00627	DNA_length		327bp		
2558669959	DRAFT_00627	Protein_length		108aa		

2558669959	DRAFT_00627	GC		0.55
2558669959	DRAFT_00627	Transmembrane		Yes
2558669960	DRAFT_00628	Locus_type		CDS
2558669960	DRAFT_00628	Product_name		hypothetical protein
2558669960	DRAFT_00628	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9
2558669960	DRAFT_00628	Coordinates		991..1473(+)
2558669960	DRAFT_00628	DNA_length		483bp
2558669960	DRAFT_00628	Protein_length		160aa
2558669960	DRAFT_00628	GC		0.56
2558669960	DRAFT_00628	Transmembrane		Yes
2558669961	DRAFT_00629	Locus_type		CDS
2558669961	DRAFT_00629	Product_name		hypothetical protein
2558669961	DRAFT_00629	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9
2558669961	DRAFT_00629	Coordinates		1524..1931(+)
2558669961	DRAFT_00629	DNA_length		408bp
2558669961	DRAFT_00629	Protein_length		135aa
2558669961	DRAFT_00629	GC		0.54
2558669961	DRAFT_00629	Transmembrane		Yes
2558669962	DRAFT_00630	KEGG_module	M00364: C10-C20 isoprenoid biosynthesis, bacteria	
2558669962	DRAFT_00630	KEGG_module	M00365: C10-C20 isoprenoid biosynthesis, archaea	
2558669962	DRAFT_00630	Metacyc	PWY-7141: linalool biosynthesis II	
2558669962	DRAFT_00630	Metacyc	PWY-7102: bisabolene biosynthesis	
2558669962	DRAFT_00630	Metacyc	PWY-6859: <i>all-trans</i>-farnesol biosynthesis	
2558669962	DRAFT_00630	Metacyc	PWY-6691: plaunotol biosynthesis	
2558669962	DRAFT_00630	Metacyc	PWY-5122: geranyl diphosphate biosynthesis	
2558669962	DRAFT_00630	Metacyc	PWY2OL-4: superpathway of linalool biosynthesis	
2558669962	DRAFT_00630	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis	
2558669962	DRAFT_00630	Metacyc	PWY-5123: <i>trans, trans</i>-farnesyl diphosphate biosynthesis	
2558669962	DRAFT_00630	Metacyc	PWY-6659: fusicoccins biosynthesis	
2558669962	DRAFT_00630	Metacyc	PWY-7182: linalool biosynthesis I	
2558669962	DRAFT_00630	Metacyc	PWY-5120: geranylgeranyldiphosphate biosynthesis	

2558669962	DRAFT_00630	COG_category	[H] Coenzyme transport and metabolism			
2558669962	DRAFT_00630	COG0142	Geranylgeranyl pyrophosphate synthase			4.00E-59
2558669962	DRAFT_00630	pfam00348	polyprenyl_synt			1.60E-50
2558669962	DRAFT_00630	EC:2.5.1.29	Geranylgeranyl diphosphate synthase.			
2558669962	DRAFT_00630	EC:2.5.1.1	Dimethylallyltranstransferase.			
2558669962	DRAFT_00630	EC:2.5.1.10	(2E,6E)-farnesyl diphosphate synthase.			
2558669962	DRAFT_00630	KO:K13787	geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10 2.5.1.			0.00E+00
2558669962	DRAFT_00630	Locus_type		CDS		
2558669962	DRAFT_00630	Product_name		Geranylgeranyl pyrophosphate synthase		
2558669962	DRAFT_00630	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669962	DRAFT_00630	Coordinates		2103..3074(-)		
2558669962	DRAFT_00630	DNA_length		972bp		
2558669962	DRAFT_00630	Protein_length		323aa		
2558669962	DRAFT_00630	GC			0.55	
2558669963	DRAFT_00631	COG_category	[R] General function prediction only			
2558669963	DRAFT_00631	COG3975	Predicted protease with the C-terminal PDZ domain			7.00E-112
2558669963	DRAFT_00631	pfam13180	PDZ_2			9.90E-08
2558669963	DRAFT_00631	pfam05299	Peptidase_M61			1.20E-38
2558669963	DRAFT_00631	Locus_type		CDS		
2558669963	DRAFT_00631	Product_name		Predicted protease with the C-terminal PDZ domain		
2558669963	DRAFT_00631	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669963	DRAFT_00631	Coordinates		3293..5077(-)		
2558669963	DRAFT_00631	DNA_length		1785bp		
2558669963	DRAFT_00631	Protein_length		594aa		
2558669963	DRAFT_00631	GC			0.57	
2558669964	DRAFT_00632	COG_category	[C] Energy production and conversion			
2558669964	DRAFT_00632	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)			4.00E-86
2558669964	DRAFT_00632	pfam00248	Aldo_ket_red			2.10E-72
2558669964	DRAFT_00632	Locus_type		CDS		
2558669964	DRAFT_00632	Product_name		Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)		
2558669964	DRAFT_00632	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669964	DRAFT_00632	Coordinates		5235..6218(-)		

2558669964	DRAFT_00632	DNA_length		984bp		
2558669964	DRAFT_00632	Protein_length		327aa		
2558669964	DRAFT_00632	GC			0.55	
2558669965	DRAFT_00633	COG_category	[R] General function prediction only			
2558669965	DRAFT_00633	COG1451	Predicted metal-dependent hydrolase			1.00E-19
2558669965	DRAFT_00633	pfam01863	DUF45			1.50E-38
2558669965	DRAFT_00633	Locus_type		CDS		
2558669965	DRAFT_00633	Product_name		Predicted metal-dependent hydrolase		
2558669965	DRAFT_00633	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669965	DRAFT_00633	Coordinates		6582..7271(+)		
2558669965	DRAFT_00633	DNA_length		690bp		
2558669965	DRAFT_00633	Protein_length		229aa		
2558669965	DRAFT_00633	GC			0.56	
2558669966	DRAFT_00634	COG_category	[S] Function unknown			
2558669966	DRAFT_00634	COG3832	Uncharacterized conserved protein			2.00E-11
2558669966	DRAFT_00634	pfam08327	AHSA1			1.40E-18
2558669966	DRAFT_00634	Locus_type		CDS		
2558669966	DRAFT_00634	Product_name		Uncharacterized conserved protein		
2558669966	DRAFT_00634	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669966	DRAFT_00634	Coordinates		7305..7841(-)		
2558669966	DRAFT_00634	DNA_length		537bp		
2558669966	DRAFT_00634	Protein_length		178aa		
2558669966	DRAFT_00634	GC			0.58	
2558669967	DRAFT_00635	Locus_type		CDS		
2558669967	DRAFT_00635	Product_name		hypothetical protein		
2558669967	DRAFT_00635	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669967	DRAFT_00635	Coordinates		7808..8032(-)		
2558669967	DRAFT_00635	DNA_length		225bp		
2558669967	DRAFT_00635	Protein_length		74aa		
2558669967	DRAFT_00635	GC			0.55	
2558669967	DRAFT_00635	Transmembrane		Yes		

2558669968	DRAFT_00636	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558669968	DRAFT_00636	COG1225	Peroxiredoxin			8.00E-09
2558669968	DRAFT_00636	pfam00578	AhpC-TSA			2.20E-20
2558669968	DRAFT_00636	Locus_type		CDS		
2558669968	DRAFT_00636	Product_name		Peroxiredoxin		
2558669968	DRAFT_00636	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669968	DRAFT_00636	Coordinates		8130..8657(+)		
2558669968	DRAFT_00636	DNA_length		528bp		
2558669968	DRAFT_00636	Protein_length		175aa		
2558669968	DRAFT_00636	GC			0.58	
2558669969	DRAFT_00637	Locus_type		CDS		
2558669969	DRAFT_00637	Product_name		hypothetical protein		
2558669969	DRAFT_00637	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669969	DRAFT_00637	Coordinates		8893..9069(+)		
2558669969	DRAFT_00637	DNA_length		177bp		
2558669969	DRAFT_00637	Protein_length		58aa		
2558669969	DRAFT_00637	GC			0.56	
2558669970	DRAFT_00638	COG_category	[R] General function prediction only			
2558669970	DRAFT_00638	COG0705	Uncharacterized membrane protein (homolog of Drosophila rhomboid			4.00E-03
2558669970	DRAFT_00638	pfam01694	Rhomboid			1.70E-16
2558669970	DRAFT_00638	Locus_type		CDS		
2558669970	DRAFT_00638	Product_name		Uncharacterized membrane protein (homolog of Drosophila rhomboi		
2558669970	DRAFT_00638	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669970	DRAFT_00638	Coordinates		9184..9741(+)		
2558669970	DRAFT_00638	DNA_length		558bp		
2558669970	DRAFT_00638	Protein_length		185aa		
2558669970	DRAFT_00638	GC			0.58	
2558669970	DRAFT_00638	Transmembrane		Yes		
2558669971	DRAFT_00639	Locus_type		CDS		
2558669971	DRAFT_00639	Product_name		hypothetical protein		

2558669971	DRAFT_00639	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669971	DRAFT_00639	Coordinates		9822..10133(+)		
2558669971	DRAFT_00639	DNA_length		312bp		
2558669971	DRAFT_00639	Protein_length		103aa		
2558669971	DRAFT_00639	GC			0.51	
2558669972	DRAFT_00640	Locus_type		CDS		
2558669972	DRAFT_00640	Product_name		hypothetical protein		
2558669972	DRAFT_00640	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669972	DRAFT_00640	Coordinates		10165..10530(-)		
2558669972	DRAFT_00640	DNA_length		366bp		
2558669972	DRAFT_00640	Protein_length		121aa		
2558669972	DRAFT_00640	GC			0.54	
2558669973	DRAFT_00641	Locus_type		CDS		
2558669973	DRAFT_00641	Product_name		hypothetical protein		
2558669973	DRAFT_00641	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669973	DRAFT_00641	Coordinates		10739..10936(-)		
2558669973	DRAFT_00641	DNA_length		198bp		
2558669973	DRAFT_00641	Protein_length		65aa		
2558669973	DRAFT_00641	GC			0.52	
2558669973	DRAFT_00641	Transmembrane		Yes		
2558669974	DRAFT_00642	COG_category	[C] Energy production and conversion			
2558669974	DRAFT_00642	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)			7.00E-79
2558669974	DRAFT_00642	pfam00248	Aldo_ket_red			5.00E-71
2558669974	DRAFT_00642	TIGR01293	voltage-dependent potassium channel beta subunit, animal			1.20E-117
2558669974	DRAFT_00642	Locus_type		CDS		
2558669974	DRAFT_00642	Product_name		voltage-dependent potassium channel beta subunit, animal		
2558669974	DRAFT_00642	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669974	DRAFT_00642	Coordinates		11014..11994(+)		
2558669974	DRAFT_00642	DNA_length		981bp		
2558669974	DRAFT_00642	Protein_length		326aa		
2558669974	DRAFT_00642	GC			0.59	

2558669975	DRAFT_00643	COG_category	[C] Energy production and conversion		
2558669975	DRAFT_00643	COG0778	Nitroreductase		4.00E-13
2558669975	DRAFT_00643	pfam00881	Nitroreductase		6.20E-19
2558669975	DRAFT_00643	Locus_type		CDS	
2558669975	DRAFT_00643	Product_name		Nitroreductase	
2558669975	DRAFT_00643	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669975	DRAFT_00643	Coordinates		12079..12597(+)	
2558669975	DRAFT_00643	DNA_length		519bp	
2558669975	DRAFT_00643	Protein_length		172aa	
2558669975	DRAFT_00643	GC		0.57	
2558669976	DRAFT_00644	pfam02195	ParBc		7.10E-21
2558669976	DRAFT_00644	TIGR00180	ParB/RepB/Spo0J family partition protein		2.40E-33
2558669976	DRAFT_00644	KO:K03497	chromosome partitioning protein, ParB family		1.30E-22
2558669976	DRAFT_00644	Locus_type		CDS	
2558669976	DRAFT_00644	Product_name		ParB/RepB/Spo0J family partition protein	
2558669976	DRAFT_00644	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669976	DRAFT_00644	Coordinates		12635..13537(-)	
2558669976	DRAFT_00644	DNA_length		903bp	
2558669976	DRAFT_00644	Protein_length		300aa	
2558669976	DRAFT_00644	GC		0.6	
2558669977	DRAFT_00645	KEGG_module	M00023: Tryptophan biosynthesis, chorismate => tryptophan		
2558669977	DRAFT_00645	COG_category	[R] General function prediction only		
2558669977	DRAFT_00645	COG1350	Predicted alternative tryptophan synthase beta-subunit (paralog of Trp		0.00E+00
2558669977	DRAFT_00645	pfam00291	PALP		2.40E-36
2558669977	DRAFT_00645	EC:4.2.1.20	Tryptophan synthase.		
2558669977	DRAFT_00645	TIGR01415	pyridoxal-phosphate dependent TrpB-like enzyme		0.00E+00
2558669977	DRAFT_00645	KO:K06001	tryptophan synthase beta chain [EC:4.2.1.20]		0.00E+00
2558669977	DRAFT_00645	Locus_type		CDS	
2558669977	DRAFT_00645	Product_name		pyridoxal-phosphate dependent TrpB-like enzyme	
2558669977	DRAFT_00645	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669977	DRAFT_00645	Coordinates		13669..14970(-)	

2558669977	DRAFT_00645	DNA_length		1302bp		
2558669977	DRAFT_00645	Protein_length		433aa		
2558669977	DRAFT_00645	GC			0.6	
2558669978	DRAFT_00646	Locus_type		CDS		
2558669978	DRAFT_00646	Product_name		hypothetical protein		
2558669978	DRAFT_00646	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669978	DRAFT_00646	Coordinates		15139..15321(+)		
2558669978	DRAFT_00646	DNA_length		183bp		
2558669978	DRAFT_00646	Protein_length		60aa		
2558669978	DRAFT_00646	GC			0.54	
2558669979	DRAFT_00647	Locus_type		CDS		
2558669979	DRAFT_00647	Product_name		hypothetical protein		
2558669979	DRAFT_00647	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669979	DRAFT_00647	Coordinates		15348..15467(+)		
2558669979	DRAFT_00647	DNA_length		120bp		
2558669979	DRAFT_00647	Protein_length		39aa		
2558669979	DRAFT_00647	GC			0.64	
2558669979	DRAFT_00647	Transmembrane		Yes		
2558669980	DRAFT_00648	Locus_type		CDS		
2558669980	DRAFT_00648	Product_name		hypothetical protein		
2558669980	DRAFT_00648	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669980	DRAFT_00648	Coordinates		15672..15920(+)		
2558669980	DRAFT_00648	DNA_length		249bp		
2558669980	DRAFT_00648	Protein_length		82aa		
2558669980	DRAFT_00648	GC			0.53	
2558669980	DRAFT_00648	Transmembrane		Yes		
2558669981	DRAFT_00649	COG_category	[L] Replication, recombination and repair			
2558669981	DRAFT_00649	COG3316	Transposase and inactivated derivatives			5.00E-12
2558669981	DRAFT_00649	pfam13610	DDE_Tnp_IS240			3.40E-22
2558669981	DRAFT_00649	Locus_type		CDS		

2558669981	DRAFT_00649	Product_name		Transposase and inactivated derivatives	
2558669981	DRAFT_00649	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669981	DRAFT_00649	Coordinates		15904..17046(-)	
2558669981	DRAFT_00649	DNA_length		1143bp	
2558669981	DRAFT_00649	Protein_length		380aa	
2558669981	DRAFT_00649	GC			0.54
2558669982	DRAFT_00650	Locus_type		CDS	
2558669982	DRAFT_00650	Product_name		hypothetical protein	
2558669982	DRAFT_00650	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669982	DRAFT_00650	Coordinates		17182..17430(+)	
2558669982	DRAFT_00650	DNA_length		249bp	
2558669982	DRAFT_00650	Protein_length		82aa	
2558669982	DRAFT_00650	GC			0.54
2558669983	DRAFT_00651	Locus_type		CDS	
2558669983	DRAFT_00651	Product_name		hypothetical protein	
2558669983	DRAFT_00651	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669983	DRAFT_00651	Coordinates		17427..17774(+)	
2558669983	DRAFT_00651	DNA_length		348bp	
2558669983	DRAFT_00651	Protein_length		115aa	
2558669983	DRAFT_00651	GC			0.51
2558669984	DRAFT_00652	Locus_type		CDS	
2558669984	DRAFT_00652	Product_name		hypothetical protein	
2558669984	DRAFT_00652	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669984	DRAFT_00652	Coordinates		17764..18162(+)	
2558669984	DRAFT_00652	DNA_length		399bp	
2558669984	DRAFT_00652	Protein_length		132aa	
2558669984	DRAFT_00652	GC			0.5
2558669985	DRAFT_00653	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558669985	DRAFT_00653	COG0229	Conserved domain frequently associated with peptide methionine sulf		3.00E-48
2558669985	DRAFT_00653	pfam01641	SelR		5.50E-48

2558669985	DRAFT_00653	TIGR00357	methionine-R-sulfoxide reductase			2.80E-56
2558669985	DRAFT_00653	Locus_type		CDS		
2558669985	DRAFT_00653	Product_name		methionine-R-sulfoxide reductase		
2558669985	DRAFT_00653	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669985	DRAFT_00653	Coordinates		18152..18937(+)		
2558669985	DRAFT_00653	DNA_length		786bp		
2558669985	DRAFT_00653	Protein_length		261aa		
2558669985	DRAFT_00653	GC			0.54	
2558669986	DRAFT_00654	Locus_type		CDS		
2558669986	DRAFT_00654	Product_name		hypothetical protein		
2558669986	DRAFT_00654	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669986	DRAFT_00654	Coordinates		19243..19779(+)		
2558669986	DRAFT_00654	DNA_length		537bp		
2558669986	DRAFT_00654	Protein_length		178aa		
2558669986	DRAFT_00654	GC			0.56	
2558669987	DRAFT_00655	pfam00027	cNMP_binding			1.70E-19
2558669987	DRAFT_00655	Locus_type		CDS		
2558669987	DRAFT_00655	Product_name		Cyclic nucleotide-binding domain		
2558669987	DRAFT_00655	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669987	DRAFT_00655	Coordinates		20123..20548(+)		
2558669987	DRAFT_00655	DNA_length		426bp		
2558669987	DRAFT_00655	Protein_length		141aa		
2558669987	DRAFT_00655	GC			0.57	
2558669988	DRAFT_00656	COG_category	[G] Carbohydrate transport and metabolism			
2558669988	DRAFT_00656	COG1082	Sugar phosphate isomerases/epimerases			2.00E-21
2558669988	DRAFT_00656	pfam01261	AP_endonuc_2			5.00E-25
2558669988	DRAFT_00656	Locus_type		CDS		
2558669988	DRAFT_00656	Product_name		Sugar phosphate isomerases/epimerases		
2558669988	DRAFT_00656	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669988	DRAFT_00656	Coordinates		20599..21408(+)		
2558669988	DRAFT_00656	DNA_length		810bp		

2558669988	DRAFT_00656	Protein_length		269aa		
2558669988	DRAFT_00656	GC			0.59	
2558669989	DRAFT_00657	Locus_type		CDS		
2558669989	DRAFT_00657	Product_name		hypothetical protein		
2558669989	DRAFT_00657	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669989	DRAFT_00657	Coordinates		21620..21892(+)		
2558669989	DRAFT_00657	DNA_length		273bp		
2558669989	DRAFT_00657	Protein_length		90aa		
2558669989	DRAFT_00657	GC			0.58	
2558669990	DRAFT_00658	pfam00571	CBS			2.10E-13
2558669990	DRAFT_00658	pfam00571	CBS			6.10E-09
2558669990	DRAFT_00658	Locus_type		CDS		
2558669990	DRAFT_00658	Product_name		Predicted signal-transduction protein containing cAMP-binding and Cl		
2558669990	DRAFT_00658	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669990	DRAFT_00658	Coordinates		21975..22487(+)		
2558669990	DRAFT_00658	DNA_length		513bp		
2558669990	DRAFT_00658	Protein_length		170aa		
2558669990	DRAFT_00658	GC			0.57	
2558669991	DRAFT_00659	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP			
2558669991	DRAFT_00659	Metacyc	PWY-5686: UMP biosynthesis			
2558669991	DRAFT_00659	IMG_pathway	321: Uridine 5'-monophosphate biosynthesis			
2558669991	DRAFT_00659	COG_category	[F] Nucleotide transport and metabolism			
2558669991	DRAFT_00659	COG0284	Orotidine-5'-phosphate decarboxylase			1.00E-25
2558669991	DRAFT_00659	pfam00215	OMPdecase			5.30E-25
2558669991	DRAFT_00659	EC:4.1.1.23	Orotidine-5'-phosphate decarboxylase.			
2558669991	DRAFT_00659	TIGR01740	orotidine 5'-phosphate decarboxylase, subfamily 1			5.20E-29
2558669991	DRAFT_00659	KO:K01591	orotidine-5'-phosphate decarboxylase [EC:4.1.1.23]			7.00E-45
2558669991	DRAFT_00659	ITERM:01394	orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)			
2558669991	DRAFT_00659	Locus_type		CDS		
2558669991	DRAFT_00659	Product_name		orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)		
2558669991	DRAFT_00659	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		

2558669991	DRAFT_00659	Coordinates		23246..23974(-)	
2558669991	DRAFT_00659	DNA_length		729bp	
2558669991	DRAFT_00659	Protein_length		242aa	
2558669991	DRAFT_00659	GC		0.58	
2558669992	DRAFT_00660	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP		
2558669992	DRAFT_00660	COG_category	[F] Nucleotide transport and metabolism		
2558669992	DRAFT_00660	COG0167	Dihydroorotate dehydrogenase		2.00E-71
2558669992	DRAFT_00660	pfam01180	DHO_dh		3.40E-57
2558669992	DRAFT_00660	EC:1.3.98.1	Dihydroorotate oxidase (fumarate).		
2558669992	DRAFT_00660	TIGR01037	dihydroorotate dehydrogenase (subfamily 1) family protein		8.90E-106
2558669992	DRAFT_00660	KO:K00226	dihydroorotate dehydrogenase (fumarate) [EC:1.3.98.1]		0.00E+00
2558669992	DRAFT_00660	Locus_type		CDS	
2558669992	DRAFT_00660	Product_name		dihydroorotate oxidase B, catalytic subunit (EC 1.3.3.1)	
2558669992	DRAFT_00660	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669992	DRAFT_00660	Coordinates		23971..24894(-)	
2558669992	DRAFT_00660	DNA_length		924bp	
2558669992	DRAFT_00660	Protein_length		307aa	
2558669992	DRAFT_00660	GC		0.59	
2558669993	DRAFT_00661	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP		
2558669993	DRAFT_00661	Metacyc	PWY-5686: UMP biosynthesis		
2558669993	DRAFT_00661	IMG_pathway	321: Uridine 5'-monophosphate biosynthesis		
2558669993	DRAFT_00661	COG_category	[F] Nucleotide transport and metabolism		
2558669993	DRAFT_00661	COG0461	Orotate phosphoribosyltransferase		3.00E-43
2558669993	DRAFT_00661	pfam00156	Pribosyltran		2.00E-14
2558669993	DRAFT_00661	EC:2.4.2.10	Orotate phosphoribosyltransferase.		
2558669993	DRAFT_00661	TIGR00336	orotate phosphoribosyltransferase		1.80E-44
2558669993	DRAFT_00661	KO:K00762	orotate phosphoribosyltransferase [EC:2.4.2.10]		8.30E-44
2558669993	DRAFT_00661	ITERM:01392	orotate phosphoribosyltransferase (EC 2.4.2.10)		
2558669993	DRAFT_00661	Locus_type		CDS	
2558669993	DRAFT_00661	Product_name		orotate phosphoribosyltransferase (EC 2.4.2.10)	
2558669993	DRAFT_00661	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669993	DRAFT_00661	Coordinates		24918..25544(-)	

2558669993	DRAFT_00661	DNA_length		627bp	
2558669993	DRAFT_00661	Protein_length		208aa	
2558669993	DRAFT_00661	GC			0.57
2558669994	DRAFT_00662	Locus_type		CDS	
2558669994	DRAFT_00662	Product_name		hypothetical protein	
2558669994	DRAFT_00662	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669994	DRAFT_00662	Coordinates		25570..26289(-)	
2558669994	DRAFT_00662	DNA_length		720bp	
2558669994	DRAFT_00662	Protein_length		239aa	
2558669994	DRAFT_00662	GC			0.55
2558669995	DRAFT_00663	COG_category	[R] General function prediction only		
2558669995	DRAFT_00663	COG1926	Predicted phosphoribosyltransferases		8.00E-53
2558669995	DRAFT_00663	pfam00156	Pribosyltran		1.30E-27
2558669995	DRAFT_00663	Locus_type		CDS	
2558669995	DRAFT_00663	Product_name		Predicted phosphoribosyltransferases	
2558669995	DRAFT_00663	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669995	DRAFT_00663	Coordinates		26334..26987(-)	
2558669995	DRAFT_00663	DNA_length		654bp	
2558669995	DRAFT_00663	Protein_length		217aa	
2558669995	DRAFT_00663	GC			0.59
2558669996	DRAFT_00664	Locus_type		CDS	
2558669996	DRAFT_00664	Product_name		hypothetical protein	
2558669996	DRAFT_00664	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558669996	DRAFT_00664	Coordinates		27361..27489(-)	
2558669996	DRAFT_00664	DNA_length		129bp	
2558669996	DRAFT_00664	Protein_length		42aa	
2558669996	DRAFT_00664	GC			0.5
2558669997	DRAFT_00665	Locus_type		CDS	
2558669997	DRAFT_00665	Product_name		hypothetical protein	
2558669997	DRAFT_00665	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	

2558669997	DRAFT_00665	Coordinates		28022..28324(-)		
2558669997	DRAFT_00665	DNA_length		303bp		
2558669997	DRAFT_00665	Protein_length		100aa		
2558669997	DRAFT_00665	GC			0.56	
2558669997	DRAFT_00665	Transmembrane		Yes		
2558669998	DRAFT_00666	Locus_type		CDS		
2558669998	DRAFT_00666	Product_name		hypothetical protein		
2558669998	DRAFT_00666	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669998	DRAFT_00666	Coordinates		28475..28717(+)		
2558669998	DRAFT_00666	DNA_length		243bp		
2558669998	DRAFT_00666	Protein_length		80aa		
2558669998	DRAFT_00666	GC			0.56	
2558669998	DRAFT_00666	Transmembrane		Yes		
2558669999	DRAFT_00667	pfam00571	CBS			3.20E-13
2558669999	DRAFT_00667	pfam00571	CBS			1.90E-14
2558669999	DRAFT_00667	Locus_type		CDS		
2558669999	DRAFT_00667	Product_name		Predicted signal-transduction protein containing cAMP-binding and C		
2558669999	DRAFT_00667	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558669999	DRAFT_00667	Coordinates		28896..29414(-)		
2558669999	DRAFT_00667	DNA_length		519bp		
2558669999	DRAFT_00667	Protein_length		172aa		
2558669999	DRAFT_00667	GC			0.56	
2558670000	DRAFT_00668	Locus_type		CDS		
2558670000	DRAFT_00668	Product_name		hypothetical protein		
2558670000	DRAFT_00668	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670000	DRAFT_00668	Coordinates		29550..30332(+)		
2558670000	DRAFT_00668	DNA_length		783bp		
2558670000	DRAFT_00668	Protein_length		260aa		
2558670000	DRAFT_00668	GC			0.51	
2558670001	DRAFT_00669	pfam00254	FKBP_C			5.50E-23

2558670001	DRAFT_00669	Locus_type		CDS		
2558670001	DRAFT_00669	Product_name		FKBP-type peptidyl-prolyl cis-trans isomerases 2		
2558670001	DRAFT_00669	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670001	DRAFT_00669	Coordinates		30841..31257(+)		
2558670001	DRAFT_00669	DNA_length		417bp		
2558670001	DRAFT_00669	Protein_length		138aa		
2558670001	DRAFT_00669	GC			0.59	

2558670002	DRAFT_00670	Locus_type		CDS		
2558670002	DRAFT_00670	Product_name		hypothetical protein		
2558670002	DRAFT_00670	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670002	DRAFT_00670	Coordinates		31358..31639(+)		
2558670002	DRAFT_00670	DNA_length		282bp		
2558670002	DRAFT_00670	Protein_length		93aa		
2558670002	DRAFT_00670	GC			0.56	

2558670003	DRAFT_00671	pfam01780	Ribosomal_L37ae			7.60E-05
2558670003	DRAFT_00671	Locus_type		CDS		
2558670003	DRAFT_00671	Product_name		Ribosomal L37ae protein family		
2558670003	DRAFT_00671	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670003	DRAFT_00671	Coordinates		31682..31873(+)		
2558670003	DRAFT_00671	DNA_length		192bp		
2558670003	DRAFT_00671	Protein_length		63aa		
2558670003	DRAFT_00671	GC			0.6	

2558670004	DRAFT_00672	Locus_type		CDS		
2558670004	DRAFT_00672	Product_name		hypothetical protein		
2558670004	DRAFT_00672	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670004	DRAFT_00672	Coordinates		31987..32208(-)		
2558670004	DRAFT_00672	DNA_length		222bp		
2558670004	DRAFT_00672	Protein_length		73aa		
2558670004	DRAFT_00672	GC			0.58	

2558670005	DRAFT_00673	COG_category	[S] Function unknown			

2558670005	DRAFT_00673	COG4260	Putative virion core protein (lumpy skin disease virus)		5.00E-38
2558670005	DRAFT_00673	pfam12773	DZR		3.30E-10
2558670005	DRAFT_00673	pfam13421	Band_7_1		2.70E-37
2558670005	DRAFT_00673	Locus_type		CDS	
2558670005	DRAFT_00673	Product_name		Putative virion core protein (lumpy skin disease virus)	
2558670005	DRAFT_00673	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558670005	DRAFT_00673	Coordinates		32412..33485(-)	
2558670005	DRAFT_00673	DNA_length		1074bp	
2558670005	DRAFT_00673	Protein_length		357aa	
2558670005	DRAFT_00673	GC		0.56	
2558670006	DRAFT_00674	Locus_type		CDS	
2558670006	DRAFT_00674	Product_name		hypothetical protein	
2558670006	DRAFT_00674	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558670006	DRAFT_00674	Coordinates		33497..34042(-)	
2558670006	DRAFT_00674	DNA_length		546bp	
2558670006	DRAFT_00674	Protein_length		181aa	
2558670006	DRAFT_00674	GC		0.57	
2558670007	DRAFT_00675	pfam01904	DUF72		4.20E-22
2558670007	DRAFT_00675	Locus_type		CDS	
2558670007	DRAFT_00675	Product_name		Uncharacterized conserved protein	
2558670007	DRAFT_00675	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558670007	DRAFT_00675	Coordinates		34122..34418(+)	
2558670007	DRAFT_00675	DNA_length		297bp	
2558670007	DRAFT_00675	Protein_length		98aa	
2558670007	DRAFT_00675	GC		0.53	
2558670008	DRAFT_00676	pfam11799	IMS_C		6.60E-20
2558670008	DRAFT_00676	Locus_type		CDS	
2558670008	DRAFT_00676	Product_name		Nucleotidyltransferase/DNA polymerase involved in DNA repair	
2558670008	DRAFT_00676	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558670008	DRAFT_00676	Coordinates		34532..35218(+)	
2558670008	DRAFT_00676	DNA_length		687bp	

2558670008	DRAFT_00676	Protein_length		228aa		
2558670008	DRAFT_00676	GC			0.61	
2558670009	DRAFT_00677	COG_category	[G] Carbohydrate transport and metabolism			
2558670009	DRAFT_00677	COG2814	Arabinose efflux permease			3.00E-08
2558670009	DRAFT_00677	pfam07690	MFS_1			8.30E-27
2558670009	DRAFT_00677	Locus_type		CDS		
2558670009	DRAFT_00677	Product_name		Arabinose efflux permease		
2558670009	DRAFT_00677	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670009	DRAFT_00677	Coordinates		35167..36426(-)		
2558670009	DRAFT_00677	DNA_length		1260bp		
2558670009	DRAFT_00677	Protein_length		419aa		
2558670009	DRAFT_00677	GC			0.59	
2558670009	DRAFT_00677	Transmembrane		Yes		
2558670010	DRAFT_00678	Metacyc	PWY-4722: creatinine degradation II			
2558670010	DRAFT_00678	COG_category	[E] Amino acid transport and metabolism			
2558670010	DRAFT_00678	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2558670010	DRAFT_00678	COG0145	N-methylhydantoinase A/acetone carboxylase, beta subunit			0.00E+00
2558670010	DRAFT_00678	pfam05378	Hydant_A_N			2.80E-45
2558670010	DRAFT_00678	pfam01968	Hydantoinase_A			5.00E-86
2558670010	DRAFT_00678	EC:3.5.2.14	N-methylhydantoinase (ATP-hydrolyzing).			
2558670010	DRAFT_00678	KO:K01473	N-methylhydantoinase A [EC:3.5.2.14]			0.00E+00
2558670010	DRAFT_00678	Locus_type		CDS		
2558670010	DRAFT_00678	Product_name		N-methylhydantoinase A/acetone carboxylase, beta subunit		
2558670010	DRAFT_00678	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670010	DRAFT_00678	Coordinates		36513..38594(+)		
2558670010	DRAFT_00678	DNA_length		2082bp		
2558670010	DRAFT_00678	Protein_length		693aa		
2558670010	DRAFT_00678	GC			0.63	
2558670011	DRAFT_00679	Metacyc	PWY-4722: creatinine degradation II			
2558670011	DRAFT_00679	COG_category	[E] Amino acid transport and metabolism			
2558670011	DRAFT_00679	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			

2558670011	DRAFT_00679	COG0146	N-methylhydantoinase B/acetone carboxylase, alpha subunit			0.00E+00
2558670011	DRAFT_00679	pfam02538	Hydantoinase_B			0.00E+00
2558670011	DRAFT_00679	EC:3.5.2.14	N-methylhydantoinase (ATP-hydrolyzing).			
2558670011	DRAFT_00679	KO:K01474	N-methylhydantoinase B [EC:3.5.2.14]			0.00E+00
2558670011	DRAFT_00679	Locus_type		CDS		
2558670011	DRAFT_00679	Product_name		N-methylhydantoinase B/acetone carboxylase, alpha subunit		
2558670011	DRAFT_00679	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670011	DRAFT_00679	Coordinates		38591..40279(+)		
2558670011	DRAFT_00679	DNA_length		1689bp		
2558670011	DRAFT_00679	Protein_length		562aa		
2558670011	DRAFT_00679	GC			0.62	

2558670012	DRAFT_00680	Locus_type		CDS		
2558670012	DRAFT_00680	Product_name		hypothetical protein		
2558670012	DRAFT_00680	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670012	DRAFT_00680	Coordinates		40314..40496(-)		
2558670012	DRAFT_00680	DNA_length		183bp		
2558670012	DRAFT_00680	Protein_length		60aa		
2558670012	DRAFT_00680	GC			0.52	
2558670012	DRAFT_00680	Transmembrane		Yes		

2558670013	DRAFT_00681	Locus_type		CDS		
2558670013	DRAFT_00681	Product_name		hypothetical protein		
2558670013	DRAFT_00681	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9		
2558670013	DRAFT_00681	Coordinates		40671..40847(-)		
2558670013	DRAFT_00681	DNA_length		177bp		
2558670013	DRAFT_00681	Protein_length		58aa		
2558670013	DRAFT_00681	GC			0.53	

2558670014	DRAFT_00682	COG_category	[S] Function unknown			
2558670014	DRAFT_00682	COG0062	Uncharacterized conserved protein			3.00E-39
2558670014	DRAFT_00682	pfam03853	YjeF_N			8.10E-40
2558670014	DRAFT_00682	TIGR00197	yjeF N-terminal region			8.50E-45
2558670014	DRAFT_00682	Locus_type		CDS		

2558670014	DRAFT_00682	Product_name		yjeF N-terminal region	
2558670014	DRAFT_00682	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558670014	DRAFT_00682	Coordinates		40941..41651(-)	
2558670014	DRAFT_00682	DNA_length		711bp	
2558670014	DRAFT_00682	Protein_length		236aa	
2558670014	DRAFT_00682	GC		0.58	
2558670015	DRAFT_00683	Locus_type		CDS	
2558670015	DRAFT_00683	Product_name		hypothetical protein	
2558670015	DRAFT_00683	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558670015	DRAFT_00683	Coordinates		41931..45953(+)	
2558670015	DRAFT_00683	DNA_length		4023bp	
2558670015	DRAFT_00683	Protein_length		1340aa	
2558670015	DRAFT_00683	GC		0.58	
2558670015	DRAFT_00683	Transmembrane		Yes	
2558670016	DRAFT_00684	COG_category	[N] Cell motility		
2558670016	DRAFT_00684	COG5491	Conserved protein implicated in secretion		1.00E-14
2558670016	DRAFT_00684	Locus_type		CDS	
2558670016	DRAFT_00684	Product_name		Conserved protein implicated in secretion	
2558670016	DRAFT_00684	Scaffold		DRAFT_contig_70_57_len_46680_read_count_840764.9	
2558670016	DRAFT_00684	Coordinates		46059..46679(+)	
2558670016	DRAFT_00684	DNA_length		621bp	
2558670016	DRAFT_00684	Protein_length		207aa	
2558670016	DRAFT_00684	GC		0.58	
2558670017	DRAFT_00685	pfam07726	AAA_3		5.00E-62
2558670017	DRAFT_00685	Locus_type		CDS	
2558670017	DRAFT_00685	Product_name		ATPase family associated with various cellular activities (AAA)	
2558670017	DRAFT_00685	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670017	DRAFT_00685	Coordinates		2..625(-)	
2558670017	DRAFT_00685	DNA_length		624bp	
2558670017	DRAFT_00685	Protein_length		208aa	
2558670017	DRAFT_00685	GC		0.59	

2558670018	DRAFT_00686	Locus_type		CDS	
2558670018	DRAFT_00686	Product_name		hypothetical protein	
2558670018	DRAFT_00686	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670018	DRAFT_00686	Coordinates		710..1156(-)	
2558670018	DRAFT_00686	DNA_length		447bp	
2558670018	DRAFT_00686	Protein_length		148aa	
2558670018	DRAFT_00686	GC		0.62	
2558670018	DRAFT_00686	Transmembrane		Yes	
2558670019	DRAFT_00687	pfam13559	DUF4129		7.30E-06
2558670019	DRAFT_00687	Locus_type		CDS	
2558670019	DRAFT_00687	Product_name		Domain of unknown function (DUF4129)	
2558670019	DRAFT_00687	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670019	DRAFT_00687	Coordinates		1143..1862(-)	
2558670019	DRAFT_00687	DNA_length		720bp	
2558670019	DRAFT_00687	Protein_length		239aa	
2558670019	DRAFT_00687	GC		0.58	
2558670019	DRAFT_00687	Transmembrane		Yes	
2558670020	DRAFT_00688	Metacyc	PWY-6549: glutamine biosynthesis III		
2558670020	DRAFT_00688	Metacyc	PWY-5675: nitrate reduction V (assimilatory)		
2558670020	DRAFT_00688	Metacyc	GLNSYN-PWY: glutamine biosynthesis I		
2558670020	DRAFT_00688	Metacyc	PWY-6963: ammonia assimilation cycle I		
2558670020	DRAFT_00688	Metacyc	PWY490-3: nitrate reduction VI (assimilatory)		
2558670020	DRAFT_00688	Metacyc	PWY-6964: ammonia assimilation cycle II		
2558670020	DRAFT_00688	Metacyc	PWY-381: nitrate reduction II (assimilatory)		
2558670020	DRAFT_00688	COG_category	[E] Amino acid transport and metabolism		
2558670020	DRAFT_00688	COG0174	Glutamine synthetase		9.00E-120
2558670020	DRAFT_00688	pfam00120	Gln-synt_C		6.10E-83
2558670020	DRAFT_00688	pfam03951	Gln-synt_N		1.10E-25
2558670020	DRAFT_00688	EC:6.3.1.2	Glutamate--ammonia ligase.		
2558670020	DRAFT_00688	TIGR00653	glutamine synthetase, type I		0.00E+00
2558670020	DRAFT_00688	KO:K01915	glutamine synthetase [EC:6.3.1.2]		0.00E+00

2558670020	DRAFT_00688	Locus_type	CDS
2558670020	DRAFT_00688	Product_name	glutamine synthetase, type I
2558670020	DRAFT_00688	Scaffold	DRAFT_contig_70_60_len_46101_read_count_777516.10
2558670020	DRAFT_00688	Coordinates	2174..3646(-)
2558670020	DRAFT_00688	DNA_length	1473bp
2558670020	DRAFT_00688	Protein_length	490aa
2558670020	DRAFT_00688	GC	0.59

2558670021	DRAFT_00689	Locus_type	CDS
2558670021	DRAFT_00689	Product_name	hypothetical protein
2558670021	DRAFT_00689	Scaffold	DRAFT_contig_70_60_len_46101_read_count_777516.10
2558670021	DRAFT_00689	Coordinates	3832..4344(+)
2558670021	DRAFT_00689	DNA_length	513bp
2558670021	DRAFT_00689	Protein_length	170aa
2558670021	DRAFT_00689	GC	0.6

2558670022	DRAFT_00690	Locus_type	CDS
2558670022	DRAFT_00690	Product_name	hypothetical protein
2558670022	DRAFT_00690	Scaffold	DRAFT_contig_70_60_len_46101_read_count_777516.10
2558670022	DRAFT_00690	Coordinates	4385..4909(+)
2558670022	DRAFT_00690	DNA_length	525bp
2558670022	DRAFT_00690	Protein_length	174aa
2558670022	DRAFT_00690	GC	0.58

2558670023	DRAFT_00691	Locus_type	CDS
2558670023	DRAFT_00691	Product_name	hypothetical protein
2558670023	DRAFT_00691	Scaffold	DRAFT_contig_70_60_len_46101_read_count_777516.10
2558670023	DRAFT_00691	Coordinates	4973..6058(-)
2558670023	DRAFT_00691	DNA_length	1086bp
2558670023	DRAFT_00691	Protein_length	361aa
2558670023	DRAFT_00691	GC	0.55
2558670023	DRAFT_00691	Transmembrane	Yes

2558670024	DRAFT_00692	Locus_type	CDS

2558670024	DRAFT_00692	Product_name		hypothetical protein	
2558670024	DRAFT_00692	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670024	DRAFT_00692	Coordinates		6216..6644(-)	
2558670024	DRAFT_00692	DNA_length		429bp	
2558670024	DRAFT_00692	Protein_length		142aa	
2558670024	DRAFT_00692	GC		0.61	
2558670025	DRAFT_00693	Locus_type		CDS	
2558670025	DRAFT_00693	Product_name		hypothetical protein	
2558670025	DRAFT_00693	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670025	DRAFT_00693	Coordinates		6844..7839(+)	
2558670025	DRAFT_00693	DNA_length		996bp	
2558670025	DRAFT_00693	Protein_length		331aa	
2558670025	DRAFT_00693	GC		0.6	
2558670026	DRAFT_00694	COG_category	[R] General function prediction only		
2558670026	DRAFT_00694	COG0433	Predicted ATPase		1.00E-09
2558670026	DRAFT_00694	pfam01935	DUF87		3.90E-07
2558670026	DRAFT_00694	pfam12846	AAA_10		6.50E-07
2558670026	DRAFT_00694	Locus_type		CDS	
2558670026	DRAFT_00694	Product_name		Predicted ATPase	
2558670026	DRAFT_00694	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670026	DRAFT_00694	Coordinates		7948..9303(+)	
2558670026	DRAFT_00694	DNA_length		1356bp	
2558670026	DRAFT_00694	Protein_length		451aa	
2558670026	DRAFT_00694	GC		0.61	
2558670027	DRAFT_00695	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670027	DRAFT_00695	COG1247	Sortase and related acyltransferases		2.00E-06
2558670027	DRAFT_00695	pfam00583	Acetyltransf_1		3.20E-14
2558670027	DRAFT_00695	Locus_type		CDS	
2558670027	DRAFT_00695	Product_name		Sortase and related acyltransferases	
2558670027	DRAFT_00695	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670027	DRAFT_00695	Coordinates		9405..9884(-)	

2558670027	DRAFT_00695	DNA_length		480bp		
2558670027	DRAFT_00695	Protein_length		159aa		
2558670027	DRAFT_00695	GC			0.53	
2558670028	DRAFT_00696	pfam04909	Amidohydro_2			1.40E-16
2558670028	DRAFT_00696	Locus_type		CDS		
2558670028	DRAFT_00696	Product_name		Predicted metal-dependent hydrolase of the TIM-barrel fold		
2558670028	DRAFT_00696	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670028	DRAFT_00696	Coordinates		9902..10189(-)		
2558670028	DRAFT_00696	DNA_length		288bp		
2558670028	DRAFT_00696	Protein_length		95aa		
2558670028	DRAFT_00696	GC			0.5	
2558670029	DRAFT_00697	COG_category	[R] General function prediction only			
2558670029	DRAFT_00697	COG2159	Predicted metal-dependent hydrolase of the TIM-barrel fold			2.00E-32
2558670029	DRAFT_00697	pfam04909	Amidohydro_2			2.10E-36
2558670029	DRAFT_00697	Locus_type		CDS		
2558670029	DRAFT_00697	Product_name		Predicted metal-dependent hydrolase of the TIM-barrel fold		
2558670029	DRAFT_00697	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670029	DRAFT_00697	Coordinates		10784..11644(+)		
2558670029	DRAFT_00697	DNA_length		861bp		
2558670029	DRAFT_00697	Protein_length		286aa		
2558670029	DRAFT_00697	GC			0.5	
2558670030	DRAFT_00698	Locus_type		CDS		
2558670030	DRAFT_00698	Product_name		hypothetical protein		
2558670030	DRAFT_00698	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670030	DRAFT_00698	Coordinates		11662..11820(-)		
2558670030	DRAFT_00698	DNA_length		159bp		
2558670030	DRAFT_00698	Protein_length		52aa		
2558670030	DRAFT_00698	GC			0.5	
2558670031	DRAFT_00699	Locus_type		CDS		
2558670031	DRAFT_00699	Product_name		hypothetical protein		

2558670031	DRAFT_00699	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670031	DRAFT_00699	Coordinates		12023..12298(+)		
2558670031	DRAFT_00699	DNA_length		276bp		
2558670031	DRAFT_00699	Protein_length		91aa		
2558670031	DRAFT_00699	GC			0.51	
2558670032	DRAFT_00700	Locus_type		CDS		
2558670032	DRAFT_00700	Product_name		hypothetical protein		
2558670032	DRAFT_00700	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670032	DRAFT_00700	Coordinates		12386..12778(-)		
2558670032	DRAFT_00700	DNA_length		393bp		
2558670032	DRAFT_00700	Protein_length		130aa		
2558670032	DRAFT_00700	GC			0.53	
2558670033	DRAFT_00701	COG_category	[S] Function unknown			
2558670033	DRAFT_00701	COG1839	Uncharacterized conserved protein			9.00E-58
2558670033	DRAFT_00701	pfam04008	Adenosine_kin			5.80E-68
2558670033	DRAFT_00701	KO:K09129	hypothetical protein			0.00E+00
2558670033	DRAFT_00701	Locus_type		CDS		
2558670033	DRAFT_00701	Product_name		Uncharacterized conserved protein		
2558670033	DRAFT_00701	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670033	DRAFT_00701	Coordinates		12953..13435(+)		
2558670033	DRAFT_00701	DNA_length		483bp		
2558670033	DRAFT_00701	Protein_length		160aa		
2558670033	DRAFT_00701	GC			0.59	
2558670034	DRAFT_00702	Locus_type		CDS		
2558670034	DRAFT_00702	Product_name		hypothetical protein		
2558670034	DRAFT_00702	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670034	DRAFT_00702	Coordinates		13530..13772(-)		
2558670034	DRAFT_00702	DNA_length		243bp		
2558670034	DRAFT_00702	Protein_length		80aa		
2558670034	DRAFT_00702	GC			0.47	
2558670034	DRAFT_00702	Transmembrane		Yes		

2558670035	DRAFT_00703	COG_category	[L] Replication, recombination and repair		
2558670035	DRAFT_00703	COG3316	Transposase and inactivated derivatives		1.00E-12
2558670035	DRAFT_00703	pfam13610	DDE_Tnp_IS240		2.40E-21
2558670035	DRAFT_00703	Locus_type		CDS	
2558670035	DRAFT_00703	Product_name		Transposase and inactivated derivatives	
2558670035	DRAFT_00703	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670035	DRAFT_00703	Coordinates		13782..15014(-)	
2558670035	DRAFT_00703	DNA_length		1233bp	
2558670035	DRAFT_00703	Protein_length		410aa	
2558670035	DRAFT_00703	GC		0.55	
2558670036	DRAFT_00704	Locus_type		CDS	
2558670036	DRAFT_00704	Product_name		hypothetical protein	
2558670036	DRAFT_00704	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670036	DRAFT_00704	Coordinates		15033..15254(+)	
2558670036	DRAFT_00704	DNA_length		222bp	
2558670036	DRAFT_00704	Protein_length		73aa	
2558670036	DRAFT_00704	GC		0.49	
2558670037	DRAFT_00705	Locus_type		CDS	
2558670037	DRAFT_00705	Product_name		hypothetical protein	
2558670037	DRAFT_00705	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670037	DRAFT_00705	Coordinates		15251..15658(+)	
2558670037	DRAFT_00705	DNA_length		408bp	
2558670037	DRAFT_00705	Protein_length		135aa	
2558670037	DRAFT_00705	GC		0.57	
2558670038	DRAFT_00706	pfam05014	Nuc_deoxyrib_tr		1.90E-10
2558670038	DRAFT_00706	Locus_type		CDS	
2558670038	DRAFT_00706	Product_name		Nucleoside 2-deoxyribosyltransferase	
2558670038	DRAFT_00706	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670038	DRAFT_00706	Coordinates		16216..16608(+)	
2558670038	DRAFT_00706	DNA_length		393bp	

2558670038	DRAFT_00706	Protein_length		130aa		
2558670038	DRAFT_00706	GC			0.54	
2558670039	DRAFT_00707	KEGG_module	M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine			
2558670039	DRAFT_00707	Metacyc	DAPLYSINESYN-PWY: lysine biosynthesis I			
2558670039	DRAFT_00707	COG_category	[E] Amino acid transport and metabolism			
2558670039	DRAFT_00707	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase a			1.00E-55
2558670039	DRAFT_00707	pfam07687	M20_dimer			1.90E-18
2558670039	DRAFT_00707	pfam01546	Peptidase_M20			1.50E-23
2558670039	DRAFT_00707	EC:3.5.1.18	Succinyl-diaminopimelate desuccinylase.			
2558670039	DRAFT_00707	TIGR01910	acetylornithine deacetylase or succinyl-diaminopimelate desuccinylase			1.80E-83
2558670039	DRAFT_00707	KO:K01439	succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]			0.00E+00
2558670039	DRAFT_00707	Locus_type		CDS		
2558670039	DRAFT_00707	Product_name		acetylornithine deacetylase or succinyl-diaminopimelate desuccinylas		
2558670039	DRAFT_00707	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670039	DRAFT_00707	Coordinates		16863..18095(-)		
2558670039	DRAFT_00707	DNA_length		1233bp		
2558670039	DRAFT_00707	Protein_length		410aa		
2558670039	DRAFT_00707	GC			0.57	
2558670040	DRAFT_00708	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670040	DRAFT_00708	COG0251	Putative translation initiation inhibitor, yjgF family			3.00E-27
2558670040	DRAFT_00708	pfam01042	Ribonuc_L-PSP			1.30E-36
2558670040	DRAFT_00708	TIGR00004	reactive intermediate/imine deaminase			1.80E-46
2558670040	DRAFT_00708	KO:K07567	TdcF protein			1.60E-31
2558670040	DRAFT_00708	Locus_type		CDS		
2558670040	DRAFT_00708	Product_name		endoribonuclease L-PSP		
2558670040	DRAFT_00708	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670040	DRAFT_00708	Coordinates		18304..18675(+)		
2558670040	DRAFT_00708	DNA_length		372bp		
2558670040	DRAFT_00708	Protein_length		123aa		
2558670040	DRAFT_00708	GC			0.6	
2558670041	DRAFT_00709	COG_category	[T] Signal transduction mechanisms			

2558670041	DRAFT_00709	COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)		5.00E-24
2558670041	DRAFT_00709	pfam14947	HTH_45		5.20E-09
2558670041	DRAFT_00709	pfam00211	Guanylate_cyc		4.60E-20
2558670041	DRAFT_00709	Locus_type		CDS	
2558670041	DRAFT_00709	Product_name		Adenylate cyclase, family 3 (some proteins contain HAMP domain)	
2558670041	DRAFT_00709	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670041	DRAFT_00709	Coordinates		18925..19749(-)	
2558670041	DRAFT_00709	DNA_length		825bp	
2558670041	DRAFT_00709	Protein_length		274aa	
2558670041	DRAFT_00709	GC		0.56	
2558670042	DRAFT_00710	Locus_type		CDS	
2558670042	DRAFT_00710	Product_name		hypothetical protein	
2558670042	DRAFT_00710	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670042	DRAFT_00710	Coordinates		19781..20950(-)	
2558670042	DRAFT_00710	DNA_length		1170bp	
2558670042	DRAFT_00710	Protein_length		389aa	
2558670042	DRAFT_00710	GC		0.61	
2558670043	DRAFT_00711	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670043	DRAFT_00711	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins		8.00E-20
2558670043	DRAFT_00711	pfam13302	Acetyltransf_3		4.40E-23
2558670043	DRAFT_00711	Locus_type		CDS	
2558670043	DRAFT_00711	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins	
2558670043	DRAFT_00711	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670043	DRAFT_00711	Coordinates		21121..21699(-)	
2558670043	DRAFT_00711	DNA_length		579bp	
2558670043	DRAFT_00711	Protein_length		192aa	
2558670043	DRAFT_00711	GC		0.51	
2558670044	DRAFT_00712	Locus_type		CDS	
2558670044	DRAFT_00712	Product_name		hypothetical protein	
2558670044	DRAFT_00712	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670044	DRAFT_00712	Coordinates		21784..21987(-)	

2558670044	DRAFT_00712	DNA_length		204bp		
2558670044	DRAFT_00712	Protein_length		67aa		
2558670044	DRAFT_00712	GC			0.53	
2558670045	DRAFT_00713	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2558670045	DRAFT_00713	COG0489	ATPases involved in chromosome partitioning			7.00E-57
2558670045	DRAFT_00713	pfam01883	DUF59			4.80E-23
2558670045	DRAFT_00713	pfam13614	AAA_31			2.40E-09
2558670045	DRAFT_00713	pfam10609	ParA			1.20E-34
2558670045	DRAFT_00713	KO:K03593	ATP-binding protein involved in chromosome partitioning			0.00E+00
2558670045	DRAFT_00713	Locus_type		CDS		
2558670045	DRAFT_00713	Product_name		ATPases involved in chromosome partitioning		
2558670045	DRAFT_00713	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670045	DRAFT_00713	Coordinates		21984..23039(-)		
2558670045	DRAFT_00713	DNA_length		1056bp		
2558670045	DRAFT_00713	Protein_length		351aa		
2558670045	DRAFT_00713	GC			0.61	
2558670046	DRAFT_00714	KEGG_module	M00378: F420 biosynthesis			
2558670046	DRAFT_00714	Metacyc	PWY-5199: factor 420 polyglutamylation			
2558670046	DRAFT_00714	COG_category	[S] Function unknown			
2558670046	DRAFT_00714	COG1478	Uncharacterized conserved protein			2.00E-63
2558670046	DRAFT_00714	pfam01996	F420_ligase			1.40E-69
2558670046	DRAFT_00714	EC:6.3.2.34	Coenzyme F420-1:gamma-L-glutamate ligase.			
2558670046	DRAFT_00714	EC:6.3.2.31	Coenzyme F420-0:L-glutamate ligase.			
2558670046	DRAFT_00714	TIGR01916	F420-0:gamma-glutamyl ligase			2.10E-86
2558670046	DRAFT_00714	KO:K12234	coenzyme F420-0:L-glutamate ligase / coenzyme F420-1:gamma-L-glut			0.00E+00
2558670046	DRAFT_00714	Locus_type		CDS		
2558670046	DRAFT_00714	Product_name		coenzyme F420-0 gamma-glutamyl ligase (EC 6.3.2.31)		
2558670046	DRAFT_00714	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670046	DRAFT_00714	Coordinates		23142..23891(+)		
2558670046	DRAFT_00714	DNA_length		750bp		
2558670046	DRAFT_00714	Protein_length		249aa		
2558670046	DRAFT_00714	GC			0.6	

2558670047	DRAFT_00715	KEGG_module	M00378: F420 biosynthesis			
2558670047	DRAFT_00715	Metacyc	PWY-5198: factor 420 biosynthesis			
2558670047	DRAFT_00715	IMG_pathway	357: Coenzyme F420 synthesis			
2558670047	DRAFT_00715	COG_category	[S] Function unknown			
2558670047	DRAFT_00715	COG0391	Uncharacterized conserved protein			2.00E-53
2558670047	DRAFT_00715	pfam01933	UPF0052			6.80E-48
2558670047	DRAFT_00715	EC:2.7.8.28	2-phospho-L-lactate transferase.			
2558670047	DRAFT_00715	TIGR01819	LPPG:FO 2-phospho-L-lactate transferase			8.50E-102
2558670047	DRAFT_00715	KO:K11212	LPPG:FO 2-phospho-L-lactate transferase [EC:2.7.8.28]			0.00E+00
2558670047	DRAFT_00715	ITERM:01551	LPPG:FO 2-phospho-L-lactate transferase (EC 2.7.8.28)			
2558670047	DRAFT_00715	Locus_type		CDS		
2558670047	DRAFT_00715	Product_name		LPPG:FO 2-phospho-L-lactate transferase (EC 2.7.8.28)		
2558670047	DRAFT_00715	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670047	DRAFT_00715	Coordinates		23896..24810(+)		
2558670047	DRAFT_00715	DNA_length		915bp		
2558670047	DRAFT_00715	Protein_length		304aa		
2558670047	DRAFT_00715	GC			0.62	
2558670048	DRAFT_00716	KEGG_module	M00378: F420 biosynthesis			
2558670048	DRAFT_00716	Metacyc	PWY-5198: factor 420 biosynthesis			
2558670048	DRAFT_00716	COG_category	[S] Function unknown			
2558670048	DRAFT_00716	COG1920	Uncharacterized conserved protein			3.00E-18
2558670048	DRAFT_00716	pfam01983	CofC			1.70E-22
2558670048	DRAFT_00716	EC:2.7.7.68	2-phospho-L-lactate guanylyltransferase.			
2558670048	DRAFT_00716	TIGR03552	2-phospho-L-lactate guanylyltransferase			1.50E-38
2558670048	DRAFT_00716	KO:K14941	2-phospho-L-lactate guanylyltransferase [EC:2.7.7.68]			3.40E-20
2558670048	DRAFT_00716	Locus_type		CDS		
2558670048	DRAFT_00716	Product_name		2-phospho-L-lactate guanylyltransferase		
2558670048	DRAFT_00716	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670048	DRAFT_00716	Coordinates		24873..25448(+)		
2558670048	DRAFT_00716	DNA_length		576bp		
2558670048	DRAFT_00716	Protein_length		191aa		
2558670048	DRAFT_00716	GC			0.6	

2558670049	DRAFT_00717	COG_category	[R] General function prediction only		
2558670049	DRAFT_00717	COG1574	Predicted metal-dependent hydrolase with the TIM-barrel fold		2.00E-87
2558670049	DRAFT_00717	pfam07969	Amidohydro_3		1.60E-61
2558670049	DRAFT_00717	Locus_type		CDS	
2558670049	DRAFT_00717	Product_name		Predicted metal-dependent hydrolase with the TIM-barrel fold	
2558670049	DRAFT_00717	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670049	DRAFT_00717	Coordinates		25490..26974(+)	
2558670049	DRAFT_00717	DNA_length		1485bp	
2558670049	DRAFT_00717	Protein_length		494aa	
2558670049	DRAFT_00717	GC		0.62	

2558670050	DRAFT_00718	COG_category	[S] Function unknown		
2558670050	DRAFT_00718	COG4754	Uncharacterized conserved protein		1.00E-15
2558670050	DRAFT_00718	pfam09821	AAA_assoc_C		3.70E-17
2558670050	DRAFT_00718	Locus_type		CDS	
2558670050	DRAFT_00718	Product_name		Uncharacterized conserved protein	
2558670050	DRAFT_00718	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670050	DRAFT_00718	Coordinates		26971..27498(-)	
2558670050	DRAFT_00718	DNA_length		528bp	
2558670050	DRAFT_00718	Protein_length		175aa	
2558670050	DRAFT_00718	GC		0.58	

2558670051	DRAFT_00719	KEGG_module	M00188: NitT/TauT family transport system		
2558670051	DRAFT_00719	COG_category	[P] Inorganic ion transport and metabolism		
2558670051	DRAFT_00719	COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase com		1.00E-77
2558670051	DRAFT_00719	pfam00005	ABC_tran		6.40E-30
2558670051	DRAFT_00719	KO:K02049	NitT/TauT family transport system ATP-binding protein		0.00E+00
2558670051	DRAFT_00719	Locus_type		CDS	
2558670051	DRAFT_00719	Product_name		ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase co	
2558670051	DRAFT_00719	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670051	DRAFT_00719	Coordinates		27533..28318(-)	
2558670051	DRAFT_00719	DNA_length		786bp	
2558670051	DRAFT_00719	Protein_length		261aa	

2558670051	DRAFT_00719	GC			0.58

2558670052	DRAFT_00720	pfam14321	DUF4382		1.50E-07
2558670052	DRAFT_00720	Locus_type		CDS	
2558670052	DRAFT_00720	Product_name		Domain of unknown function (DUF4382)	
2558670052	DRAFT_00720	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670052	DRAFT_00720	Coordinates		28627..29358(+)	
2558670052	DRAFT_00720	DNA_length		732bp	
2558670052	DRAFT_00720	Protein_length		243aa	
2558670052	DRAFT_00720	GC			0.57
2558670052	DRAFT_00720	Transmembrane		Yes	

2558670053	DRAFT_00721	pfam12840	HTH_20		1.20E-06
2558670053	DRAFT_00721	Locus_type		CDS	
2558670053	DRAFT_00721	Product_name		Helix-turn-helix domain	
2558670053	DRAFT_00721	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670053	DRAFT_00721	Coordinates		29360..29632(+)	
2558670053	DRAFT_00721	DNA_length		273bp	
2558670053	DRAFT_00721	Protein_length		90aa	
2558670053	DRAFT_00721	GC			0.58

2558670054	DRAFT_00722	Locus_type		CDS	
2558670054	DRAFT_00722	Product_name		hypothetical protein	
2558670054	DRAFT_00722	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670054	DRAFT_00722	Coordinates		29935..30660(-)	
2558670054	DRAFT_00722	DNA_length		726bp	
2558670054	DRAFT_00722	Protein_length		241aa	
2558670054	DRAFT_00722	GC			0.51
2558670054	DRAFT_00722	Signal_peptide		Yes	
2558670054	DRAFT_00722	Transmembrane		Yes	

2558670055	DRAFT_00723	pfam01022	HTH_5		2.90E-05
2558670055	DRAFT_00723	Locus_type		CDS	
2558670055	DRAFT_00723	Product_name		Bacterial regulatory protein, arsR family	

2558670055	DRAFT_00723	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670055	DRAFT_00723	Coordinates		30735..31178(-)	
2558670055	DRAFT_00723	DNA_length		444bp	
2558670055	DRAFT_00723	Protein_length		147aa	
2558670055	DRAFT_00723	GC		0.56	
2558670055	DRAFT_00723	Transmembrane		Yes	

2558670056	DRAFT_00724	KEGG_module	M00188: NitT/TauT family transport system		
2558670056	DRAFT_00724	COG_category	[P] Inorganic ion transport and metabolism		
2558670056	DRAFT_00724	COG4986	ABC-type anion transport system, duplicated permease component		5.00E-63
2558670056	DRAFT_00724	pfam00528	BPD_transp_1		1.10E-12
2558670056	DRAFT_00724	pfam00528	BPD_transp_1		6.70E-16
2558670056	DRAFT_00724	KO:K02050	NitT/TauT family transport system permease protein		0.00E+00
2558670056	DRAFT_00724	Locus_type		CDS	
2558670056	DRAFT_00724	Product_name		ABC-type anion transport system, duplicated permease component	
2558670056	DRAFT_00724	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670056	DRAFT_00724	Coordinates		31561..33111(-)	
2558670056	DRAFT_00724	DNA_length		1551bp	
2558670056	DRAFT_00724	Protein_length		516aa	
2558670056	DRAFT_00724	GC		0.55	
2558670056	DRAFT_00724	Transmembrane		Yes	

2558670057	DRAFT_00725	Locus_type		CDS	
2558670057	DRAFT_00725	Product_name		hypothetical protein	
2558670057	DRAFT_00725	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670057	DRAFT_00725	Coordinates		33219..33650(-)	
2558670057	DRAFT_00725	DNA_length		432bp	
2558670057	DRAFT_00725	Protein_length		143aa	
2558670057	DRAFT_00725	GC		0.56	

2558670058	DRAFT_00726	Locus_type		CDS	
2558670058	DRAFT_00726	Product_name		hypothetical protein	
2558670058	DRAFT_00726	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670058	DRAFT_00726	Coordinates		33781..34137(-)	

2558670058	DRAFT_00726	DNA_length		357bp		
2558670058	DRAFT_00726	Protein_length		118aa		
2558670058	DRAFT_00726	GC			0.59	
2558670059	DRAFT_00727	pfam04014	Antitoxin-MazE			3.30E-08
2558670059	DRAFT_00727	Locus_type		CDS		
2558670059	DRAFT_00727	Product_name		Antidote-toxin recognition MazE		
2558670059	DRAFT_00727	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670059	DRAFT_00727	Coordinates		34344..34544(+)		
2558670059	DRAFT_00727	DNA_length		201bp		
2558670059	DRAFT_00727	Protein_length		66aa		
2558670059	DRAFT_00727	GC			0.56	
2558670060	DRAFT_00728	COG_category	[E] Amino acid transport and metabolism			
2558670060	DRAFT_00728	COG0346	Lactoylglutathione lyase and related lyases			5.00E-04
2558670060	DRAFT_00728	pfam12681	Glyoxalase_2			2.80E-14
2558670060	DRAFT_00728	Locus_type		CDS		
2558670060	DRAFT_00728	Product_name		Lactoylglutathione lyase and related lyases		
2558670060	DRAFT_00728	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670060	DRAFT_00728	Coordinates		34619..34960(+)		
2558670060	DRAFT_00728	DNA_length		342bp		
2558670060	DRAFT_00728	Protein_length		113aa		
2558670060	DRAFT_00728	GC			0.56	
2558670061	DRAFT_00729	Metacyc	PWY-5770: phenazine-1-carboxylate biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5365: linear furanocoumarin biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5808: hyperforin and adhyperforin biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5816: all <i>trans</i> undecaprenyl diphosphate biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-4681: kievitone biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5132: humulone biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-6834: spermidine biosynthesis III			
2558670061	DRAFT_00729	Metacyc	PWY-2681: <i>trans</i>-zeatin biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5802: alizarin biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-6681: neurosporaxanthin biosynthesis			

2558670061	DRAFT_00729	Metacyc	PWY-5893: tridecaprenyl diphosphate biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-6262: demethylmenaquinol-8 biosynthesis II			
2558670061	DRAFT_00729	Metacyc	PWY-5817: dodecaprenyl diphosphate biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5027: phylloquinol biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-702: methionine biosynthesis II			
2558670061	DRAFT_00729	Metacyc	PWY-5135: xanthohumol biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5133: cohumulone biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-6936: seleno-amino acid biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5064: chlorophyll <i>a</i> biosynthesis II			
2558670061	DRAFT_00729	Metacyc	PWY-4502: wighteone and luteone biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-7169: hyperxanthone E biosynthesis			
2558670061	DRAFT_00729	Metacyc	PWY-5068: chlorophyll cycle			
2558670061	DRAFT_00729	Metacyc	PWY-6793: demethylmenaquinol-8 biosynthesis III			
2558670061	DRAFT_00729	Metacyc	PWY-6403: carrageenan biosynthesis			
2558670061	DRAFT_00729	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670061	DRAFT_00729	COG0109	Polyprenyltransferase (cytochrome oxidase assembly factor)			2.00E-60
2558670061	DRAFT_00729	pfam01040	UbiA			2.00E-28
2558670061	DRAFT_00729	EC:2.5.1.-	Transferases. Transferring alkyl or aryl groups, other than methyl groups. Transferring alkyl or			
2558670061	DRAFT_00729	TIGR01473	protoheme IX farnesyltransferase			2.30E-82
2558670061	DRAFT_00729	KO:K02301	protoheme IX farnesyltransferase [EC:2.5.1.-]			0.00E+00
2558670061	DRAFT_00729	Locus_type		CDS		
2558670061	DRAFT_00729	Product_name		protoheme IX farnesyltransferase		
2558670061	DRAFT_00729	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10		
2558670061	DRAFT_00729	Coordinates		35197..36075(+)		
2558670061	DRAFT_00729	DNA_length		879bp		
2558670061	DRAFT_00729	Protein_length		292aa		
2558670061	DRAFT_00729	GC			0.58	
2558670061	DRAFT_00729	Transmembrane		Yes		
2558670062	DRAFT_00730	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670062	DRAFT_00730	COG4346	Predicted membrane-bound dolichyl-phosphate-mannose-protein mar			6.00E-15
2558670062	DRAFT_00730	pfam02366	PMT			4.90E-14
2558670062	DRAFT_00730	Locus_type		CDS		
2558670062	DRAFT_00730	Product_name		Predicted membrane-bound dolichyl-phosphate-mannose-protein ma		

2558670062	DRAFT_00730	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670062	DRAFT_00730	Coordinates		36118..37719(-)	
2558670062	DRAFT_00730	DNA_length		1602bp	
2558670062	DRAFT_00730	Protein_length		533aa	
2558670062	DRAFT_00730	GC			0.58
2558670062	DRAFT_00730	Transmembrane		Yes	
2558670063	DRAFT_00731	Locus_type		CDS	
2558670063	DRAFT_00731	Product_name		hypothetical protein	
2558670063	DRAFT_00731	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670063	DRAFT_00731	Coordinates		37999..38316(+)	
2558670063	DRAFT_00731	DNA_length		318bp	
2558670063	DRAFT_00731	Protein_length		105aa	
2558670063	DRAFT_00731	GC			0.51
2558670063	DRAFT_00731	Transmembrane		Yes	
2558670064	DRAFT_00732	Locus_type		CDS	
2558670064	DRAFT_00732	Product_name		hypothetical protein	
2558670064	DRAFT_00732	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670064	DRAFT_00732	Coordinates		38532..38864(-)	
2558670064	DRAFT_00732	DNA_length		333bp	
2558670064	DRAFT_00732	Protein_length		110aa	
2558670064	DRAFT_00732	GC			0.55
2558670065	DRAFT_00733	COG_category	[K] Transcription		
2558670065	DRAFT_00733	COG3432	Predicted transcriptional regulator		2.00E-11
2558670065	DRAFT_00733	pfam14947	HTH_45		7.40E-17
2558670065	DRAFT_00733	Locus_type		CDS	
2558670065	DRAFT_00733	Product_name		Predicted transcriptional regulator	
2558670065	DRAFT_00733	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670065	DRAFT_00733	Coordinates		39084..39422(+)	
2558670065	DRAFT_00733	DNA_length		339bp	
2558670065	DRAFT_00733	Protein_length		112aa	
2558670065	DRAFT_00733	GC			0.53

2558670066	DRAFT_00734	Locus_type		CDS	
2558670066	DRAFT_00734	Product_name		hypothetical protein	
2558670066	DRAFT_00734	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670066	DRAFT_00734	Coordinates		39490..40917(-)	
2558670066	DRAFT_00734	DNA_length		1428bp	
2558670066	DRAFT_00734	Protein_length		475aa	
2558670066	DRAFT_00734	GC			0.57
2558670066	DRAFT_00734	Transmembrane		Yes	
2558670067	DRAFT_00735	KEGG_module	M00365: C10-C20 isoprenoid biosynthesis, archaea		
2558670067	DRAFT_00735	KEGG_module	M00364: C10-C20 isoprenoid biosynthesis, bacteria		
2558670067	DRAFT_00735	Metacyc	PWY-6659: fusicoccins biosynthesis		
2558670067	DRAFT_00735	Metacyc	PWY2OL-4: superpathway of linalool biosynthesis		
2558670067	DRAFT_00735	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis		
2558670067	DRAFT_00735	Metacyc	PWY-6859: <i>all-trans</i>-farnesol biosynthesis		
2558670067	DRAFT_00735	Metacyc	PWY-6691: plaunotol biosynthesis		
2558670067	DRAFT_00735	Metacyc	PWY-5123: <i>trans, trans</i>-farnesyl diphosphate biosynthesis		
2558670067	DRAFT_00735	Metacyc	PWY-5122: geranyl diphosphate biosynthesis		
2558670067	DRAFT_00735	Metacyc	PWY-7182: linalool biosynthesis I		
2558670067	DRAFT_00735	Metacyc	PWY-7141: linalool biosynthesis II		
2558670067	DRAFT_00735	Metacyc	PWY-5120: geranylgeranyldiphosphate biosynthesis		
2558670067	DRAFT_00735	Metacyc	PWY-7102: bisabolene biosynthesis		
2558670067	DRAFT_00735	COG_category	[H] Coenzyme transport and metabolism		
2558670067	DRAFT_00735	COG0142	Geranylgeranyl pyrophosphate synthase		2.00E-55
2558670067	DRAFT_00735	pfam00348	polyprenyl_synt		8.40E-52
2558670067	DRAFT_00735	EC:2.5.1.29	Geranylgeranyl diphosphate synthase.		
2558670067	DRAFT_00735	EC:2.5.1.1	Dimethylallyltranstransferase.		
2558670067	DRAFT_00735	EC:2.5.1.10	(2E,6E)-farnesyl diphosphate synthase.		
2558670067	DRAFT_00735	KO:K13787	geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10 2.5.1.		0.00E+00
2558670067	DRAFT_00735	ITERM:00778	farnesyl-diphosphate synthase (EC 2.5.1.10)		
2558670067	DRAFT_00735	ITERM:05618	geranylgeranyl-diphosphate synthase (EC 2.5.1.29)		
2558670067	DRAFT_00735	Locus_type		CDS	
2558670067	DRAFT_00735	Product_name		farnesyl-diphosphate synthase (EC 2.5.1.10)/geranylgeranyl-diphosph	

2558670067	DRAFT_00735	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670067	DRAFT_00735	Coordinates		40967..41992(-)	
2558670067	DRAFT_00735	DNA_length		1026bp	
2558670067	DRAFT_00735	Protein_length		341aa	
2558670067	DRAFT_00735	GC		0.59	
2558670068	DRAFT_00736	COG_category	[H] Coenzyme transport and metabolism		
2558670068	DRAFT_00736	COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferas		2.00E-09
2558670068	DRAFT_00736	pfam01040	UbiA		3.40E-24
2558670068	DRAFT_00736	Locus_type		CDS	
2558670068	DRAFT_00736	Product_name		4-hydroxybenzoate polyprenyltransferase and related prenyltransfera	
2558670068	DRAFT_00736	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670068	DRAFT_00736	Coordinates		41979..42896(-)	
2558670068	DRAFT_00736	DNA_length		918bp	
2558670068	DRAFT_00736	Protein_length		305aa	
2558670068	DRAFT_00736	GC		0.59	
2558670068	DRAFT_00736	Transmembrane		Yes	
2558670069	DRAFT_00737	Locus_type		CDS	
2558670069	DRAFT_00737	Product_name		hypothetical protein	
2558670069	DRAFT_00737	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670069	DRAFT_00737	Coordinates		42836..43927(-)	
2558670069	DRAFT_00737	DNA_length		1092bp	
2558670069	DRAFT_00737	Protein_length		363aa	
2558670069	DRAFT_00737	GC		0.54	
2558670070	DRAFT_00738	COG_category	[T] Signal transduction mechanisms		
2558670070	DRAFT_00738	COG0467	RecA-superfamily ATPases implicated in signal transduction		2.00E-30
2558670070	DRAFT_00738	pfam06745	KaiC		3.30E-48
2558670070	DRAFT_00738	Locus_type		CDS	
2558670070	DRAFT_00738	Product_name		RecA-superfamily ATPases implicated in signal transduction	
2558670070	DRAFT_00738	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670070	DRAFT_00738	Coordinates		44104..44796(+)	
2558670070	DRAFT_00738	DNA_length		693bp	

2558670070	DRAFT_00738	Protein_length		230aa	
2558670070	DRAFT_00738	GC		0.53	
2558670071	DRAFT_00739	Locus_type		CDS	
2558670071	DRAFT_00739	Product_name		hypothetical protein	
2558670071	DRAFT_00739	Scaffold		DRAFT_contig_70_60_len_46101_read_count_777516.10	
2558670071	DRAFT_00739	Coordinates		44876..45922(+)	
2558670071	DRAFT_00739	DNA_length		1047bp	
2558670071	DRAFT_00739	Protein_length		348aa	
2558670071	DRAFT_00739	GC		0.59	
2558670071	DRAFT_00739	Signal_peptide		Yes	
2558670071	DRAFT_00739	Transmembrane		Yes	
2558670072	DRAFT_00740	COG_category	[R] General function prediction only		
2558670072	DRAFT_00740	COG1011	Predicted hydrolase (HAD superfamily)		3.00E-22
2558670072	DRAFT_00740	pfam13419	HAD_2		1.10E-22
2558670072	DRAFT_00740	TIGR01549	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third		5.60E-11
2558670072	DRAFT_00740	TIGR01509	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third		9.10E-14
2558670072	DRAFT_00740	KO:K07025	putative hydrolase of the HAD superfamily		5.40E-20
2558670072	DRAFT_00740	Locus_type		CDS	
2558670072	DRAFT_00740	Product_name		haloacid dehalogenase superfamily, subfamily IA, variant 3 with third	
2558670072	DRAFT_00740	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670072	DRAFT_00740	Coordinates		156..911(+)	
2558670072	DRAFT_00740	DNA_length		756bp	
2558670072	DRAFT_00740	Protein_length		251aa	
2558670072	DRAFT_00740	GC		0.54	
2558670073	DRAFT_00741	pfam00583	Acetyltransf_1		3.80E-12
2558670073	DRAFT_00741	Locus_type		CDS	
2558670073	DRAFT_00741	Product_name		Acetyltransferases	
2558670073	DRAFT_00741	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670073	DRAFT_00741	Coordinates		979..1464(-)	
2558670073	DRAFT_00741	DNA_length		486bp	
2558670073	DRAFT_00741	Protein_length		161aa	

2558670073	DRAFT_00741	GC	0.52
2558670074	DRAFT_00742	Locus_type	CDS
2558670074	DRAFT_00742	Product_name	hypothetical protein
2558670074	DRAFT_00742	Scaffold	DRAFT_contig_70_77_len_39784_read_count_688219.11
2558670074	DRAFT_00742	Coordinates	1809..2336(+)
2558670074	DRAFT_00742	DNA_length	528bp
2558670074	DRAFT_00742	Protein_length	175aa
2558670074	DRAFT_00742	GC	0.55
2558670074	DRAFT_00742	Transmembrane	Yes
2558670075	DRAFT_00743	Locus_type	CDS
2558670075	DRAFT_00743	Product_name	hypothetical protein
2558670075	DRAFT_00743	Scaffold	DRAFT_contig_70_77_len_39784_read_count_688219.11
2558670075	DRAFT_00743	Coordinates	2429..2989(+)
2558670075	DRAFT_00743	DNA_length	561bp
2558670075	DRAFT_00743	Protein_length	186aa
2558670075	DRAFT_00743	GC	0.54
2558670076	DRAFT_00744	Locus_type	CDS
2558670076	DRAFT_00744	Product_name	hypothetical protein
2558670076	DRAFT_00744	Scaffold	DRAFT_contig_70_77_len_39784_read_count_688219.11
2558670076	DRAFT_00744	Coordinates	3108..3428(+)
2558670076	DRAFT_00744	DNA_length	321bp
2558670076	DRAFT_00744	Protein_length	106aa
2558670076	DRAFT_00744	GC	0.55
2558670076	DRAFT_00744	Transmembrane	Yes
2558670077	DRAFT_00745	Locus_type	CDS
2558670077	DRAFT_00745	Product_name	hypothetical protein
2558670077	DRAFT_00745	Scaffold	DRAFT_contig_70_77_len_39784_read_count_688219.11
2558670077	DRAFT_00745	Coordinates	3467..3715(-)
2558670077	DRAFT_00745	DNA_length	249bp
2558670077	DRAFT_00745	Protein_length	82aa

2558670077	DRAFT_00745	GC			0.57	
2558670078	DRAFT_00746	KEGG_module	M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone			
2558670078	DRAFT_00746	Metacyc	PWY-6627: salinosporamide A biosynthesis			
2558670078	DRAFT_00746	Metacyc	PWY-7007: methyl ketone biosynthesis			
2558670078	DRAFT_00746	Metacyc	PWY-5113: UDP-D-apiose biosynthesis (from UDP-D-glucuronate)			
2558670078	DRAFT_00746	Metacyc	PWY3O-19: ubiquinol-6 biosynthesis (eukaryotic)			
2558670078	DRAFT_00746	Metacyc	PWY-181: photorespiration			
2558670078	DRAFT_00746	Metacyc	PWY-6585: 2-tridecanone biosynthesis			
2558670078	DRAFT_00746	Metacyc	PWY-5856: ubiquinol-9 biosynthesis (prokaryotic)			
2558670078	DRAFT_00746	Metacyc	PWY-5855: ubiquinol-7 biosynthesis (prokaryotic)			
2558670078	DRAFT_00746	Metacyc	PWY-5870: ubiquinol-8 biosynthesis (eukaryotic)			
2558670078	DRAFT_00746	Metacyc	PWY-3385: choline biosynthesis I			
2558670078	DRAFT_00746	Metacyc	PWY-5163: <I>p</I>-cumate degradation to 2-oxopent-4-enoate			
2558670078	DRAFT_00746	Metacyc	PWY-6559: spermidine biosynthesis II			
2558670078	DRAFT_00746	Metacyc	PWY-5826: hypoglycin biosynthesis			
2558670078	DRAFT_00746	Metacyc	PWY-5873: ubiquinol-7 biosynthesis (eukaryotic)			
2558670078	DRAFT_00746	Metacyc	PWY-5871: ubiquinol-9 biosynthesis (eukaryotic)			
2558670078	DRAFT_00746	Metacyc	PWY-6708: ubiquinol-8 biosynthesis (prokaryotic)			
2558670078	DRAFT_00746	Metacyc	PWY-5857: ubiquinol-10 biosynthesis (prokaryotic)			
2558670078	DRAFT_00746	Metacyc	PWY-5872: ubiquinol-10 biosynthesis (eukaryotic)			
2558670078	DRAFT_00746	COG_category	[H] Coenzyme transport and metabolism			
2558670078	DRAFT_00746	COG0163	3-polyprenyl-4-hydroxybenzoate decarboxylase			4.00E-69
2558670078	DRAFT_00746	pfam02441	Flavoprotein			8.60E-25
2558670078	DRAFT_00746	EC:4.1.1.-	Lyases. Carbon-carbon lyases. Carboxy-lyases.			
2558670078	DRAFT_00746	TIGR00421	polyprenyl P-hydroxybenzoate and phenylacrylic acid decarboxylases			8.10E-72
2558670078	DRAFT_00746	KO:K03186	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiX [EC:4.1.1.-]			0.00E+00
2558670078	DRAFT_00746	Locus_type		CDS		
2558670078	DRAFT_00746	Product_name		polyprenyl P-hydroxybenzoate and phenylacrylic acid decarboxylases		
2558670078	DRAFT_00746	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670078	DRAFT_00746	Coordinates		5075..5659(+)		
2558670078	DRAFT_00746	DNA_length		585bp		
2558670078	DRAFT_00746	Protein_length		194aa		
2558670078	DRAFT_00746	GC			0.58	

2558670079	DRAFT_00747	COG_category	[S] Function unknown			
2558670079	DRAFT_00747	COG1786	Uncharacterized conserved protein			5.00E-33
2558670079	DRAFT_00747	pfam01989	DUF126			2.40E-34
2558670079	DRAFT_00747	KO:K09128	hypothetical protein			6.50E-34
2558670079	DRAFT_00747	ITERM:01401	predicted aconitase subunit 2 (EC 4.2.1.3)			
2558670079	DRAFT_00747	Locus_type		CDS		
2558670079	DRAFT_00747	Product_name		predicted aconitase subunit 2 (EC 4.2.1.3)		
2558670079	DRAFT_00747	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670079	DRAFT_00747	Coordinates		5731..6138(-)		
2558670079	DRAFT_00747	DNA_length		408bp		
2558670079	DRAFT_00747	Protein_length		135aa		
2558670079	DRAFT_00747	GC			0.58	

2558670080	DRAFT_00748	COG_category	[S] Function unknown			
2558670080	DRAFT_00748	COG1679	Uncharacterized conserved protein			4.00E-129
2558670080	DRAFT_00748	pfam04412	DUF521			0.00E+00
2558670080	DRAFT_00748	KO:K09123	hypothetical protein			0.00E+00
2558670080	DRAFT_00748	ITERM:01400	predicted aconitase subunit 1 (EC 4.2.1.3)			
2558670080	DRAFT_00748	Locus_type		CDS		
2558670080	DRAFT_00748	Product_name		predicted aconitase subunit 1 (EC 4.2.1.3)		
2558670080	DRAFT_00748	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670080	DRAFT_00748	Coordinates		6108..7292(-)		
2558670080	DRAFT_00748	DNA_length		1185bp		
2558670080	DRAFT_00748	Protein_length		394aa		
2558670080	DRAFT_00748	GC			0.59	

2558670081	DRAFT_00749	COG_category	[H] Coenzyme transport and metabolism			
2558670081	DRAFT_00749	COG0043	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxy			2.00E-97
2558670081	DRAFT_00749	pfam01977	UbiD			3.10E-109
2558670081	DRAFT_00749	TIGR00148	UbiD family decarboxylase			9.00E-107
2558670081	DRAFT_00749	Locus_type		CDS		
2558670081	DRAFT_00749	Product_name		UbiD family decarboxylase		
2558670081	DRAFT_00749	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		

2558670081	DRAFT_00749	Coordinates		7300..8598(-)		
2558670081	DRAFT_00749	DNA_length		1299bp		
2558670081	DRAFT_00749	Protein_length		432aa		
2558670081	DRAFT_00749	GC			0.57	

2558670082	DRAFT_00750	Locus_type		CDS		
2558670082	DRAFT_00750	Product_name		hypothetical protein		
2558670082	DRAFT_00750	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670082	DRAFT_00750	Coordinates		8763..9203(+)		
2558670082	DRAFT_00750	DNA_length		441bp		
2558670082	DRAFT_00750	Protein_length		146aa		
2558670082	DRAFT_00750	GC			0.52	
2558670082	DRAFT_00750	Transmembrane		Yes		

2558670083	DRAFT_00751	KEGG_module	M00133: Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine			
2558670083	DRAFT_00751	Metacyc	PWY-6834: spermidine biosynthesis III			
2558670083	DRAFT_00751	Metacyc	PWY0-823: arginine degradation III (arginine decarboxylase/agmatinase pathway)			
2558670083	DRAFT_00751	Metacyc	PWY0-1299: arginine dependent acid resistance			
2558670083	DRAFT_00751	Metacyc	PWY-40: putrescine biosynthesis I			
2558670083	DRAFT_00751	Metacyc	PWY-6305: putrescine biosynthesis IV			
2558670083	DRAFT_00751	Metacyc	ARGDEG-III-PWY: arginine degradation IV (arginine decarboxylase/agmatine deiminase pathwa			
2558670083	DRAFT_00751	Metacyc	PWY-43: putrescine biosynthesis II			
2558670083	DRAFT_00751	IMG_pathway	186: L-arginine degradation by Arg decarboxylase pathway			
2558670083	DRAFT_00751	IMG_pathway	524: Spermidine synthesis via aminopropylagmatine			
2558670083	DRAFT_00751	IMG_pathway	823: Putrescine synthesis from L-arginine			
2558670083	DRAFT_00751	COG_category	[S] Function unknown			
2558670083	DRAFT_00751	COG1945	Uncharacterized conserved protein			8.00E-37
2558670083	DRAFT_00751	pfam01862	PvlArgDC			1.30E-57
2558670083	DRAFT_00751	EC:4.1.1.19	Arginine decarboxylase.			
2558670083	DRAFT_00751	TIGR00286	arginine decarboxylase, pyruvoyl-dependent			5.00E-35
2558670083	DRAFT_00751	KO:K02626	arginine decarboxylase [EC:4.1.1.19]			0.00E+00
2558670083	DRAFT_00751	ITERM:00488	arginine decarboxylase (EC 4.1.1.19)			
2558670083	DRAFT_00751	Locus_type		CDS		
2558670083	DRAFT_00751	Product_name		arginine decarboxylase (EC 4.1.1.19)		

2558670083	DRAFT_00751	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670083	DRAFT_00751	Coordinates		9353..9922(-)	
2558670083	DRAFT_00751	DNA_length		570bp	
2558670083	DRAFT_00751	Protein_length		189aa	
2558670083	DRAFT_00751	GC		0.56	
2558670084	DRAFT_00752	KEGG_module	M00555: Betaine biosynthesis, choline => betaine		
2558670084	DRAFT_00752	Metacyc	PWY-3722: glycine betaine biosynthesis II (Gram-positive bacteria)		
2558670084	DRAFT_00752	Metacyc	BETSYN-PWY: glycine betaine biosynthesis I (Gram-negative bacteria)		
2558670084	DRAFT_00752	Metacyc	CHOLINE-BETAINE-ANA-PWY: choline degradation I		
2558670084	DRAFT_00752	Metacyc	PWY1F-353: glycine betaine biosynthesis III (plants)		
2558670084	DRAFT_00752	COG_category	[C] Energy production and conversion		
2558670084	DRAFT_00752	COG1012	NAD-dependent aldehyde dehydrogenases		0.00E+00
2558670084	DRAFT_00752	pfam00171	Aldedh		0.00E+00
2558670084	DRAFT_00752	EC:1.2.1.8	Betaine-aldehyde dehydrogenase.		
2558670084	DRAFT_00752	TIGR03374	1-pyrroline dehydrogenase		0.00E+00
2558670084	DRAFT_00752	KO:K00130	betaine-aldehyde dehydrogenase [EC:1.2.1.8]		0.00E+00
2558670084	DRAFT_00752	Locus_type		CDS	
2558670084	DRAFT_00752	Product_name		NAD-dependent aldehyde dehydrogenases	
2558670084	DRAFT_00752	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670084	DRAFT_00752	Coordinates		10113..11615(-)	
2558670084	DRAFT_00752	DNA_length		1503bp	
2558670084	DRAFT_00752	Protein_length		500aa	
2558670084	DRAFT_00752	GC		0.56	
2558670085	DRAFT_00753	KEGG_module	M00239: Peptides/nickel transport system		
2558670085	DRAFT_00753	COG_category	[E] Amino acid transport and metabolism		
2558670085	DRAFT_00753	COG0747	ABC-type dipeptide transport system, periplasmic component		4.00E-45
2558670085	DRAFT_00753	pfam00496	SBP_bac_5		1.10E-57
2558670085	DRAFT_00753	KO:K02035	peptide/nickel transport system substrate-binding protein		0.00E+00
2558670085	DRAFT_00753	Locus_type		CDS	
2558670085	DRAFT_00753	Product_name		ABC-type dipeptide transport system, periplasmic component	
2558670085	DRAFT_00753	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670085	DRAFT_00753	Coordinates		11891..13756(+)	

2558670085	DRAFT_00753	DNA_length		1866bp		
2558670085	DRAFT_00753	Protein_length		621aa		
2558670085	DRAFT_00753	GC			0.54	
2558670085	DRAFT_00753	Transmembrane		Yes		
2558670086	DRAFT_00754	pfam00528	BPD_transp_1			1.40E-33
2558670086	DRAFT_00754	Locus_type		CDS		
2558670086	DRAFT_00754	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease		
2558670086	DRAFT_00754	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670086	DRAFT_00754	Coordinates		14105..14803(+)		
2558670086	DRAFT_00754	DNA_length		699bp		
2558670086	DRAFT_00754	Protein_length		232aa		
2558670086	DRAFT_00754	GC			0.52	
2558670086	DRAFT_00754	Transmembrane		Yes		
2558670087	DRAFT_00755	KEGG_module	M00239: Peptides/nickel transport system			
2558670087	DRAFT_00755	COG_category	[E] Amino acid transport and metabolism			
2558670087	DRAFT_00755	COG_category	[P] Inorganic ion transport and metabolism			
2558670087	DRAFT_00755	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c			9.00E-57
2558670087	DRAFT_00755	pfam00528	BPD_transp_1			2.50E-21
2558670087	DRAFT_00755	KO:K02034	peptide/nickel transport system permease protein			0.00E+00
2558670087	DRAFT_00755	Locus_type		CDS		
2558670087	DRAFT_00755	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease		
2558670087	DRAFT_00755	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670087	DRAFT_00755	Coordinates		14800..15801(+)		
2558670087	DRAFT_00755	DNA_length		1002bp		
2558670087	DRAFT_00755	Protein_length		333aa		
2558670087	DRAFT_00755	GC			0.55	
2558670087	DRAFT_00755	Transmembrane		Yes		
2558670088	DRAFT_00756	KEGG_module	M00439: Oligopeptide transport system			
2558670088	DRAFT_00756	pfam00005	ABC_tran			2.40E-33
2558670088	DRAFT_00756	pfam08352	oligo_HPY			7.90E-11
2558670088	DRAFT_00756	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termin			5.90E-16

2558670088	DRAFT_00756	KO:K10823	oligopeptide transport system ATP-binding protein			0.00E+00
2558670088	DRAFT_00756	Locus_type		CDS		
2558670088	DRAFT_00756	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termi		
2558670088	DRAFT_00756	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670088	DRAFT_00756	Coordinates		15757..16725(-)		
2558670088	DRAFT_00756	DNA_length		969bp		
2558670088	DRAFT_00756	Protein_length		322aa		
2558670088	DRAFT_00756	GC			0.54	
2558670089	DRAFT_00757	KEGG_module	M00439: Oligopeptide transport system			
2558670089	DRAFT_00757	COG_category	[P] Inorganic ion transport and metabolism			
2558670089	DRAFT_00757	COG_category	[E] Amino acid transport and metabolism			
2558670089	DRAFT_00757	COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase com			4.00E-108
2558670089	DRAFT_00757	pfam00005	ABC_tran			2.10E-27
2558670089	DRAFT_00757	pfam08352	oligo_HPY			4.50E-17
2558670089	DRAFT_00757	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termin			2.90E-27
2558670089	DRAFT_00757	KO:K15583	oligopeptide transport system ATP-binding protein			0.00E+00
2558670089	DRAFT_00757	Locus_type		CDS		
2558670089	DRAFT_00757	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termi		
2558670089	DRAFT_00757	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670089	DRAFT_00757	Coordinates		16703..17779(-)		
2558670089	DRAFT_00757	DNA_length		1077bp		
2558670089	DRAFT_00757	Protein_length		358aa		
2558670089	DRAFT_00757	GC			0.53	
2558670090	DRAFT_00758	Locus_type		CDS		
2558670090	DRAFT_00758	Product_name		hypothetical protein		
2558670090	DRAFT_00758	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670090	DRAFT_00758	Coordinates		17857..18543(-)		
2558670090	DRAFT_00758	DNA_length		687bp		
2558670090	DRAFT_00758	Protein_length		228aa		
2558670090	DRAFT_00758	GC			0.48	
2558670091	DRAFT_00759	COG_category	[L] Replication, recombination and repair			

2558670091	DRAFT_00759	COG3316	Transposase and inactivated derivatives		1.00E-09
2558670091	DRAFT_00759	pfam13610	DDE_Tnp_IS240		1.90E-19
2558670091	DRAFT_00759	pfam04434	SWIM		4.30E-06
2558670091	DRAFT_00759	Locus_type		CDS	
2558670091	DRAFT_00759	Product_name		Transposase and inactivated derivatives	
2558670091	DRAFT_00759	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670091	DRAFT_00759	Coordinates		18515..19657(-)	
2558670091	DRAFT_00759	DNA_length		1143bp	
2558670091	DRAFT_00759	Protein_length		380aa	
2558670091	DRAFT_00759	GC		0.57	
2558670092	DRAFT_00760	Locus_type		CDS	
2558670092	DRAFT_00760	Product_name		hypothetical protein	
2558670092	DRAFT_00760	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670092	DRAFT_00760	Coordinates		19815..19958(+)	
2558670092	DRAFT_00760	DNA_length		144bp	
2558670092	DRAFT_00760	Protein_length		47aa	
2558670092	DRAFT_00760	GC		0.51	
2558670093	DRAFT_00761	Locus_type		CDS	
2558670093	DRAFT_00761	Product_name		hypothetical protein	
2558670093	DRAFT_00761	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670093	DRAFT_00761	Coordinates		19965..21323(+)	
2558670093	DRAFT_00761	DNA_length		1359bp	
2558670093	DRAFT_00761	Protein_length		452aa	
2558670093	DRAFT_00761	GC		0.5	
2558670093	DRAFT_00761	Transmembrane		Yes	
2558670094	DRAFT_00762	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme		
2558670094	DRAFT_00762	Metacyc	PWY-5188: tetrapyrrole biosynthesis I (from glutamate)		
2558670094	DRAFT_00762	COG_category	[H] Coenzyme transport and metabolism		
2558670094	DRAFT_00762	COG0001	Glutamate-1-semialdehyde aminotransferase		0.00E+00
2558670094	DRAFT_00762	pfam00202	Aminotran_3		5.60E-65
2558670094	DRAFT_00762	EC:5.4.3.8	Glutamate-1-semialdehyde 2,1-aminomutase.		

2558670094	DRAFT_00762	TIGR00713	glutamate-1-semialdehyde-2,1-aminomutase			0.00E+00
2558670094	DRAFT_00762	KO:K01845	glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]			0.00E+00
2558670094	DRAFT_00762	Locus_type		CDS		
2558670094	DRAFT_00762	Product_name		Glutamate-1-semialdehyde aminotransferase		
2558670094	DRAFT_00762	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670094	DRAFT_00762	Coordinates		21667..23085(-)		
2558670094	DRAFT_00762	DNA_length		1419bp		
2558670094	DRAFT_00762	Protein_length		472aa		
2558670094	DRAFT_00762	GC			0.54	
2558670095	DRAFT_00763	Locus_type		CDS		
2558670095	DRAFT_00763	Product_name		hypothetical protein		
2558670095	DRAFT_00763	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670095	DRAFT_00763	Coordinates		23066..23305(-)		
2558670095	DRAFT_00763	DNA_length		240bp		
2558670095	DRAFT_00763	Protein_length		79aa		
2558670095	DRAFT_00763	GC			0.51	
2558670096	DRAFT_00764	Locus_type		CDS		
2558670096	DRAFT_00764	Product_name		hypothetical protein		
2558670096	DRAFT_00764	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670096	DRAFT_00764	Coordinates		23247..23378(-)		
2558670096	DRAFT_00764	DNA_length		132bp		
2558670096	DRAFT_00764	Protein_length		43aa		
2558670096	DRAFT_00764	GC			0.48	
2558670097	DRAFT_00765	Locus_type		CDS		
2558670097	DRAFT_00765	Product_name		hypothetical protein		
2558670097	DRAFT_00765	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670097	DRAFT_00765	Coordinates		23652..23930(+)		
2558670097	DRAFT_00765	DNA_length		279bp		
2558670097	DRAFT_00765	Protein_length		92aa		
2558670097	DRAFT_00765	GC			0.51	

2558670098	DRAFT_00766	KEGG_module	M00033: Ectoine biosynthesis, aspartate => ectoine			
2558670098	DRAFT_00766	Metacyc	P101-PWY: ectoine biosynthesis			
2558670098	DRAFT_00766	Metacyc	PWY-761: rhizobactin 1021 biosynthesis			
2558670098	DRAFT_00766	Metacyc	PWY-6409: pyoverdine I biosynthesis			
2558670098	DRAFT_00766	Metacyc	PWY-6562: norspermidine biosynthesis			
2558670098	DRAFT_00766	COG_category	[E] Amino acid transport and metabolism			
2558670098	DRAFT_00766	COG0160	4-aminobutyrate aminotransferase and related aminotransferases			4.00E-121
2558670098	DRAFT_00766	pfam00202	Aminotran_3			1.00E-85
2558670098	DRAFT_00766	EC:2.6.1.76	Diaminobutyrate--2-oxoglutarate transaminase.			
2558670098	DRAFT_00766	KO:K00836	diaminobutyrate-2-oxoglutarate transaminase [EC:2.6.1.76]			0.00E+00
2558670098	DRAFT_00766	Locus_type		CDS		
2558670098	DRAFT_00766	Product_name		4-aminobutyrate aminotransferase and related aminotransferases		
2558670098	DRAFT_00766	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670098	DRAFT_00766	Coordinates		24097..25458(-)		
2558670098	DRAFT_00766	DNA_length		1362bp		
2558670098	DRAFT_00766	Protein_length		453aa		
2558670098	DRAFT_00766	GC			0.56	
2558670099	DRAFT_00767	COG_category	[E] Amino acid transport and metabolism			
2558670099	DRAFT_00767	COG1748	Saccharopine dehydrogenase and related proteins			1.00E-37
2558670099	DRAFT_00767	pfam03435	Saccharop_dh			6.00E-39
2558670099	DRAFT_00767	Locus_type		CDS		
2558670099	DRAFT_00767	Product_name		Saccharopine dehydrogenase and related proteins		
2558670099	DRAFT_00767	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670099	DRAFT_00767	Coordinates		25738..26931(+)		
2558670099	DRAFT_00767	DNA_length		1194bp		
2558670099	DRAFT_00767	Protein_length		397aa		
2558670099	DRAFT_00767	GC			0.53	
2558670100	DRAFT_00768	pfam09594	DUF2029			6.40E-08
2558670100	DRAFT_00768	Locus_type		CDS		
2558670100	DRAFT_00768	Product_name		Predicted membrane-bound dolichyl-phosphate-mannose-protein ma		
2558670100	DRAFT_00768	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670100	DRAFT_00768	Coordinates		27304..28656(-)		

2558670100	DRAFT_00768	DNA_length		1353bp		
2558670100	DRAFT_00768	Protein_length		450aa		
2558670100	DRAFT_00768	GC			0.55	
2558670100	DRAFT_00768	Transmembrane		Yes		

2558670101	DRAFT_00769	Locus_type		CDS		
2558670101	DRAFT_00769	Product_name		hypothetical protein		
2558670101	DRAFT_00769	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670101	DRAFT_00769	Coordinates		28729..29037(+)		
2558670101	DRAFT_00769	DNA_length		309bp		
2558670101	DRAFT_00769	Protein_length		102aa		
2558670101	DRAFT_00769	GC			0.55	
2558670101	DRAFT_00769	Transmembrane		Yes		

2558670102	DRAFT_00770	Locus_type		CDS		
2558670102	DRAFT_00770	Product_name		hypothetical protein		
2558670102	DRAFT_00770	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670102	DRAFT_00770	Coordinates		29143..29409(-)		
2558670102	DRAFT_00770	DNA_length		267bp		
2558670102	DRAFT_00770	Protein_length		88aa		
2558670102	DRAFT_00770	GC			0.59	

2558670103	DRAFT_00771	COG_category	[F] Nucleotide transport and metabolism			
2558670103	DRAFT_00771	COG1457	Purine-cytosine permease and related proteins			1.00E-52
2558670103	DRAFT_00771	pfam02133	Transp_cyt_pur			7.50E-31
2558670103	DRAFT_00771	TIGR00800	NCS1 nucleoside transporter family			8.60E-40
2558670103	DRAFT_00771	KO:K03457	nucleobase:cation symporter-1, NCS1 family			0.00E+00
2558670103	DRAFT_00771	Locus_type		CDS		
2558670103	DRAFT_00771	Product_name		Purine-cytosine permease and related proteins		
2558670103	DRAFT_00771	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670103	DRAFT_00771	Coordinates		29550..30905(-)		
2558670103	DRAFT_00771	DNA_length		1356bp		
2558670103	DRAFT_00771	Protein_length		451aa		
2558670103	DRAFT_00771	GC			0.58	

2558670103	DRAFT_00771	Transmembrane		Yes		
2558670104	DRAFT_00772	pfam03551	PadR			7.80E-11
2558670104	DRAFT_00772	Locus_type		CDS		
2558670104	DRAFT_00772	Product_name		Predicted transcriptional regulators		
2558670104	DRAFT_00772	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670104	DRAFT_00772	Coordinates		30958..31335(-)		
2558670104	DRAFT_00772	DNA_length		378bp		
2558670104	DRAFT_00772	Protein_length		125aa		
2558670104	DRAFT_00772	GC			0.58	
2558670105	DRAFT_00773	COG_category	[E] Amino acid transport and metabolism			
2558670105	DRAFT_00773	COG1446	Asparaginase			4.00E-54
2558670105	DRAFT_00773	pfam01112	Asparaginase_2			1.10E-57
2558670105	DRAFT_00773	EC:3.4.19.5	Beta-aspartyl-peptidase.			
2558670105	DRAFT_00773	KO:K13051	beta-aspartyl-peptidase (threonine type) [EC:3.4.19.5]			0.00E+00
2558670105	DRAFT_00773	Locus_type		CDS		
2558670105	DRAFT_00773	Product_name		Asparaginase		
2558670105	DRAFT_00773	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670105	DRAFT_00773	Coordinates		31533..32435(+)		
2558670105	DRAFT_00773	DNA_length		903bp		
2558670105	DRAFT_00773	Protein_length		300aa		
2558670105	DRAFT_00773	GC			0.64	
2558670106	DRAFT_00774	COG_category	[L] Replication, recombination and repair			
2558670106	DRAFT_00774	COG0608	Single-stranded DNA-specific exonuclease			5.00E-09
2558670106	DRAFT_00774	pfam02272	DHHA1			3.50E-08
2558670106	DRAFT_00774	KO:K07463	archaea-specific RecJ-like exonuclease			0.00E+00
2558670106	DRAFT_00774	Locus_type		CDS		
2558670106	DRAFT_00774	Product_name		Single-stranded DNA-specific exonuclease		
2558670106	DRAFT_00774	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670106	DRAFT_00774	Coordinates		32533..33489(+)		
2558670106	DRAFT_00774	DNA_length		957bp		
2558670106	DRAFT_00774	Protein_length		318aa		

2558670106	DRAFT_00774	GC			0.61
2558670107	DRAFT_00775	KEGG_module	M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone		
2558670107	DRAFT_00775	KEGG_module	M00116: Menaquinone biosynthesis, chorismate => menaquinone		
2558670107	DRAFT_00775	Metacyc	PWY3O-19: ubiquinol-6 biosynthesis (eukaryotic)		
2558670107	DRAFT_00775	Metacyc	PWY-6708: ubiquinol-8 biosynthesis (prokaryotic)		
2558670107	DRAFT_00775	Metacyc	PWY-5890: menaquinol-10 biosynthesis		
2558670107	DRAFT_00775	Metacyc	PWY-5844: menaquinol-9 biosynthesis		
2558670107	DRAFT_00775	Metacyc	PWY-5891: menaquinol-11 biosynthesis		
2558670107	DRAFT_00775	Metacyc	PWY-5849: menaquinol-6 biosynthesis		
2558670107	DRAFT_00775	Metacyc	PWY-5872: ubiquinol-10 biosynthesis (eukaryotic)		
2558670107	DRAFT_00775	Metacyc	MENAQUINONESYN-PWY: menaquinol-8 biosynthesis		
2558670107	DRAFT_00775	Metacyc	PWY-5857: ubiquinol-10 biosynthesis (prokaryotic)		
2558670107	DRAFT_00775	Metacyc	PWY-5892: menaquinol-12 biosynthesis		
2558670107	DRAFT_00775	Metacyc	PWY-5873: ubiquinol-7 biosynthesis (eukaryotic)		
2558670107	DRAFT_00775	Metacyc	PWY-5871: ubiquinol-9 biosynthesis (eukaryotic)		
2558670107	DRAFT_00775	Metacyc	PWY-5856: ubiquinol-9 biosynthesis (prokaryotic)		
2558670107	DRAFT_00775	Metacyc	PWY-5895: menaquinol-13 biosynthesis		
2558670107	DRAFT_00775	Metacyc	PWY-5839: menaquinol-7 biosynthesis		
2558670107	DRAFT_00775	Metacyc	PWY-5855: ubiquinol-7 biosynthesis (prokaryotic)		
2558670107	DRAFT_00775	Metacyc	PWY-5870: ubiquinol-8 biosynthesis (eukaryotic)		
2558670107	DRAFT_00775	COG_category	[H] Coenzyme transport and metabolism		
2558670107	DRAFT_00775	COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis		2.00E-18
2558670107	DRAFT_00775	pfam08241	Methyltransf_11		4.50E-12
2558670107	DRAFT_00775	EC:2.1.1.163	Demethylmenaquinone methyltransferase.		
2558670107	DRAFT_00775	EC:2.1.1.201	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase.		
2558670107	DRAFT_00775	KO:K03183	ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.16		3.80E-34
2558670107	DRAFT_00775	Locus_type		CDS	
2558670107	DRAFT_00775	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	
2558670107	DRAFT_00775	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670107	DRAFT_00775	Coordinates		33486..34172(-)	
2558670107	DRAFT_00775	DNA_length		687bp	
2558670107	DRAFT_00775	Protein_length		228aa	
2558670107	DRAFT_00775	GC			0.61

2558670107	DRAFT_00775	Transmembrane		Yes		
2558670108	DRAFT_00776	COG_category	[G] Carbohydrate transport and metabolism			
2558670108	DRAFT_00776	COG0063	Predicted sugar kinase			2.00E-52
2558670108	DRAFT_00776	pfam01256	Carb_kinase			8.10E-50
2558670108	DRAFT_00776	TIGR00196	yjeF C-terminal region, hydroxyethylthiazole kinase-related			2.00E-71
2558670108	DRAFT_00776	Locus_type		CDS		
2558670108	DRAFT_00776	Product_name		yjeF C-terminal region, hydroxyethylthiazole kinase-related		
2558670108	DRAFT_00776	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670108	DRAFT_00776	Coordinates		34259..35125(-)		
2558670108	DRAFT_00776	DNA_length		867bp		
2558670108	DRAFT_00776	Protein_length		288aa		
2558670108	DRAFT_00776	GC			0.64	
2558670109	DRAFT_00777	Metacyc	PWY-6610: adenine and adenosine salvage IV			
2558670109	DRAFT_00777	Metacyc	PWY-6605: adenine and adenosine salvage II			
2558670109	DRAFT_00777	Metacyc	P121-PWY: adenine and adenosine salvage I			
2558670109	DRAFT_00777	COG_category	[F] Nucleotide transport and metabolism			
2558670109	DRAFT_00777	COG0503	Adenine/guanine phosphoribosyltransferases and related PRPP-binding			6.00E-20
2558670109	DRAFT_00777	pfam00156	Pribosyltran			2.30E-16
2558670109	DRAFT_00777	EC:2.4.2.7	Adenine phosphoribosyltransferase.			
2558670109	DRAFT_00777	KO:K00759	adenine phosphoribosyltransferase [EC:2.4.2.7]			8.50E-40
2558670109	DRAFT_00777	Locus_type		CDS		
2558670109	DRAFT_00777	Product_name		Adenine/guanine phosphoribosyltransferases and related PRPP-bindi		
2558670109	DRAFT_00777	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670109	DRAFT_00777	Coordinates		35131..35871(-)		
2558670109	DRAFT_00777	DNA_length		741bp		
2558670109	DRAFT_00777	Protein_length		246aa		
2558670109	DRAFT_00777	GC			0.6	
2558670110	DRAFT_00778	Locus_type		CDS		
2558670110	DRAFT_00778	Product_name		hypothetical protein		
2558670110	DRAFT_00778	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670110	DRAFT_00778	Coordinates		35942..36139(-)		

2558670110	DRAFT_00778	DNA_length		198bp		
2558670110	DRAFT_00778	Protein_length		65aa		
2558670110	DRAFT_00778	GC			0.66	
2558670110	DRAFT_00778	Transmembrane		Yes		
2558670111	DRAFT_00779	Metacyc	PWY-6700: queuosine biosynthesis			
2558670111	DRAFT_00779	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670111	DRAFT_00779	COG0343	Queuine/archaeosine tRNA-ribosyltransferase			1.00E-76
2558670111	DRAFT_00779	pfam01702	TGT			5.80E-44
2558670111	DRAFT_00779	EC:2.4.2.29	tRNA-guanine(34) transglycosylase.			
2558670111	DRAFT_00779	TIGR00449	tRNA-guanine family transglycosylase			2.50E-70
2558670111	DRAFT_00779	TIGR00432	tRNA-guanine transglycosylase, archaeosine-15-forming			6.20E-116
2558670111	DRAFT_00779	KO:K00773	queuine tRNA-ribosyltransferase [EC:2.4.2.29]			0.00E+00
2558670111	DRAFT_00779	Locus_type		CDS		
2558670111	DRAFT_00779	Product_name		tRNA-guanine family transglycosylase		
2558670111	DRAFT_00779	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670111	DRAFT_00779	Coordinates		36189..37733(+)		
2558670111	DRAFT_00779	DNA_length		1545bp		
2558670111	DRAFT_00779	Protein_length		514aa		
2558670111	DRAFT_00779	GC			0.59	
2558670112	DRAFT_00780	COG_category	[R] General function prediction only			
2558670112	DRAFT_00780	COG1938	Archaeal enzymes of ATP-grasp superfamily			1.00E-32
2558670112	DRAFT_00780	pfam09754	PAC2			9.50E-26
2558670112	DRAFT_00780	KO:K06869	uncharacterized protein			3.30E-25
2558670112	DRAFT_00780	Locus_type		CDS		
2558670112	DRAFT_00780	Product_name		Archaeal enzymes of ATP-grasp superfamily		
2558670112	DRAFT_00780	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11		
2558670112	DRAFT_00780	Coordinates		37651..38352(-)		
2558670112	DRAFT_00780	DNA_length		702bp		
2558670112	DRAFT_00780	Protein_length		233aa		
2558670112	DRAFT_00780	GC			0.61	
2558670113	DRAFT_00781	COG_category	[L] Replication, recombination and repair			

2558670113	DRAFT_00781	COG3316	Transposase and inactivated derivatives		4.00E-15
2558670113	DRAFT_00781	pfam13610	DDE_Tnp_IS240		1.10E-22
2558670113	DRAFT_00781	Locus_type		CDS	
2558670113	DRAFT_00781	Product_name		Transposase and inactivated derivatives	
2558670113	DRAFT_00781	Scaffold		DRAFT_contig_70_77_len_39784_read_count_688219.11	
2558670113	DRAFT_00781	Coordinates		38745..39698(+)	
2558670113	DRAFT_00781	DNA_length		954bp	
2558670113	DRAFT_00781	Protein_length		317aa	
2558670113	DRAFT_00781	GC		0.52	
2558670114	DRAFT_00782	Locus_type		CDS	
2558670114	DRAFT_00782	Product_name		hypothetical protein	
2558670114	DRAFT_00782	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670114	DRAFT_00782	Coordinates		1..228(+)	
2558670114	DRAFT_00782	DNA_length		228bp	
2558670114	DRAFT_00782	Protein_length		75aa	
2558670114	DRAFT_00782	GC		0.5	
2558670115	DRAFT_00783	Locus_type		CDS	
2558670115	DRAFT_00783	Product_name		hypothetical protein	
2558670115	DRAFT_00783	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670115	DRAFT_00783	Coordinates		347..1213(-)	
2558670115	DRAFT_00783	DNA_length		867bp	
2558670115	DRAFT_00783	Protein_length		288aa	
2558670115	DRAFT_00783	GC		0.53	
2558670115	DRAFT_00783	Transmembrane		Yes	
2558670116	DRAFT_00784	Locus_type		CDS	
2558670116	DRAFT_00784	Product_name		hypothetical protein	
2558670116	DRAFT_00784	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670116	DRAFT_00784	Coordinates		1613..1957(-)	
2558670116	DRAFT_00784	DNA_length		345bp	
2558670116	DRAFT_00784	Protein_length		114aa	
2558670116	DRAFT_00784	GC		0.46	

2558670117	DRAFT_00785	pfam00583	Acetyltransf_1			2.80E-08
2558670117	DRAFT_00785	Locus_type		CDS		
2558670117	DRAFT_00785	Product_name		Acetyltransferases		
2558670117	DRAFT_00785	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670117	DRAFT_00785	Coordinates		2403..2834(+)		
2558670117	DRAFT_00785	DNA_length		432bp		
2558670117	DRAFT_00785	Protein_length		143aa		
2558670117	DRAFT_00785	GC			0.51	
2558670118	DRAFT_00786	COG_category	[S] Function unknown			
2558670118	DRAFT_00786	COG5616	Predicted integral membrane protein			1.00E-38
2558670118	DRAFT_00786	pfam00211	Guanylate_cyc			5.40E-20
2558670118	DRAFT_00786	EC:4.6.1.1	Adenylate cyclase.			
2558670118	DRAFT_00786	KO:K01768	adenylate cyclase [EC:4.6.1.1]			0.00E+00
2558670118	DRAFT_00786	Locus_type		CDS		
2558670118	DRAFT_00786	Product_name		Predicted integral membrane protein		
2558670118	DRAFT_00786	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670118	DRAFT_00786	Coordinates		3076..5001(-)		
2558670118	DRAFT_00786	DNA_length		1926bp		
2558670118	DRAFT_00786	Protein_length		641aa		
2558670118	DRAFT_00786	GC			0.57	
2558670119	DRAFT_00787	Locus_type		tRNA		
2558670119	DRAFT_00787	Product_name		tRNA_Asn_GTT		
2558670119	DRAFT_00787	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670119	DRAFT_00787	Coordinates		5229..5337(-)		
2558670119	DRAFT_00787	DNA_length		82bp		
2558670119	DRAFT_00787	GC			0.63	
2558670120	DRAFT_00788	Locus_type		CDS		
2558670120	DRAFT_00788	Product_name		hypothetical protein		
2558670120	DRAFT_00788	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670120	DRAFT_00788	Coordinates		5414..5662(+)		

2558670120	DRAFT_00788	DNA_length		249bp	
2558670120	DRAFT_00788	Protein_length		82aa	
2558670120	DRAFT_00788	GC		0.59	
2558670121	DRAFT_00789	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670121	DRAFT_00789	COG0023	Translation initiation factor 1 (eIF-1/SUI1) and related proteins		4.00E-16
2558670121	DRAFT_00789	pfam01253	SUI1		1.30E-19
2558670121	DRAFT_00789	TIGR01158	translation initation factor SUI1, putative, prokaryotic		4.40E-29
2558670121	DRAFT_00789	KO:K03113	translation initiation factor 1		2.10E-18
2558670121	DRAFT_00789	Locus_type		CDS	
2558670121	DRAFT_00789	Product_name		Translation initiation factor 1 (eIF-1/SUI1) and related proteins	
2558670121	DRAFT_00789	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670121	DRAFT_00789	Coordinates		5948..6244(+)	
2558670121	DRAFT_00789	DNA_length		297bp	
2558670121	DRAFT_00789	Protein_length		98aa	
2558670121	DRAFT_00789	GC		0.56	
2558670122	DRAFT_00790	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes		
2558670122	DRAFT_00790	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer		
2558670122	DRAFT_00790	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)		
2558670122	DRAFT_00790	Metacyc	PWY-6692: Fe(II) oxidation		
2558670122	DRAFT_00790	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation		
2558670122	DRAFT_00790	Metacyc	PWY-3781: aerobic respiration (cytochrome c)		
2558670122	DRAFT_00790	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer		
2558670122	DRAFT_00790	COG_category	[C] Energy production and conversion		
2558670122	DRAFT_00790	COG1005	NADH:ubiquinone oxidoreductase subunit 1 (chain H)		7.00E-64
2558670122	DRAFT_00790	pfam00146	NADHdh		1.70E-78
2558670122	DRAFT_00790	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).		
2558670122	DRAFT_00790	KO:K00337	NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]		0.00E+00
2558670122	DRAFT_00790	ITERM:05535	NADH dehydrogenase subunit H (EC 1.6.5.3)		
2558670122	DRAFT_00790	Locus_type		CDS	
2558670122	DRAFT_00790	Product_name		NADH dehydrogenase subunit H (EC 1.6.5.3)	
2558670122	DRAFT_00790	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670122	DRAFT_00790	Coordinates		6336..7520(+)	

2558670122	DRAFT_00790	DNA_length		1185bp		
2558670122	DRAFT_00790	Protein_length		394aa		
2558670122	DRAFT_00790	GC			0.57	
2558670122	DRAFT_00790	Transmembrane		Yes		
2558670123	DRAFT_00791	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2558670123	DRAFT_00791	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558670123	DRAFT_00791	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558670123	DRAFT_00791	Metacyc	PWY-6692: Fe(II) oxidation			
2558670123	DRAFT_00791	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558670123	DRAFT_00791	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558670123	DRAFT_00791	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558670123	DRAFT_00791	COG_category	[C] Energy production and conversion			
2558670123	DRAFT_00791	COG1143	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 2			7.00E-28
2558670123	DRAFT_00791	pfam12838	Fer4_7			4.20E-10
2558670123	DRAFT_00791	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558670123	DRAFT_00791	KO:K00338	NADH-quinone oxidoreductase subunit I [EC:1.6.5.3]			0.00E+00
2558670123	DRAFT_00791	Locus_type		CDS		
2558670123	DRAFT_00791	Product_name		Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase		
2558670123	DRAFT_00791	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670123	DRAFT_00791	Coordinates		7521..8036(+)		
2558670123	DRAFT_00791	DNA_length		516bp		
2558670123	DRAFT_00791	Protein_length		171aa		
2558670123	DRAFT_00791	GC			0.57	
2558670124	DRAFT_00792	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2558670124	DRAFT_00792	Metacyc	PWY-6692: Fe(II) oxidation			
2558670124	DRAFT_00792	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558670124	DRAFT_00792	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558670124	DRAFT_00792	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558670124	DRAFT_00792	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558670124	DRAFT_00792	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558670124	DRAFT_00792	COG_category	[C] Energy production and conversion			
2558670124	DRAFT_00792	COG0839	NADH:ubiquinone oxidoreductase subunit 6 (chain J)			8.00E-10

2558670124	DRAFT_00792	pfam00499	Oxidored_q3			6.60E-17
2558670124	DRAFT_00792	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558670124	DRAFT_00792	KO:K00339	NADH-quinone oxidoreductase subunit J [EC:1.6.5.3]			6.90E-33
2558670124	DRAFT_00792	Locus_type		CDS		
2558670124	DRAFT_00792	Product_name		NADH:ubiquinone oxidoreductase subunit 6 (chain J)		
2558670124	DRAFT_00792	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670124	DRAFT_00792	Coordinates		8029..8535(+)		
2558670124	DRAFT_00792	DNA_length		507bp		
2558670124	DRAFT_00792	Protein_length		168aa		
2558670124	DRAFT_00792	GC			0.59	
2558670124	DRAFT_00792	Transmembrane		Yes		
2558670125	DRAFT_00793	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2558670125	DRAFT_00793	Metacyc	PWY-6692: Fe(II) oxidation			
2558670125	DRAFT_00793	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558670125	DRAFT_00793	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558670125	DRAFT_00793	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558670125	DRAFT_00793	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558670125	DRAFT_00793	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558670125	DRAFT_00793	COG_category	[C] Energy production and conversion			
2558670125	DRAFT_00793	COG0713	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)			1.00E-16
2558670125	DRAFT_00793	pfam00420	Oxidored_q2			1.40E-24
2558670125	DRAFT_00793	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558670125	DRAFT_00793	KO:K00340	NADH-quinone oxidoreductase subunit K [EC:1.6.5.3]			2.10E-23
2558670125	DRAFT_00793	Locus_type		CDS		
2558670125	DRAFT_00793	Product_name		NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)		
2558670125	DRAFT_00793	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670125	DRAFT_00793	Coordinates		8553..8837(+)		
2558670125	DRAFT_00793	DNA_length		285bp		
2558670125	DRAFT_00793	Protein_length		94aa		
2558670125	DRAFT_00793	GC			0.51	
2558670125	DRAFT_00793	Transmembrane		Yes		
2558670126	DRAFT_00794	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			

2558670126	DRAFT_00794	Metacyc	PWY-6692: Fe(II) oxidation		
2558670126	DRAFT_00794	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer		
2558670126	DRAFT_00794	Metacyc	PWY-3781: aerobic respiration (cytochrome c)		
2558670126	DRAFT_00794	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation		
2558670126	DRAFT_00794	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer		
2558670126	DRAFT_00794	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)		
2558670126	DRAFT_00794	COG_category	[C] Energy production and conversion		
2558670126	DRAFT_00794	COG1008	NADH:ubiquinone oxidoreductase subunit 4 (chain M)		1.00E-57
2558670126	DRAFT_00794	pfam00361	Oxidored_q1		7.60E-52
2558670126	DRAFT_00794	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).		
2558670126	DRAFT_00794	TIGR01972	proton-translocating NADH-quinone oxidoreductase, chain M		9.50E-79
2558670126	DRAFT_00794	KO:K00342	NADH-quinone oxidoreductase subunit M [EC:1.6.5.3]		0.00E+00
2558670126	DRAFT_00794	Locus_type		CDS	
2558670126	DRAFT_00794	Product_name		NADH:ubiquinone oxidoreductase subunit 4 (chain M)	
2558670126	DRAFT_00794	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670126	DRAFT_00794	Coordinates		8915..10414(+)	
2558670126	DRAFT_00794	DNA_length		1500bp	
2558670126	DRAFT_00794	Protein_length		499aa	
2558670126	DRAFT_00794	GC		0.55	
2558670126	DRAFT_00794	Transmembrane		Yes	

2558670127	DRAFT_00795	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes		
2558670127	DRAFT_00795	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation		
2558670127	DRAFT_00795	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)		
2558670127	DRAFT_00795	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer		
2558670127	DRAFT_00795	Metacyc	PWY-6692: Fe(II) oxidation		
2558670127	DRAFT_00795	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer		
2558670127	DRAFT_00795	Metacyc	PWY-3781: aerobic respiration (cytochrome c)		
2558670127	DRAFT_00795	COG_category	[C] Energy production and conversion		
2558670127	DRAFT_00795	COG_category	[P] Inorganic ion transport and metabolism		
2558670127	DRAFT_00795	COG1009	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na		8.00E-107
2558670127	DRAFT_00795	pfam00361	Oxidored_q1		6.70E-59
2558670127	DRAFT_00795	pfam00662	Oxidored_q1_N		7.90E-09
2558670127	DRAFT_00795	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).		

2558670127	DRAFT_00795	TIGR01974	proton-translocating NADH-quinone oxidoreductase, chain L		0.00E+00
2558670127	DRAFT_00795	KO:K00341	NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]		0.00E+00
2558670127	DRAFT_00795	Locus_type		CDS	
2558670127	DRAFT_00795	Product_name		proton-translocating NADH-quinone oxidoreductase, chain L	
2558670127	DRAFT_00795	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670127	DRAFT_00795	Coordinates		10411..12588(+)	
2558670127	DRAFT_00795	DNA_length		2178bp	
2558670127	DRAFT_00795	Protein_length		725aa	
2558670127	DRAFT_00795	GC		0.56	
2558670127	DRAFT_00795	Transmembrane		Yes	

2558670128	DRAFT_00796	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes		
2558670128	DRAFT_00796	Metacyc	PWY-6692: Fe(II) oxidation		
2558670128	DRAFT_00796	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer		
2558670128	DRAFT_00796	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)		
2558670128	DRAFT_00796	Metacyc	PWY-3781: aerobic respiration (cytochrome c)		
2558670128	DRAFT_00796	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation		
2558670128	DRAFT_00796	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer		
2558670128	DRAFT_00796	COG_category	[C] Energy production and conversion		
2558670128	DRAFT_00796	COG1008	NADH:ubiquinone oxidoreductase subunit 4 (chain M)		4.00E-102
2558670128	DRAFT_00796	pfam00361	Oxidored_q1		4.40E-66
2558670128	DRAFT_00796	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).		
2558670128	DRAFT_00796	TIGR01972	proton-translocating NADH-quinone oxidoreductase, chain M		0.00E+00
2558670128	DRAFT_00796	KO:K00342	NADH-quinone oxidoreductase subunit M [EC:1.6.5.3]		0.00E+00
2558670128	DRAFT_00796	Locus_type		CDS	
2558670128	DRAFT_00796	Product_name		proton-translocating NADH-quinone oxidoreductase, chain M	
2558670128	DRAFT_00796	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670128	DRAFT_00796	Coordinates		12585..14060(+)	
2558670128	DRAFT_00796	DNA_length		1476bp	
2558670128	DRAFT_00796	Protein_length		491aa	
2558670128	DRAFT_00796	GC		0.56	
2558670128	DRAFT_00796	Transmembrane		Yes	

2558670129	DRAFT_00797	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes		

2558670129	DRAFT_00797	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558670129	DRAFT_00797	Metacyc	PWY-6692: Fe(II) oxidation			
2558670129	DRAFT_00797	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558670129	DRAFT_00797	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558670129	DRAFT_00797	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558670129	DRAFT_00797	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558670129	DRAFT_00797	COG_category	[C] Energy production and conversion			
2558670129	DRAFT_00797	COG1007	NADH:ubiquinone oxidoreductase subunit 2 (chain N)			7.00E-69
2558670129	DRAFT_00797	pfam00361	Oxidored_q1			9.00E-63
2558670129	DRAFT_00797	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558670129	DRAFT_00797	TIGR01770	proton-translocating NADH-quinone oxidoreductase, chain N			2.90E-96
2558670129	DRAFT_00797	KO:K00343	NADH-quinone oxidoreductase subunit N [EC:1.6.5.3]			0.00E+00
2558670129	DRAFT_00797	Locus_type		CDS		
2558670129	DRAFT_00797	Product_name		NADH:ubiquinone oxidoreductase subunit 2 (chain N)		
2558670129	DRAFT_00797	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670129	DRAFT_00797	Coordinates		14123..15520(+)		
2558670129	DRAFT_00797	DNA_length		1398bp		
2558670129	DRAFT_00797	Protein_length		465aa		
2558670129	DRAFT_00797	GC			0.56	
2558670129	DRAFT_00797	Transmembrane		Yes		
2558670130	DRAFT_00798	KEGG_module	M00159: V-type ATPase, prokaryotes			
2558670130	DRAFT_00798	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558670130	DRAFT_00798	COG_category	[C] Energy production and conversion			
2558670130	DRAFT_00798	COG1269	Archaeal/vacuolar-type H+-ATPase subunit I			2.00E-67
2558670130	DRAFT_00798	pfam01496	V_ATPase_I			2.80E-51
2558670130	DRAFT_00798	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2558670130	DRAFT_00798	KO:K02123	V-type H+-transporting ATPase subunit I [EC:3.6.3.14]			0.00E+00
2558670130	DRAFT_00798	Locus_type		CDS		
2558670130	DRAFT_00798	Product_name		Archaeal/vacuolar-type H+-ATPase subunit I		
2558670130	DRAFT_00798	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670130	DRAFT_00798	Coordinates		15524..17569(-)		
2558670130	DRAFT_00798	DNA_length		2046bp		
2558670130	DRAFT_00798	Protein_length		681aa		

2558670130	DRAFT_00798	GC			0.55	
2558670130	DRAFT_00798	Transmembrane		Yes		
2558670131	DRAFT_00799	KEGG_module	M00159: V-type ATPase, prokaryotes			
2558670131	DRAFT_00799	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558670131	DRAFT_00799	COG_category	[C] Energy production and conversion			
2558670131	DRAFT_00799	COG1527	Archaeal/vacuolar-type H+-ATPase subunit C			9.00E-21
2558670131	DRAFT_00799	pfam01992	vATP-synt_AC39			5.20E-24
2558670131	DRAFT_00799	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2558670131	DRAFT_00799	KO:K02119	V-type H+-transporting ATPase subunit C [EC:3.6.3.14]			0.00E+00
2558670131	DRAFT_00799	Locus_type		CDS		
2558670131	DRAFT_00799	Product_name		Archaeal/vacuolar-type H+-ATPase subunit C		
2558670131	DRAFT_00799	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670131	DRAFT_00799	Coordinates		17692..18744(+)		
2558670131	DRAFT_00799	DNA_length		1053bp		
2558670131	DRAFT_00799	Protein_length		350aa		
2558670131	DRAFT_00799	GC			0.55	
2558670132	DRAFT_00800	Locus_type		CDS		
2558670132	DRAFT_00800	Product_name		hypothetical protein		
2558670132	DRAFT_00800	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670132	DRAFT_00800	Coordinates		18859..19299(-)		
2558670132	DRAFT_00800	DNA_length		441bp		
2558670132	DRAFT_00800	Protein_length		146aa		
2558670132	DRAFT_00800	GC			0.49	
2558670133	DRAFT_00801	COG_category	[L] Replication, recombination and repair			
2558670133	DRAFT_00801	COG3316	Transposase and inactivated derivatives			4.00E-11
2558670133	DRAFT_00801	pfam13610	DDE_Tnp_IS240			3.60E-22
2558670133	DRAFT_00801	Locus_type		CDS		
2558670133	DRAFT_00801	Product_name		Transposase and inactivated derivatives		
2558670133	DRAFT_00801	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670133	DRAFT_00801	Coordinates		19296..20429(-)		
2558670133	DRAFT_00801	DNA_length		1134bp		

2558670133	DRAFT_00801	Protein_length		377aa		
2558670133	DRAFT_00801	GC			0.53	
2558670134	DRAFT_00802	Locus_type		CDS		
2558670134	DRAFT_00802	Product_name		hypothetical protein		
2558670134	DRAFT_00802	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670134	DRAFT_00802	Coordinates		20645..20818(+)		
2558670134	DRAFT_00802	DNA_length		174bp		
2558670134	DRAFT_00802	Protein_length		57aa		
2558670134	DRAFT_00802	GC			0.49	
2558670135	DRAFT_00803	Locus_type		CDS		
2558670135	DRAFT_00803	Product_name		hypothetical protein		
2558670135	DRAFT_00803	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670135	DRAFT_00803	Coordinates		20799..21353(+)		
2558670135	DRAFT_00803	DNA_length		555bp		
2558670135	DRAFT_00803	Protein_length		184aa		
2558670135	DRAFT_00803	GC			0.5	
2558670136	DRAFT_00804	Locus_type		CDS		
2558670136	DRAFT_00804	Product_name		hypothetical protein		
2558670136	DRAFT_00804	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670136	DRAFT_00804	Coordinates		21350..21610(+)		
2558670136	DRAFT_00804	DNA_length		261bp		
2558670136	DRAFT_00804	Protein_length		86aa		
2558670136	DRAFT_00804	GC			0.47	
2558670137	DRAFT_00805	KEGG_module	M00159: V-type ATPase, prokaryotes			
2558670137	DRAFT_00805	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558670137	DRAFT_00805	pfam00137	ATP-synt_C			2.90E-21
2558670137	DRAFT_00805	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2558670137	DRAFT_00805	KO:K02124	V-type H+-transporting ATPase subunit K [EC:3.6.3.14]			7.80E-16
2558670137	DRAFT_00805	Locus_type		CDS		
2558670137	DRAFT_00805	Product_name		ATP synthase subunit C		

2558670137	DRAFT_00805	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670137	DRAFT_00805	Coordinates		21636..21962(+)		
2558670137	DRAFT_00805	DNA_length		327bp		
2558670137	DRAFT_00805	Protein_length		108aa		
2558670137	DRAFT_00805	GC			0.54	
2558670137	DRAFT_00805	Signal_peptide		Yes		
2558670137	DRAFT_00805	Transmembrane		Yes		
2558670138	DRAFT_00806	Metacyc	PWY-5783: octaprenyl diphosphate biosynthesis			
2558670138	DRAFT_00806	COG_category	[H] Coenzyme transport and metabolism			
2558670138	DRAFT_00806	COG0142	Geranylgeranyl pyrophosphate synthase			3.00E-41
2558670138	DRAFT_00806	pfam00348	polyprenyl_synt			5.20E-43
2558670138	DRAFT_00806	EC:2.5.1.90	All-trans-octaprenyl-diphosphate synthase.			
2558670138	DRAFT_00806	KO:K02523	octaprenyl-diphosphate synthase [EC:2.5.1.90]			0.00E+00
2558670138	DRAFT_00806	Locus_type		CDS		
2558670138	DRAFT_00806	Product_name		Geranylgeranyl pyrophosphate synthase		
2558670138	DRAFT_00806	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670138	DRAFT_00806	Coordinates		22104..22961(-)		
2558670138	DRAFT_00806	DNA_length		858bp		
2558670138	DRAFT_00806	Protein_length		285aa		
2558670138	DRAFT_00806	GC			0.55	
2558670138	DRAFT_00806	Transmembrane		Yes		
2558670139	DRAFT_00807	Locus_type		tRNA		
2558670139	DRAFT_00807	Product_name		tRNA_Pseudo_TTC		
2558670139	DRAFT_00807	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670139	DRAFT_00807	Coordinates		23327..23398(+)		
2558670139	DRAFT_00807	DNA_length		72bp		
2558670139	DRAFT_00807	GC			0.67	
2558670140	DRAFT_00808	Locus_type		CDS		
2558670140	DRAFT_00808	Product_name		hypothetical protein		
2558670140	DRAFT_00808	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670140	DRAFT_00808	Coordinates		23454..24824(+)		

2558670140	DRAFT_00808	DNA_length		1371bp	
2558670140	DRAFT_00808	Protein_length		456aa	
2558670140	DRAFT_00808	GC		0.56	
2558670141	DRAFT_00809	Locus_type		CDS	
2558670141	DRAFT_00809	Product_name		hypothetical protein	
2558670141	DRAFT_00809	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670141	DRAFT_00809	Coordinates		25126..26250(+)	
2558670141	DRAFT_00809	DNA_length		1125bp	
2558670141	DRAFT_00809	Protein_length		374aa	
2558670141	DRAFT_00809	GC		0.59	
2558670141	DRAFT_00809	Signal_peptide		Yes	
2558670142	DRAFT_00810	Locus_type		CDS	
2558670142	DRAFT_00810	Product_name		hypothetical protein	
2558670142	DRAFT_00810	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670142	DRAFT_00810	Coordinates		26367..26915(-)	
2558670142	DRAFT_00810	DNA_length		549bp	
2558670142	DRAFT_00810	Protein_length		182aa	
2558670142	DRAFT_00810	GC		0.51	
2558670142	DRAFT_00810	Transmembrane		Yes	
2558670143	DRAFT_00811	pfam00096	zf-C2H2		3.10E-04
2558670143	DRAFT_00811	Locus_type		CDS	
2558670143	DRAFT_00811	Product_name		Zinc finger, C2H2 type	
2558670143	DRAFT_00811	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670143	DRAFT_00811	Coordinates		26992..27480(+)	
2558670143	DRAFT_00811	DNA_length		489bp	
2558670143	DRAFT_00811	Protein_length		162aa	
2558670143	DRAFT_00811	GC		0.52	
2558670143	DRAFT_00811	Transmembrane		Yes	
2558670144	DRAFT_00812	Locus_type		CDS	
2558670144	DRAFT_00812	Product_name		hypothetical protein	

2558670144	DRAFT_00812	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670144	DRAFT_00812	Coordinates		28067..30187(+)	
2558670144	DRAFT_00812	DNA_length		2121bp	
2558670144	DRAFT_00812	Protein_length		706aa	
2558670144	DRAFT_00812	GC		0.56	
2558670144	DRAFT_00812	Signal_peptide		Yes	
2558670144	DRAFT_00812	Transmembrane		Yes	
2558670145	DRAFT_00813	pfam13392	HNH_3		9.60E-08
2558670145	DRAFT_00813	Locus_type		CDS	
2558670145	DRAFT_00813	Product_name		HNH endonuclease	
2558670145	DRAFT_00813	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670145	DRAFT_00813	Coordinates		30376..30954(-)	
2558670145	DRAFT_00813	DNA_length		579bp	
2558670145	DRAFT_00813	Protein_length		192aa	
2558670145	DRAFT_00813	GC		0.58	
2558670146	DRAFT_00814	Locus_type		CDS	
2558670146	DRAFT_00814	Product_name		hypothetical protein	
2558670146	DRAFT_00814	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670146	DRAFT_00814	Coordinates		31056..31250(-)	
2558670146	DRAFT_00814	DNA_length		195bp	
2558670146	DRAFT_00814	Protein_length		64aa	
2558670146	DRAFT_00814	GC		0.52	
2558670147	DRAFT_00815	Locus_type		CDS	
2558670147	DRAFT_00815	Product_name		hypothetical protein	
2558670147	DRAFT_00815	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12	
2558670147	DRAFT_00815	Coordinates		31325..32203(+)	
2558670147	DRAFT_00815	DNA_length		879bp	
2558670147	DRAFT_00815	Protein_length		292aa	
2558670147	DRAFT_00815	GC		0.56	
2558670148	DRAFT_00816	Locus_type		CDS	

2558670148	DRAFT_00816	Product_name		hypothetical protein		
2558670148	DRAFT_00816	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670148	DRAFT_00816	Coordinates		32811..33320(-)		
2558670148	DRAFT_00816	DNA_length		510bp		
2558670148	DRAFT_00816	Protein_length		169aa		
2558670148	DRAFT_00816	GC			0.5	
2558670149	DRAFT_00817	pfam00149	Metallophos			2.10E-06
2558670149	DRAFT_00817	Locus_type		CDS		
2558670149	DRAFT_00817	Product_name		Calcineurin-like phosphoesterase		
2558670149	DRAFT_00817	Scaffold		DRAFT_contig_70_78_len_38919_read_count_721921.12		
2558670149	DRAFT_00817	Coordinates		33464..38476(+)		
2558670149	DRAFT_00817	DNA_length		5013bp		
2558670149	DRAFT_00817	Protein_length		1670aa		
2558670149	DRAFT_00817	GC			0.55	
2558670149	DRAFT_00817	Transmembrane		Yes		
2558670150	DRAFT_00818	pfam13240	zinc_ribbon_2			6.80E-08
2558670150	DRAFT_00818	Locus_type		CDS		
2558670150	DRAFT_00818	Product_name		Predicted ferric reductase		
2558670150	DRAFT_00818	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670150	DRAFT_00818	Coordinates		2..526(+)		
2558670150	DRAFT_00818	DNA_length		525bp		
2558670150	DRAFT_00818	Protein_length		174aa		
2558670150	DRAFT_00818	GC			0.55	
2558670150	DRAFT_00818	Transmembrane		Yes		
2558670151	DRAFT_00819	pfam01243	Pyridox_oxidase			3.90E-13
2558670151	DRAFT_00819	TIGR03618	PPOX class probable F420-dependent enzyme			9.30E-31
2558670151	DRAFT_00819	Locus_type		CDS		
2558670151	DRAFT_00819	Product_name		PPOX class probable F420-dependent enzyme		
2558670151	DRAFT_00819	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670151	DRAFT_00819	Coordinates		603..992(-)		
2558670151	DRAFT_00819	DNA_length		390bp		

2558670151	DRAFT_00819	Protein_length		129aa	
2558670151	DRAFT_00819	GC		0.5	
2558670152	DRAFT_00820	COG_category	[S] Function unknown		
2558670152	DRAFT_00820	COG4280	Predicted membrane protein		2.00E-20
2558670152	DRAFT_00820	Locus_type		CDS	
2558670152	DRAFT_00820	Product_name		Predicted membrane protein	
2558670152	DRAFT_00820	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670152	DRAFT_00820	Coordinates		1101..1781(+)	
2558670152	DRAFT_00820	DNA_length		681bp	
2558670152	DRAFT_00820	Protein_length		226aa	
2558670152	DRAFT_00820	GC		0.5	
2558670152	DRAFT_00820	Transmembrane		Yes	
2558670153	DRAFT_00821	Locus_type		CDS	
2558670153	DRAFT_00821	Product_name		hypothetical protein	
2558670153	DRAFT_00821	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670153	DRAFT_00821	Coordinates		1798..1965(+)	
2558670153	DRAFT_00821	DNA_length		168bp	
2558670153	DRAFT_00821	Protein_length		55aa	
2558670153	DRAFT_00821	GC		0.51	
2558670154	DRAFT_00822	pfam07690	MFS_1		7.10E-16
2558670154	DRAFT_00822	Locus_type		CDS	
2558670154	DRAFT_00822	Product_name		Major Facilitator Superfamily	
2558670154	DRAFT_00822	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670154	DRAFT_00822	Coordinates		1987..3291(+)	
2558670154	DRAFT_00822	DNA_length		1305bp	
2558670154	DRAFT_00822	Protein_length		434aa	
2558670154	DRAFT_00822	GC		0.55	
2558670154	DRAFT_00822	Transmembrane		Yes	
2558670155	DRAFT_00823	COG_category	[S] Function unknown		
2558670155	DRAFT_00823	COG4095	Uncharacterized conserved protein		7.00E-08

2558670155	DRAFT_00823	pfam04193	PQ-loop		2.00E-09
2558670155	DRAFT_00823	KO:K15383	MtN3 and saliva related transmembrane protein		8.70E-14
2558670155	DRAFT_00823	Locus_type		CDS	
2558670155	DRAFT_00823	Product_name		Uncharacterized conserved protein	
2558670155	DRAFT_00823	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670155	DRAFT_00823	Coordinates		3440..3718(+)	
2558670155	DRAFT_00823	DNA_length		279bp	
2558670155	DRAFT_00823	Protein_length		92aa	
2558670155	DRAFT_00823	GC		0.5	
2558670155	DRAFT_00823	Transmembrane		Yes	

2558670156	DRAFT_00824	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670156	DRAFT_00824	COG5257	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)		0.00E+00
2558670156	DRAFT_00824	pfam00009	GTP_EFTU		3.60E-42
2558670156	DRAFT_00824	pfam03144	GTP_EFTU_D2		4.90E-06
2558670156	DRAFT_00824	pfam09173	eIF2_C		1.50E-23
2558670156	DRAFT_00824	TIGR00231	small GTP-binding protein domain		2.60E-17
2558670156	DRAFT_00824	TIGR03680	translation initiation factor 2 subunit gamma		0.00E+00
2558670156	DRAFT_00824	KO:K03242	translation initiation factor 2 subunit 3		0.00E+00
2558670156	DRAFT_00824	ITERM:02577	translation initiation factor 2 subunit gamma (aeIF-2g)		
2558670156	DRAFT_00824	Locus_type		CDS	
2558670156	DRAFT_00824	Product_name		translation initiation factor 2 subunit gamma (aeIF-2g)	
2558670156	DRAFT_00824	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670156	DRAFT_00824	Coordinates		3903..5165(+)	
2558670156	DRAFT_00824	DNA_length		1263bp	
2558670156	DRAFT_00824	Protein_length		420aa	
2558670156	DRAFT_00824	GC		0.62	

2558670157	DRAFT_00825	COG_category	[R] General function prediction only		
2558670157	DRAFT_00825	COG1412	Uncharacterized proteins of PilT N-term./Vapc superfamily		2.00E-07
2558670157	DRAFT_00825	Locus_type		CDS	
2558670157	DRAFT_00825	Product_name		Uncharacterized proteins of PilT N-term./Vapc superfamily	
2558670157	DRAFT_00825	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670157	DRAFT_00825	Coordinates		5169..5537(+)	

2558670157	DRAFT_00825	DNA_length		369bp	
2558670157	DRAFT_00825	Protein_length		122aa	
2558670157	DRAFT_00825	GC		0.6	
2558670158	DRAFT_00826	KEGG_module	M00115: NAD biosynthesis, aspartate => NAD		
2558670158	DRAFT_00826	Metacyc	PYRIDNUCSYN-PWY: NAD biosynthesis I (from aspartate)		
2558670158	DRAFT_00826	COG_category	[H] Coenzyme transport and metabolism		
2558670158	DRAFT_00826	COG0171	NAD synthase		3.00E-68
2558670158	DRAFT_00826	pfam02540	NAD_synthase		2.30E-71
2558670158	DRAFT_00826	EC:6.3.1.5	NAD(+) synthase.		
2558670158	DRAFT_00826	TIGR00552	NAD+ synthetase		1.40E-69
2558670158	DRAFT_00826	KO:K01916	NAD+ synthase [EC:6.3.1.5]		0.00E+00
2558670158	DRAFT_00826	Locus_type		CDS	
2558670158	DRAFT_00826	Product_name		NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	
2558670158	DRAFT_00826	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670158	DRAFT_00826	Coordinates		5584..6375(+)	
2558670158	DRAFT_00826	DNA_length		792bp	
2558670158	DRAFT_00826	Protein_length		263aa	
2558670158	DRAFT_00826	GC		0.61	
2558670159	DRAFT_00827	KEGG_module	M00184: RNA polymerase, archaea		
2558670159	DRAFT_00827	COG_category	[K] Transcription		
2558670159	DRAFT_00827	COG1095	DNA-directed RNA polymerase, subunit E'		1.00E-48
2558670159	DRAFT_00827	pfam00575	S1		5.50E-14
2558670159	DRAFT_00827	pfam03876	SHS2_Rpb7-N		6.90E-16
2558670159	DRAFT_00827	EC:2.7.7.6	DNA-directed RNA polymerase.		
2558670159	DRAFT_00827	TIGR00448	DNA-directed RNA polymerase (rpoE), archaeal and eukaryotic form		7.30E-61
2558670159	DRAFT_00827	KO:K03049	DNA-directed RNA polymerase subunit E' [EC:2.7.7.6]		0.00E+00
2558670159	DRAFT_00827	Locus_type		CDS	
2558670159	DRAFT_00827	Product_name		DNA-directed RNA polymerase (rpoE), archaeal and eukaryotic form	
2558670159	DRAFT_00827	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670159	DRAFT_00827	Coordinates		6443..7027(+)	
2558670159	DRAFT_00827	DNA_length		585bp	
2558670159	DRAFT_00827	Protein_length		194aa	

2558670159	DRAFT_00827	GC			0.56	
2558670160	DRAFT_00828	KEGG_module	M00184: RNA polymerase, archaea			
2558670160	DRAFT_00828	COG_category	[K] Transcription			
2558670160	DRAFT_00828	COG2093	DNA-directed RNA polymerase, subunit E''			1.00E-15
2558670160	DRAFT_00828	pfam06093	Spt4			9.00E-14
2558670160	DRAFT_00828	EC:2.7.7.6	DNA-directed RNA polymerase.			
2558670160	DRAFT_00828	KO:K03050	DNA-directed RNA polymerase subunit E" [EC:2.7.7.6]			2.60E-14
2558670160	DRAFT_00828	Locus_type		CDS		
2558670160	DRAFT_00828	Product_name		DNA-directed RNA polymerase, subunit E'' (EC 2.7.7.6)		
2558670160	DRAFT_00828	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670160	DRAFT_00828	Coordinates		7039..7224(+)		
2558670160	DRAFT_00828	DNA_length		186bp		
2558670160	DRAFT_00828	Protein_length		61aa		
2558670160	DRAFT_00828	GC			0.55	
2558670161	DRAFT_00829	COG_category	[S] Function unknown			
2558670161	DRAFT_00829	COG1909	Uncharacterized protein conserved in archaea			3.00E-32
2558670161	DRAFT_00829	pfam04019	DUF359			1.20E-32
2558670161	DRAFT_00829	KO:K09735	hypothetical protein			1.00E-26
2558670161	DRAFT_00829	Locus_type		CDS		
2558670161	DRAFT_00829	Product_name		Uncharacterized protein conserved in archaea		
2558670161	DRAFT_00829	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670161	DRAFT_00829	Coordinates		7229..7762(+)		
2558670161	DRAFT_00829	DNA_length		534bp		
2558670161	DRAFT_00829	Protein_length		177aa		
2558670161	DRAFT_00829	GC			0.6	
2558670162	DRAFT_00830	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670162	DRAFT_00830	COG2004	Ribosomal protein S24E			5.00E-05
2558670162	DRAFT_00830	pfam01282	Ribosomal_S24e			5.80E-08
2558670162	DRAFT_00830	Locus_type		CDS		
2558670162	DRAFT_00830	Product_name		Ribosomal protein S24E		
2558670162	DRAFT_00830	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		

2558670162	DRAFT_00830	Coordinates		7795..8139(+)		
2558670162	DRAFT_00830	DNA_length		345bp		
2558670162	DRAFT_00830	Protein_length		114aa		
2558670162	DRAFT_00830	GC			0.59	

2558670163	DRAFT_00831	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670163	DRAFT_00831	COG1998	Ribosomal protein S27AE			1.00E-12
2558670163	DRAFT_00831	pfam01599	Ribosomal_S27			2.50E-17
2558670163	DRAFT_00831	Locus_type		CDS		
2558670163	DRAFT_00831	Product_name		Ribosomal protein S27AE		
2558670163	DRAFT_00831	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670163	DRAFT_00831	Coordinates		8142..8447(+)		
2558670163	DRAFT_00831	DNA_length		306bp		
2558670163	DRAFT_00831	Protein_length		101aa		
2558670163	DRAFT_00831	GC			0.55	

2558670164	DRAFT_00832	Locus_type		CDS		
2558670164	DRAFT_00832	Product_name		hypothetical protein		
2558670164	DRAFT_00832	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670164	DRAFT_00832	Coordinates		8609..9643(-)		
2558670164	DRAFT_00832	DNA_length		1035bp		
2558670164	DRAFT_00832	Protein_length		344aa		
2558670164	DRAFT_00832	GC			0.56	
2558670164	DRAFT_00832	Signal_peptide		Yes		
2558670164	DRAFT_00832	Transmembrane		Yes		

2558670165	DRAFT_00833	COG_category	[L] Replication, recombination and repair			
2558670165	DRAFT_00833	COG3316	Transposase and inactivated derivatives			7.00E-10
2558670165	DRAFT_00833	pfam13610	DDE_Tnp_IS240			9.60E-21
2558670165	DRAFT_00833	Locus_type		CDS		
2558670165	DRAFT_00833	Product_name		Transposase and inactivated derivatives		
2558670165	DRAFT_00833	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670165	DRAFT_00833	Coordinates		9718..10893(-)		
2558670165	DRAFT_00833	DNA_length		1176bp		

2558670165	DRAFT_00833	Protein_length		391aa	
2558670165	DRAFT_00833	GC		0.53	
2558670166	DRAFT_00834	Locus_type		CDS	
2558670166	DRAFT_00834	Product_name		hypothetical protein	
2558670166	DRAFT_00834	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670166	DRAFT_00834	Coordinates		11155..11946(-)	
2558670166	DRAFT_00834	DNA_length		792bp	
2558670166	DRAFT_00834	Protein_length		263aa	
2558670166	DRAFT_00834	GC		0.5	
2558670167	DRAFT_00835	Locus_type		CDS	
2558670167	DRAFT_00835	Product_name		Mn2+-dependent serine/threonine protein kinase	
2558670167	DRAFT_00835	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670167	DRAFT_00835	Coordinates		12281..13906(-)	
2558670167	DRAFT_00835	DNA_length		1626bp	
2558670167	DRAFT_00835	Protein_length		541aa	
2558670167	DRAFT_00835	GC		0.61	
2558670168	DRAFT_00836	Locus_type		CDS	
2558670168	DRAFT_00836	Product_name		hypothetical protein	
2558670168	DRAFT_00836	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670168	DRAFT_00836	Coordinates		13903..14589(-)	
2558670168	DRAFT_00836	DNA_length		687bp	
2558670168	DRAFT_00836	Protein_length		228aa	
2558670168	DRAFT_00836	GC		0.6	
2558670169	DRAFT_00837	COG_category	[K] Transcription		
2558670169	DRAFT_00837	COG1522	Transcriptional regulators		9.00E-18
2558670169	DRAFT_00837	pfam13412	HTH_24		3.10E-11
2558670169	DRAFT_00837	pfam01037	AsnC_trans_reg		2.40E-07
2558670169	DRAFT_00837	KO:K03718	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and		1.20E-34
2558670169	DRAFT_00837	Locus_type		CDS	
2558670169	DRAFT_00837	Product_name		Transcriptional regulators	

2558670169	DRAFT_00837	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670169	DRAFT_00837	Coordinates		14631..15107(-)	
2558670169	DRAFT_00837	DNA_length		477bp	
2558670169	DRAFT_00837	Protein_length		158aa	
2558670169	DRAFT_00837	GC		0.59	
2558670170	DRAFT_00838	KEGG_module	M00179: Ribosome, archaea		
2558670170	DRAFT_00838	KEGG_module	M00177: Ribosome, eukaryotes		
2558670170	DRAFT_00838	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670170	DRAFT_00838	COG2125	Ribosomal protein S6E (S10)		2.00E-28
2558670170	DRAFT_00838	pfam01092	Ribosomal_S6e		4.50E-24
2558670170	DRAFT_00838	KO:K02991	small subunit ribosomal protein S6e		1.60E-28
2558670170	DRAFT_00838	Locus_type		CDS	
2558670170	DRAFT_00838	Product_name		SSU ribosomal protein S6E	
2558670170	DRAFT_00838	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670170	DRAFT_00838	Coordinates		15189..15548(-)	
2558670170	DRAFT_00838	DNA_length		360bp	
2558670170	DRAFT_00838	Protein_length		119aa	
2558670170	DRAFT_00838	GC		0.59	
2558670171	DRAFT_00839	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670171	DRAFT_00839	COG0532	Translation initiation factor 2 (IF-2; GTPase)		7.00E-95
2558670171	DRAFT_00839	pfam00009	GTP_EFTU		2.30E-27
2558670171	DRAFT_00839	pfam11987	IF-2		7.10E-15
2558670171	DRAFT_00839	pfam14578	GTP_EFTU_D4		7.60E-17
2558670171	DRAFT_00839	TIGR00491	translation initiation factor aIF-2/yIF-2		0.00E+00
2558670171	DRAFT_00839	TIGR00231	small GTP-binding protein domain		5.30E-19
2558670171	DRAFT_00839	KO:K03243	translation initiation factor 5B		0.00E+00
2558670171	DRAFT_00839	Locus_type		CDS	
2558670171	DRAFT_00839	Product_name		translation initiation factor aIF-2/yIF-2	
2558670171	DRAFT_00839	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670171	DRAFT_00839	Coordinates		15631..17424(-)	
2558670171	DRAFT_00839	DNA_length		1794bp	
2558670171	DRAFT_00839	Protein_length		597aa	

2558670171	DRAFT_00839	GC			0.6
2558670172	DRAFT_00840	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP		
2558670172	DRAFT_00840	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP		
2558670172	DRAFT_00840	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP		
2558670172	DRAFT_00840	KEGG_module	M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP		
2558670172	DRAFT_00840	Metacyc	PWY-7198: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis IV		
2558670172	DRAFT_00840	Metacyc	PWY-7187: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis II		
2558670172	DRAFT_00840	Metacyc	PWY-7184: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis I		
2558670172	DRAFT_00840	Metacyc	PWY-6545: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis III		
2558670172	DRAFT_00840	Metacyc	PPGPPMET-PWY: ppGpp biosynthesis		
2558670172	DRAFT_00840	Metacyc	PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP		
2558670172	DRAFT_00840	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis		
2558670172	DRAFT_00840	Metacyc	PWY-7197: pyrimidine deoxyribonucleotide phosphorylation		
2558670172	DRAFT_00840	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis		
2558670172	DRAFT_00840	Metacyc	PWY-7205: CMP phosphorylation		
2558670172	DRAFT_00840	Metacyc	PWY-7176: UTP and CTP <i>de novo</i> biosynthesis		
2558670172	DRAFT_00840	Metacyc	PWY0-166: superpathway of pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis (E.		
2558670172	DRAFT_00840	IMG_pathway	296: GTP biosynthesis		
2558670172	DRAFT_00840	IMG_pathway	323: UTP synthesis		
2558670172	DRAFT_00840	IMG_pathway	332: dTTP synthesis		
2558670172	DRAFT_00840	IMG_pathway	476: Cytidine conversion to CTP		
2558670172	DRAFT_00840	COG_category	[F] Nucleotide transport and metabolism		
2558670172	DRAFT_00840	COG0105	Nucleoside diphosphate kinase		2.00E-45
2558670172	DRAFT_00840	pfam00334	NDK		1.10E-48
2558670172	DRAFT_00840	EC:2.7.4.6	Nucleoside-diphosphate kinase.		
2558670172	DRAFT_00840	KO:K00940	nucleoside-diphosphate kinase [EC:2.7.4.6]		3.90E-42
2558670172	DRAFT_00840	ITERM:01287	nucleoside diphosphate kinase (EC 2.7.4.6)		
2558670172	DRAFT_00840	Locus_type		CDS	
2558670172	DRAFT_00840	Product_name		nucleoside diphosphate kinase (EC 2.7.4.6)	
2558670172	DRAFT_00840	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670172	DRAFT_00840	Coordinates		17454..17873(-)	
2558670172	DRAFT_00840	DNA_length		420bp	
2558670172	DRAFT_00840	Protein_length		139aa	

2558670172	DRAFT_00840	GC			0.59	
2558670173	DRAFT_00841	KEGG_module	M00179: Ribosome, archaea			
2558670173	DRAFT_00841	KEGG_module	M00177: Ribosome, eukaryotes			
2558670173	DRAFT_00841	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670173	DRAFT_00841	COG2075	Ribosomal protein L24E			8.00E-09
2558670173	DRAFT_00841	pfam01246	Ribosomal_L24e			5.90E-13
2558670173	DRAFT_00841	KO:K02896	large subunit ribosomal protein L24e			7.70E-11
2558670173	DRAFT_00841	ITERM:00247	LSU ribosomal protein L24E			
2558670173	DRAFT_00841	Locus_type		CDS		
2558670173	DRAFT_00841	Product_name		LSU ribosomal protein L24E		
2558670173	DRAFT_00841	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670173	DRAFT_00841	Coordinates		17870..18052(-)		
2558670173	DRAFT_00841	DNA_length		183bp		
2558670173	DRAFT_00841	Protein_length		60aa		
2558670173	DRAFT_00841	GC			0.5	
2558670174	DRAFT_00842	KEGG_module	M00179: Ribosome, archaea			
2558670174	DRAFT_00842	KEGG_module	M00177: Ribosome, eukaryotes			
2558670174	DRAFT_00842	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670174	DRAFT_00842	COG2053	Ribosomal protein S28E/S33			1.00E-15
2558670174	DRAFT_00842	pfam01200	Ribosomal_S28e			6.60E-30
2558670174	DRAFT_00842	KO:K02979	small subunit ribosomal protein S28e			1.80E-22
2558670174	DRAFT_00842	Locus_type		CDS		
2558670174	DRAFT_00842	Product_name		Ribosomal protein S28E/S33		
2558670174	DRAFT_00842	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670174	DRAFT_00842	Coordinates		18167..18382(-)		
2558670174	DRAFT_00842	DNA_length		216bp		
2558670174	DRAFT_00842	Protein_length		71aa		
2558670174	DRAFT_00842	GC			0.52	
2558670175	DRAFT_00843	KEGG_module	M00177: Ribosome, eukaryotes			
2558670175	DRAFT_00843	KEGG_module	M00179: Ribosome, archaea			
2558670175	DRAFT_00843	COG_category	[J] Translation, ribosomal structure and biogenesis			

2558670175	DRAFT_00843	COG1358	Ribosomal protein HS6-type (S12/L30/L7a)			8.00E-24
2558670175	DRAFT_00843	pfam01248	Ribosomal_L7Ae			8.40E-29
2558670175	DRAFT_00843	TIGR03677	50S ribosomal protein L7Ae			5.50E-52
2558670175	DRAFT_00843	KO:K02936	large subunit ribosomal protein L7Ae			1.60E-37
2558670175	DRAFT_00843	ITERM:00224	LSU ribosomal protein L7AE			
2558670175	DRAFT_00843	Locus_type		CDS		
2558670175	DRAFT_00843	Product_name		LSU ribosomal protein L7AE		
2558670175	DRAFT_00843	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670175	DRAFT_00843	Coordinates		18379..18759(-)		
2558670175	DRAFT_00843	DNA_length		381bp		
2558670175	DRAFT_00843	Protein_length		126aa		
2558670175	DRAFT_00843	GC			0.59	

2558670176	DRAFT_00844	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme			
2558670176	DRAFT_00844	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2558670176	DRAFT_00844	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2558670176	DRAFT_00844	Metacyc	PWY-5188: tetrapyrrole biosynthesis I (from glutamate)			
2558670176	DRAFT_00844	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558670176	DRAFT_00844	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670176	DRAFT_00844	COG0008	Glutamyl- and glutaminyl-tRNA synthetases			9.00E-69
2558670176	DRAFT_00844	pfam03950	tRNA-synt_1c_C			1.40E-26
2558670176	DRAFT_00844	pfam00749	tRNA-synt_1c			1.00E-65
2558670176	DRAFT_00844	EC:6.1.1.17	Glutamate--tRNA ligase.			
2558670176	DRAFT_00844	TIGR00463	glutamyl-tRNA synthetase, archaeal and eukaryotic family			0.00E+00
2558670176	DRAFT_00844	KO:K01885	glutamyl-tRNA synthetase [EC:6.1.1.17]			0.00E+00
2558670176	DRAFT_00844	Locus_type		CDS		
2558670176	DRAFT_00844	Product_name		glutamyl-tRNA synthetase, archaeal and eukaryotic family		
2558670176	DRAFT_00844	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670176	DRAFT_00844	Coordinates		18917..20635(-)		
2558670176	DRAFT_00844	DNA_length		1719bp		
2558670176	DRAFT_00844	Protein_length		572aa		
2558670176	DRAFT_00844	GC			0.57	

2558670177	DRAFT_00845	KEGG_module	M00364: C10-C20 isoprenoid biosynthesis, bacteria

2558670177	DRAFT_00845	KEGG_module	M00366: C10-C20 isoprenoid biosynthesis, plants			
2558670177	DRAFT_00845	Metacyc	PWY-6659: fusicoccins biosynthesis			
2558670177	DRAFT_00845	Metacyc	PWY-5122: geranyl diphosphate biosynthesis			
2558670177	DRAFT_00845	Metacyc	PWY-6859: <i>all-trans</i>-farnesol biosynthesis			
2558670177	DRAFT_00845	Metacyc	PWY-6691: plaunotol biosynthesis			
2558670177	DRAFT_00845	Metacyc	PWY-5123: <i>trans, trans</i>-farnesyl diphosphate biosynthesis			
2558670177	DRAFT_00845	Metacyc	PWY-7141: linalool biosynthesis II			
2558670177	DRAFT_00845	Metacyc	PWY-5120: geranylgeranyldiphosphate biosynthesis			
2558670177	DRAFT_00845	Metacyc	PWY2OL-4: superpathway of linalool biosynthesis			
2558670177	DRAFT_00845	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis			
2558670177	DRAFT_00845	Metacyc	PWY-7182: linalool biosynthesis I			
2558670177	DRAFT_00845	Metacyc	PWY-7102: bisabolene biosynthesis			
2558670177	DRAFT_00845	COG_category	[H] Coenzyme transport and metabolism			
2558670177	DRAFT_00845	COG0142	Geranylgeranyl pyrophosphate synthase			4.00E-55
2558670177	DRAFT_00845	pfam00348	polyprenyl_synt			1.60E-52
2558670177	DRAFT_00845	EC:2.5.1.29	Geranylgeranyl diphosphate synthase.			
2558670177	DRAFT_00845	EC:2.5.1.1	Dimethylallyltranstransferase.			
2558670177	DRAFT_00845	EC:2.5.1.10	(2E,6E)-farnesyl diphosphate synthase.			
2558670177	DRAFT_00845	KO:K13789	geranylgeranyl diphosphate synthase, type II [EC:2.5.1.1 2.5.1.10 2.5.1.			0.00E+00
2558670177	DRAFT_00845	Locus_type		CDS		
2558670177	DRAFT_00845	Product_name		Geranylgeranyl pyrophosphate synthase		
2558670177	DRAFT_00845	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670177	DRAFT_00845	Coordinates		20629..21660(-)		
2558670177	DRAFT_00845	DNA_length		1032bp		
2558670177	DRAFT_00845	Protein_length		343aa		
2558670177	DRAFT_00845	GC			0.59	

2558670178	DRAFT_00846	Metacyc	PWY-6174: mevalonate pathway II (archaea)	
2558670178	DRAFT_00846	IMG_pathway	591: Archaeal mevalonate pathway for isopentenyl pyrophosphate synthesis	
2558670178	DRAFT_00846	COG_category	[R] General function prediction only	
2558670178	DRAFT_00846	COG1608	Predicted archaeal kinase	2.00E-48
2558670178	DRAFT_00846	pfam00696	AA_kinase	2.40E-29
2558670178	DRAFT_00846	EC:2.7.4.26	Isopentenyl phosphate kinase.	
2558670178	DRAFT_00846	KO:K06981	isopentenyl phosphate kinase [EC:2.7.4.26]	2.10E-38

2558670178	DRAFT_00846	ITERM:05321	isopentenyl phosphate kinase (EC 2.7.4.-)			
2558670178	DRAFT_00846	Locus_type		CDS		
2558670178	DRAFT_00846	Product_name		isopentenyl phosphate kinase (EC 2.7.4.-)		
2558670178	DRAFT_00846	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670178	DRAFT_00846	Coordinates		21686..22432(-)		
2558670178	DRAFT_00846	DNA_length		747bp		
2558670178	DRAFT_00846	Protein_length		248aa		
2558670178	DRAFT_00846	GC			0.59	
2558670179	DRAFT_00847	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			
2558670179	DRAFT_00847	Metacyc	PWY-6174: mevalonate pathway II (archaea)			
2558670179	DRAFT_00847	Metacyc	PWY-922: mevalonate pathway I			
2558670179	DRAFT_00847	IMG_pathway	178: Mevalonate pathway for isopentenyl pyrophopsphate synthesis			
2558670179	DRAFT_00847	IMG_pathway	591: Archaeal mevalonate pathway for isopentenyl pyrophosphate synthesis			
2558670179	DRAFT_00847	COG_category	[I] Lipid transport and metabolism			
2558670179	DRAFT_00847	COG1577	Mevalonate kinase			2.00E-52
2558670179	DRAFT_00847	pfam00288	GHMP_kinases_N			6.30E-18
2558670179	DRAFT_00847	pfam08544	GHMP_kinases_C			7.90E-14
2558670179	DRAFT_00847	EC:2.7.1.36	Mevalonate kinase.			
2558670179	DRAFT_00847	TIGR00549	mevalonate kinase			9.60E-69
2558670179	DRAFT_00847	KO:K00869	mevalonate kinase [EC:2.7.1.36]			0.00E+00
2558670179	DRAFT_00847	ITERM:00464	mevalonate kinase (EC 2.7.1.36)			
2558670179	DRAFT_00847	Locus_type		CDS		
2558670179	DRAFT_00847	Product_name		mevalonate kinase (EC 2.7.1.36)		
2558670179	DRAFT_00847	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670179	DRAFT_00847	Coordinates		22417..23346(-)		
2558670179	DRAFT_00847	DNA_length		930bp		
2558670179	DRAFT_00847	Protein_length		309aa		
2558670179	DRAFT_00847	GC			0.62	
2558670180	DRAFT_00848	COG_category	[R] General function prediction only			
2558670180	DRAFT_00848	COG1355	Predicted dioxygenase			2.00E-84
2558670180	DRAFT_00848	pfam01875	Memo			1.90E-76
2558670180	DRAFT_00848	TIGR04336	AmmeMemoRadiSam system protein B			6.20E-94

2558670180	DRAFT_00848	Locus_type		CDS	
2558670180	DRAFT_00848	Product_name		AmmeMemoRadiSam system protein B	
2558670180	DRAFT_00848	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670180	DRAFT_00848	Coordinates		23350..24225(-)	
2558670180	DRAFT_00848	DNA_length		876bp	
2558670180	DRAFT_00848	Protein_length		291aa	
2558670180	DRAFT_00848	GC			0.57
2558670181	DRAFT_00849	KEGG_module	M00179: Ribosome, archaea		
2558670181	DRAFT_00849	KEGG_module	M00178: Ribosome, bacteria		
2558670181	DRAFT_00849	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670181	DRAFT_00849	COG0052	Ribosomal protein S2		2.00E-33
2558670181	DRAFT_00849	pfam00318	Ribosomal_S2		7.60E-12
2558670181	DRAFT_00849	pfam00318	Ribosomal_S2		1.10E-17
2558670181	DRAFT_00849	TIGR01012	ribosomal protein Sa(cytosolic)/S2(archaeal)		3.50E-64
2558670181	DRAFT_00849	KO:K02967	small subunit ribosomal protein S2		0.00E+00
2558670181	DRAFT_00849	Locus_type		CDS	
2558670181	DRAFT_00849	Product_name		Ribosomal protein S2	
2558670181	DRAFT_00849	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670181	DRAFT_00849	Coordinates		24225..24893(-)	
2558670181	DRAFT_00849	DNA_length		669bp	
2558670181	DRAFT_00849	Protein_length		222aa	
2558670181	DRAFT_00849	GC			0.59
2558670182	DRAFT_00850	KEGG_module	M00184: RNA polymerase, archaea		
2558670182	DRAFT_00850	COG_category	[K] Transcription		
2558670182	DRAFT_00850	COG1644	DNA-directed RNA polymerase, subunit N (RpoN/RPB10)		9.00E-23
2558670182	DRAFT_00850	pfam01194	RNA_pol_N		1.00E-28
2558670182	DRAFT_00850	EC:2.7.7.6	DNA-directed RNA polymerase.		
2558670182	DRAFT_00850	KO:K03058	DNA-directed RNA polymerase subunit N [EC:2.7.7.6]		3.60E-20
2558670182	DRAFT_00850	ITERM:01913	DNA-directed RNA polymerase, subunit N (EC 2.7.7.6)		
2558670182	DRAFT_00850	Locus_type		CDS	
2558670182	DRAFT_00850	Product_name		DNA-directed RNA polymerase, subunit N (EC 2.7.7.6)	
2558670182	DRAFT_00850	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	

2558670182	DRAFT_00850	Coordinates		24913..25125(-)		
2558670182	DRAFT_00850	DNA_length		213bp		
2558670182	DRAFT_00850	Protein_length		70aa		
2558670182	DRAFT_00850	GC			0.54	
2558670183	DRAFT_00851	KEGG_module	M00179: Ribosome, archaea			
2558670183	DRAFT_00851	KEGG_module	M00178: Ribosome, bacteria			
2558670183	DRAFT_00851	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670183	DRAFT_00851	COG0103	Ribosomal protein S9			4.00E-28
2558670183	DRAFT_00851	pfam00380	Ribosomal_S9			1.60E-30
2558670183	DRAFT_00851	KO:K02996	small subunit ribosomal protein S9			8.50E-32
2558670183	DRAFT_00851	Locus_type		CDS		
2558670183	DRAFT_00851	Product_name		Ribosomal protein S9		
2558670183	DRAFT_00851	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670183	DRAFT_00851	Coordinates		25132..25563(-)		
2558670183	DRAFT_00851	DNA_length		432bp		
2558670183	DRAFT_00851	Protein_length		143aa		
2558670183	DRAFT_00851	GC			0.58	
2558670184	DRAFT_00852	KEGG_module	M00178: Ribosome, bacteria			
2558670184	DRAFT_00852	KEGG_module	M00179: Ribosome, archaea			
2558670184	DRAFT_00852	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670184	DRAFT_00852	COG0102	Ribosomal protein L13			2.00E-19
2558670184	DRAFT_00852	pfam00572	Ribosomal_L13			1.80E-22
2558670184	DRAFT_00852	TIGR01077	ribosomal protein L13, archaeal/eukaryotic			7.30E-45
2558670184	DRAFT_00852	KO:K02871	large subunit ribosomal protein L13			3.10E-37
2558670184	DRAFT_00852	Locus_type		CDS		
2558670184	DRAFT_00852	Product_name		ribosomal protein L13, archaeal/eukaryotic		
2558670184	DRAFT_00852	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670184	DRAFT_00852	Coordinates		25566..26006(-)		
2558670184	DRAFT_00852	DNA_length		441bp		
2558670184	DRAFT_00852	Protein_length		146aa		
2558670184	DRAFT_00852	GC			0.56	

2558670185	DRAFT_00853	KEGG_module	M00179: Ribosome, archaea			
2558670185	DRAFT_00853	KEGG_module	M00177: Ribosome, eukaryotes			
2558670185	DRAFT_00853	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670185	DRAFT_00853	COG1727	Ribosomal protein L18E			1.00E-25
2558670185	DRAFT_00853	pfam00828	Ribosomal_L18e			4.60E-11
2558670185	DRAFT_00853	KO:K02883	large subunit ribosomal protein L18e			3.80E-22
2558670185	DRAFT_00853	Locus_type		CDS		
2558670185	DRAFT_00853	Product_name		Ribosomal protein L18E		
2558670185	DRAFT_00853	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670185	DRAFT_00853	Coordinates		25996..26349(-)		
2558670185	DRAFT_00853	DNA_length		354bp		
2558670185	DRAFT_00853	Protein_length		117aa		
2558670185	DRAFT_00853	GC			0.58	
2558670186	DRAFT_00854	KEGG_module	M00184: RNA polymerase, archaea			
2558670186	DRAFT_00854	pfam01000	RNA_pol_A_bac			2.20E-27
2558670186	DRAFT_00854	pfam01193	RNA_pol_L			2.60E-11
2558670186	DRAFT_00854	EC:2.7.7.6	DNA-directed RNA polymerase.			
2558670186	DRAFT_00854	KO:K03047	DNA-directed RNA polymerase subunit D [EC:2.7.7.6]			0.00E+00
2558670186	DRAFT_00854	Locus_type		CDS		
2558670186	DRAFT_00854	Product_name		DNA-directed RNA polymerase, alpha subunit/40 kD subunit		
2558670186	DRAFT_00854	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670186	DRAFT_00854	Coordinates		26346..26984(-)		
2558670186	DRAFT_00854	DNA_length		639bp		
2558670186	DRAFT_00854	Protein_length		212aa		
2558670186	DRAFT_00854	GC			0.58	
2558670187	DRAFT_00855	KEGG_module	M00178: Ribosome, bacteria			
2558670187	DRAFT_00855	KEGG_module	M00179: Ribosome, archaea			
2558670187	DRAFT_00855	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670187	DRAFT_00855	COG0099	Ribosomal protein S13			1.00E-23
2558670187	DRAFT_00855	pfam00416	Ribosomal_S13			2.10E-28
2558670187	DRAFT_00855	TIGR03629	archaeal ribosomal protein S13P			1.00E-58
2558670187	DRAFT_00855	KO:K02952	small subunit ribosomal protein S13			1.60E-42

2558670187	DRAFT_00855	Locus_type		CDS		
2558670187	DRAFT_00855	Product_name		archaeal ribosomal protein S13P		
2558670187	DRAFT_00855	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670187	DRAFT_00855	Coordinates		27173..27667(+)		
2558670187	DRAFT_00855	DNA_length		495bp		
2558670187	DRAFT_00855	Protein_length		164aa		
2558670187	DRAFT_00855	GC			0.57	
2558670188	DRAFT_00856	KEGG_module	M00179: Ribosome, archaea			
2558670188	DRAFT_00856	KEGG_module	M00178: Ribosome, bacteria			
2558670188	DRAFT_00856	pfam01479	S4			2.00E-13
2558670188	DRAFT_00856	TIGR01018	ribosomal protein S4(archaeal type)/S9(eukaryote cytosolic type)			9.80E-59
2558670188	DRAFT_00856	KO:K02986	small subunit ribosomal protein S4			2.80E-45
2558670188	DRAFT_00856	Locus_type		CDS		
2558670188	DRAFT_00856	Product_name		SSU ribosomal protein S4P		
2558670188	DRAFT_00856	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670188	DRAFT_00856	Coordinates		27671..28255(+)		
2558670188	DRAFT_00856	DNA_length		585bp		
2558670188	DRAFT_00856	Protein_length		194aa		
2558670188	DRAFT_00856	GC			0.59	
2558670189	DRAFT_00857	KEGG_module	M00179: Ribosome, archaea			
2558670189	DRAFT_00857	KEGG_module	M00178: Ribosome, bacteria			
2558670189	DRAFT_00857	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670189	DRAFT_00857	COG0100	Ribosomal protein S11			2.00E-32
2558670189	DRAFT_00857	pfam00411	Ribosomal_S11			8.10E-40
2558670189	DRAFT_00857	TIGR03628	archaeal ribosomal protein S11P			3.10E-62
2558670189	DRAFT_00857	KO:K02948	small subunit ribosomal protein S11			0.00E+00
2558670189	DRAFT_00857	Locus_type		CDS		
2558670189	DRAFT_00857	Product_name		SSU ribosomal protein S11P		
2558670189	DRAFT_00857	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670189	DRAFT_00857	Coordinates		28262..28669(+)		
2558670189	DRAFT_00857	DNA_length		408bp		
2558670189	DRAFT_00857	Protein_length		135aa		

2558670189	DRAFT_00857	GC			0.56	
2558670190	DRAFT_00858	COG_category	[K] Transcription			
2558670190	DRAFT_00858	COG1695	Predicted transcriptional regulators			2.00E-06
2558670190	DRAFT_00858	pfam12840	HTH_20			1.30E-09
2558670190	DRAFT_00858	pfam05124	S_layer_C			8.70E-07
2558670190	DRAFT_00858	Locus_type		CDS		
2558670190	DRAFT_00858	Product_name		Predicted transcriptional regulators		
2558670190	DRAFT_00858	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670190	DRAFT_00858	Coordinates		28673..29620(-)		
2558670190	DRAFT_00858	DNA_length		948bp		
2558670190	DRAFT_00858	Protein_length		315aa		
2558670190	DRAFT_00858	GC			0.59	
2558670191	DRAFT_00859	Metacyc	UDPNAGSYN-PWY: UDP-<i>N</i>-acetyl-D-glucosamine biosynthesis I			
2558670191	DRAFT_00859	Metacyc	PWY-6749: CMP-legionaminate biosynthesis I			
2558670191	DRAFT_00859	Metacyc	UDPNACETYLGALSYN-PWY: UDP-<i>N</i>-acetyl-D-glucosamine biosynthesis II			
2558670191	DRAFT_00859	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558670191	DRAFT_00859	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and			0.00E+00
2558670191	DRAFT_00859	pfam01380	SIS			3.50E-29
2558670191	DRAFT_00859	pfam13522	GATase_6			3.50E-23
2558670191	DRAFT_00859	pfam01380	SIS			5.70E-20
2558670191	DRAFT_00859	EC:2.6.1.16	Glutamine--fructose-6-phosphate transaminase (isomerizing).			
2558670191	DRAFT_00859	TIGR01135	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)			0.00E+00
2558670191	DRAFT_00859	KO:K00820	glucosamine--fructose-6-phosphate aminotransferase (isomerizing) [E			0.00E+00
2558670191	DRAFT_00859	Locus_type		CDS		
2558670191	DRAFT_00859	Product_name		glucosamine--fructose-6-phosphate aminotransferase (isomerizing)		
2558670191	DRAFT_00859	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670191	DRAFT_00859	Coordinates		29712..31538(+)		
2558670191	DRAFT_00859	DNA_length		1827bp		
2558670191	DRAFT_00859	Protein_length		608aa		
2558670191	DRAFT_00859	GC			0.58	
2558670192	DRAFT_00860	Metacyc	PWY-5905: hypusine biosynthesis			

2558670192	DRAFT_00860	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670192	DRAFT_00860	COG1899	Deoxyhypusine synthase			6.00E-84
2558670192	DRAFT_00860	pfam01916	DS			4.10E-70
2558670192	DRAFT_00860	EC:2.5.1.46	Deoxyhypusine synthase.			
2558670192	DRAFT_00860	TIGR00321	deoxyhypusine synthase			2.60E-94
2558670192	DRAFT_00860	KO:K00809	deoxyhypusine synthase [EC:2.5.1.46]			0.00E+00
2558670192	DRAFT_00860	Locus_type		CDS		
2558670192	DRAFT_00860	Product_name		deoxyhypusine synthase (EC 2.5.1.46)		
2558670192	DRAFT_00860	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670192	DRAFT_00860	Coordinates		31574..32593(+)		
2558670192	DRAFT_00860	DNA_length		1020bp		
2558670192	DRAFT_00860	Protein_length		339aa		
2558670192	DRAFT_00860	GC			0.57	
2558670193	DRAFT_00861	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP			
2558670193	DRAFT_00861	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP			
2558670193	DRAFT_00861	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2558670193	DRAFT_00861	Metacyc	PWY-6124: inosine-5'-phosphate biosynthesis II			
2558670193	DRAFT_00861	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558670193	DRAFT_00861	Metacyc	PWY-6123: inosine-5'-phosphate biosynthesis I			
2558670193	DRAFT_00861	COG_category	[F] Nucleotide transport and metabolism			
2558670193	DRAFT_00861	COG0015	Adenylosuccinate lyase			6.00E-60
2558670193	DRAFT_00861	pfam08328	ASL_C			1.80E-20
2558670193	DRAFT_00861	pfam00206	Lyase_1			4.20E-31
2558670193	DRAFT_00861	EC:4.3.2.2	Adenylosuccinate lyase.			
2558670193	DRAFT_00861	KO:K01756	adenylosuccinate lyase [EC:4.3.2.2]			0.00E+00
2558670193	DRAFT_00861	Locus_type		CDS		
2558670193	DRAFT_00861	Product_name		Adenylosuccinate lyase		
2558670193	DRAFT_00861	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670193	DRAFT_00861	Coordinates		32583..33866(-)		
2558670193	DRAFT_00861	DNA_length		1284bp		
2558670193	DRAFT_00861	Protein_length		427aa		
2558670193	DRAFT_00861	GC			0.58	

2558670194	DRAFT_00862	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP			
2558670194	DRAFT_00862	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558670194	DRAFT_00862	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2558670194	DRAFT_00862	IMG_pathway	236: AMP anabolism via adenylosuccinate			
2558670194	DRAFT_00862	COG_category	[F] Nucleotide transport and metabolism			
2558670194	DRAFT_00862	COG0104	Adenylosuccinate synthase			2.00E-122
2558670194	DRAFT_00862	pfam00709	Adenylsucc_synt			3.20E-124
2558670194	DRAFT_00862	EC:6.3.4.4	Adenylosuccinate synthase.			
2558670194	DRAFT_00862	TIGR00184	adenylosuccinate synthase			1.40E-120
2558670194	DRAFT_00862	KO:K01939	adenylosuccinate synthase [EC:6.3.4.4]			0.00E+00
2558670194	DRAFT_00862	ITERM:00630	Adenylosuccinate synthetase (EC 6.3.4.4)			
2558670194	DRAFT_00862	Locus_type		CDS		
2558670194	DRAFT_00862	Product_name		Adenylosuccinate synthetase (EC 6.3.4.4)		
2558670194	DRAFT_00862	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13		
2558670194	DRAFT_00862	Coordinates		33856..35070(-)		
2558670194	DRAFT_00862	DNA_length		1215bp		
2558670194	DRAFT_00862	Protein_length		404aa		
2558670194	DRAFT_00862	GC			0.61	
2558670195	DRAFT_00863	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP			
2558670195	DRAFT_00863	Metacyc	PWY-5695: urate biosynthesis/inosine 5'-phosphate degradation			
2558670195	DRAFT_00863	Metacyc	PWY-6596: adenosine nucleotides degradation I			
2558670195	DRAFT_00863	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2558670195	DRAFT_00863	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2558670195	DRAFT_00863	COG_category	[F] Nucleotide transport and metabolism			
2558670195	DRAFT_00863	COG0516	IMP dehydrogenase/GMP reductase			2.00E-24
2558670195	DRAFT_00863	pfam00571	CBS			1.10E-08
2558670195	DRAFT_00863	pfam00571	CBS			2.70E-08
2558670195	DRAFT_00863	pfam00478	IMPDH			0.00E+00
2558670195	DRAFT_00863	EC:1.1.1.205	IMP dehydrogenase.			
2558670195	DRAFT_00863	TIGR01302	inosine-5'-monophosphate dehydrogenase			0.00E+00
2558670195	DRAFT_00863	KO:K00088	IMP dehydrogenase [EC:1.1.1.205]			0.00E+00
2558670195	DRAFT_00863	Locus_type		CDS		
2558670195	DRAFT_00863	Product_name		inosine-5'-monophosphate dehydrogenase		

2558670195	DRAFT_00863	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670195	DRAFT_00863	Coordinates		35072..36547(-)	
2558670195	DRAFT_00863	DNA_length		1476bp	
2558670195	DRAFT_00863	Protein_length		491aa	
2558670195	DRAFT_00863	GC		0.58	
2558670196	DRAFT_00864	Locus_type		tRNA	
2558670196	DRAFT_00864	Product_name		tRNA_Undet_???	
2558670196	DRAFT_00864	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670196	DRAFT_00864	Coordinates		36634..36750(-)	
2558670196	DRAFT_00864	DNA_length		117bp	
2558670196	DRAFT_00864	GC		0.66	
2558670197	DRAFT_00865	Locus_type		CDS	
2558670197	DRAFT_00865	Product_name		hypothetical protein	
2558670197	DRAFT_00865	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670197	DRAFT_00865	Coordinates		36911..37759(-)	
2558670197	DRAFT_00865	DNA_length		849bp	
2558670197	DRAFT_00865	Protein_length		282aa	
2558670197	DRAFT_00865	GC		0.59	
2558670197	DRAFT_00865	Transmembrane		Yes	
2558670198	DRAFT_00866	pfam12730	ABC2_membrane_4		1.60E-07
2558670198	DRAFT_00866	Locus_type		CDS	
2558670198	DRAFT_00866	Product_name		ABC-2 family transporter protein	
2558670198	DRAFT_00866	Scaffold		DRAFT_contig_70_80_len_38341_read_count_650701.13	
2558670198	DRAFT_00866	Coordinates		37759..38340(-)	
2558670198	DRAFT_00866	DNA_length		582bp	
2558670198	DRAFT_00866	Protein_length		193aa	
2558670198	DRAFT_00866	GC		0.63	
2558670198	DRAFT_00866	Transmembrane		Yes	
2558670199	DRAFT_00867	COG_category	[S] Function unknown		
2558670199	DRAFT_00867	COG3371	Predicted membrane protein		2.00E-03

2558670199	DRAFT_00867	pfam06197	DUF998			6.20E-13
2558670199	DRAFT_00867	Locus_type		CDS		
2558670199	DRAFT_00867	Product_name		Predicted membrane protein		
2558670199	DRAFT_00867	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670199	DRAFT_00867	Coordinates		237..917(+)		
2558670199	DRAFT_00867	DNA_length		681bp		
2558670199	DRAFT_00867	Protein_length		226aa		
2558670199	DRAFT_00867	GC			0.57	
2558670199	DRAFT_00867	Transmembrane		Yes		
2558670200	DRAFT_00868	COG_category	[R] General function prediction only			
2558670200	DRAFT_00868	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa			2.00E-30
2558670200	DRAFT_00868	pfam12697	Abhydrolase_6			5.90E-37
2558670200	DRAFT_00868	Locus_type		CDS		
2558670200	DRAFT_00868	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super		
2558670200	DRAFT_00868	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670200	DRAFT_00868	Coordinates		1043..1885(+)		
2558670200	DRAFT_00868	DNA_length		843bp		
2558670200	DRAFT_00868	Protein_length		280aa		
2558670200	DRAFT_00868	GC			0.57	
2558670201	DRAFT_00869	COG_category	[R] General function prediction only			
2558670201	DRAFT_00869	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa			2.00E-32
2558670201	DRAFT_00869	pfam12697	Abhydrolase_6			2.10E-37
2558670201	DRAFT_00869	Locus_type		CDS		
2558670201	DRAFT_00869	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super		
2558670201	DRAFT_00869	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670201	DRAFT_00869	Coordinates		2037..2837(-)		
2558670201	DRAFT_00869	DNA_length		801bp		
2558670201	DRAFT_00869	Protein_length		266aa		
2558670201	DRAFT_00869	GC			0.52	
2558670202	DRAFT_00870	Locus_type		CDS		
2558670202	DRAFT_00870	Product_name		hypothetical protein		

2558670202	DRAFT_00870	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670202	DRAFT_00870	Coordinates		3192..3566(-)	
2558670202	DRAFT_00870	DNA_length		375bp	
2558670202	DRAFT_00870	Protein_length		124aa	
2558670202	DRAFT_00870	GC		0.48	
2558670203	DRAFT_00871	Locus_type		CDS	
2558670203	DRAFT_00871	Product_name		hypothetical protein	
2558670203	DRAFT_00871	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670203	DRAFT_00871	Coordinates		3599..3931(-)	
2558670203	DRAFT_00871	DNA_length		333bp	
2558670203	DRAFT_00871	Protein_length		110aa	
2558670203	DRAFT_00871	GC		0.6	
2558670204	DRAFT_00872	COG_category	[K] Transcription		
2558670204	DRAFT_00872	COG0195	Transcription elongation factor		3.00E-07
2558670204	DRAFT_00872	Locus_type		CDS	
2558670204	DRAFT_00872	Product_name		Transcription elongation factor	
2558670204	DRAFT_00872	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670204	DRAFT_00872	Coordinates		3977..4513(+)	
2558670204	DRAFT_00872	DNA_length		537bp	
2558670204	DRAFT_00872	Protein_length		178aa	
2558670204	DRAFT_00872	GC		0.61	
2558670205	DRAFT_00873	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558670205	DRAFT_00873	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558670205	DRAFT_00873	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558670205	DRAFT_00873	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670205	DRAFT_00873	COG0017	Aspartyl/asparaginyl-tRNA synthetases		5.00E-113
2558670205	DRAFT_00873	pfam00152	tRNA-synt_2		9.60E-72
2558670205	DRAFT_00873	pfam01336	tRNA_anti-codon		2.40E-11
2558670205	DRAFT_00873	EC:6.1.1.12	Aspartate--tRNA ligase.		
2558670205	DRAFT_00873	TIGR00458	nondiscriminating aspartyl-tRNA synthetase		2.30E-128
2558670205	DRAFT_00873	KO:K01876	aspartyl-tRNA synthetase [EC:6.1.1.12]		0.00E+00

2558670205	DRAFT_00873	Locus_type		CDS		
2558670205	DRAFT_00873	Product_name		nondiscriminating aspartyl-tRNA synthetase		
2558670205	DRAFT_00873	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670205	DRAFT_00873	Coordinates		4510..5823(-)		
2558670205	DRAFT_00873	DNA_length		1314bp		
2558670205	DRAFT_00873	Protein_length		437aa		
2558670205	DRAFT_00873	GC			0.6	

2558670206	DRAFT_00874	pfam04212	MIT			4.80E-09
2558670206	DRAFT_00874	pfam00004	AAA			1.70E-36
2558670206	DRAFT_00874	Locus_type		CDS		
2558670206	DRAFT_00874	Product_name		ATPases of the AAA+ class		
2558670206	DRAFT_00874	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670206	DRAFT_00874	Coordinates		5856..7076(-)		
2558670206	DRAFT_00874	DNA_length		1221bp		
2558670206	DRAFT_00874	Protein_length		406aa		
2558670206	DRAFT_00874	GC			0.6	

2558670207	DRAFT_00875	COG_category	[N] Cell motility			
2558670207	DRAFT_00875	COG5491	Conserved protein implicated in secretion			5.00E-07
2558670207	DRAFT_00875	pfam03357	Snf7			1.10E-05
2558670207	DRAFT_00875	Locus_type		CDS		
2558670207	DRAFT_00875	Product_name		Conserved protein implicated in secretion		
2558670207	DRAFT_00875	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670207	DRAFT_00875	Coordinates		7073..7936(-)		
2558670207	DRAFT_00875	DNA_length		864bp		
2558670207	DRAFT_00875	Protein_length		287aa		
2558670207	DRAFT_00875	GC			0.6	

2558670208	DRAFT_00876	COG_category	[N] Cell motility			
2558670208	DRAFT_00876	COG5491	Conserved protein implicated in secretion			5.00E-16
2558670208	DRAFT_00876	Locus_type		CDS		
2558670208	DRAFT_00876	Product_name		Conserved protein implicated in secretion		
2558670208	DRAFT_00876	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		

2558670208	DRAFT_00876	Coordinates		8152..8802(-)		
2558670208	DRAFT_00876	DNA_length		651bp		
2558670208	DRAFT_00876	Protein_length		216aa		
2558670208	DRAFT_00876	GC			0.55	

2558670209	DRAFT_00877	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2558670209	DRAFT_00877	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2558670209	DRAFT_00877	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558670209	DRAFT_00877	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670209	DRAFT_00877	COG0060	Isoleucyl-tRNA synthetase			0.00E+00
2558670209	DRAFT_00877	pfam08264	Anticodon_1			7.50E-29
2558670209	DRAFT_00877	pfam00133	tRNA-synt_1			6.20E-107
2558670209	DRAFT_00877	pfam00133	tRNA-synt_1			1.80E-25
2558670209	DRAFT_00877	EC:6.1.1.5	Isoleucine--tRNA ligase.			
2558670209	DRAFT_00877	TIGR00392	isoleucyl-tRNA synthetase			0.00E+00
2558670209	DRAFT_00877	KO:K01870	isoleucyl-tRNA synthetase [EC:6.1.1.5]			0.00E+00
2558670209	DRAFT_00877	Locus_type		CDS		
2558670209	DRAFT_00877	Product_name		Isoleucyl-tRNA synthetase (EC 6.1.1.5)		
2558670209	DRAFT_00877	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670209	DRAFT_00877	Coordinates		9144..12497(+)		
2558670209	DRAFT_00877	DNA_length		3354bp		
2558670209	DRAFT_00877	Protein_length		1117aa		
2558670209	DRAFT_00877	GC			0.5	

2558670210	DRAFT_00878	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670210	DRAFT_00878	COG1236	Predicted exonuclease of the beta-lactamase fold involved in RNA proc			9.00E-19
2558670210	DRAFT_00878	KO:K07577	putative mRNA 3-end processing factor			0.00E+00
2558670210	DRAFT_00878	Locus_type		CDS		
2558670210	DRAFT_00878	Product_name		Predicted exonuclease of the beta-lactamase fold involved in RNA prc		
2558670210	DRAFT_00878	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670210	DRAFT_00878	Coordinates		12850..13911(-)		
2558670210	DRAFT_00878	DNA_length		1062bp		
2558670210	DRAFT_00878	Protein_length		353aa		
2558670210	DRAFT_00878	GC			0.61	

2558670211	DRAFT_00879	Locus_type		CDS	
2558670211	DRAFT_00879	Product_name		hypothetical protein	
2558670211	DRAFT_00879	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670211	DRAFT_00879	Coordinates		13881..16196(-)	
2558670211	DRAFT_00879	DNA_length		2316bp	
2558670211	DRAFT_00879	Protein_length		771aa	
2558670211	DRAFT_00879	GC		0.64	
2558670212	DRAFT_00880	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558670212	DRAFT_00880	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558670212	DRAFT_00880	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558670212	DRAFT_00880	IMG_pathway	488: L-cysteine ligation to tRNA(Cys)		
2558670212	DRAFT_00880	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670212	DRAFT_00880	COG0215	Cysteinyl-tRNA synthetase		0.00E+00
2558670212	DRAFT_00880	pfam09190	DALR_2		3.30E-13
2558670212	DRAFT_00880	pfam01406	tRNA-synt_1e		8.70E-104
2558670212	DRAFT_00880	EC:6.1.1.16	Cysteine--tRNA ligase.		
2558670212	DRAFT_00880	TIGR00435	cysteinyl-tRNA synthetase		0.00E+00
2558670212	DRAFT_00880	KO:K01883	cysteinyl-tRNA synthetase [EC:6.1.1.16]		0.00E+00
2558670212	DRAFT_00880	ITERM:00404	cysteinyl-tRNA synthetase (EC 6.1.1.16)		
2558670212	DRAFT_00880	Locus_type		CDS	
2558670212	DRAFT_00880	Product_name		cysteinyl-tRNA synthetase (EC 6.1.1.16)	
2558670212	DRAFT_00880	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670212	DRAFT_00880	Coordinates		16268..17668(-)	
2558670212	DRAFT_00880	DNA_length		1401bp	
2558670212	DRAFT_00880	Protein_length		466aa	
2558670212	DRAFT_00880	GC		0.6	
2558670213	DRAFT_00881	Locus_type		CDS	
2558670213	DRAFT_00881	Product_name		hypothetical protein	
2558670213	DRAFT_00881	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670213	DRAFT_00881	Coordinates		17725..17874(-)	
2558670213	DRAFT_00881	DNA_length		150bp	

2558670213	DRAFT_00881	Protein_length		49aa		
2558670213	DRAFT_00881	GC			0.48	
2558670214	DRAFT_00882	Locus_type		tRNA		
2558670214	DRAFT_00882	Product_name		tRNA_Cys_GCA		
2558670214	DRAFT_00882	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670214	DRAFT_00882	Coordinates		18367..18453(+)		
2558670214	DRAFT_00882	DNA_length		74bp		
2558670214	DRAFT_00882	GC			0.66	
2558670215	DRAFT_00883	COG_category	[C] Energy production and conversion			
2558670215	DRAFT_00883	COG3808	Inorganic pyrophosphatase			0.00E+00
2558670215	DRAFT_00883	pfam03030	H_PPase			0.00E+00
2558670215	DRAFT_00883	EC:3.6.1.1	Inorganic diphosphatase.			
2558670215	DRAFT_00883	TIGR01104	vacuolar-type H(+)-translocating pyrophosphatase			0.00E+00
2558670215	DRAFT_00883	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump [EC:3.6.1.1]			0.00E+00
2558670215	DRAFT_00883	Locus_type		CDS		
2558670215	DRAFT_00883	Product_name		vacuolar-type H(+)-translocating pyrophosphatase		
2558670215	DRAFT_00883	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670215	DRAFT_00883	Coordinates		18529..20775(+)		
2558670215	DRAFT_00883	DNA_length		2247bp		
2558670215	DRAFT_00883	Protein_length		748aa		
2558670215	DRAFT_00883	GC			0.58	
2558670215	DRAFT_00883	Transmembrane		Yes		
2558670216	DRAFT_00884	KEGG_module	M00153: Cytochrome d ubiquinol oxidase			
2558670216	DRAFT_00884	Metacyc	PWY-6824: justicidin B biosynthesis			
2558670216	DRAFT_00884	Metacyc	PWY-5466: matairesinol biosynthesis			
2558670216	DRAFT_00884	Metacyc	PWY-5404: betaxanthin biosynthesis (via dopaxanthin)			
2558670216	DRAFT_00884	Metacyc	PWY-5439: betacyanin biosynthesis (via dopamine)			
2558670216	DRAFT_00884	Metacyc	PWY-5787: oligomeric urushiol biosynthesis			
2558670216	DRAFT_00884	Metacyc	PWY-6498: eumelanin biosynthesis			
2558670216	DRAFT_00884	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558670216	DRAFT_00884	Metacyc	PWY-5476: cornusiin E biosynthesis			

2558670216	DRAFT_00884	Metacyc	PWY0-1353: succinate to cytochrome <i>bd</i> oxidase electron transfer		
2558670216	DRAFT_00884	COG_category	[C] Energy production and conversion		
2558670216	DRAFT_00884	COG1271	Cytochrome bd-type quinol oxidase, subunit 1		4.00E-84
2558670216	DRAFT_00884	pfam01654	Bac_Ubq_Cox		2.50E-81
2558670216	DRAFT_00884	EC:1.10.3.-	Oxidoreductases. Acting on diphenols and related substances as donors. With oxygen as accep		
2558670216	DRAFT_00884	KO:K00425	cytochrome d ubiquinol oxidase subunit I [EC:1.10.3.-]		0.00E+00
2558670216	DRAFT_00884	ITERM:06137	cytochrome bd-I ubiquinol oxidase subunit 1 apoprotein (EC 1.10.3.10)		
2558670216	DRAFT_00884	Locus_type		CDS	
2558670216	DRAFT_00884	Product_name		cytochrome bd-I ubiquinol oxidase subunit 1 apoprotein (EC 1.10.3.1	
2558670216	DRAFT_00884	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670216	DRAFT_00884	Coordinates		20890..22233(+)	
2558670216	DRAFT_00884	DNA_length		1344bp	
2558670216	DRAFT_00884	Protein_length		447aa	
2558670216	DRAFT_00884	GC		0.56	
2558670216	DRAFT_00884	Transmembrane		Yes	

2558670217	DRAFT_00885	KEGG_module	M00153: Cytochrome d ubiquinol oxidase		
2558670217	DRAFT_00885	Metacyc	PWY0-1353: succinate to cytochrome <i>bd</i> oxidase electron transfer		
2558670217	DRAFT_00885	Metacyc	PWY-6824: justicidin B biosynthesis		
2558670217	DRAFT_00885	Metacyc	PWY-5404: betaxanthin biosynthesis (via dopaxanthin)		
2558670217	DRAFT_00885	Metacyc	PWY-5787: oligomeric urushiol biosynthesis		
2558670217	DRAFT_00885	Metacyc	PWY-5476: cornusiin E biosynthesis		
2558670217	DRAFT_00885	Metacyc	PWY-5466: matairesinol biosynthesis		
2558670217	DRAFT_00885	Metacyc	PWY-5439: betacyanin biosynthesis (via dopamine)		
2558670217	DRAFT_00885	Metacyc	PWY-6498: eumelanin biosynthesis		
2558670217	DRAFT_00885	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer		
2558670217	DRAFT_00885	EC:1.10.3.-	Oxidoreductases. Acting on diphenols and related substances as donors. With oxygen as accep		
2558670217	DRAFT_00885	KO:K00426	cytochrome d ubiquinol oxidase subunit II [EC:1.10.3.-]		0.00E+00
2558670217	DRAFT_00885	Locus_type		CDS	
2558670217	DRAFT_00885	Product_name		hypothetical protein	
2558670217	DRAFT_00885	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670217	DRAFT_00885	Coordinates		22237..23187(+)	
2558670217	DRAFT_00885	DNA_length		951bp	
2558670217	DRAFT_00885	Protein_length		316aa	

2558670217	DRAFT_00885	GC			0.56	
2558670217	DRAFT_00885	Transmembrane		Yes		
2558670218	DRAFT_00886	Locus_type		CDS		
2558670218	DRAFT_00886	Product_name		hypothetical protein		
2558670218	DRAFT_00886	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670218	DRAFT_00886	Coordinates		23127..23345(-)		
2558670218	DRAFT_00886	DNA_length		219bp		
2558670218	DRAFT_00886	Protein_length		72aa		
2558670218	DRAFT_00886	GC			0.56	
2558670219	DRAFT_00887	Metacyc	PWY-5905: hypusine biosynthesis			
2558670219	DRAFT_00887	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670219	DRAFT_00887	COG1899	Deoxyhypusine synthase			5.00E-92
2558670219	DRAFT_00887	pfam01916	DS			6.90E-83
2558670219	DRAFT_00887	EC:2.5.1.46	Deoxyhypusine synthase.			
2558670219	DRAFT_00887	TIGR00321	deoxyhypusine synthase			1.50E-85
2558670219	DRAFT_00887	KO:K00809	deoxyhypusine synthase [EC:2.5.1.46]			0.00E+00
2558670219	DRAFT_00887	Locus_type		CDS		
2558670219	DRAFT_00887	Product_name		deoxyhypusine synthase (EC 2.5.1.46)		
2558670219	DRAFT_00887	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670219	DRAFT_00887	Coordinates		23354..24319(-)		
2558670219	DRAFT_00887	DNA_length		966bp		
2558670219	DRAFT_00887	Protein_length		321aa		
2558670219	DRAFT_00887	GC			0.6	
2558670220	DRAFT_00888	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP			
2558670220	DRAFT_00888	COG_category	[F] Nucleotide transport and metabolism			
2558670220	DRAFT_00888	COG0125	Thymidylate kinase			2.00E-21
2558670220	DRAFT_00888	pfam02223	Thymidylate_kin			9.00E-27
2558670220	DRAFT_00888	EC:2.7.4.9	dTMP kinase.			
2558670220	DRAFT_00888	KO:K00943	dTMP kinase [EC:2.7.4.9]			1.40E-32
2558670220	DRAFT_00888	Locus_type		CDS		
2558670220	DRAFT_00888	Product_name		Thymidylate kinase		

2558670220	DRAFT_00888	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670220	DRAFT_00888	Coordinates		24349..24933(-)	
2558670220	DRAFT_00888	DNA_length		585bp	
2558670220	DRAFT_00888	Protein_length		194aa	
2558670220	DRAFT_00888	GC		0.56	
2558670220	DRAFT_00888	Transmembrane		Yes	
2558670221	DRAFT_00889	COG_category	[I] Lipid transport and metabolism		
2558670221	DRAFT_00889	COG0170	Dolichol kinase		5.00E-13
2558670221	DRAFT_00889	pfam01148	CTP_transf_1		5.70E-06
2558670221	DRAFT_00889	Locus_type		CDS	
2558670221	DRAFT_00889	Product_name		Dolichol kinase	
2558670221	DRAFT_00889	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670221	DRAFT_00889	Coordinates		24947..25669(-)	
2558670221	DRAFT_00889	DNA_length		723bp	
2558670221	DRAFT_00889	Protein_length		240aa	
2558670221	DRAFT_00889	GC		0.54	
2558670221	DRAFT_00889	Transmembrane		Yes	
2558670222	DRAFT_00890	COG_category	[R] General function prediction only		
2558670222	DRAFT_00890	COG1719	Predicted hydrocarbon binding protein (contains V4R domain)		1.00E-07
2558670222	DRAFT_00890	pfam02830	V4R		3.00E-11
2558670222	DRAFT_00890	Locus_type		CDS	
2558670222	DRAFT_00890	Product_name		Predicted hydrocarbon binding protein (contains V4R domain)	
2558670222	DRAFT_00890	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670222	DRAFT_00890	Coordinates		25874..26656(-)	
2558670222	DRAFT_00890	DNA_length		783bp	
2558670222	DRAFT_00890	Protein_length		260aa	
2558670222	DRAFT_00890	GC		0.55	
2558670223	DRAFT_00891	KEGG_module	M00248: Putative antibiotic transport system		
2558670223	DRAFT_00891	pfam01061	ABC2_membrane		3.30E-16
2558670223	DRAFT_00891	KO:K09686	antibiotic transport system permease protein		0.00E+00
2558670223	DRAFT_00891	Locus_type		CDS	

2558670223	DRAFT_00891	Product_name		Predicted membrane protein		
2558670223	DRAFT_00891	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670223	DRAFT_00891	Coordinates		26789..27556(-)		
2558670223	DRAFT_00891	DNA_length		768bp		
2558670223	DRAFT_00891	Protein_length		255aa		
2558670223	DRAFT_00891	GC			0.56	
2558670223	DRAFT_00891	Transmembrane		Yes		
2558670224	DRAFT_00892	KEGG_module	M00254: ABC-2 type transport system			
2558670224	DRAFT_00892	COG_category	[V] Defense mechanisms			
2558670224	DRAFT_00892	COG1131	ABC-type multidrug transport system, ATPase component			2.00E-67
2558670224	DRAFT_00892	pfam00005	ABC_tran			4.10E-30
2558670224	DRAFT_00892	KO:K01990	ABC-2 type transport system ATP-binding protein			0.00E+00
2558670224	DRAFT_00892	Locus_type		CDS		
2558670224	DRAFT_00892	Product_name		ABC-type multidrug transport system, ATPase component		
2558670224	DRAFT_00892	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670224	DRAFT_00892	Coordinates		27561..28520(-)		
2558670224	DRAFT_00892	DNA_length		960bp		
2558670224	DRAFT_00892	Protein_length		319aa		
2558670224	DRAFT_00892	GC			0.56	
2558670225	DRAFT_00893	Locus_type		CDS		
2558670225	DRAFT_00893	Product_name		hypothetical protein		
2558670225	DRAFT_00893	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670225	DRAFT_00893	Coordinates		28558..29898(-)		
2558670225	DRAFT_00893	DNA_length		1341bp		
2558670225	DRAFT_00893	Protein_length		446aa		
2558670225	DRAFT_00893	GC			0.59	
2558670225	DRAFT_00893	Transmembrane		Yes		
2558670226	DRAFT_00894	pfam01022	HTH_5			2.20E-10
2558670226	DRAFT_00894	Locus_type		CDS		
2558670226	DRAFT_00894	Product_name		Bacterial regulatory protein, arsR family		
2558670226	DRAFT_00894	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		

2558670226	DRAFT_00894	Coordinates		29891..30454(-)	
2558670226	DRAFT_00894	DNA_length		564bp	
2558670226	DRAFT_00894	Protein_length		187aa	
2558670226	DRAFT_00894	GC		0.6	
2558670227	DRAFT_00895	COG_category	[F] Nucleotide transport and metabolism		
2558670227	DRAFT_00895	COG1936	Predicted nucleotide kinase (related to CMP and AMP kinases)		5.00E-24
2558670227	DRAFT_00895	pfam13238	AAA_18		8.00E-17
2558670227	DRAFT_00895	Locus_type		CDS	
2558670227	DRAFT_00895	Product_name		Predicted nucleotide kinase (related to CMP and AMP kinases)	
2558670227	DRAFT_00895	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670227	DRAFT_00895	Coordinates		30683..31264(-)	
2558670227	DRAFT_00895	DNA_length		582bp	
2558670227	DRAFT_00895	Protein_length		193aa	
2558670227	DRAFT_00895	GC		0.6	
2558670228	DRAFT_00896	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558670228	DRAFT_00896	COG0225	Peptide methionine sulfoxide reductase		2.00E-62
2558670228	DRAFT_00896	pfam01625	PMSR		2.90E-63
2558670228	DRAFT_00896	EC:1.8.4.11	Peptide-methionine (S)-S-oxide reductase.		
2558670228	DRAFT_00896	TIGR00401	methionine-S-sulfoxide reductase		7.50E-64
2558670228	DRAFT_00896	KO:K07304	peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]		0.00E+00
2558670228	DRAFT_00896	Locus_type		CDS	
2558670228	DRAFT_00896	Product_name		methionine-S-sulfoxide reductase	
2558670228	DRAFT_00896	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670228	DRAFT_00896	Coordinates		31285..31848(-)	
2558670228	DRAFT_00896	DNA_length		564bp	
2558670228	DRAFT_00896	Protein_length		187aa	
2558670228	DRAFT_00896	GC		0.6	
2558670229	DRAFT_00897	Locus_type		CDS	
2558670229	DRAFT_00897	Product_name		hypothetical protein	
2558670229	DRAFT_00897	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670229	DRAFT_00897	Coordinates		32052..32204(+)	

2558670229	DRAFT_00897	DNA_length		153bp	
2558670229	DRAFT_00897	Protein_length		50aa	
2558670229	DRAFT_00897	GC		0.54	
2558670229	DRAFT_00897	Transmembrane		Yes	
2558670230	DRAFT_00898	COG_category	[H] Coenzyme transport and metabolism		
2558670230	DRAFT_00898	COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis		2.00E-11
2558670230	DRAFT_00898	pfam08241	Methyltransf_11		1.80E-14
2558670230	DRAFT_00898	Locus_type		CDS	
2558670230	DRAFT_00898	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	
2558670230	DRAFT_00898	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670230	DRAFT_00898	Coordinates		32256..33206(-)	
2558670230	DRAFT_00898	DNA_length		951bp	
2558670230	DRAFT_00898	Protein_length		316aa	
2558670230	DRAFT_00898	GC		0.51	
2558670231	DRAFT_00899	pfam00082	Peptidase_S8		2.30E-06
2558670231	DRAFT_00899	Locus_type		CDS	
2558670231	DRAFT_00899	Product_name		Predicted protease	
2558670231	DRAFT_00899	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670231	DRAFT_00899	Coordinates		33387..34862(-)	
2558670231	DRAFT_00899	DNA_length		1476bp	
2558670231	DRAFT_00899	Protein_length		491aa	
2558670231	DRAFT_00899	GC		0.52	
2558670231	DRAFT_00899	Transmembrane		Yes	
2558670232	DRAFT_00900	COG_category	[E] Amino acid transport and metabolism		
2558670232	DRAFT_00900	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases		3.00E-105
2558670232	DRAFT_00900	pfam00326	Peptidase_S9		8.70E-54
2558670232	DRAFT_00900	pfam10647	Gmad1		1.20E-05
2558670232	DRAFT_00900	Locus_type		CDS	
2558670232	DRAFT_00900	Product_name		Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	
2558670232	DRAFT_00900	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14	
2558670232	DRAFT_00900	Coordinates		35038..36855(-)	

2558670232	DRAFT_00900	DNA_length		1818bp		
2558670232	DRAFT_00900	Protein_length		605aa		
2558670232	DRAFT_00900	GC			0.59	

2558670233	DRAFT_00901	pfam13229	Beta_helix			2.50E-17
2558670233	DRAFT_00901	TIGR03804	parallel beta-helix repeat (two copies)			9.60E-14
2558670233	DRAFT_00901	Locus_type		CDS		
2558670233	DRAFT_00901	Product_name		parallel beta-helix repeat (two copies)		
2558670233	DRAFT_00901	Scaffold		DRAFT_contig_70_81_len_37990_read_count_630184.14		
2558670233	DRAFT_00901	Coordinates		37202..37987(+)		
2558670233	DRAFT_00901	DNA_length		786bp		
2558670233	DRAFT_00901	Protein_length		262aa		
2558670233	DRAFT_00901	GC			0.54	
2558670233	DRAFT_00901	Transmembrane		Yes		

2558670234	DRAFT_00902	Locus_type		CDS		
2558670234	DRAFT_00902	Product_name		hypothetical protein		
2558670234	DRAFT_00902	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670234	DRAFT_00902	Coordinates		294..503(-)		
2558670234	DRAFT_00902	DNA_length		210bp		
2558670234	DRAFT_00902	Protein_length		69aa		
2558670234	DRAFT_00902	GC			0.48	
2558670234	DRAFT_00902	Transmembrane		Yes		

2558670235	DRAFT_00903	KEGG_module	M00020: Serine biosynthesis, glycerate-3P => serine			
2558670235	DRAFT_00903	Metacyc	SERSYN-PWY: serine biosynthesis			
2558670235	DRAFT_00903	COG_category	[H] Coenzyme transport and metabolism			
2558670235	DRAFT_00903	COG_category	[E] Amino acid transport and metabolism			
2558670235	DRAFT_00903	COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases			5.00E-40
2558670235	DRAFT_00903	pfam02826	2-Hacid_dh_C			3.40E-30
2558670235	DRAFT_00903	pfam00389	2-Hacid_dh			2.40E-10
2558670235	DRAFT_00903	EC:1.1.1.95	Phosphoglycerate dehydrogenase.			
2558670235	DRAFT_00903	KO:K00058	D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]			0.00E+00
2558670235	DRAFT_00903	Locus_type		CDS		

2558670235	DRAFT_00903	Product_name		Phosphoglycerate dehydrogenase and related dehydrogenases	
2558670235	DRAFT_00903	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670235	DRAFT_00903	Coordinates		646..1572(-)	
2558670235	DRAFT_00903	DNA_length		927bp	
2558670235	DRAFT_00903	Protein_length		308aa	
2558670235	DRAFT_00903	GC		0.58	
2558670236	DRAFT_00904	COG_category	[K] Transcription		
2558670236	DRAFT_00904	COG1758	DNA-directed RNA polymerase, subunit K/omega		6.00E-09
2558670236	DRAFT_00904	pfam01192	RNA_pol_Rpb6		4.00E-11
2558670236	DRAFT_00904	Locus_type		CDS	
2558670236	DRAFT_00904	Product_name		DNA-directed RNA polymerase, subunit K/omega	
2558670236	DRAFT_00904	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670236	DRAFT_00904	Coordinates		1589..1879(-)	
2558670236	DRAFT_00904	DNA_length		291bp	
2558670236	DRAFT_00904	Protein_length		96aa	
2558670236	DRAFT_00904	GC		0.55	
2558670237	DRAFT_00905	COG_category	[S] Function unknown		
2558670237	DRAFT_00905	COG2164	Uncharacterized conserved protein		3.00E-07
2558670237	DRAFT_00905	pfam04126	Cyclophil_like		1.50E-05
2558670237	DRAFT_00905	KO:K09143	hypothetical protein		9.20E-12
2558670237	DRAFT_00905	Locus_type		CDS	
2558670237	DRAFT_00905	Product_name		Uncharacterized conserved protein	
2558670237	DRAFT_00905	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670237	DRAFT_00905	Coordinates		1981..2388(+)	
2558670237	DRAFT_00905	DNA_length		408bp	
2558670237	DRAFT_00905	Protein_length		135aa	
2558670237	DRAFT_00905	GC		0.61	
2558670238	DRAFT_00906	Locus_type		CDS	
2558670238	DRAFT_00906	Product_name		hypothetical protein	
2558670238	DRAFT_00906	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670238	DRAFT_00906	Coordinates		2526..2876(-)	

2558670238	DRAFT_00906	DNA_length		351bp	
2558670238	DRAFT_00906	Protein_length		116aa	
2558670238	DRAFT_00906	GC		0.59	
2558670239	DRAFT_00907	COG_category	[T] Signal transduction mechanisms		
2558670239	DRAFT_00907	COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)		4.00E-27
2558670239	DRAFT_00907	pfam00211	Guanylate_cyc		6.00E-24
2558670239	DRAFT_00907	Locus_type		CDS	
2558670239	DRAFT_00907	Product_name		Adenylate cyclase, family 3 (some proteins contain HAMP domain)	
2558670239	DRAFT_00907	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670239	DRAFT_00907	Coordinates		2998..4662(-)	
2558670239	DRAFT_00907	DNA_length		1665bp	
2558670239	DRAFT_00907	Protein_length		554aa	
2558670239	DRAFT_00907	GC		0.57	
2558670240	DRAFT_00908	Locus_type		CDS	
2558670240	DRAFT_00908	Product_name		hypothetical protein	
2558670240	DRAFT_00908	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670240	DRAFT_00908	Coordinates		4911..6131(+)	
2558670240	DRAFT_00908	DNA_length		1221bp	
2558670240	DRAFT_00908	Protein_length		406aa	
2558670240	DRAFT_00908	GC		0.6	
2558670240	DRAFT_00908	Transmembrane		Yes	
2558670241	DRAFT_00909	Metacyc	PWY-5386: methylglyoxal degradation I		
2558670241	DRAFT_00909	COG_category	[E] Amino acid transport and metabolism		
2558670241	DRAFT_00909	COG0346	Lactoylglutathione lyase and related lyases		2.00E-09
2558670241	DRAFT_00909	pfam12681	Glyoxalase_2		5.10E-17
2558670241	DRAFT_00909	EC:4.4.1.5	Lactoylglutathione lyase.		
2558670241	DRAFT_00909	TIGR00068	lactoylglutathione lyase		5.00E-24
2558670241	DRAFT_00909	KO:K01759	lactoylglutathione lyase [EC:4.4.1.5]		2.10E-12
2558670241	DRAFT_00909	Locus_type		CDS	
2558670241	DRAFT_00909	Product_name		Lactoylglutathione lyase and related lyases	
2558670241	DRAFT_00909	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	

2558670241	DRAFT_00909	Coordinates		6404..6793(+)		
2558670241	DRAFT_00909	DNA_length		390bp		
2558670241	DRAFT_00909	Protein_length		129aa		
2558670241	DRAFT_00909	GC			0.52	
2558670242	DRAFT_00910	Locus_type		CDS		
2558670242	DRAFT_00910	Product_name		hypothetical protein		
2558670242	DRAFT_00910	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670242	DRAFT_00910	Coordinates		6951..7478(-)		
2558670242	DRAFT_00910	DNA_length		528bp		
2558670242	DRAFT_00910	Protein_length		175aa		
2558670242	DRAFT_00910	GC			0.56	
2558670242	DRAFT_00910	Transmembrane		Yes		
2558670243	DRAFT_00911	Locus_type		CDS		
2558670243	DRAFT_00911	Product_name		hypothetical protein		
2558670243	DRAFT_00911	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670243	DRAFT_00911	Coordinates		7609..7764(-)		
2558670243	DRAFT_00911	DNA_length		156bp		
2558670243	DRAFT_00911	Protein_length		51aa		
2558670243	DRAFT_00911	GC			0.56	
2558670244	DRAFT_00912	COG_category	[L] Replication, recombination and repair			
2558670244	DRAFT_00912	COG1793	ATP-dependent DNA ligase			9.00E-81
2558670244	DRAFT_00912	pfam04679	DNA_ligase_A_C			5.30E-22
2558670244	DRAFT_00912	pfam01068	DNA_ligase_A_M			5.50E-48
2558670244	DRAFT_00912	pfam04675	DNA_ligase_A_N			1.50E-41
2558670244	DRAFT_00912	EC:6.5.1.1	DNA ligase (ATP).			
2558670244	DRAFT_00912	TIGR00574	DNA ligase I, ATP-dependent (dnl1)			0.00E+00
2558670244	DRAFT_00912	KO:K10747	DNA ligase 1 [EC:6.5.1.1]			0.00E+00
2558670244	DRAFT_00912	Locus_type		CDS		
2558670244	DRAFT_00912	Product_name		DNA ligase I, ATP-dependent (dnl1)		
2558670244	DRAFT_00912	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670244	DRAFT_00912	Coordinates		7774..9528(+)		

2558670244	DRAFT_00912	DNA_length		1755bp		
2558670244	DRAFT_00912	Protein_length		584aa		
2558670244	DRAFT_00912	GC			0.58	
2558670245	DRAFT_00913	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670245	DRAFT_00913	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal			1.00E-38
2558670245	DRAFT_00913	pfam13180	PDZ_2			8.40E-12
2558670245	DRAFT_00913	pfam13365	Trypsin_2			2.20E-17
2558670245	DRAFT_00913	EC:1.3.1.74	2-alkenal reductase.			
2558670245	DRAFT_00913	KO:K08070	2-alkenal reductase [EC:1.3.1.74]			0.00E+00
2558670245	DRAFT_00913	Locus_type		CDS		
2558670245	DRAFT_00913	Product_name		Trypsin-like serine proteases, typically periplasmic, contain C-termina		
2558670245	DRAFT_00913	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670245	DRAFT_00913	Coordinates		9749..10960(+)		
2558670245	DRAFT_00913	DNA_length		1212bp		
2558670245	DRAFT_00913	Protein_length		403aa		
2558670245	DRAFT_00913	GC			0.56	
2558670245	DRAFT_00913	Transmembrane		Yes		
2558670246	DRAFT_00914	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670246	DRAFT_00914	COG1030	Membrane-bound serine protease (ClpP class)			3.00E-51
2558670246	DRAFT_00914	pfam01957	NfeD			1.50E-22
2558670246	DRAFT_00914	KO:K07403	membrane-bound serine protease (ClpP class)			0.00E+00
2558670246	DRAFT_00914	Locus_type		CDS		
2558670246	DRAFT_00914	Product_name		Membrane-bound serine protease (ClpP class)		
2558670246	DRAFT_00914	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670246	DRAFT_00914	Coordinates		11095..12420(+)		
2558670246	DRAFT_00914	DNA_length		1326bp		
2558670246	DRAFT_00914	Protein_length		441aa		
2558670246	DRAFT_00914	GC			0.57	
2558670246	DRAFT_00914	Signal_peptide		Yes		
2558670246	DRAFT_00914	Transmembrane		Yes		
2558670247	DRAFT_00915	COG_category	[O] Posttranslational modification, protein turnover, chaperones			

2558670247	DRAFT_00915	COG0330	Membrane protease subunits, stomatin/prohibitin homologs			7.00E-39
2558670247	DRAFT_00915	pfam01145	Band_7			2.40E-33
2558670247	DRAFT_00915	Locus_type		CDS		
2558670247	DRAFT_00915	Product_name		SPFH domain, Band 7 family protein		
2558670247	DRAFT_00915	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670247	DRAFT_00915	Coordinates		12417..13322(+)		
2558670247	DRAFT_00915	DNA_length		906bp		
2558670247	DRAFT_00915	Protein_length		301aa		
2558670247	DRAFT_00915	GC			0.57	
2558670247	DRAFT_00915	Transmembrane		Yes		

2558670248	DRAFT_00916	pfam00583	Acetyltransf_1			1.20E-13
2558670248	DRAFT_00916	Locus_type		CDS		
2558670248	DRAFT_00916	Product_name		Acetyltransferases		
2558670248	DRAFT_00916	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670248	DRAFT_00916	Coordinates		13376..13819(+)		
2558670248	DRAFT_00916	DNA_length		444bp		
2558670248	DRAFT_00916	Protein_length		147aa		
2558670248	DRAFT_00916	GC			0.48	

2558670249	DRAFT_00917	Locus_type		CDS		
2558670249	DRAFT_00917	Product_name		hypothetical protein		
2558670249	DRAFT_00917	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670249	DRAFT_00917	Coordinates		14036..14305(+)		
2558670249	DRAFT_00917	DNA_length		270bp		
2558670249	DRAFT_00917	Protein_length		89aa		
2558670249	DRAFT_00917	GC			0.51	
2558670249	DRAFT_00917	Transmembrane		Yes		

2558670250	DRAFT_00918	Locus_type		CDS		
2558670250	DRAFT_00918	Product_name		hypothetical protein		
2558670250	DRAFT_00918	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670250	DRAFT_00918	Coordinates		14702..15220(-)		
2558670250	DRAFT_00918	DNA_length		519bp		

2558670250	DRAFT_00918	Protein_length	172aa
2558670250	DRAFT_00918	GC	0.52
2558670251	DRAFT_00919	Locus_type	CDS
2558670251	DRAFT_00919	Product_name	hypothetical protein
2558670251	DRAFT_00919	Scaffold	DRAFT_contig_70_88_len_36701_read_count_592636.15
2558670251	DRAFT_00919	Coordinates	15342..15686(+)
2558670251	DRAFT_00919	DNA_length	345bp
2558670251	DRAFT_00919	Protein_length	114aa
2558670251	DRAFT_00919	GC	0.55
2558670252	DRAFT_00920	Locus_type	CDS
2558670252	DRAFT_00920	Product_name	hypothetical protein
2558670252	DRAFT_00920	Scaffold	DRAFT_contig_70_88_len_36701_read_count_592636.15
2558670252	DRAFT_00920	Coordinates	15736..15945(-)
2558670252	DRAFT_00920	DNA_length	210bp
2558670252	DRAFT_00920	Protein_length	69aa
2558670252	DRAFT_00920	GC	0.5
2558670252	DRAFT_00920	Transmembrane	Yes
2558670253	DRAFT_00921	Locus_type	CDS
2558670253	DRAFT_00921	Product_name	hypothetical protein
2558670253	DRAFT_00921	Scaffold	DRAFT_contig_70_88_len_36701_read_count_592636.15
2558670253	DRAFT_00921	Coordinates	16158..16565(+)
2558670253	DRAFT_00921	DNA_length	408bp
2558670253	DRAFT_00921	Protein_length	135aa
2558670253	DRAFT_00921	GC	0.48
2558670254	DRAFT_00922	Locus_type	CDS
2558670254	DRAFT_00922	Product_name	hypothetical protein
2558670254	DRAFT_00922	Scaffold	DRAFT_contig_70_88_len_36701_read_count_592636.15
2558670254	DRAFT_00922	Coordinates	16798..16917(+)
2558670254	DRAFT_00922	DNA_length	120bp
2558670254	DRAFT_00922	Protein_length	39aa

2558670254	DRAFT_00922	GC			0.54	

2558670255	DRAFT_00923	Locus_type		CDS		
2558670255	DRAFT_00923	Product_name		hypothetical protein		
2558670255	DRAFT_00923	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670255	DRAFT_00923	Coordinates		17037..17252(-)		
2558670255	DRAFT_00923	DNA_length		216bp		
2558670255	DRAFT_00923	Protein_length		71aa		
2558670255	DRAFT_00923	GC			0.56	

2558670256	DRAFT_00924	COG_category	[P] Inorganic ion transport and metabolism			
2558670256	DRAFT_00924	COG1392	Phosphate transport regulator (distant homolog of PhoU)			1.00E-05
2558670256	DRAFT_00924	pfam01865	PhoU_div			3.70E-10
2558670256	DRAFT_00924	KO:K07220	hypothetical protein			1.20E-36
2558670256	DRAFT_00924	Locus_type		CDS		
2558670256	DRAFT_00924	Product_name		Phosphate transport regulator (distant homolog of PhoU)		
2558670256	DRAFT_00924	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670256	DRAFT_00924	Coordinates		17480..18070(+)		
2558670256	DRAFT_00924	DNA_length		591bp		
2558670256	DRAFT_00924	Protein_length		196aa		
2558670256	DRAFT_00924	GC			0.56	

2558670257	DRAFT_00925	Metacyc	PWY-6689: tRNA splicing			
2558670257	DRAFT_00925	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670257	DRAFT_00925	COG1676	tRNA splicing endonuclease			2.00E-26
2558670257	DRAFT_00925	pfam02778	tRNA_int_endo_N			1.40E-15
2558670257	DRAFT_00925	pfam01974	tRNA_int_endo			1.80E-26
2558670257	DRAFT_00925	EC:3.1.27.9	tRNA-intron endonuclease.			
2558670257	DRAFT_00925	TIGR00324	tRNA-intron endonuclease			2.20E-28
2558670257	DRAFT_00925	KO:K01170	tRNA-intron endonuclease, archaea type [EC:3.1.27.9]			0.00E+00
2558670257	DRAFT_00925	Locus_type		CDS		
2558670257	DRAFT_00925	Product_name		tRNA-intron endonuclease		
2558670257	DRAFT_00925	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670257	DRAFT_00925	Coordinates		18073..18630(+)		

2558670257	DRAFT_00925	DNA_length		558bp	
2558670257	DRAFT_00925	Protein_length		185aa	
2558670257	DRAFT_00925	GC		0.57	
2558670258	DRAFT_00926	Metacyc	PWY-6829: tRNA methylation (yeast)		
2558670258	DRAFT_00926	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670258	DRAFT_00926	COG2519	tRNA(1-methyladenosine) methyltransferase and related methyltransf		6.00E-65
2558670258	DRAFT_00926	pfam08704	GCD14		3.80E-29
2558670258	DRAFT_00926	EC:2.1.1.220	tRNA (adenine(58)-N(1))-methyltransferase.		
2558670258	DRAFT_00926	EC:2.1.1.219	tRNA (adenine(57)-N(1)/adenine(58)-N(1))-methyltransferase.		
2558670258	DRAFT_00926	KO:K07442	tRNA (adenine57-N1/adenine58-N1)-methyltransferase [EC:2.1.1.219 2		0.00E+00
2558670258	DRAFT_00926	Locus_type		CDS	
2558670258	DRAFT_00926	Product_name		tRNA(1-methyladenosine) methyltransferase and related methyltrans	
2558670258	DRAFT_00926	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670258	DRAFT_00926	Coordinates		18665..19450(+)	
2558670258	DRAFT_00926	DNA_length		786bp	
2558670258	DRAFT_00926	Protein_length		261aa	
2558670258	DRAFT_00926	GC		0.58	
2558670259	DRAFT_00927	Locus_type		CDS	
2558670259	DRAFT_00927	Product_name		hypothetical protein	
2558670259	DRAFT_00927	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670259	DRAFT_00927	Coordinates		19549..20178(+)	
2558670259	DRAFT_00927	DNA_length		630bp	
2558670259	DRAFT_00927	Protein_length		209aa	
2558670259	DRAFT_00927	GC		0.57	
2558670259	DRAFT_00927	Transmembrane		Yes	
2558670260	DRAFT_00928	COG_category	[S] Function unknown		
2558670260	DRAFT_00928	COG2119	Predicted membrane protein		2.00E-08
2558670260	DRAFT_00928	pfam01169	UPF0016		1.20E-09
2558670260	DRAFT_00928	pfam01169	UPF0016		4.00E-08
2558670260	DRAFT_00928	Locus_type		CDS	
2558670260	DRAFT_00928	Product_name		Predicted membrane protein	

2558670260	DRAFT_00928	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670260	DRAFT_00928	Coordinates		20372..20974(+)	
2558670260	DRAFT_00928	DNA_length		603bp	
2558670260	DRAFT_00928	Protein_length		200aa	
2558670260	DRAFT_00928	GC		0.57	
2558670260	DRAFT_00928	Transmembrane		Yes	
2558670261	DRAFT_00929	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558670261	DRAFT_00929	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558670261	DRAFT_00929	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558670261	DRAFT_00929	IMG_pathway	500: L-proline ligation to tRNA(Pro)		
2558670261	DRAFT_00929	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670261	DRAFT_00929	COG0442	Prolyl-tRNA synthetase		2.00E-104
2558670261	DRAFT_00929	pfam00587	tRNA-synt_2b		7.60E-19
2558670261	DRAFT_00929	pfam03129	HGTP_anticodon		1.70E-17
2558670261	DRAFT_00929	pfam09180	ProRS-C_1		1.30E-16
2558670261	DRAFT_00929	EC:6.1.1.15	Proline--tRNA ligase.		
2558670261	DRAFT_00929	TIGR00408	prolyl-tRNA synthetase, family I		0.00E+00
2558670261	DRAFT_00929	KO:K01881	prolyl-tRNA synthetase [EC:6.1.1.15]		0.00E+00
2558670261	DRAFT_00929	ITERM:01944	prolyl-tRNA synthetase (EC 6.1.1.15)		
2558670261	DRAFT_00929	Locus_type		CDS	
2558670261	DRAFT_00929	Product_name		prolyl-tRNA synthetase (EC 6.1.1.15)	
2558670261	DRAFT_00929	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670261	DRAFT_00929	Coordinates		21095..22540(+)	
2558670261	DRAFT_00929	DNA_length		1446bp	
2558670261	DRAFT_00929	Protein_length		481aa	
2558670261	DRAFT_00929	GC		0.58	
2558670262	DRAFT_00930	COG_category	[G] Carbohydrate transport and metabolism		
2558670262	DRAFT_00930	COG0524	Sugar kinases, ribokinase family		3.00E-18
2558670262	DRAFT_00930	pfam00294	PfkB		4.30E-23
2558670262	DRAFT_00930	Locus_type		CDS	
2558670262	DRAFT_00930	Product_name		Sugar kinases, ribokinase family	
2558670262	DRAFT_00930	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	

2558670262	DRAFT_00930	Coordinates		22564..23469(-)		
2558670262	DRAFT_00930	DNA_length		906bp		
2558670262	DRAFT_00930	Protein_length		301aa		
2558670262	DRAFT_00930	GC			0.59	
2558670263	DRAFT_00931	KEGG_module	M00179: Ribosome, archaea			
2558670263	DRAFT_00931	KEGG_module	M00177: Ribosome, eukaryotes			
2558670263	DRAFT_00931	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670263	DRAFT_00931	COG4830	Ribosomal protein S26			9.00E-18
2558670263	DRAFT_00931	pfam01283	Ribosomal_S26e			1.20E-28
2558670263	DRAFT_00931	KO:K02976	small subunit ribosomal protein S26e			7.80E-31
2558670263	DRAFT_00931	Locus_type		CDS		
2558670263	DRAFT_00931	Product_name		Ribosomal protein S26		
2558670263	DRAFT_00931	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670263	DRAFT_00931	Coordinates		23597..23872(+)		
2558670263	DRAFT_00931	DNA_length		276bp		
2558670263	DRAFT_00931	Protein_length		91aa		
2558670263	DRAFT_00931	GC			0.55	
2558670264	DRAFT_00932	Locus_type		CDS		
2558670264	DRAFT_00932	Product_name		hypothetical protein		
2558670264	DRAFT_00932	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670264	DRAFT_00932	Coordinates		24030..24335(+)		
2558670264	DRAFT_00932	DNA_length		306bp		
2558670264	DRAFT_00932	Protein_length		101aa		
2558670264	DRAFT_00932	GC			0.56	
2558670265	DRAFT_00933	Metacyc	PWY-5668: cardiolipin biosynthesis I			
2558670265	DRAFT_00933	Metacyc	PWY4FS-7: phosphatidylglycerol biosynthesis I (plastidic)			
2558670265	DRAFT_00933	Metacyc	PWY4FS-8: phosphatidylglycerol biosynthesis II (non-plastidic)			
2558670265	DRAFT_00933	Metacyc	PWY-5269: cardiolipin biosynthesis II			
2558670265	DRAFT_00933	Metacyc	PWY0-1545: cardiolipin biosynthesis III			
2558670265	DRAFT_00933	COG_category	[I] Lipid transport and metabolism			
2558670265	DRAFT_00933	COG0558	Phosphatidylglycerophosphate synthase			2.00E-10

2558670265	DRAFT_00933	pfam01066	CDP-OH_P_transf		1.30E-12
2558670265	DRAFT_00933	EC:2.7.8.5	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase.		
2558670265	DRAFT_00933	KO:K00995	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [E		0.00E+00
2558670265	DRAFT_00933	Locus_type		CDS	
2558670265	DRAFT_00933	Product_name		Phosphatidylglycerophosphate synthase	
2558670265	DRAFT_00933	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670265	DRAFT_00933	Coordinates		24326..24919(-)	
2558670265	DRAFT_00933	DNA_length		594bp	
2558670265	DRAFT_00933	Protein_length		197aa	
2558670265	DRAFT_00933	GC		0.59	
2558670265	DRAFT_00933	Transmembrane		Yes	
2558670266	DRAFT_00934	Locus_type		CDS	
2558670266	DRAFT_00934	Product_name		hypothetical protein	
2558670266	DRAFT_00934	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670266	DRAFT_00934	Coordinates		24956..25159(+)	
2558670266	DRAFT_00934	DNA_length		204bp	
2558670266	DRAFT_00934	Protein_length		67aa	
2558670266	DRAFT_00934	GC		0.57	
2558670267	DRAFT_00935	IMG_pathway	504: L-threonine ligation to tRNA(Thr)		
2558670267	DRAFT_00935	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670267	DRAFT_00935	COG0441	Threonyl-tRNA synthetase		0.00E+00
2558670267	DRAFT_00935	pfam03129	HGTP_anticodon		1.90E-16
2558670267	DRAFT_00935	pfam08915	tRNA-Thr_ED		2.00E-38
2558670267	DRAFT_00935	pfam00587	tRNA-synt_2b		7.60E-36
2558670267	DRAFT_00935	TIGR00418	threonyl-tRNA synthetase		0.00E+00
2558670267	DRAFT_00935	ITERM:00389	threonyl-tRNA synthetase (EC 6.1.1.3)		
2558670267	DRAFT_00935	Locus_type		CDS	
2558670267	DRAFT_00935	Product_name		threonyl-tRNA synthetase (EC 6.1.1.3)	
2558670267	DRAFT_00935	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670267	DRAFT_00935	Coordinates		25191..26864(+)	
2558670267	DRAFT_00935	DNA_length		1674bp	
2558670267	DRAFT_00935	Protein_length		557aa	

2558670267	DRAFT_00935	GC		0.57	
2558670268	DRAFT_00936	KEGG_module	M00133: Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine		
2558670268	DRAFT_00936	Metacyc	PWY-40: putrescine biosynthesis I		
2558670268	DRAFT_00936	Metacyc	PWY-6305: putrescine biosynthesis IV		
2558670268	DRAFT_00936	Metacyc	PWY0-823: arginine degradation III (arginine decarboxylase/agmatinase pathway)		
2558670268	DRAFT_00936	COG_category	[E] Amino acid transport and metabolism		
2558670268	DRAFT_00936	COG0010	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family		2.00E-54
2558670268	DRAFT_00936	pfam00491	Arginase		2.40E-67
2558670268	DRAFT_00936	EC:3.5.3.11	Agmatinase.		
2558670268	DRAFT_00936	TIGR01230	agmatinase		5.70E-70
2558670268	DRAFT_00936	KO:K01480	agmatinase [EC:3.5.3.11]		0.00E+00
2558670268	DRAFT_00936	Locus_type		CDS	
2558670268	DRAFT_00936	Product_name		agmatinase	
2558670268	DRAFT_00936	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670268	DRAFT_00936	Coordinates		26870..27823(-)	
2558670268	DRAFT_00936	DNA_length		954bp	
2558670268	DRAFT_00936	Protein_length		317aa	
2558670268	DRAFT_00936	GC		0.6	
2558670269	DRAFT_00937	Locus_type		CDS	
2558670269	DRAFT_00937	Product_name		hypothetical protein	
2558670269	DRAFT_00937	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670269	DRAFT_00937	Coordinates		27829..27948(+)	
2558670269	DRAFT_00937	DNA_length		120bp	
2558670269	DRAFT_00937	Protein_length		39aa	
2558670269	DRAFT_00937	GC		0.52	
2558670270	DRAFT_00938	Locus_type		CDS	
2558670270	DRAFT_00938	Product_name		hypothetical protein	
2558670270	DRAFT_00938	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15	
2558670270	DRAFT_00938	Coordinates		28271..29164(+)	
2558670270	DRAFT_00938	DNA_length		894bp	
2558670270	DRAFT_00938	Protein_length		297aa	

2558670270	DRAFT_00938	GC			0.56	
2558670270	DRAFT_00938	Transmembrane		Yes		
2558670271	DRAFT_00939	KEGG_module	M00534: Naphthalene degradataion, naphthalene => salicylate			
2558670271	DRAFT_00939	Metacyc	PWY-5427: naphthalene degradation			
2558670271	DRAFT_00939	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2558670271	DRAFT_00939	COG3917	2-hydroxychromene-2-carboxylate isomerase			2.00E-27
2558670271	DRAFT_00939	pfam01323	DSBA			1.40E-36
2558670271	DRAFT_00939	EC:5.99.1.4	2-hydroxychromene-2-carboxylate isomerase.			
2558670271	DRAFT_00939	KO:K14584	2-hydroxychromene-2-carboxylate isomerase [EC:5.99.1.4]			4.10E-28
2558670271	DRAFT_00939	Locus_type		CDS		
2558670271	DRAFT_00939	Product_name		2-hydroxychromene-2-carboxylate isomerase		
2558670271	DRAFT_00939	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670271	DRAFT_00939	Coordinates		29300..29893(+)		
2558670271	DRAFT_00939	DNA_length		594bp		
2558670271	DRAFT_00939	Protein_length		197aa		
2558670271	DRAFT_00939	GC			0.52	
2558670272	DRAFT_00940	Locus_type		CDS		
2558670272	DRAFT_00940	Product_name		hypothetical protein		
2558670272	DRAFT_00940	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670272	DRAFT_00940	Coordinates		30157..33690(+)		
2558670272	DRAFT_00940	DNA_length		3534bp		
2558670272	DRAFT_00940	Protein_length		1177aa		
2558670272	DRAFT_00940	GC			0.57	
2558670272	DRAFT_00940	Transmembrane		Yes		
2558670273	DRAFT_00941	Locus_type		CDS		
2558670273	DRAFT_00941	Product_name		hypothetical protein		
2558670273	DRAFT_00941	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670273	DRAFT_00941	Coordinates		33988..34386(-)		
2558670273	DRAFT_00941	DNA_length		399bp		
2558670273	DRAFT_00941	Protein_length		132aa		
2558670273	DRAFT_00941	GC			0.55	

2558670274	DRAFT_00942	pfam02195	ParBc			2.10E-06
2558670274	DRAFT_00942	Locus_type		CDS		
2558670274	DRAFT_00942	Product_name		ParB-like nuclease domain		
2558670274	DRAFT_00942	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670274	DRAFT_00942	Coordinates		34513..35004(+)		
2558670274	DRAFT_00942	DNA_length		492bp		
2558670274	DRAFT_00942	Protein_length		163aa		
2558670274	DRAFT_00942	GC			0.44	
2558670275	DRAFT_00943	COG_category	[E] Amino acid transport and metabolism			
2558670275	DRAFT_00943	COG2309	Leucyl aminopeptidase (aminopeptidase T)			2.00E-28
2558670275	DRAFT_00943	pfam02073	Peptidase_M29			1.40E-27
2558670275	DRAFT_00943	Locus_type		CDS		
2558670275	DRAFT_00943	Product_name		Leucyl aminopeptidase (aminopeptidase T)		
2558670275	DRAFT_00943	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670275	DRAFT_00943	Coordinates		35088..36173(-)		
2558670275	DRAFT_00943	DNA_length		1086bp		
2558670275	DRAFT_00943	Protein_length		361aa		
2558670275	DRAFT_00943	GC			0.55	
2558670276	DRAFT_00944	pfam00211	Guanylate_cyc			2.40E-14
2558670276	DRAFT_00944	Locus_type		CDS		
2558670276	DRAFT_00944	Product_name		Adenylate cyclase, family 3 (some proteins contain HAMP domain)		
2558670276	DRAFT_00944	Scaffold		DRAFT_contig_70_88_len_36701_read_count_592636.15		
2558670276	DRAFT_00944	Coordinates		36354..36698(+)		
2558670276	DRAFT_00944	DNA_length		345bp		
2558670276	DRAFT_00944	Protein_length		115aa		
2558670276	DRAFT_00944	GC			0.56	
2558670277	DRAFT_00945	Locus_type		tRNA		
2558670277	DRAFT_00945	Product_name		tRNA_Pseudo_CTC		
2558670277	DRAFT_00945	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670277	DRAFT_00945	Coordinates		1..60(-)		

2558670277	DRAFT_00945	DNA_length		60bp		
2558670277	DRAFT_00945	GC			0.6	
2558670278	DRAFT_00946	COG_category	[S] Function unknown			
2558670278	DRAFT_00946	COG5513	Predicted secreted protein			1.00E-05
2558670278	DRAFT_00946	pfam09394	Inhibitor_I42			2.00E-13
2558670278	DRAFT_00946	Locus_type		CDS		
2558670278	DRAFT_00946	Product_name		Predicted secreted protein		
2558670278	DRAFT_00946	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670278	DRAFT_00946	Coordinates		548..2440(-)		
2558670278	DRAFT_00946	DNA_length		1893bp		
2558670278	DRAFT_00946	Protein_length		630aa		
2558670278	DRAFT_00946	GC			0.58	
2558670278	DRAFT_00946	Transmembrane		Yes		
2558670279	DRAFT_00947	IMG_pathway	433: Archaeal nucleoid proteins			
2558670279	DRAFT_00947	COG_category	[B] Chromatin structure and dynamics			
2558670279	DRAFT_00947	COG2036	Histones H3 and H4			2.00E-10
2558670279	DRAFT_00947	pfam00808	CBFD_NFYB_HMF			5.70E-11
2558670279	DRAFT_00947	ITERM:00140	archaeal histone			
2558670279	DRAFT_00947	Locus_type		CDS		
2558670279	DRAFT_00947	Product_name		archaeal histone		
2558670279	DRAFT_00947	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670279	DRAFT_00947	Coordinates		2844..3071(-)		
2558670279	DRAFT_00947	DNA_length		228bp		
2558670279	DRAFT_00947	Protein_length		75aa		
2558670279	DRAFT_00947	GC			0.56	
2558670280	DRAFT_00948	COG_category	[L] Replication, recombination and repair			
2558670280	DRAFT_00948	COG0084	Mg-dependent DNase			3.00E-32
2558670280	DRAFT_00948	pfam01026	TatD_DNase			1.70E-33
2558670280	DRAFT_00948	EC:3.1.21.-	Hydrolases. Acting on ester bonds. Endodeoxyribonucleases producing 5'-phosphomonoesters			
2558670280	DRAFT_00948	KO:K03424	TatD DNase family protein [EC:3.1.21.-]			6.40E-31
2558670280	DRAFT_00948	Locus_type		CDS		

2558670280	DRAFT_00948	Product_name		Mg-dependent DNase		
2558670280	DRAFT_00948	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670280	DRAFT_00948	Coordinates		3324..3980(+)		
2558670280	DRAFT_00948	DNA_length		657bp		
2558670280	DRAFT_00948	Protein_length		218aa		
2558670280	DRAFT_00948	GC			0.59	
2558670281	DRAFT_00949	KEGG_module	M00179: Ribosome, archaea			
2558670281	DRAFT_00949	KEGG_module	M00177: Ribosome, eukaryotes			
2558670281	DRAFT_00949	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670281	DRAFT_00949	COG1383	Ribosomal protein S17E			8.00E-09
2558670281	DRAFT_00949	pfam00833	Ribosomal_S17e			4.00E-14
2558670281	DRAFT_00949	KO:K02962	small subunit ribosomal protein S17e			3.20E-08
2558670281	DRAFT_00949	Locus_type		CDS		
2558670281	DRAFT_00949	Product_name		Ribosomal protein S17E		
2558670281	DRAFT_00949	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670281	DRAFT_00949	Coordinates		4010..4219(+)		
2558670281	DRAFT_00949	DNA_length		210bp		
2558670281	DRAFT_00949	Protein_length		69aa		
2558670281	DRAFT_00949	GC			0.51	
2558670282	DRAFT_00950	pfam02195	ParBc			2.90E-06
2558670282	DRAFT_00950	Locus_type		CDS		
2558670282	DRAFT_00950	Product_name		Predicted transcriptional regulators		
2558670282	DRAFT_00950	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670282	DRAFT_00950	Coordinates		4223..5041(+)		
2558670282	DRAFT_00950	DNA_length		819bp		
2558670282	DRAFT_00950	Protein_length		272aa		
2558670282	DRAFT_00950	GC			0.58	
2558670283	DRAFT_00951	Locus_type		CDS		
2558670283	DRAFT_00951	Product_name		hypothetical protein		
2558670283	DRAFT_00951	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670283	DRAFT_00951	Coordinates		5038..5295(+)		

2558670283	DRAFT_00951	DNA_length		258bp		
2558670283	DRAFT_00951	Protein_length		85aa		
2558670283	DRAFT_00951	GC			0.6	
2558670284	DRAFT_00952	pfam08617	CGI-121			4.10E-07
2558670284	DRAFT_00952	KO:K09119	hypothetical protein			5.30E-08
2558670284	DRAFT_00952	Locus_type		CDS		
2558670284	DRAFT_00952	Product_name		Uncharacterized conserved protein		
2558670284	DRAFT_00952	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670284	DRAFT_00952	Coordinates		5300..5761(+)		
2558670284	DRAFT_00952	DNA_length		462bp		
2558670284	DRAFT_00952	Protein_length		153aa		
2558670284	DRAFT_00952	GC			0.58	
2558670285	DRAFT_00953	COG_category	[R] General function prediction only			
2558670285	DRAFT_00953	COG1818	Predicted RNA-binding protein, contains THUMP domain			3.00E-14
2558670285	DRAFT_00953	pfam02926	THUMP			9.20E-11
2558670285	DRAFT_00953	KO:K06963	tRNA acetyltransferase TAN1			6.30E-26
2558670285	DRAFT_00953	Locus_type		CDS		
2558670285	DRAFT_00953	Product_name		Predicted RNA-binding protein, contains THUMP domain		
2558670285	DRAFT_00953	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670285	DRAFT_00953	Coordinates		5730..6242(-)		
2558670285	DRAFT_00953	DNA_length		513bp		
2558670285	DRAFT_00953	Protein_length		170aa		
2558670285	DRAFT_00953	GC			0.56	
2558670286	DRAFT_00954	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670286	DRAFT_00954	COG0009	Putative translation factor (SUA5)			2.00E-48
2558670286	DRAFT_00954	pfam01300	Sua5_yciO_yrdC			9.90E-52
2558670286	DRAFT_00954	TIGR00057	tRNA threonylcarbamoyl adenosine modification protein, Sua5/YciO/Yr			9.60E-53
2558670286	DRAFT_00954	KO:K07566	tRNA threonylcarbamoyladenosine biosynthesis protein			2.00E-42
2558670286	DRAFT_00954	ITERM:02777	translation factor SUA5			
2558670286	DRAFT_00954	Locus_type		CDS		
2558670286	DRAFT_00954	Product_name		translation factor SUA5		

2558670286	DRAFT_00954	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670286	DRAFT_00954	Coordinates		6239..6847(-)	
2558670286	DRAFT_00954	DNA_length		609bp	
2558670286	DRAFT_00954	Protein_length		202aa	
2558670286	DRAFT_00954	GC		0.59	
2558670287	DRAFT_00955	pfam13489	Methyltransf_23		2.50E-10
2558670287	DRAFT_00955	Locus_type		CDS	
2558670287	DRAFT_00955	Product_name		Methyltransferase domain	
2558670287	DRAFT_00955	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670287	DRAFT_00955	Coordinates		6989..7771(+)	
2558670287	DRAFT_00955	DNA_length		783bp	
2558670287	DRAFT_00955	Protein_length		260aa	
2558670287	DRAFT_00955	GC		0.5	
2558670288	DRAFT_00956	Locus_type		CDS	
2558670288	DRAFT_00956	Product_name		hypothetical protein	
2558670288	DRAFT_00956	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670288	DRAFT_00956	Coordinates		7923..8321(-)	
2558670288	DRAFT_00956	DNA_length		399bp	
2558670288	DRAFT_00956	Protein_length		132aa	
2558670288	DRAFT_00956	GC		0.56	
2558670289	DRAFT_00957	Locus_type		CDS	
2558670289	DRAFT_00957	Product_name		hypothetical protein	
2558670289	DRAFT_00957	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670289	DRAFT_00957	Coordinates		8336..8818(-)	
2558670289	DRAFT_00957	DNA_length		483bp	
2558670289	DRAFT_00957	Protein_length		160aa	
2558670289	DRAFT_00957	GC		0.49	
2558670290	DRAFT_00958	Locus_type		CDS	
2558670290	DRAFT_00958	Product_name		hypothetical protein	
2558670290	DRAFT_00958	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	

2558670290	DRAFT_00958	Coordinates		8827..9009(-)		
2558670290	DRAFT_00958	DNA_length		183bp		
2558670290	DRAFT_00958	Protein_length		60aa		
2558670290	DRAFT_00958	GC			0.55	
2558670291	DRAFT_00959	COG_category	[L] Replication, recombination and repair			
2558670291	DRAFT_00959	COG3316	Transposase and inactivated derivatives			9.00E-08
2558670291	DRAFT_00959	pfam13610	DDE_Tnp_IS240			2.80E-19
2558670291	DRAFT_00959	Locus_type		CDS		
2558670291	DRAFT_00959	Product_name		Transposase and inactivated derivatives		
2558670291	DRAFT_00959	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670291	DRAFT_00959	Coordinates		9139..10359(+)		
2558670291	DRAFT_00959	DNA_length		1221bp		
2558670291	DRAFT_00959	Protein_length		406aa		
2558670291	DRAFT_00959	GC			0.57	
2558670292	DRAFT_00960	Locus_type		CDS		
2558670292	DRAFT_00960	Product_name		hypothetical protein		
2558670292	DRAFT_00960	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670292	DRAFT_00960	Coordinates		10381..10758(+)		
2558670292	DRAFT_00960	DNA_length		378bp		
2558670292	DRAFT_00960	Protein_length		125aa		
2558670292	DRAFT_00960	GC			0.5	
2558670292	DRAFT_00960	Transmembrane		Yes		
2558670293	DRAFT_00961	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds			
2558670293	DRAFT_00961	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2558670293	DRAFT_00961	KEGG_module	M00003: Gluconeogenesis, oxaloacetate => fructose-6P			
2558670293	DRAFT_00961	Metacyc	PWY-7003: glycerol degradation to butanol			
2558670293	DRAFT_00961	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2558670293	DRAFT_00961	Metacyc	GLYCOLYSIS: glycolysis I			
2558670293	DRAFT_00961	Metacyc	P341-PWY: glycolysis V (Pyrococcus)			
2558670293	DRAFT_00961	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			
2558670293	DRAFT_00961	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			

2558670293	DRAFT_00961	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2558670293	DRAFT_00961	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2558670293	DRAFT_00961	Metacyc	PWY66-373: sucrose degradation V (mammalian)			
2558670293	DRAFT_00961	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)			
2558670293	DRAFT_00961	Metacyc	PWY-1042: glycolysis IV (plant cytosol)			
2558670293	DRAFT_00961	IMG_pathway	336: Standard Embden-Meyerhof pathway			
2558670293	DRAFT_00961	IMG_pathway	337: Embden-Meyerhof pathway without bisphosphoglycerate			
2558670293	DRAFT_00961	IMG_pathway	527: Calvin cycle			
2558670293	DRAFT_00961	COG_category	[G] Carbohydrate transport and metabolism			
2558670293	DRAFT_00961	COG0149	Triosephosphate isomerase			6.00E-27
2558670293	DRAFT_00961	pfam00121	TIM			2.40E-08
2558670293	DRAFT_00961	pfam00121	TIM			3.50E-08
2558670293	DRAFT_00961	EC:5.3.1.1	Triose-phosphate isomerase.			
2558670293	DRAFT_00961	TIGR00419	triosephosphate isomerase			8.90E-41
2558670293	DRAFT_00961	KO:K01803	triosephosphate isomerase (TIM) [EC:5.3.1.1]			0.00E+00
2558670293	DRAFT_00961	ITERM:01475	triosephosphate isomerase (EC 5.3.1.1)			
2558670293	DRAFT_00961	Locus_type		CDS		
2558670293	DRAFT_00961	Product_name		triosephosphate isomerase (EC 5.3.1.1)		
2558670293	DRAFT_00961	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670293	DRAFT_00961	Coordinates		11490..12152(+)		
2558670293	DRAFT_00961	DNA_length		663bp		
2558670293	DRAFT_00961	Protein_length		220aa		
2558670293	DRAFT_00961	GC			0.6	
2558670294	DRAFT_00962	KEGG_module	M00344: Formaldehyde assimilation, xylulose monophosphate pathway			
2558670294	DRAFT_00962	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)			
2558670294	DRAFT_00962	KEGG_module	M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP			
2558670294	DRAFT_00962	KEGG_module	M00003: Gluconeogenesis, oxaloacetate => fructose-6P			
2558670294	DRAFT_00962	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2558670294	DRAFT_00962	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2558670294	DRAFT_00962	Metacyc	GLYCOLYSIS: glycolysis I			
2558670294	DRAFT_00962	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2558670294	DRAFT_00962	Metacyc	SUCSYN-PWY: sucrose biosynthesis			
2558670294	DRAFT_00962	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			

2558670294	DRAFT_00962	COG_category	[G] Carbohydrate transport and metabolism		
2558670294	DRAFT_00962	COG0158	Fructose-1,6-bisphosphatase		9.00E-62
2558670294	DRAFT_00962	pfam00316	FBPase		7.70E-63
2558670294	DRAFT_00962	EC:3.1.3.11	Fructose-bisphosphatase.		
2558670294	DRAFT_00962	KO:K03841	fructose-1,6-bisphosphatase I [EC:3.1.3.11]		0.00E+00
2558670294	DRAFT_00962	Locus_type		CDS	
2558670294	DRAFT_00962	Product_name		Fructose-1,6-bisphosphatase	
2558670294	DRAFT_00962	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670294	DRAFT_00962	Coordinates		12284..13180(-)	
2558670294	DRAFT_00962	DNA_length		897bp	
2558670294	DRAFT_00962	Protein_length		298aa	
2558670294	DRAFT_00962	GC		0.6	
2558670295	DRAFT_00963	Metacyc	ARGININE-SYN4-PWY: arginine biosynthesis IV		
2558670295	DRAFT_00963	Metacyc	GLUTAMATE-SYN2-PWY: glutamate biosynthesis II		
2558670295	DRAFT_00963	Metacyc	PWY-5766: glutamate degradation X		
2558670295	DRAFT_00963	COG_category	[E] Amino acid transport and metabolism		
2558670295	DRAFT_00963	COG0334	Glutamate dehydrogenase/leucine dehydrogenase		0.00E+00
2558670295	DRAFT_00963	pfam00208	ELFV_dehydrog		4.10E-69
2558670295	DRAFT_00963	pfam02812	ELFV_dehydrog_N		8.40E-52
2558670295	DRAFT_00963	EC:1.4.1.3	Glutamate dehydrogenase (NAD(P)(+)).		
2558670295	DRAFT_00963	KO:K00261	glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]		0.00E+00
2558670295	DRAFT_00963	Locus_type		CDS	
2558670295	DRAFT_00963	Product_name		glutamate dehydrogenase (NAD/NADP) (EC 1.4.1.3)	
2558670295	DRAFT_00963	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670295	DRAFT_00963	Coordinates		13659..14912(+)	
2558670295	DRAFT_00963	DNA_length		1254bp	
2558670295	DRAFT_00963	Protein_length		417aa	
2558670295	DRAFT_00963	GC		0.6	
2558670296	DRAFT_00964	Metacyc	PWY-1042: glycolysis IV (plant cytosol)		
2558670296	DRAFT_00964	Metacyc	P341-PWY: glycolysis V (Pyrococcus)		
2558670296	DRAFT_00964	Metacyc	GLUCONEO-PWY: gluconeogenesis I		
2558670296	DRAFT_00964	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)		

2558670296	DRAFT_00964	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle		
2558670296	DRAFT_00964	Metacyc	PWY66-373: sucrose degradation V (mammalian)		
2558670296	DRAFT_00964	Metacyc	SUCSYN-PWY: sucrose biosynthesis		
2558670296	DRAFT_00964	Metacyc	GLYCOLYSIS: glycolysis I		
2558670296	DRAFT_00964	Metacyc	PWY-5484: glycolysis II (from fructose-6P)		
2558670296	DRAFT_00964	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)		
2558670296	DRAFT_00964	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2558670296	DRAFT_00964	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)		
2558670296	DRAFT_00964	COG_category	[G] Carbohydrate transport and metabolism		
2558670296	DRAFT_00964	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes		3.00E-59
2558670296	DRAFT_00964	pfam01791	DeoC		2.50E-35
2558670296	DRAFT_00964	EC:4.1.2.13	Fructose-bisphosphate aldolase.		
2558670296	DRAFT_00964	KO:K11645	fructose-bisphosphate aldolase, class I [EC:4.1.2.13]		0.00E+00
2558670296	DRAFT_00964	Locus_type		CDS	
2558670296	DRAFT_00964	Product_name		fructose-bisphosphate aldolase (EC 4.1.2.13)	
2558670296	DRAFT_00964	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670296	DRAFT_00964	Coordinates		15056..15835(+)	
2558670296	DRAFT_00964	DNA_length		780bp	
2558670296	DRAFT_00964	Protein_length		259aa	
2558670296	DRAFT_00964	GC		0.62	

2558670297	DRAFT_00965	KEGG_module	M00248: Putative antibiotic transport system		
2558670297	DRAFT_00965	COG_category	[V] Defense mechanisms		
2558670297	DRAFT_00965	COG0842	ABC-type multidrug transport system, permease component		1.00E-10
2558670297	DRAFT_00965	pfam01061	ABC2_membrane		2.00E-29
2558670297	DRAFT_00965	TIGR00025	ABC transporter efflux protein, DrrB family		2.30E-22
2558670297	DRAFT_00965	TIGR01247	daunorubicin resistance ABC transporter membrane protein		1.60E-43
2558670297	DRAFT_00965	KO:K09686	antibiotic transport system permease protein		0.00E+00
2558670297	DRAFT_00965	Locus_type		CDS	
2558670297	DRAFT_00965	Product_name		ABC-type multidrug transport system, permease component	
2558670297	DRAFT_00965	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670297	DRAFT_00965	Coordinates		15900..16862(-)	
2558670297	DRAFT_00965	DNA_length		963bp	
2558670297	DRAFT_00965	Protein_length		320aa	

2558670297	DRAFT_00965	GC			0.56	
2558670297	DRAFT_00965	Transmembrane		Yes		
2558670298	DRAFT_00966	KEGG_module	M00248: Putative antibiotic transport system			
2558670298	DRAFT_00966	COG_category	[V] Defense mechanisms			
2558670298	DRAFT_00966	COG1131	ABC-type multidrug transport system, ATPase component			8.00E-79
2558670298	DRAFT_00966	pfam00005	ABC_tran			6.10E-29
2558670298	DRAFT_00966	pfam13732	DUF4162			3.20E-08
2558670298	DRAFT_00966	TIGR01188	daunorubicin resistance ABC transporter ATP-binding subunit			9.20E-120
2558670298	DRAFT_00966	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2558670298	DRAFT_00966	Locus_type		CDS		
2558670298	DRAFT_00966	Product_name		daunorubicin resistance ABC transporter ATP-binding subunit		
2558670298	DRAFT_00966	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670298	DRAFT_00966	Coordinates		16872..17882(-)		
2558670298	DRAFT_00966	DNA_length		1011bp		
2558670298	DRAFT_00966	Protein_length		336aa		
2558670298	DRAFT_00966	GC			0.57	
2558670299	DRAFT_00967	COG_category	[K] Transcription			
2558670299	DRAFT_00967	COG1695	Predicted transcriptional regulators			2.00E-06
2558670299	DRAFT_00967	pfam03551	PadR			4.10E-08
2558670299	DRAFT_00967	Locus_type		CDS		
2558670299	DRAFT_00967	Product_name		Predicted transcriptional regulators		
2558670299	DRAFT_00967	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670299	DRAFT_00967	Coordinates		17879..18214(-)		
2558670299	DRAFT_00967	DNA_length		336bp		
2558670299	DRAFT_00967	Protein_length		111aa		
2558670299	DRAFT_00967	GC			0.59	
2558670300	DRAFT_00968	Locus_type		CDS		
2558670300	DRAFT_00968	Product_name		hypothetical protein		
2558670300	DRAFT_00968	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670300	DRAFT_00968	Coordinates		18857..19060(+)		
2558670300	DRAFT_00968	DNA_length		204bp		

2558670300	DRAFT_00968	Protein_length		67aa		
2558670300	DRAFT_00968	GC			0.52	
2558670300	DRAFT_00968	Transmembrane		Yes		

2558670301	DRAFT_00969	Locus_type		CDS		
2558670301	DRAFT_00969	Product_name		hypothetical protein		
2558670301	DRAFT_00969	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670301	DRAFT_00969	Coordinates		19183..19941(+)		
2558670301	DRAFT_00969	DNA_length		759bp		
2558670301	DRAFT_00969	Protein_length		252aa		
2558670301	DRAFT_00969	GC			0.51	

2558670302	DRAFT_00970	COG_category	[L] Replication, recombination and repair			
2558670302	DRAFT_00970	COG3316	Transposase and inactivated derivatives			2.00E-13
2558670302	DRAFT_00970	pfam13610	DDE_Tnp_IS240			1.60E-18
2558670302	DRAFT_00970	Locus_type		CDS		
2558670302	DRAFT_00970	Product_name		Transposase and inactivated derivatives		
2558670302	DRAFT_00970	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670302	DRAFT_00970	Coordinates		19896..21056(+)		
2558670302	DRAFT_00970	DNA_length		1161bp		
2558670302	DRAFT_00970	Protein_length		386aa		
2558670302	DRAFT_00970	GC			0.51	

2558670303	DRAFT_00971	Metacyc	PWY-5386: methylglyoxal degradation I			
2558670303	DRAFT_00971	COG_category	[R] General function prediction only			
2558670303	DRAFT_00971	COG0491	Zn-dependent hydrolases, including glyoxylases			6.00E-24
2558670303	DRAFT_00971	pfam00753	Lactamase_B			4.20E-23
2558670303	DRAFT_00971	EC:3.1.2.6	Hydroxyacylglutathione hydrolase.			
2558670303	DRAFT_00971	KO:K01069	hydroxyacylglutathione hydrolase [EC:3.1.2.6]			3.80E-37
2558670303	DRAFT_00971	Locus_type		CDS		
2558670303	DRAFT_00971	Product_name		Zn-dependent hydrolases, including glyoxylases		
2558670303	DRAFT_00971	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670303	DRAFT_00971	Coordinates		21270..21875(-)		
2558670303	DRAFT_00971	DNA_length		606bp		

2558670303	DRAFT_00971	Protein_length		201aa	
2558670303	DRAFT_00971	GC		0.58	
2558670304	DRAFT_00972	Locus_type		CDS	
2558670304	DRAFT_00972	Product_name		hypothetical protein	
2558670304	DRAFT_00972	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670304	DRAFT_00972	Coordinates		22111..22293(-)	
2558670304	DRAFT_00972	DNA_length		183bp	
2558670304	DRAFT_00972	Protein_length		60aa	
2558670304	DRAFT_00972	GC		0.51	
2558670305	DRAFT_00973	COG_category	[P] Inorganic ion transport and metabolism		
2558670305	DRAFT_00973	COG1392	Phosphate transport regulator (distant homolog of PhoU)		7.00E-18
2558670305	DRAFT_00973	pfam01865	PhoU_div		7.00E-20
2558670305	DRAFT_00973	KO:K07220	hypothetical protein		0.00E+00
2558670305	DRAFT_00973	Locus_type		CDS	
2558670305	DRAFT_00973	Product_name		Phosphate transport regulator (distant homolog of PhoU)	
2558670305	DRAFT_00973	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670305	DRAFT_00973	Coordinates		22490..23113(+)	
2558670305	DRAFT_00973	DNA_length		624bp	
2558670305	DRAFT_00973	Protein_length		207aa	
2558670305	DRAFT_00973	GC		0.52	
2558670306	DRAFT_00974	COG_category	[P] Inorganic ion transport and metabolism		
2558670306	DRAFT_00974	COG0306	Phosphate/sulphate permeases		1.00E-54
2558670306	DRAFT_00974	pfam01384	PHO4		1.90E-93
2558670306	DRAFT_00974	KO:K03306	inorganic phosphate transporter, PiT family		0.00E+00
2558670306	DRAFT_00974	Locus_type		CDS	
2558670306	DRAFT_00974	Product_name		Phosphate/sulphate permeases	
2558670306	DRAFT_00974	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670306	DRAFT_00974	Coordinates		23124..24110(+)	
2558670306	DRAFT_00974	DNA_length		987bp	
2558670306	DRAFT_00974	Protein_length		328aa	
2558670306	DRAFT_00974	GC		0.58	

2558670306	DRAFT_00974	Transmembrane		Yes	
2558670307	DRAFT_00975	pfam03551	PadR		7.00E-17
2558670307	DRAFT_00975	ITERM:01890	transcriptional regulator, PadR family		
2558670307	DRAFT_00975	Locus_type		CDS	
2558670307	DRAFT_00975	Product_name		transcriptional regulator, PadR family	
2558670307	DRAFT_00975	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670307	DRAFT_00975	Coordinates		24209..24721(+)	
2558670307	DRAFT_00975	DNA_length		513bp	
2558670307	DRAFT_00975	Protein_length		170aa	
2558670307	DRAFT_00975	GC		0.55	
2558670308	DRAFT_00976	Metacyc	PWY-7076: 3,5-dimethoxytoluene biosynthesis		
2558670308	DRAFT_00976	Metacyc	PWY-6334: L-dopa degradation		
2558670308	DRAFT_00976	Metacyc	PWY-5426: betaxanthin biosynthesis		
2558670308	DRAFT_00976	Metacyc	PWY-6342: noradrenaline and adrenaline degradation		
2558670308	DRAFT_00976	Metacyc	PWY6666-2: dopamine degradation		
2558670308	DRAFT_00976	COG_category	[R] General function prediction only		
2558670308	DRAFT_00976	COG4122	Predicted O-methyltransferase		2.00E-32
2558670308	DRAFT_00976	pfam01596	Methyltransf_3		2.50E-27
2558670308	DRAFT_00976	EC:2.1.1.6	Catechol O-methyltransferase.		
2558670308	DRAFT_00976	KO:K00545	catechol O-methyltransferase [EC:2.1.1.6]		1.20E-25
2558670308	DRAFT_00976	Locus_type		CDS	
2558670308	DRAFT_00976	Product_name		Predicted O-methyltransferase	
2558670308	DRAFT_00976	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670308	DRAFT_00976	Coordinates		24737..25321(+)	
2558670308	DRAFT_00976	DNA_length		585bp	
2558670308	DRAFT_00976	Protein_length		194aa	
2558670308	DRAFT_00976	GC		0.58	
2558670309	DRAFT_00977	Locus_type		CDS	
2558670309	DRAFT_00977	Product_name		hypothetical protein	
2558670309	DRAFT_00977	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670309	DRAFT_00977	Coordinates		25474..25854(-)	

2558670309	DRAFT_00977	DNA_length		381bp		
2558670309	DRAFT_00977	Protein_length		126aa		
2558670309	DRAFT_00977	GC			0.57	
2558670310	DRAFT_00978	COG_category	[R] General function prediction only			
2558670310	DRAFT_00978	COG3324	Predicted enzyme related to lactoylglutathione lyase			8.00E-17
2558670310	DRAFT_00978	pfam12681	Glyoxalase_2			1.20E-12
2558670310	DRAFT_00978	Locus_type		CDS		
2558670310	DRAFT_00978	Product_name		Predicted enzyme related to lactoylglutathione lyase		
2558670310	DRAFT_00978	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670310	DRAFT_00978	Coordinates		26061..26450(+)		
2558670310	DRAFT_00978	DNA_length		390bp		
2558670310	DRAFT_00978	Protein_length		129aa		
2558670310	DRAFT_00978	GC			0.56	
2558670311	DRAFT_00979	COG_category	[E] Amino acid transport and metabolism			
2558670311	DRAFT_00979	COG0006	Xaa-Pro aminopeptidase			6.00E-50
2558670311	DRAFT_00979	pfam00557	Peptidase_M24			1.60E-28
2558670311	DRAFT_00979	pfam01321	Creatinase_N			1.30E-10
2558670311	DRAFT_00979	Locus_type		CDS		
2558670311	DRAFT_00979	Product_name		Xaa-Pro aminopeptidase		
2558670311	DRAFT_00979	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670311	DRAFT_00979	Coordinates		26655..27743(-)		
2558670311	DRAFT_00979	DNA_length		1089bp		
2558670311	DRAFT_00979	Protein_length		362aa		
2558670311	DRAFT_00979	GC			0.57	
2558670312	DRAFT_00980	pfam03745	DUF309			2.50E-20
2558670312	DRAFT_00980	KO:K09763	hypothetical protein			5.90E-25
2558670312	DRAFT_00980	Locus_type		CDS		
2558670312	DRAFT_00980	Product_name		Uncharacterized conserved protein		
2558670312	DRAFT_00980	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670312	DRAFT_00980	Coordinates		27884..28444(+)		
2558670312	DRAFT_00980	DNA_length		561bp		

2558670312	DRAFT_00980	Protein_length		186aa	
2558670312	DRAFT_00980	GC			0.57
2558670313	DRAFT_00981	Locus_type		CDS	
2558670313	DRAFT_00981	Product_name		hypothetical protein	
2558670313	DRAFT_00981	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670313	DRAFT_00981	Coordinates		28617..29267(-)	
2558670313	DRAFT_00981	DNA_length		651bp	
2558670313	DRAFT_00981	Protein_length		216aa	
2558670313	DRAFT_00981	GC			0.54
2558670314	DRAFT_00982	Locus_type		CDS	
2558670314	DRAFT_00982	Product_name		hypothetical protein	
2558670314	DRAFT_00982	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670314	DRAFT_00982	Coordinates		29301..29771(-)	
2558670314	DRAFT_00982	DNA_length		471bp	
2558670314	DRAFT_00982	Protein_length		156aa	
2558670314	DRAFT_00982	GC			0.55
2558670314	DRAFT_00982	Transmembrane		Yes	
2558670315	DRAFT_00983	Locus_type		CDS	
2558670315	DRAFT_00983	Product_name		hypothetical protein	
2558670315	DRAFT_00983	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670315	DRAFT_00983	Coordinates		29740..30111(-)	
2558670315	DRAFT_00983	DNA_length		372bp	
2558670315	DRAFT_00983	Protein_length		123aa	
2558670315	DRAFT_00983	GC			0.51
2558670315	DRAFT_00983	Transmembrane		Yes	
2558670316	DRAFT_00984	pfam12730	ABC2_membrane_4		2.10E-06
2558670316	DRAFT_00984	Locus_type		CDS	
2558670316	DRAFT_00984	Product_name		ABC-2 family transporter protein	
2558670316	DRAFT_00984	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16	
2558670316	DRAFT_00984	Coordinates		30321..31967(-)	

2558670316	DRAFT_00984	DNA_length		1647bp		
2558670316	DRAFT_00984	Protein_length		548aa		
2558670316	DRAFT_00984	GC			0.57	
2558670316	DRAFT_00984	Transmembrane		Yes		

2558670317	DRAFT_00985	KEGG_module	M00254: ABC-2 type transport system			
2558670317	DRAFT_00985	COG_category	[V] Defense mechanisms			
2558670317	DRAFT_00985	COG1131	ABC-type multidrug transport system, ATPase component			6.00E-65
2558670317	DRAFT_00985	pfam00005	ABC_tran			1.30E-28
2558670317	DRAFT_00985	KO:K01990	ABC-2 type transport system ATP-binding protein			0.00E+00
2558670317	DRAFT_00985	Locus_type		CDS		
2558670317	DRAFT_00985	Product_name		ABC-type multidrug transport system, ATPase component		
2558670317	DRAFT_00985	Scaffold		DRAFT_contig_70_97_len_33135_read_count_580268.16		
2558670317	DRAFT_00985	Coordinates		31964..32755(-)		
2558670317	DRAFT_00985	DNA_length		792bp		
2558670317	DRAFT_00985	Protein_length		263aa		
2558670317	DRAFT_00985	GC			0.55	

2558670318	DRAFT_00986	pfam12695	Abhydrolase_5			1.00E-11
2558670318	DRAFT_00986	Locus_type		CDS		
2558670318	DRAFT_00986	Product_name		Dienelactone hydrolase and related enzymes		
2558670318	DRAFT_00986	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670318	DRAFT_00986	Coordinates		1..450(+)		
2558670318	DRAFT_00986	DNA_length		450bp		
2558670318	DRAFT_00986	Protein_length		149aa		
2558670318	DRAFT_00986	GC			0.64	

2558670319	DRAFT_00987	Locus_type		CDS		
2558670319	DRAFT_00987	Product_name		hypothetical protein		
2558670319	DRAFT_00987	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670319	DRAFT_00987	Coordinates		647..1195(+)		
2558670319	DRAFT_00987	DNA_length		549bp		
2558670319	DRAFT_00987	Protein_length		182aa		
2558670319	DRAFT_00987	GC			0.52	

2558670320	DRAFT_00988	pfam00583	Acetyltransf_1		4.70E-05
2558670320	DRAFT_00988	Locus_type		CDS	
2558670320	DRAFT_00988	Product_name		Acetyltransferase (GNAT) family	
2558670320	DRAFT_00988	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670320	DRAFT_00988	Coordinates		1281..2069(-)	
2558670320	DRAFT_00988	DNA_length		789bp	
2558670320	DRAFT_00988	Protein_length		262aa	
2558670320	DRAFT_00988	GC		0.55	

2558670321	DRAFT_00989	Locus_type		CDS	
2558670321	DRAFT_00989	Product_name		hypothetical protein	
2558670321	DRAFT_00989	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670321	DRAFT_00989	Coordinates		2063..3235(-)	
2558670321	DRAFT_00989	DNA_length		1173bp	
2558670321	DRAFT_00989	Protein_length		390aa	
2558670321	DRAFT_00989	GC		0.55	

2558670322	DRAFT_00990	Locus_type		CDS	
2558670322	DRAFT_00990	Product_name		hypothetical protein	
2558670322	DRAFT_00990	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670322	DRAFT_00990	Coordinates		3311..4387(-)	
2558670322	DRAFT_00990	DNA_length		1077bp	
2558670322	DRAFT_00990	Protein_length		358aa	
2558670322	DRAFT_00990	GC		0.58	
2558670322	DRAFT_00990	Signal_peptide		Yes	
2558670322	DRAFT_00990	Transmembrane		Yes	

2558670323	DRAFT_00991	Locus_type		CDS	
2558670323	DRAFT_00991	Product_name		hypothetical protein	
2558670323	DRAFT_00991	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670323	DRAFT_00991	Coordinates		4377..5942(-)	
2558670323	DRAFT_00991	DNA_length		1566bp	
2558670323	DRAFT_00991	Protein_length		521aa	

2558670323	DRAFT_00991	GC			0.57	
2558670324	DRAFT_00992	Locus_type		CDS		
2558670324	DRAFT_00992	Product_name		hypothetical protein		
2558670324	DRAFT_00992	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670324	DRAFT_00992	Coordinates		6416..7789(+)		
2558670324	DRAFT_00992	DNA_length		1374bp		
2558670324	DRAFT_00992	Protein_length		457aa		
2558670324	DRAFT_00992	GC			0.54	
2558670324	DRAFT_00992	Transmembrane		Yes		
2558670325	DRAFT_00993	COG_category	[E] Amino acid transport and metabolism			
2558670325	DRAFT_00993	COG1164	Oligoendopeptidase F			3.00E-58
2558670325	DRAFT_00993	pfam01432	Peptidase_M3			5.60E-33
2558670325	DRAFT_00993	EC:3.4.24.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Metalloendopeptidases.			
2558670325	DRAFT_00993	TIGR02289	oligoendopeptidase, M3 family			0.00E+00
2558670325	DRAFT_00993	KO:K08602	oligoendopeptidase F [EC:3.4.24.-]			0.00E+00
2558670325	DRAFT_00993	Locus_type		CDS		
2558670325	DRAFT_00993	Product_name		oligoendopeptidase, M3 family		
2558670325	DRAFT_00993	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670325	DRAFT_00993	Coordinates		7878..9608(-)		
2558670325	DRAFT_00993	DNA_length		1731bp		
2558670325	DRAFT_00993	Protein_length		576aa		
2558670325	DRAFT_00993	GC			0.57	
2558670325	DRAFT_00993	Transmembrane		Yes		
2558670326	DRAFT_00994	pfam06224	HTH_42			2.20E-49
2558670326	DRAFT_00994	Locus_type		CDS		
2558670326	DRAFT_00994	Product_name		Winged helix DNA-binding domain		
2558670326	DRAFT_00994	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670326	DRAFT_00994	Coordinates		9906..11027(+)		
2558670326	DRAFT_00994	DNA_length		1122bp		
2558670326	DRAFT_00994	Protein_length		373aa		
2558670326	DRAFT_00994	GC			0.62	

2558670327	DRAFT_00995	Locus_type		CDS		
2558670327	DRAFT_00995	Product_name		hypothetical protein		
2558670327	DRAFT_00995	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670327	DRAFT_00995	Coordinates		11096..11698(-)		
2558670327	DRAFT_00995	DNA_length		603bp		
2558670327	DRAFT_00995	Protein_length		200aa		
2558670327	DRAFT_00995	GC			0.54	

2558670328	DRAFT_00996	pfam05977	MFS_3			3.80E-41
2558670328	DRAFT_00996	Locus_type		CDS		
2558670328	DRAFT_00996	Product_name		Sugar phosphate permease		
2558670328	DRAFT_00996	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670328	DRAFT_00996	Coordinates		11743..13011(+)		
2558670328	DRAFT_00996	DNA_length		1269bp		
2558670328	DRAFT_00996	Protein_length		422aa		
2558670328	DRAFT_00996	GC			0.6	
2558670328	DRAFT_00996	Transmembrane		Yes		

2558670329	DRAFT_00997	KEGG_module	M00236: Putative polar amino acid transport system			
2558670329	DRAFT_00997	COG_category	[T] Signal transduction mechanisms			
2558670329	DRAFT_00997	COG_category	[E] Amino acid transport and metabolism			
2558670329	DRAFT_00997	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmi			7.00E-32
2558670329	DRAFT_00997	pfam00497	SBP_bac_3			1.40E-56
2558670329	DRAFT_00997	KO:K02030	polar amino acid transport system substrate-binding protein			0.00E+00
2558670329	DRAFT_00997	ITERM:05951	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)			
2558670329	DRAFT_00997	Locus_type		CDS		
2558670329	DRAFT_00997	Product_name		amino acid ABC transporter substrate-binding protein, PAAT family (T		
2558670329	DRAFT_00997	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670329	DRAFT_00997	Coordinates		13325..14095(+)		
2558670329	DRAFT_00997	DNA_length		771bp		
2558670329	DRAFT_00997	Protein_length		256aa		
2558670329	DRAFT_00997	GC			0.59	
2558670329	DRAFT_00997	Transmembrane		Yes		

2558670330	DRAFT_00998	KEGG_module	M00236: Putative polar amino acid transport system		
2558670330	DRAFT_00998	COG_category	[E] Amino acid transport and metabolism		
2558670330	DRAFT_00998	COG0765	ABC-type amino acid transport system, permease component		1.00E-41
2558670330	DRAFT_00998	pfam00528	BPD_transp_1		2.60E-15
2558670330	DRAFT_00998	TIGR01726	amine acid ABC transporter, permease protein, 3-TM region, His/Glu/G		2.50E-27
2558670330	DRAFT_00998	KO:K02029	polar amino acid transport system permease protein		6.70E-44
2558670330	DRAFT_00998	ITERM:06081	amino acid ABC transporter membrane protein 1, PAAT family (TC 3.A.1.3.-)		
2558670330	DRAFT_00998	Locus_type		CDS	
2558670330	DRAFT_00998	Product_name		amino acid ABC transporter membrane protein 1, PAAT family (TC 3.A	
2558670330	DRAFT_00998	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670330	DRAFT_00998	Coordinates		14118..14789(+)	
2558670330	DRAFT_00998	DNA_length		672bp	
2558670330	DRAFT_00998	Protein_length		223aa	
2558670330	DRAFT_00998	GC		0.6	
2558670330	DRAFT_00998	Transmembrane		Yes	
2558670331	DRAFT_00999	KEGG_module	M00236: Putative polar amino acid transport system		
2558670331	DRAFT_00999	COG_category	[E] Amino acid transport and metabolism		
2558670331	DRAFT_00999	COG1126	ABC-type polar amino acid transport system, ATPase component		4.00E-87
2558670331	DRAFT_00999	pfam00005	ABC_tran		3.00E-33
2558670331	DRAFT_00999	EC:3.6.3.21	Polar-amino-acid-transporting ATPase.		
2558670331	DRAFT_00999	KO:K02028	polar amino acid transport system ATP-binding protein [EC:3.6.3.21]		0.00E+00
2558670331	DRAFT_00999	Locus_type		CDS	
2558670331	DRAFT_00999	Product_name		amino acid ABC transporter ATP-binding protein, PAAT family (TC 3.A.	
2558670331	DRAFT_00999	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670331	DRAFT_00999	Coordinates		14786..15556(+)	
2558670331	DRAFT_00999	DNA_length		771bp	
2558670331	DRAFT_00999	Protein_length		256aa	
2558670331	DRAFT_00999	GC		0.61	
2558670332	DRAFT_01000	KEGG_module	M00236: Putative polar amino acid transport system		
2558670332	DRAFT_01000	COG_category	[E] Amino acid transport and metabolism		
2558670332	DRAFT_01000	COG0765	ABC-type amino acid transport system, permease component		4.00E-48

2558670332	DRAFT_01000	pfam00528	BPD_transp_1		4.00E-12
2558670332	DRAFT_01000	TIGR01726	amine acid ABC transporter, permease protein, 3-TM region, His/Glu/G		4.70E-37
2558670332	DRAFT_01000	KO:K02029	polar amino acid transport system permease protein		0.00E+00
2558670332	DRAFT_01000	Locus_type		CDS	
2558670332	DRAFT_01000	Product_name		amine acid ABC transporter, permease protein, 3-TM region, His/Glu/	
2558670332	DRAFT_01000	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670332	DRAFT_01000	Coordinates		15575..16234(+)	
2558670332	DRAFT_01000	DNA_length		660bp	
2558670332	DRAFT_01000	Protein_length		219aa	
2558670332	DRAFT_01000	GC		0.58	
2558670332	DRAFT_01000	Transmembrane		Yes	
2558670333	DRAFT_01001	Locus_type		CDS	
2558670333	DRAFT_01001	Product_name		hypothetical protein	
2558670333	DRAFT_01001	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670333	DRAFT_01001	Coordinates		16590..18500(-)	
2558670333	DRAFT_01001	DNA_length		1911bp	
2558670333	DRAFT_01001	Protein_length		636aa	
2558670333	DRAFT_01001	GC		0.58	
2558670333	DRAFT_01001	Transmembrane		Yes	
2558670334	DRAFT_01002	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670334	DRAFT_01002	COG4591	ABC-type transport system, involved in lipoprotein release, permease c		1.00E-08
2558670334	DRAFT_01002	pfam02687	FtsX		7.30E-11
2558670334	DRAFT_01002	pfam12704	MacB_PCD		6.60E-18
2558670334	DRAFT_01002	Locus_type		CDS	
2558670334	DRAFT_01002	Product_name		ABC-type transport system, involved in lipoprotein release, permease	
2558670334	DRAFT_01002	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670334	DRAFT_01002	Coordinates		18558..19682(+)	
2558670334	DRAFT_01002	DNA_length		1125bp	
2558670334	DRAFT_01002	Protein_length		374aa	
2558670334	DRAFT_01002	GC		0.57	
2558670334	DRAFT_01002	Transmembrane		Yes	

2558670335	DRAFT_01003	KEGG_module	M00258: Putative ABC transport system		
2558670335	DRAFT_01003	COG_category	[V] Defense mechanisms		
2558670335	DRAFT_01003	COG1136	ABC-type antimicrobial peptide transport system, ATPase component		3.00E-58
2558670335	DRAFT_01003	pfam00005	ABC_tran		5.70E-29
2558670335	DRAFT_01003	KO:K02003	putative ABC transport system ATP-binding protein		0.00E+00
2558670335	DRAFT_01003	Locus_type		CDS	
2558670335	DRAFT_01003	Product_name		ABC-type antimicrobial peptide transport system, ATPase component	
2558670335	DRAFT_01003	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670335	DRAFT_01003	Coordinates		19679..20371(+)	
2558670335	DRAFT_01003	DNA_length		693bp	
2558670335	DRAFT_01003	Protein_length		230aa	
2558670335	DRAFT_01003	GC		0.59	

2558670336	DRAFT_01004	COG_category	[K] Transcription		
2558670336	DRAFT_01004	COG_category	[L] Replication, recombination and repair		
2558670336	DRAFT_01004	COG1199	Rad3-related DNA helicases		2.00E-41
2558670336	DRAFT_01004	pfam13307	Helicase_C_2		4.60E-18
2558670336	DRAFT_01004	pfam06733	DEAD_2		4.40E-08
2558670336	DRAFT_01004	Locus_type		CDS	
2558670336	DRAFT_01004	Product_name		Helicase C-terminal domain/DEAD_2	
2558670336	DRAFT_01004	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670336	DRAFT_01004	Coordinates		20772..22520(-)	
2558670336	DRAFT_01004	DNA_length		1749bp	
2558670336	DRAFT_01004	Protein_length		582aa	
2558670336	DRAFT_01004	GC		0.58	

2558670337	DRAFT_01005	pfam04041	DUF377		2.70E-32
2558670337	DRAFT_01005	Locus_type		CDS	
2558670337	DRAFT_01005	Product_name		Predicted glycosylase	
2558670337	DRAFT_01005	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670337	DRAFT_01005	Coordinates		22663..24132(-)	
2558670337	DRAFT_01005	DNA_length		1470bp	
2558670337	DRAFT_01005	Protein_length		489aa	
2558670337	DRAFT_01005	GC		0.64	

2558670338	DRAFT_01006	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670338	DRAFT_01006	COG0438	Glycosyltransferase		3.00E-23
2558670338	DRAFT_01006	pfam00534	Glycos_transf_1		2.20E-18
2558670338	DRAFT_01006	Locus_type		CDS	
2558670338	DRAFT_01006	Product_name		Glycosyltransferase	
2558670338	DRAFT_01006	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670338	DRAFT_01006	Coordinates		24167..26362(-)	
2558670338	DRAFT_01006	DNA_length		2196bp	
2558670338	DRAFT_01006	Protein_length		731aa	
2558670338	DRAFT_01006	GC		0.61	
2558670338	DRAFT_01006	Fused_gene		Yes	
2558670339	DRAFT_01007	Locus_type		CDS	
2558670339	DRAFT_01007	Product_name		hypothetical protein	
2558670339	DRAFT_01007	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670339	DRAFT_01007	Coordinates		26641..27024(+)	
2558670339	DRAFT_01007	DNA_length		384bp	
2558670339	DRAFT_01007	Protein_length		127aa	
2558670339	DRAFT_01007	GC		0.49	
2558670339	DRAFT_01007	Transmembrane		Yes	
2558670340	DRAFT_01008	COG_category	[P] Inorganic ion transport and metabolism		
2558670340	DRAFT_01008	COG2608	Copper chaperone		1.00E-03
2558670340	DRAFT_01008	Locus_type		CDS	
2558670340	DRAFT_01008	Product_name		Copper chaperone	
2558670340	DRAFT_01008	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670340	DRAFT_01008	Coordinates		27407..27739(-)	
2558670340	DRAFT_01008	DNA_length		333bp	
2558670340	DRAFT_01008	Protein_length		110aa	
2558670340	DRAFT_01008	GC		0.55	
2558670341	DRAFT_01009	pfam01402	RHH_1		2.00E-04
2558670341	DRAFT_01009	Locus_type		CDS	

2558670341	DRAFT_01009	Product_name		Ribbon-helix-helix protein, copG family	
2558670341	DRAFT_01009	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670341	DRAFT_01009	Coordinates		27848..28366(-)	
2558670341	DRAFT_01009	DNA_length		519bp	
2558670341	DRAFT_01009	Protein_length		172aa	
2558670341	DRAFT_01009	GC		0.56	
2558670342	DRAFT_01010	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558670342	DRAFT_01010	COG0071	Molecular chaperone (small heat shock protein)		7.00E-20
2558670342	DRAFT_01010	pfam00011	HSP20		9.70E-18
2558670342	DRAFT_01010	KO:K13993	HSP20 family protein		6.10E-19
2558670342	DRAFT_01010	Locus_type		CDS	
2558670342	DRAFT_01010	Product_name		Molecular chaperone (small heat shock protein)	
2558670342	DRAFT_01010	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670342	DRAFT_01010	Coordinates		28623..29168(+)	
2558670342	DRAFT_01010	DNA_length		546bp	
2558670342	DRAFT_01010	Protein_length		181aa	
2558670342	DRAFT_01010	GC		0.53	
2558670343	DRAFT_01011	Locus_type		CDS	
2558670343	DRAFT_01011	Product_name		hypothetical protein	
2558670343	DRAFT_01011	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670343	DRAFT_01011	Coordinates		29258..29386(-)	
2558670343	DRAFT_01011	DNA_length		129bp	
2558670343	DRAFT_01011	Protein_length		42aa	
2558670343	DRAFT_01011	GC		0.6	
2558670344	DRAFT_01012	Locus_type		CDS	
2558670344	DRAFT_01012	Product_name		hypothetical protein	
2558670344	DRAFT_01012	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670344	DRAFT_01012	Coordinates		29496..29714(-)	
2558670344	DRAFT_01012	DNA_length		219bp	
2558670344	DRAFT_01012	Protein_length		72aa	
2558670344	DRAFT_01012	GC		0.53	

2558670344	DRAFT_01012	Transmembrane		Yes	
2558670345	DRAFT_01013	COG_category	[L] Replication, recombination and repair		
2558670345	DRAFT_01013	COG3316	Transposase and inactivated derivatives		7.00E-15
2558670345	DRAFT_01013	pfam04434	SWIM		9.50E-07
2558670345	DRAFT_01013	pfam13610	DDE_Tnp_IS240		1.30E-24
2558670345	DRAFT_01013	Locus_type		CDS	
2558670345	DRAFT_01013	Product_name		Transposase and inactivated derivatives	
2558670345	DRAFT_01013	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670345	DRAFT_01013	Coordinates		29720..30838(-)	
2558670345	DRAFT_01013	DNA_length		1119bp	
2558670345	DRAFT_01013	Protein_length		372aa	
2558670345	DRAFT_01013	GC		0.53	
2558670346	DRAFT_01014	Locus_type		CDS	
2558670346	DRAFT_01014	Product_name		hypothetical protein	
2558670346	DRAFT_01014	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670346	DRAFT_01014	Coordinates		30979..31176(+)	
2558670346	DRAFT_01014	DNA_length		198bp	
2558670346	DRAFT_01014	Protein_length		65aa	
2558670346	DRAFT_01014	GC		0.46	
2558670347	DRAFT_01015	Locus_type		CDS	
2558670347	DRAFT_01015	Product_name		hypothetical protein	
2558670347	DRAFT_01015	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670347	DRAFT_01015	Coordinates		31173..31589(+)	
2558670347	DRAFT_01015	DNA_length		417bp	
2558670347	DRAFT_01015	Protein_length		138aa	
2558670347	DRAFT_01015	GC		0.48	
2558670348	DRAFT_01016	Locus_type		CDS	
2558670348	DRAFT_01016	Product_name		hypothetical protein	
2558670348	DRAFT_01016	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17	
2558670348	DRAFT_01016	Coordinates		31564..31965(+)	

2558670348	DRAFT_01016	DNA_length		402bp		
2558670348	DRAFT_01016	Protein_length		133aa		
2558670348	DRAFT_01016	GC			0.48	
2558670349	DRAFT_01017	pfam12874	zf-met			1.90E-04
2558670349	DRAFT_01017	pfam00301	Rubredoxin			9.70E-06
2558670349	DRAFT_01017	pfam13912	zf-C2H2_6			5.50E-06
2558670349	DRAFT_01017	Locus_type		CDS		
2558670349	DRAFT_01017	Product_name		Zinc-finger of C2H2 type/C2H2-type zinc finger		
2558670349	DRAFT_01017	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670349	DRAFT_01017	Coordinates		31904..32149(+)		
2558670349	DRAFT_01017	DNA_length		246bp		
2558670349	DRAFT_01017	Protein_length		81aa		
2558670349	DRAFT_01017	GC			0.52	
2558670350	DRAFT_01018	Locus_type		CDS		
2558670350	DRAFT_01018	Product_name		hypothetical protein		
2558670350	DRAFT_01018	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670350	DRAFT_01018	Coordinates		32146..32325(+)		
2558670350	DRAFT_01018	DNA_length		180bp		
2558670350	DRAFT_01018	Protein_length		59aa		
2558670350	DRAFT_01018	GC			0.45	
2558670351	DRAFT_01019	Locus_type		CDS		
2558670351	DRAFT_01019	Product_name		hypothetical protein		
2558670351	DRAFT_01019	Scaffold		DRAFT_contig_70_99_len_32598_read_count_581408.17		
2558670351	DRAFT_01019	Coordinates		32332..32595(+)		
2558670351	DRAFT_01019	DNA_length		264bp		
2558670351	DRAFT_01019	Protein_length		88aa		
2558670351	DRAFT_01019	GC			0.54	
2558670352	DRAFT_01020	Locus_type		CDS		
2558670352	DRAFT_01020	Product_name		hypothetical protein		
2558670352	DRAFT_01020	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		

2558670352	DRAFT_01020	Coordinates		3..173(+)		
2558670352	DRAFT_01020	DNA_length		171bp		
2558670352	DRAFT_01020	Protein_length		56aa		
2558670352	DRAFT_01020	GC			0.58	
2558670352	DRAFT_01020	Transmembrane		Yes		
2558670353	DRAFT_01021	Locus_type		CDS		
2558670353	DRAFT_01021	Product_name		hypothetical protein		
2558670353	DRAFT_01021	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670353	DRAFT_01021	Coordinates		107..385(-)		
2558670353	DRAFT_01021	DNA_length		279bp		
2558670353	DRAFT_01021	Protein_length		92aa		
2558670353	DRAFT_01021	GC			0.57	
2558670354	DRAFT_01022	pfam07758	DUF1614			1.20E-07
2558670354	DRAFT_01022	Locus_type		CDS		
2558670354	DRAFT_01022	Product_name		Protein of unknown function (DUF1614)		
2558670354	DRAFT_01022	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670354	DRAFT_01022	Coordinates		345..953(-)		
2558670354	DRAFT_01022	DNA_length		609bp		
2558670354	DRAFT_01022	Protein_length		202aa		
2558670354	DRAFT_01022	GC			0.52	
2558670354	DRAFT_01022	Transmembrane		Yes		
2558670355	DRAFT_01023	Locus_type		CDS		
2558670355	DRAFT_01023	Product_name		hypothetical protein		
2558670355	DRAFT_01023	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670355	DRAFT_01023	Coordinates		1122..1763(-)		
2558670355	DRAFT_01023	DNA_length		642bp		
2558670355	DRAFT_01023	Protein_length		213aa		
2558670355	DRAFT_01023	GC			0.51	
2558670356	DRAFT_01024	Locus_type		CDS		
2558670356	DRAFT_01024	Product_name		hypothetical protein		

2558670356	DRAFT_01024	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670356	DRAFT_01024	Coordinates		1898..2809(-)	
2558670356	DRAFT_01024	DNA_length		912bp	
2558670356	DRAFT_01024	Protein_length		303aa	
2558670356	DRAFT_01024	GC		0.5	
2558670357	DRAFT_01025	Locus_type		CDS	
2558670357	DRAFT_01025	Product_name		hypothetical protein	
2558670357	DRAFT_01025	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670357	DRAFT_01025	Coordinates		3209..5209(+)	
2558670357	DRAFT_01025	DNA_length		2001bp	
2558670357	DRAFT_01025	Protein_length		666aa	
2558670357	DRAFT_01025	GC		0.51	
2558670358	DRAFT_01026	pfam08123	DOT1		2.30E-05
2558670358	DRAFT_01026	Locus_type		CDS	
2558670358	DRAFT_01026	Product_name		Histone methylation protein DOT1	
2558670358	DRAFT_01026	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670358	DRAFT_01026	Coordinates		5253..5501(-)	
2558670358	DRAFT_01026	DNA_length		249bp	
2558670358	DRAFT_01026	Protein_length		82aa	
2558670358	DRAFT_01026	GC		0.58	
2558670359	DRAFT_01027	Locus_type		CDS	
2558670359	DRAFT_01027	Product_name		hypothetical protein	
2558670359	DRAFT_01027	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670359	DRAFT_01027	Coordinates		5547..5675(-)	
2558670359	DRAFT_01027	DNA_length		129bp	
2558670359	DRAFT_01027	Protein_length		42aa	
2558670359	DRAFT_01027	GC		0.6	
2558670360	DRAFT_01028	Locus_type		CDS	
2558670360	DRAFT_01028	Product_name		hypothetical protein	
2558670360	DRAFT_01028	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	

2558670360	DRAFT_01028	Coordinates		5860..6390(-)	
2558670360	DRAFT_01028	DNA_length		531bp	
2558670360	DRAFT_01028	Protein_length		176aa	
2558670360	DRAFT_01028	GC		0.53	
2558670360	DRAFT_01028	Transmembrane		Yes	
2558670361	DRAFT_01029	Locus_type		CDS	
2558670361	DRAFT_01029	Product_name		hypothetical protein	
2558670361	DRAFT_01029	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670361	DRAFT_01029	Coordinates		6510..7445(+)	
2558670361	DRAFT_01029	DNA_length		936bp	
2558670361	DRAFT_01029	Protein_length		311aa	
2558670361	DRAFT_01029	GC		0.51	
2558670362	DRAFT_01030	Locus_type		CDS	
2558670362	DRAFT_01030	Product_name		hypothetical protein	
2558670362	DRAFT_01030	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670362	DRAFT_01030	Coordinates		7549..8766(+)	
2558670362	DRAFT_01030	DNA_length		1218bp	
2558670362	DRAFT_01030	Protein_length		405aa	
2558670362	DRAFT_01030	GC		0.54	
2558670362	DRAFT_01030	Transmembrane		Yes	
2558670363	DRAFT_01031	Locus_type		CDS	
2558670363	DRAFT_01031	Product_name		hypothetical protein	
2558670363	DRAFT_01031	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670363	DRAFT_01031	Coordinates		8867..9028(+)	
2558670363	DRAFT_01031	DNA_length		162bp	
2558670363	DRAFT_01031	Protein_length		53aa	
2558670363	DRAFT_01031	GC		0.57	
2558670364	DRAFT_01032	pfam06094	AIG2		1.90E-12
2558670364	DRAFT_01032	Locus_type		CDS	
2558670364	DRAFT_01032	Product_name		Uncharacterized protein involved in cation transport	

2558670364	DRAFT_01032	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670364	DRAFT_01032	Coordinates		9025..10074(+)	
2558670364	DRAFT_01032	DNA_length		1050bp	
2558670364	DRAFT_01032	Protein_length		349aa	
2558670364	DRAFT_01032	GC		0.56	
2558670365	DRAFT_01033	COG_category	[S] Function unknown		
2558670365	DRAFT_01033	COG3832	Uncharacterized conserved protein		4.00E-11
2558670365	DRAFT_01033	pfam08327	AHSA1		7.60E-17
2558670365	DRAFT_01033	Locus_type		CDS	
2558670365	DRAFT_01033	Product_name		Uncharacterized conserved protein	
2558670365	DRAFT_01033	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670365	DRAFT_01033	Coordinates		10254..10769(-)	
2558670365	DRAFT_01033	DNA_length		516bp	
2558670365	DRAFT_01033	Protein_length		171aa	
2558670365	DRAFT_01033	GC		0.55	
2558670366	DRAFT_01034	COG_category	[R] General function prediction only		
2558670366	DRAFT_01034	COG0730	Predicted permeases		2.00E-14
2558670366	DRAFT_01034	pfam01925	TauE		1.40E-39
2558670366	DRAFT_01034	Locus_type		CDS	
2558670366	DRAFT_01034	Product_name		Predicted permeases	
2558670366	DRAFT_01034	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670366	DRAFT_01034	Coordinates		10994..11821(+)	
2558670366	DRAFT_01034	DNA_length		828bp	
2558670366	DRAFT_01034	Protein_length		275aa	
2558670366	DRAFT_01034	GC		0.57	
2558670366	DRAFT_01034	Transmembrane		Yes	
2558670367	DRAFT_01035	COG_category	[S] Function unknown		
2558670367	DRAFT_01035	COG4272	Predicted membrane protein		3.00E-08
2558670367	DRAFT_01035	pfam07843	DUF1634		1.20E-16
2558670367	DRAFT_01035	Locus_type		CDS	
2558670367	DRAFT_01035	Product_name		Predicted membrane protein	

2558670367	DRAFT_01035	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670367	DRAFT_01035	Coordinates		11818..12201(+)		
2558670367	DRAFT_01035	DNA_length		384bp		
2558670367	DRAFT_01035	Protein_length		127aa		
2558670367	DRAFT_01035	GC			0.55	
2558670367	DRAFT_01035	Transmembrane		Yes		

2558670368	DRAFT_01036	COG_category	[S] Function unknown			
2558670368	DRAFT_01036	COG3885	Uncharacterized conserved protein			2.00E-54
2558670368	DRAFT_01036	pfam02900	LigB			1.30E-19
2558670368	DRAFT_01036	Locus_type		CDS		
2558670368	DRAFT_01036	Product_name		Uncharacterized conserved protein		
2558670368	DRAFT_01036	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670368	DRAFT_01036	Coordinates		12450..13289(-)		
2558670368	DRAFT_01036	DNA_length		840bp		
2558670368	DRAFT_01036	Protein_length		279aa		
2558670368	DRAFT_01036	GC			0.59	

2558670369	DRAFT_01037	COG_category	[R] General function prediction only			
2558670369	DRAFT_01037	COG0491	Zn-dependent hydrolases, including glyoxylases			3.00E-14
2558670369	DRAFT_01037	pfam00753	Lactamase_B			3.60E-20
2558670369	DRAFT_01037	Locus_type		CDS		
2558670369	DRAFT_01037	Product_name		Zn-dependent hydrolases, including glyoxylases		
2558670369	DRAFT_01037	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670369	DRAFT_01037	Coordinates		13315..14217(-)		
2558670369	DRAFT_01037	DNA_length		903bp		
2558670369	DRAFT_01037	Protein_length		300aa		
2558670369	DRAFT_01037	GC			0.59	

2558670370	DRAFT_01038	Metacyc	PWY-6842: glutathione-mediated detoxification II			
2558670370	DRAFT_01038	COG_category	[R] General function prediction only			
2558670370	DRAFT_01038	COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase			5.00E-118
2558670370	DRAFT_01038	pfam07687	M20_dimer			2.30E-14
2558670370	DRAFT_01038	pfam01546	Peptidase_M20			6.40E-32

2558670370	DRAFT_01038	EC:3.4.17.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Metallocarboxypeptidases.		
2558670370	DRAFT_01038	TIGR01891	amidohydrolase		1.00E-123
2558670370	DRAFT_01038	KO:K13048	carboxypeptidase Ss1 [EC:3.4.17.-]		0.00E+00
2558670370	DRAFT_01038	Locus_type		CDS	
2558670370	DRAFT_01038	Product_name		carboxypeptidase Ss1. Metallo peptidase. MEROPS family M20D	
2558670370	DRAFT_01038	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670370	DRAFT_01038	Coordinates		14227..15417(-)	
2558670370	DRAFT_01038	DNA_length		1191bp	
2558670370	DRAFT_01038	Protein_length		396aa	
2558670370	DRAFT_01038	GC		0.57	
2558670371	DRAFT_01039	COG_category	[S] Function unknown		
2558670371	DRAFT_01039	COG2410	Uncharacterized conserved protein		2.00E-17
2558670371	DRAFT_01039	pfam04250	DUF429		1.10E-27
2558670371	DRAFT_01039	KO:K09147	hypothetical protein		2.00E-31
2558670371	DRAFT_01039	Locus_type		CDS	
2558670371	DRAFT_01039	Product_name		Uncharacterized conserved protein	
2558670371	DRAFT_01039	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670371	DRAFT_01039	Coordinates		15473..16081(+)	
2558670371	DRAFT_01039	DNA_length		609bp	
2558670371	DRAFT_01039	Protein_length		202aa	
2558670371	DRAFT_01039	GC		0.58	
2558670372	DRAFT_01040	Locus_type		tRNA	
2558670372	DRAFT_01040	Product_name		tRNA_Leu_TAA	
2558670372	DRAFT_01040	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670372	DRAFT_01040	Coordinates		16337..16446(-)	
2558670372	DRAFT_01040	DNA_length		87bp	
2558670372	DRAFT_01040	GC		0.63	
2558670373	DRAFT_01041	COG_category	[L] Replication, recombination and repair		
2558670373	DRAFT_01041	COG1796	DNA polymerase IV (family X)		4.00E-65
2558670373	DRAFT_01041	pfam02811	PHP		1.00E-09
2558670373	DRAFT_01041	pfam14716	HHH_8		1.20E-18

2558670373	DRAFT_01041	pfam14791	DNA_pol_B_thumb			2.50E-24
2558670373	DRAFT_01041	KO:K02347	DNA polymerase (family X)			0.00E+00
2558670373	DRAFT_01041	Locus_type		CDS		
2558670373	DRAFT_01041	Product_name		DNA polymerase IV (family X)		
2558670373	DRAFT_01041	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670373	DRAFT_01041	Coordinates		16491..18179(-)		
2558670373	DRAFT_01041	DNA_length		1689bp		
2558670373	DRAFT_01041	Protein_length		562aa		
2558670373	DRAFT_01041	GC			0.58	
2558670374	DRAFT_01042	COG_category	[E] Amino acid transport and metabolism			
2558670374	DRAFT_01042	COG0006	Xaa-Pro aminopeptidase			1.00E-62
2558670374	DRAFT_01042	pfam01321	Creatinase_N			1.40E-15
2558670374	DRAFT_01042	pfam00557	Peptidase_M24			4.20E-47
2558670374	DRAFT_01042	EC:3.4.13.9	Xaa-Pro dipeptidase.			
2558670374	DRAFT_01042	KO:K01271	Xaa-Pro dipeptidase [EC:3.4.13.9]			0.00E+00
2558670374	DRAFT_01042	Locus_type		CDS		
2558670374	DRAFT_01042	Product_name		Xaa-Pro aminopeptidase		
2558670374	DRAFT_01042	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670374	DRAFT_01042	Coordinates		18255..19355(-)		
2558670374	DRAFT_01042	DNA_length		1101bp		
2558670374	DRAFT_01042	Protein_length		366aa		
2558670374	DRAFT_01042	GC			0.59	
2558670375	DRAFT_01043	Metacyc	PWY-5737: (5<i>R</i>)-carbapenem biosynthesis			
2558670375	DRAFT_01043	Metacyc	PROUT-PWY: proline degradation			
2558670375	DRAFT_01043	Metacyc	PWY-6922: <i>L-N^{δ}</i>-acetylornithine biosynthesis			
2558670375	DRAFT_01043	Metacyc	CITRULBIO-PWY: citrulline biosynthesis			
2558670375	DRAFT_01043	IMG_pathway	181: L-proline oxidation to L-glutamate			
2558670375	DRAFT_01043	COG_category	[E] Amino acid transport and metabolism			
2558670375	DRAFT_01043	COG0506	Proline dehydrogenase			6.00E-28
2558670375	DRAFT_01043	pfam01619	Pro_dh			1.70E-37
2558670375	DRAFT_01043	EC:1.5.99.8	Proline dehydrogenase.			
2558670375	DRAFT_01043	KO:K00318	proline dehydrogenase [EC:1.5.99.8]			0.00E+00

2558670375	DRAFT_01043	ITERM:00470	L-proline dehydrogenase (EC 1.5.99.8)		
2558670375	DRAFT_01043	Locus_type		CDS	
2558670375	DRAFT_01043	Product_name		L-proline dehydrogenase (EC 1.5.99.8)	
2558670375	DRAFT_01043	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670375	DRAFT_01043	Coordinates		19370..20257(+)	
2558670375	DRAFT_01043	DNA_length		888bp	
2558670375	DRAFT_01043	Protein_length		295aa	
2558670375	DRAFT_01043	GC			0.59
2558670376	DRAFT_01044	Locus_type		CDS	
2558670376	DRAFT_01044	Product_name		hypothetical protein	
2558670376	DRAFT_01044	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670376	DRAFT_01044	Coordinates		20369..20545(+)	
2558670376	DRAFT_01044	DNA_length		177bp	
2558670376	DRAFT_01044	Protein_length		58aa	
2558670376	DRAFT_01044	GC			0.54
2558670377	DRAFT_01045	pfam12840	HTH_20		9.70E-08
2558670377	DRAFT_01045	KO:K07721	ArsR family transcriptional regulator		3.90E-12
2558670377	DRAFT_01045	Locus_type		CDS	
2558670377	DRAFT_01045	Product_name		Predicted transcriptional regulators	
2558670377	DRAFT_01045	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670377	DRAFT_01045	Coordinates		20570..21232(-)	
2558670377	DRAFT_01045	DNA_length		663bp	
2558670377	DRAFT_01045	Protein_length		220aa	
2558670377	DRAFT_01045	GC			0.57
2558670378	DRAFT_01046	Metacyc	PWY-4041: γ-glutamyl cycle		
2558670378	DRAFT_01046	Metacyc	PWY-5826: hypoglycin biosynthesis		
2558670378	DRAFT_01046	Metacyc	PWY66-375: leukotriene biosynthesis		
2558670378	DRAFT_01046	COG_category	[E] Amino acid transport and metabolism		
2558670378	DRAFT_01046	COG0405	Gamma-glutamyltransferase		3.00E-115
2558670378	DRAFT_01046	pfam01019	G_glu_transpept		6.80E-108
2558670378	DRAFT_01046	EC:2.3.2.2	Gamma-glutamyltransferase.		

2558670378	DRAFT_01046	TIGR00066	gamma-glutamyltranspeptidase			6.60E-91
2558670378	DRAFT_01046	KO:K00681	gamma-glutamyltranspeptidase [EC:2.3.2.2]			0.00E+00
2558670378	DRAFT_01046	Locus_type		CDS		
2558670378	DRAFT_01046	Product_name		Gamma-glutamyltransferase		
2558670378	DRAFT_01046	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670378	DRAFT_01046	Coordinates		21300..22823(+)		
2558670378	DRAFT_01046	DNA_length		1524bp		
2558670378	DRAFT_01046	Protein_length		507aa		
2558670378	DRAFT_01046	GC			0.6	
2558670379	DRAFT_01047	Locus_type		tRNA		
2558670379	DRAFT_01047	Product_name		tRNA_Arg_CCT		
2558670379	DRAFT_01047	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670379	DRAFT_01047	Coordinates		22855..22960(-)		
2558670379	DRAFT_01047	DNA_length		93bp		
2558670379	DRAFT_01047	GC			0.65	
2558670380	DRAFT_01048	Locus_type		CDS		
2558670380	DRAFT_01048	Product_name		Ala-tRNA(Pro) hydrolase (EC 3.1.1.-)		
2558670380	DRAFT_01048	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670380	DRAFT_01048	Coordinates		23004..23456(-)		
2558670380	DRAFT_01048	DNA_length		453bp		
2558670380	DRAFT_01048	Protein_length		150aa		
2558670380	DRAFT_01048	GC			0.57	
2558670381	DRAFT_01049	COG_category	[C] Energy production and conversion			
2558670381	DRAFT_01049	COG0644	Dehydrogenases (flavoproteins)			1.00E-18
2558670381	DRAFT_01049	Locus_type		CDS		
2558670381	DRAFT_01049	Product_name		hypothetical protein		
2558670381	DRAFT_01049	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670381	DRAFT_01049	Coordinates		23457..24467(-)		
2558670381	DRAFT_01049	DNA_length		1011bp		
2558670381	DRAFT_01049	Protein_length		336aa		
2558670381	DRAFT_01049	GC			0.57	

2558670382	DRAFT_01050	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes		
2558670382	DRAFT_01050	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation		
2558670382	DRAFT_01050	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer		
2558670382	DRAFT_01050	Metacyc	PWY-3781: aerobic respiration (cytochrome c)		
2558670382	DRAFT_01050	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)		
2558670382	DRAFT_01050	Metacyc	PWY-6692: Fe(II) oxidation		
2558670382	DRAFT_01050	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer		
2558670382	DRAFT_01050	COG_category	[C] Energy production and conversion		
2558670382	DRAFT_01050	COG0838	NADH:ubiquinone oxidoreductase subunit 3 (chain A)		1.00E-14
2558670382	DRAFT_01050	pfam00507	Oxidored_q4		2.60E-15
2558670382	DRAFT_01050	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).		
2558670382	DRAFT_01050	KO:K00330	NADH-quinone oxidoreductase subunit A [EC:1.6.5.3]		8.60E-25
2558670382	DRAFT_01050	Locus_type		CDS	
2558670382	DRAFT_01050	Product_name		NADH:ubiquinone oxidoreductase subunit 3 (chain A)	
2558670382	DRAFT_01050	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670382	DRAFT_01050	Coordinates		24694..25065(+)	
2558670382	DRAFT_01050	DNA_length		372bp	
2558670382	DRAFT_01050	Protein_length		123aa	
2558670382	DRAFT_01050	GC		0.59	
2558670382	DRAFT_01050	Transmembrane		Yes	

2558670383	DRAFT_01051	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes		
2558670383	DRAFT_01051	Metacyc	PWY-3781: aerobic respiration (cytochrome c)		
2558670383	DRAFT_01051	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation		
2558670383	DRAFT_01051	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer		
2558670383	DRAFT_01051	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)		
2558670383	DRAFT_01051	Metacyc	PWY-6692: Fe(II) oxidation		
2558670383	DRAFT_01051	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer		
2558670383	DRAFT_01051	pfam01058	Oxidored_q6		1.20E-21
2558670383	DRAFT_01051	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).		
2558670383	DRAFT_01051	TIGR01957	NADH-quinone oxidoreductase, B subunit		6.70E-63
2558670383	DRAFT_01051	KO:K00331	NADH-quinone oxidoreductase subunit B [EC:1.6.5.3]		0.00E+00
2558670383	DRAFT_01051	Locus_type		CDS	

2558670383	DRAFT_01051	Product_name		NADH dehydrogenase subunit B (EC 1.6.5.3)		
2558670383	DRAFT_01051	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670383	DRAFT_01051	Coordinates		25059..25580(+)		
2558670383	DRAFT_01051	DNA_length		522bp		
2558670383	DRAFT_01051	Protein_length		173aa		
2558670383	DRAFT_01051	GC			0.59	

2558670384	DRAFT_01052	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2558670384	DRAFT_01052	Metacyc	PWY-6692: Fe(II) oxidation			
2558670384	DRAFT_01052	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558670384	DRAFT_01052	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558670384	DRAFT_01052	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558670384	DRAFT_01052	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558670384	DRAFT_01052	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558670384	DRAFT_01052	COG_category	[C] Energy production and conversion			
2558670384	DRAFT_01052	COG0852	NADH:ubiquinone oxidoreductase 27 kD subunit			2.00E-20
2558670384	DRAFT_01052	pfam00329	Complex1_30kDa			6.90E-26
2558670384	DRAFT_01052	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2558670384	DRAFT_01052	KO:K00332	NADH-quinone oxidoreductase subunit C [EC:1.6.5.3]			3.10E-34
2558670384	DRAFT_01052	Locus_type		CDS		
2558670384	DRAFT_01052	Product_name		NADH:ubiquinone oxidoreductase 27 kD subunit		
2558670384	DRAFT_01052	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670384	DRAFT_01052	Coordinates		25588..26148(+)		
2558670384	DRAFT_01052	DNA_length		561bp		
2558670384	DRAFT_01052	Protein_length		186aa		
2558670384	DRAFT_01052	GC			0.58	

2558670385	DRAFT_01053	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2558670385	DRAFT_01053	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2558670385	DRAFT_01053	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2558670385	DRAFT_01053	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2558670385	DRAFT_01053	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2558670385	DRAFT_01053	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2558670385	DRAFT_01053	Metacyc	PWY-6692: Fe(II) oxidation			

2558670385	DRAFT_01053	COG_category	[C] Energy production and conversion		
2558670385	DRAFT_01053	COG0649	NADH:ubiquinone oxidoreductase 49 kD subunit 7		1.00E-121
2558670385	DRAFT_01053	pfam00346	Complex1_49kDa		9.90E-15
2558670385	DRAFT_01053	pfam00346	Complex1_49kDa		1.20E-44
2558670385	DRAFT_01053	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).		
2558670385	DRAFT_01053	KO:K00333	NADH-quinone oxidoreductase subunit D [EC:1.6.5.3]		0.00E+00
2558670385	DRAFT_01053	Locus_type		CDS	
2558670385	DRAFT_01053	Product_name		NADH dehydrogenase subunit D (EC 1.6.5.3)	
2558670385	DRAFT_01053	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670385	DRAFT_01053	Coordinates		26152..27270(+)	
2558670385	DRAFT_01053	DNA_length		1119bp	
2558670385	DRAFT_01053	Protein_length		372aa	
2558670385	DRAFT_01053	GC		0.58	
2558670386	DRAFT_01054	COG_category	[N] Cell motility		
2558670386	DRAFT_01054	COG5491	Conserved protein implicated in secretion		9.00E-14
2558670386	DRAFT_01054	Locus_type		CDS	
2558670386	DRAFT_01054	Product_name		Conserved protein implicated in secretion	
2558670386	DRAFT_01054	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670386	DRAFT_01054	Coordinates		27566..28216(+)	
2558670386	DRAFT_01054	DNA_length		651bp	
2558670386	DRAFT_01054	Protein_length		216aa	
2558670386	DRAFT_01054	GC		0.57	
2558670387	DRAFT_01055	COG_category	[K] Transcription		
2558670387	DRAFT_01055	COG1378	Predicted transcriptional regulators		6.00E-23
2558670387	DRAFT_01055	pfam01978	TrmB		1.90E-17
2558670387	DRAFT_01055	Locus_type		CDS	
2558670387	DRAFT_01055	Product_name		Predicted transcriptional regulators	
2558670387	DRAFT_01055	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18	
2558670387	DRAFT_01055	Coordinates		28320..29018(-)	
2558670387	DRAFT_01055	DNA_length		699bp	
2558670387	DRAFT_01055	Protein_length		232aa	
2558670387	DRAFT_01055	GC		0.61	

2558670388	DRAFT_01056	COG_category	[C] Energy production and conversion			
2558670388	DRAFT_01056	COG0644	Dehydrogenases (flavoproteins)			2.00E-36
2558670388	DRAFT_01056	Locus_type		CDS		
2558670388	DRAFT_01056	Product_name		Dehydrogenases (flavoproteins)		
2558670388	DRAFT_01056	Scaffold		DRAFT_contig_70_107_len_30580_read_count_534093.18		
2558670388	DRAFT_01056	Coordinates		29073..30548(+)		
2558670388	DRAFT_01056	DNA_length		1476bp		
2558670388	DRAFT_01056	Protein_length		491aa		
2558670388	DRAFT_01056	GC			0.58	
2558670388	DRAFT_01056	Transmembrane		Yes		
2558670389	DRAFT_01057	COG_category	[L] Replication, recombination and repair			
2558670389	DRAFT_01057	COG4974	Site-specific recombinase XerD			6.00E-05
2558670389	DRAFT_01057	Locus_type		CDS		
2558670389	DRAFT_01057	Product_name		Site-specific recombinase XerD		
2558670389	DRAFT_01057	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670389	DRAFT_01057	Coordinates		137..1474(+)		
2558670389	DRAFT_01057	DNA_length		1338bp		
2558670389	DRAFT_01057	Protein_length		445aa		
2558670389	DRAFT_01057	GC			0.63	
2558670390	DRAFT_01058	Locus_type		CDS		
2558670390	DRAFT_01058	Product_name		hypothetical protein		
2558670390	DRAFT_01058	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670390	DRAFT_01058	Coordinates		1481..1663(-)		
2558670390	DRAFT_01058	DNA_length		183bp		
2558670390	DRAFT_01058	Protein_length		60aa		
2558670390	DRAFT_01058	GC			0.65	
2558670391	DRAFT_01059	Locus_type		CDS		
2558670391	DRAFT_01059	Product_name		hypothetical protein		
2558670391	DRAFT_01059	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670391	DRAFT_01059	Coordinates		1856..3121(+)		

2558670391	DRAFT_01059	DNA_length		1266bp		
2558670391	DRAFT_01059	Protein_length		421aa		
2558670391	DRAFT_01059	GC			0.52	

2558670392	DRAFT_01060	pfam07883	Cupin_2			1.00E-10
2558670392	DRAFT_01060	Locus_type		CDS		
2558670392	DRAFT_01060	Product_name		Cupin domain		
2558670392	DRAFT_01060	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670392	DRAFT_01060	Coordinates		3569..3916(-)		
2558670392	DRAFT_01060	DNA_length		348bp		
2558670392	DRAFT_01060	Protein_length		115aa		
2558670392	DRAFT_01060	GC			0.56	

2558670393	DRAFT_01061	COG_category	[P] Inorganic ion transport and metabolism			
2558670393	DRAFT_01061	COG1914	Mn2+ and Fe2+ transporters of the NRAMP family			7.00E-32
2558670393	DRAFT_01061	pfam01566	Nramp			1.20E-40
2558670393	DRAFT_01061	TIGR01197	NRAMP (natural resistance-associated macrophage protein) metal ion			2.80E-17
2558670393	DRAFT_01061	Locus_type		CDS		
2558670393	DRAFT_01061	Product_name		Mn2+ and Fe2+ transporters of the NRAMP family		
2558670393	DRAFT_01061	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670393	DRAFT_01061	Coordinates		4019..5179(+)		
2558670393	DRAFT_01061	DNA_length		1161bp		
2558670393	DRAFT_01061	Protein_length		386aa		
2558670393	DRAFT_01061	GC			0.62	
2558670393	DRAFT_01061	Transmembrane		Yes		

2558670394	DRAFT_01062	COG_category	[V] Defense mechanisms			
2558670394	DRAFT_01062	COG0842	ABC-type multidrug transport system, permease component			1.00E-09
2558670394	DRAFT_01062	pfam12698	ABC2_membrane_3			1.20E-29
2558670394	DRAFT_01062	Locus_type		CDS		
2558670394	DRAFT_01062	Product_name		ABC-type multidrug transport system, permease component		
2558670394	DRAFT_01062	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670394	DRAFT_01062	Coordinates		5255..6382(-)		
2558670394	DRAFT_01062	DNA_length		1128bp		

2558670394	DRAFT_01062	Protein_length		375aa		
2558670394	DRAFT_01062	GC			0.54	
2558670394	DRAFT_01062	Transmembrane		Yes		

2558670395	DRAFT_01063	COG_category	[P] Inorganic ion transport and metabolism			
2558670395	DRAFT_01063	COG_category	[C] Energy production and conversion			
2558670395	DRAFT_01063	COG1668	ABC-type Na+ efflux pump, permease component			3.00E-06
2558670395	DRAFT_01063	pfam12698	ABC2_membrane_3			2.10E-29
2558670395	DRAFT_01063	Locus_type		CDS		
2558670395	DRAFT_01063	Product_name		ABC-2 family transporter protein		
2558670395	DRAFT_01063	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670395	DRAFT_01063	Coordinates		6379..7482(-)		
2558670395	DRAFT_01063	DNA_length		1104bp		
2558670395	DRAFT_01063	Protein_length		367aa		
2558670395	DRAFT_01063	GC			0.55	
2558670395	DRAFT_01063	Transmembrane		Yes		

2558670396	DRAFT_01064	KEGG_module	M00254: ABC-2 type transport system			
2558670396	DRAFT_01064	COG_category	[V] Defense mechanisms			
2558670396	DRAFT_01064	COG1131	ABC-type multidrug transport system, ATPase component			4.00E-60
2558670396	DRAFT_01064	pfam00005	ABC_tran			4.50E-33
2558670396	DRAFT_01064	KO:K01990	ABC-2 type transport system ATP-binding protein			0.00E+00
2558670396	DRAFT_01064	Locus_type		CDS		
2558670396	DRAFT_01064	Product_name		ABC-type multidrug transport system, ATPase component		
2558670396	DRAFT_01064	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670396	DRAFT_01064	Coordinates		7479..8408(-)		
2558670396	DRAFT_01064	DNA_length		930bp		
2558670396	DRAFT_01064	Protein_length		309aa		
2558670396	DRAFT_01064	GC			0.53	

2558670397	DRAFT_01065	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2558670397	DRAFT_01065	COG3267	Type II secretory pathway, component ExeA (predicted ATPase)			3.00E-06
2558670397	DRAFT_01065	pfam01637	Arch_ATPase			6.10E-18
2558670397	DRAFT_01065	Locus_type		CDS		

2558670397	DRAFT_01065	Product_name		Archaeal ATPase		
2558670397	DRAFT_01065	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670397	DRAFT_01065	Coordinates		9511..10728(+)		
2558670397	DRAFT_01065	DNA_length		1218bp		
2558670397	DRAFT_01065	Protein_length		405aa		
2558670397	DRAFT_01065	GC			0.52	

2558670398	DRAFT_01066	Locus_type		CDS		
2558670398	DRAFT_01066	Product_name		hypothetical protein		
2558670398	DRAFT_01066	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670398	DRAFT_01066	Coordinates		10715..11797(+)		
2558670398	DRAFT_01066	DNA_length		1083bp		
2558670398	DRAFT_01066	Protein_length		360aa		
2558670398	DRAFT_01066	GC			0.54	
2558670398	DRAFT_01066	Transmembrane		Yes		

2558670399	DRAFT_01067	Locus_type		CDS		
2558670399	DRAFT_01067	Product_name		hypothetical protein		
2558670399	DRAFT_01067	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670399	DRAFT_01067	Coordinates		11932..12624(-)		
2558670399	DRAFT_01067	DNA_length		693bp		
2558670399	DRAFT_01067	Protein_length		230aa		
2558670399	DRAFT_01067	GC			0.48	

2558670400	DRAFT_01068	pfam13676	TIR_2			4.10E-10
2558670400	DRAFT_01068	Locus_type		CDS		
2558670400	DRAFT_01068	Product_name		TIR domain		
2558670400	DRAFT_01068	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670400	DRAFT_01068	Coordinates		12621..13067(-)		
2558670400	DRAFT_01068	DNA_length		447bp		
2558670400	DRAFT_01068	Protein_length		148aa		
2558670400	DRAFT_01068	GC			0.51	

2558670401	DRAFT_01069	Locus_type		CDS		

2558670401	DRAFT_01069	Product_name	hypothetical protein
2558670401	DRAFT_01069	Scaffold	DRAFT_contig_70_118_len_28894_read_count_476415.19
2558670401	DRAFT_01069	Coordinates	13147..13290(+)
2558670401	DRAFT_01069	DNA_length	144bp
2558670401	DRAFT_01069	Protein_length	47aa
2558670401	DRAFT_01069	GC	0.5
2558670401	DRAFT_01069	Transmembrane	Yes
2558670402	DRAFT_01070	Locus_type	CDS
2558670402	DRAFT_01070	Product_name	hypothetical protein
2558670402	DRAFT_01070	Scaffold	DRAFT_contig_70_118_len_28894_read_count_476415.19
2558670402	DRAFT_01070	Coordinates	13287..13991(+)
2558670402	DRAFT_01070	DNA_length	705bp
2558670402	DRAFT_01070	Protein_length	234aa
2558670402	DRAFT_01070	GC	0.46
2558670403	DRAFT_01071	Locus_type	CDS
2558670403	DRAFT_01071	Product_name	hypothetical protein
2558670403	DRAFT_01071	Scaffold	DRAFT_contig_70_118_len_28894_read_count_476415.19
2558670403	DRAFT_01071	Coordinates	14288..14419(-)
2558670403	DRAFT_01071	DNA_length	132bp
2558670403	DRAFT_01071	Protein_length	43aa
2558670403	DRAFT_01071	GC	0.47
2558670403	DRAFT_01071	Transmembrane	Yes
2558670404	DRAFT_01072	Locus_type	CDS
2558670404	DRAFT_01072	Product_name	hypothetical protein
2558670404	DRAFT_01072	Scaffold	DRAFT_contig_70_118_len_28894_read_count_476415.19
2558670404	DRAFT_01072	Coordinates	14462..14800(+)
2558670404	DRAFT_01072	DNA_length	339bp
2558670404	DRAFT_01072	Protein_length	112aa
2558670404	DRAFT_01072	GC	0.5
2558670405	DRAFT_01073	COG_category	[R] General function prediction only

2558670405	DRAFT_01073	COG1672	Predicted ATPase (AAA+ superfamily)		8.00E-07
2558670405	DRAFT_01073	pfam01637	Arch_ATPase		2.30E-12
2558670405	DRAFT_01073	Locus_type		CDS	
2558670405	DRAFT_01073	Product_name		Predicted ATPase (AAA+ superfamily)	
2558670405	DRAFT_01073	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670405	DRAFT_01073	Coordinates		14848..15963(-)	
2558670405	DRAFT_01073	DNA_length		1116bp	
2558670405	DRAFT_01073	Protein_length		371aa	
2558670405	DRAFT_01073	GC		0.47	
2558670406	DRAFT_01074	Locus_type		CDS	
2558670406	DRAFT_01074	Product_name		hypothetical protein	
2558670406	DRAFT_01074	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670406	DRAFT_01074	Coordinates		16299..17021(-)	
2558670406	DRAFT_01074	DNA_length		723bp	
2558670406	DRAFT_01074	Protein_length		240aa	
2558670406	DRAFT_01074	GC		0.51	
2558670407	DRAFT_01075	Locus_type		CDS	
2558670407	DRAFT_01075	Product_name		hypothetical protein	
2558670407	DRAFT_01075	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670407	DRAFT_01075	Coordinates		17402..17572(+)	
2558670407	DRAFT_01075	DNA_length		171bp	
2558670407	DRAFT_01075	Protein_length		56aa	
2558670407	DRAFT_01075	GC		0.53	
2558670407	DRAFT_01075	Transmembrane		Yes	
2558670408	DRAFT_01076	Locus_type		CDS	
2558670408	DRAFT_01076	Product_name		hypothetical protein	
2558670408	DRAFT_01076	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670408	DRAFT_01076	Coordinates		17579..18586(+)	
2558670408	DRAFT_01076	DNA_length		1008bp	
2558670408	DRAFT_01076	Protein_length		335aa	
2558670408	DRAFT_01076	GC		0.54	

2558670408	DRAFT_01076	Transmembrane		Yes	
2558670409	DRAFT_01077	COG_category	[R] General function prediction only		
2558670409	DRAFT_01077	COG0456	Acetyltransferases		2.00E-05
2558670409	DRAFT_01077	pfam00583	Acetyltransf_1		6.10E-13
2558670409	DRAFT_01077	Locus_type		CDS	
2558670409	DRAFT_01077	Product_name		Acetyltransferases	
2558670409	DRAFT_01077	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670409	DRAFT_01077	Coordinates		19216..22482(+)	
2558670409	DRAFT_01077	DNA_length		3267bp	
2558670409	DRAFT_01077	Protein_length		1088aa	
2558670409	DRAFT_01077	GC		0.5	
2558670410	DRAFT_01078	pfam00583	Acetyltransf_1		9.60E-18
2558670410	DRAFT_01078	Locus_type		CDS	
2558670410	DRAFT_01078	Product_name		Acetyltransferases	
2558670410	DRAFT_01078	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670410	DRAFT_01078	Coordinates		22858..23334(-)	
2558670410	DRAFT_01078	DNA_length		477bp	
2558670410	DRAFT_01078	Protein_length		158aa	
2558670410	DRAFT_01078	GC		0.57	
2558670411	DRAFT_01079	Locus_type		CDS	
2558670411	DRAFT_01079	Product_name		hypothetical protein	
2558670411	DRAFT_01079	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670411	DRAFT_01079	Coordinates		23824..24249(+)	
2558670411	DRAFT_01079	DNA_length		426bp	
2558670411	DRAFT_01079	Protein_length		141aa	
2558670411	DRAFT_01079	GC		0.59	
2558670412	DRAFT_01080	pfam05048	NosD		3.30E-12
2558670412	DRAFT_01080	TIGR03804	parallel beta-helix repeat (two copies)		7.50E-14
2558670412	DRAFT_01080	Locus_type		CDS	
2558670412	DRAFT_01080	Product_name		parallel beta-helix repeat (two copies)	

2558670412	DRAFT_01080	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670412	DRAFT_01080	Coordinates		24174..24785(-)	
2558670412	DRAFT_01080	DNA_length		612bp	
2558670412	DRAFT_01080	Protein_length		203aa	
2558670412	DRAFT_01080	GC		0.56	
2558670412	DRAFT_01080	Transmembrane		Yes	
2558670413	DRAFT_01081	COG_category	[C] Energy production and conversion		
2558670413	DRAFT_01081	COG1032	Fe-S oxidoreductase		2.00E-28
2558670413	DRAFT_01081	pfam04055	Radical_SAM		6.10E-12
2558670413	DRAFT_01081	Locus_type		CDS	
2558670413	DRAFT_01081	Product_name		Fe-S oxidoreductase	
2558670413	DRAFT_01081	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19	
2558670413	DRAFT_01081	Coordinates		25184..26932(-)	
2558670413	DRAFT_01081	DNA_length		1749bp	
2558670413	DRAFT_01081	Protein_length		582aa	
2558670413	DRAFT_01081	GC		0.58	
2558670414	DRAFT_01082	Metacyc	PWY-6963: ammonia assimilation cycle I		
2558670414	DRAFT_01082	Metacyc	GLUTAMINEFUM-PWY: glutamine degradation II		
2558670414	DRAFT_01082	Metacyc	GLUGLNSYN-PWY: glutamate biosynthesis IV		
2558670414	DRAFT_01082	Metacyc	GLUTSYN-PWY: glutamate biosynthesis I		
2558670414	DRAFT_01082	COG_category	[R] General function prediction only		
2558670414	DRAFT_01082	COG_category	[E] Amino acid transport and metabolism		
2558670414	DRAFT_01082	COG0493	NADPH-dependent glutamate synthase beta chain and related oxidore		1.00E-94
2558670414	DRAFT_01082	pfam07992	Pyr_redox_2		2.40E-10
2558670414	DRAFT_01082	pfam07992	Pyr_redox_2		4.10E-07
2558670414	DRAFT_01082	pfam14691	Fer4_20		5.10E-30
2558670414	DRAFT_01082	EC:1.4.1.14	Glutamate synthase (NADH).		
2558670414	DRAFT_01082	EC:1.4.1.13	Glutamate synthase (NADPH).		
2558670414	DRAFT_01082	KO:K00266	glutamate synthase (NADPH/NADH) small chain [EC:1.4.1.13 1.4.1.14]		0.00E+00
2558670414	DRAFT_01082	ITERM:00721	sulfide dehydrogenase (flavoprotein) subunit SudA (EC 1.8.1.-)		
2558670414	DRAFT_01082	Locus_type		CDS	
2558670414	DRAFT_01082	Product_name		sulfide dehydrogenase (flavoprotein) subunit SudA (EC 1.8.1.-)	

2558670414	DRAFT_01082	Scaffold		DRAFT_contig_70_118_len_28894_read_count_476415.19		
2558670414	DRAFT_01082	Coordinates		26965..28542(+)		
2558670414	DRAFT_01082	DNA_length		1578bp		
2558670414	DRAFT_01082	Protein_length		525aa		
2558670414	DRAFT_01082	GC			0.58	

2558670415	DRAFT_01083	Locus_type		tRNA		
2558670415	DRAFT_01083	Product_name		tRNA_Glu_CTC		
2558670415	DRAFT_01083	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670415	DRAFT_01083	Coordinates		1..75(+)		
2558670415	DRAFT_01083	DNA_length		75bp		
2558670415	DRAFT_01083	GC			0.67	

2558670416	DRAFT_01084	pfam13353	Fer4_12			1.80E-10
2558670416	DRAFT_01084	Locus_type		CDS		
2558670416	DRAFT_01084	Product_name		Organic radical activating enzymes		
2558670416	DRAFT_01084	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670416	DRAFT_01084	Coordinates		131..1534(+)		
2558670416	DRAFT_01084	DNA_length		1404bp		
2558670416	DRAFT_01084	Protein_length		467aa		
2558670416	DRAFT_01084	GC			0.58	

2558670417	DRAFT_01085	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP			
2558670417	DRAFT_01085	Metacyc	PWY0-166: superpathway of pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis (E.			
2558670417	DRAFT_01085	Metacyc	PWY-7187: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis II			
2558670417	DRAFT_01085	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2558670417	DRAFT_01085	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2558670417	DRAFT_01085	COG_category	[F] Nucleotide transport and metabolism			
2558670417	DRAFT_01085	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase			5.00E-80
2558670417	DRAFT_01085	pfam13597	NRDD			7.00E-55
2558670417	DRAFT_01085	pfam13597	NRDD			1.50E-06
2558670417	DRAFT_01085	EC:1.17.4.2	Ribonucleoside-triphosphate reductase.			
2558670417	DRAFT_01085	TIGR02487	anaerobic ribonucleoside-triphosphate reductase			1.10E-91
2558670417	DRAFT_01085	KO:K00527	ribonucleoside-triphosphate reductase [EC:1.17.4.2]			0.00E+00

2558670417	DRAFT_01085	ITERM:00735	ribonucleoside-triphosphate reductase class III catalytic subunit (EC 1.17.4.2)			
2558670417	DRAFT_01085	Locus_type		CDS		
2558670417	DRAFT_01085	Product_name		ribonucleoside-triphosphate reductase class III catalytic subunit (EC 1		
2558670417	DRAFT_01085	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670417	DRAFT_01085	Coordinates		1527..3239(+)		
2558670417	DRAFT_01085	DNA_length		1713bp		
2558670417	DRAFT_01085	Protein_length		570aa		
2558670417	DRAFT_01085	GC			0.56	
2558670418	DRAFT_01086	COG_category	[F] Nucleotide transport and metabolism			
2558670418	DRAFT_01086	COG0125	Thymidylate kinase			6.00E-12
2558670418	DRAFT_01086	pfam02223	Thymidylate_kin			4.90E-15
2558670418	DRAFT_01086	Locus_type		CDS		
2558670418	DRAFT_01086	Product_name		Thymidylate kinase		
2558670418	DRAFT_01086	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670418	DRAFT_01086	Coordinates		3239..3862(+)		
2558670418	DRAFT_01086	DNA_length		624bp		
2558670418	DRAFT_01086	Protein_length		207aa		
2558670418	DRAFT_01086	GC			0.54	
2558670419	DRAFT_01087	pfam13306	LRR_5			2.90E-12
2558670419	DRAFT_01087	pfam13306	LRR_5			9.00E-22
2558670419	DRAFT_01087	pfam13306	LRR_5			4.50E-10
2558670419	DRAFT_01087	pfam13306	LRR_5			3.60E-08
2558670419	DRAFT_01087	Locus_type		CDS		
2558670419	DRAFT_01087	Product_name		Leucine rich repeats (6 copies)		
2558670419	DRAFT_01087	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670419	DRAFT_01087	Coordinates		3864..5642(+)		
2558670419	DRAFT_01087	DNA_length		1779bp		
2558670419	DRAFT_01087	Protein_length		592aa		
2558670419	DRAFT_01087	GC			0.56	
2558670420	DRAFT_01088	COG_category	[G] Carbohydrate transport and metabolism			
2558670420	DRAFT_01088	COG1082	Sugar phosphate isomerases/epimerases			3.00E-21

2558670420	DRAFT_01088	pfam01261	AP_endonuc_2			3.30E-25
2558670420	DRAFT_01088	Locus_type		CDS		
2558670420	DRAFT_01088	Product_name		Sugar phosphate isomerases/epimerases		
2558670420	DRAFT_01088	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670420	DRAFT_01088	Coordinates		5669..6442(-)		
2558670420	DRAFT_01088	DNA_length		774bp		
2558670420	DRAFT_01088	Protein_length		257aa		
2558670420	DRAFT_01088	GC			0.54	
2558670421	DRAFT_01089	pfam01555	N6_N4_Mtase			1.80E-34
2558670421	DRAFT_01089	Locus_type		CDS		
2558670421	DRAFT_01089	Product_name		Adenine specific DNA methylase Mod		
2558670421	DRAFT_01089	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670421	DRAFT_01089	Coordinates		6682..7800(+)		
2558670421	DRAFT_01089	DNA_length		1119bp		
2558670421	DRAFT_01089	Protein_length		372aa		
2558670421	DRAFT_01089	GC			0.52	
2558670422	DRAFT_01090	Locus_type		CDS		
2558670422	DRAFT_01090	Product_name		hypothetical protein		
2558670422	DRAFT_01090	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670422	DRAFT_01090	Coordinates		7915..8280(-)		
2558670422	DRAFT_01090	DNA_length		366bp		
2558670422	DRAFT_01090	Protein_length		121aa		
2558670422	DRAFT_01090	GC			0.48	
2558670423	DRAFT_01091	Locus_type		CDS		
2558670423	DRAFT_01091	Product_name		hypothetical protein		
2558670423	DRAFT_01091	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670423	DRAFT_01091	Coordinates		8424..8612(-)		
2558670423	DRAFT_01091	DNA_length		189bp		
2558670423	DRAFT_01091	Protein_length		62aa		
2558670423	DRAFT_01091	GC			0.52	

2558670424	DRAFT_01092	Locus_type	CDS	
2558670424	DRAFT_01092	Product_name	hypothetical protein	
2558670424	DRAFT_01092	Scaffold	DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670424	DRAFT_01092	Coordinates	8660..9379(-)	
2558670424	DRAFT_01092	DNA_length	720bp	
2558670424	DRAFT_01092	Protein_length	239aa	
2558670424	DRAFT_01092	GC		0.51
2558670425	DRAFT_01093	Locus_type	CDS	
2558670425	DRAFT_01093	Product_name	hypothetical protein	
2558670425	DRAFT_01093	Scaffold	DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670425	DRAFT_01093	Coordinates	9369..10184(-)	
2558670425	DRAFT_01093	DNA_length	816bp	
2558670425	DRAFT_01093	Protein_length	271aa	
2558670425	DRAFT_01093	GC		0.58
2558670425	DRAFT_01093	Transmembrane	Yes	
2558670426	DRAFT_01094	Locus_type	CDS	
2558670426	DRAFT_01094	Product_name	hypothetical protein	
2558670426	DRAFT_01094	Scaffold	DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670426	DRAFT_01094	Coordinates	10181..10717(-)	
2558670426	DRAFT_01094	DNA_length	537bp	
2558670426	DRAFT_01094	Protein_length	178aa	
2558670426	DRAFT_01094	GC		0.51
2558670427	DRAFT_01095	Locus_type	CDS	
2558670427	DRAFT_01095	Product_name	hypothetical protein	
2558670427	DRAFT_01095	Scaffold	DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670427	DRAFT_01095	Coordinates	10797..11351(-)	
2558670427	DRAFT_01095	DNA_length	555bp	
2558670427	DRAFT_01095	Protein_length	184aa	
2558670427	DRAFT_01095	GC		0.49
2558670428	DRAFT_01096	Locus_type	CDS	

2558670428	DRAFT_01096	Product_name		hypothetical protein		
2558670428	DRAFT_01096	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670428	DRAFT_01096	Coordinates		11359..11586(-)		
2558670428	DRAFT_01096	DNA_length		228bp		
2558670428	DRAFT_01096	Protein_length		75aa		
2558670428	DRAFT_01096	GC			0.53	
2558670429	DRAFT_01097	Locus_type		CDS		
2558670429	DRAFT_01097	Product_name		hypothetical protein		
2558670429	DRAFT_01097	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670429	DRAFT_01097	Coordinates		11780..12178(+)		
2558670429	DRAFT_01097	DNA_length		399bp		
2558670429	DRAFT_01097	Protein_length		132aa		
2558670429	DRAFT_01097	GC			0.5	
2558670430	DRAFT_01098	Locus_type		CDS		
2558670430	DRAFT_01098	Product_name		hypothetical protein		
2558670430	DRAFT_01098	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670430	DRAFT_01098	Coordinates		12386..13408(-)		
2558670430	DRAFT_01098	DNA_length		1023bp		
2558670430	DRAFT_01098	Protein_length		340aa		
2558670430	DRAFT_01098	GC			0.47	
2558670430	DRAFT_01098	Transmembrane		Yes		
2558670431	DRAFT_01099	pfam01909	NTP_transf_2			2.20E-06
2558670431	DRAFT_01099	Locus_type		CDS		
2558670431	DRAFT_01099	Product_name		Nucleotidyltransferase domain		
2558670431	DRAFT_01099	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670431	DRAFT_01099	Coordinates		13533..14405(+)		
2558670431	DRAFT_01099	DNA_length		873bp		
2558670431	DRAFT_01099	Protein_length		290aa		
2558670431	DRAFT_01099	GC			0.5	
2558670432	DRAFT_01100	Locus_type		CDS		

2558670432	DRAFT_01100	Product_name		hypothetical protein	
2558670432	DRAFT_01100	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670432	DRAFT_01100	Coordinates		14411..14548(-)	
2558670432	DRAFT_01100	DNA_length		138bp	
2558670432	DRAFT_01100	Protein_length		45aa	
2558670432	DRAFT_01100	GC		0.49	
2558670433	DRAFT_01101	pfam04307	DUF457		3.50E-10
2558670433	DRAFT_01101	Locus_type		CDS	
2558670433	DRAFT_01101	Product_name		Predicted membrane-bound metal-dependent hydrolase (DUF457)	
2558670433	DRAFT_01101	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670433	DRAFT_01101	Coordinates		14545..15009(-)	
2558670433	DRAFT_01101	DNA_length		465bp	
2558670433	DRAFT_01101	Protein_length		154aa	
2558670433	DRAFT_01101	GC		0.52	
2558670433	DRAFT_01101	Transmembrane		Yes	
2558670434	DRAFT_01102	Locus_type		CDS	
2558670434	DRAFT_01102	Product_name		hypothetical protein	
2558670434	DRAFT_01102	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670434	DRAFT_01102	Coordinates		15592..17382(-)	
2558670434	DRAFT_01102	DNA_length		1791bp	
2558670434	DRAFT_01102	Protein_length		596aa	
2558670434	DRAFT_01102	GC		0.49	
2558670435	DRAFT_01103	Locus_type		CDS	
2558670435	DRAFT_01103	Product_name		hypothetical protein	
2558670435	DRAFT_01103	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670435	DRAFT_01103	Coordinates		17379..18278(-)	
2558670435	DRAFT_01103	DNA_length		900bp	
2558670435	DRAFT_01103	Protein_length		299aa	
2558670435	DRAFT_01103	GC		0.51	
2558670436	DRAFT_01104	Locus_type		CDS	

2558670436	DRAFT_01104	Product_name		hypothetical protein		
2558670436	DRAFT_01104	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670436	DRAFT_01104	Coordinates		18286..18456(+)		
2558670436	DRAFT_01104	DNA_length		171bp		
2558670436	DRAFT_01104	Protein_length		56aa		
2558670436	DRAFT_01104	GC			0.52	

2558670437	DRAFT_01105	Locus_type		CDS		
2558670437	DRAFT_01105	Product_name		hypothetical protein		
2558670437	DRAFT_01105	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670437	DRAFT_01105	Coordinates		18463..19164(+)		
2558670437	DRAFT_01105	DNA_length		702bp		
2558670437	DRAFT_01105	Protein_length		233aa		
2558670437	DRAFT_01105	GC			0.53	
2558670437	DRAFT_01105	Transmembrane		Yes		

2558670438	DRAFT_01106	COG_category	[R] General function prediction only			
2558670438	DRAFT_01106	COG0433	Predicted ATPase			1.00E-08
2558670438	DRAFT_01106	pfam12846	AAA_10			1.60E-26
2558670438	DRAFT_01106	Locus_type		CDS		
2558670438	DRAFT_01106	Product_name		Predicted ATPase		
2558670438	DRAFT_01106	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670438	DRAFT_01106	Coordinates		19217..21892(+)		
2558670438	DRAFT_01106	DNA_length		2676bp		
2558670438	DRAFT_01106	Protein_length		891aa		
2558670438	DRAFT_01106	GC			0.52	

2558670439	DRAFT_01107	Locus_type		CDS		
2558670439	DRAFT_01107	Product_name		hypothetical protein		
2558670439	DRAFT_01107	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670439	DRAFT_01107	Coordinates		21905..22141(+)		
2558670439	DRAFT_01107	DNA_length		237bp		
2558670439	DRAFT_01107	Protein_length		78aa		
2558670439	DRAFT_01107	GC			0.55	

2558670440	DRAFT_01108	Locus_type		CDS	
2558670440	DRAFT_01108	Product_name		hypothetical protein	
2558670440	DRAFT_01108	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670440	DRAFT_01108	Coordinates		22189..22473(+)	
2558670440	DRAFT_01108	DNA_length		285bp	
2558670440	DRAFT_01108	Protein_length		94aa	
2558670440	DRAFT_01108	GC		0.46	

2558670441	DRAFT_01109	COG_category	[S] Function unknown		
2558670441	DRAFT_01109	COG5616	Predicted integral membrane protein		3.00E-33
2558670441	DRAFT_01109	pfam13414	TPR_11		2.30E-10
2558670441	DRAFT_01109	pfam00211	Guanylate_cyc		2.30E-28
2558670441	DRAFT_01109	EC:4.6.1.1	Adenylate cyclase.		
2558670441	DRAFT_01109	KO:K01768	adenylate cyclase [EC:4.6.1.1]		0.00E+00
2558670441	DRAFT_01109	Locus_type		CDS	
2558670441	DRAFT_01109	Product_name		Predicted integral membrane protein	
2558670441	DRAFT_01109	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670441	DRAFT_01109	Coordinates		22952..24895(+)	
2558670441	DRAFT_01109	DNA_length		1944bp	
2558670441	DRAFT_01109	Protein_length		647aa	
2558670441	DRAFT_01109	GC		0.56	
2558670441	DRAFT_01109	Fused_gene		Yes	

2558670442	DRAFT_01110	pfam13240	zinc_ribbon_2		5.40E-07
2558670442	DRAFT_01110	pfam06271	RDD		6.50E-21
2558670442	DRAFT_01110	Locus_type		CDS	
2558670442	DRAFT_01110	Product_name		zinc-ribbon domain/RDD family	
2558670442	DRAFT_01110	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20	
2558670442	DRAFT_01110	Coordinates		25081..25647(-)	
2558670442	DRAFT_01110	DNA_length		567bp	
2558670442	DRAFT_01110	Protein_length		188aa	
2558670442	DRAFT_01110	GC		0.58	
2558670442	DRAFT_01110	Transmembrane		Yes	

2558670443	DRAFT_01111	Locus_type		CDS		
2558670443	DRAFT_01111	Product_name		hypothetical protein		
2558670443	DRAFT_01111	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670443	DRAFT_01111	Coordinates		25842..26048(+)		
2558670443	DRAFT_01111	DNA_length		207bp		
2558670443	DRAFT_01111	Protein_length		68aa		
2558670443	DRAFT_01111	GC			0.52	
2558670444	DRAFT_01112	COG_category	[R] General function prediction only			
2558670444	DRAFT_01112	COG0456	Acetyltransferases			3.00E-06
2558670444	DRAFT_01112	pfam13673	Acetyltransf_10			3.90E-13
2558670444	DRAFT_01112	Locus_type		CDS		
2558670444	DRAFT_01112	Product_name		Acetyltransferases		
2558670444	DRAFT_01112	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670444	DRAFT_01112	Coordinates		26116..26610(-)		
2558670444	DRAFT_01112	DNA_length		495bp		
2558670444	DRAFT_01112	Protein_length		164aa		
2558670444	DRAFT_01112	GC			0.54	
2558670445	DRAFT_01113	Locus_type		CDS		
2558670445	DRAFT_01113	Product_name		hypothetical protein		
2558670445	DRAFT_01113	Scaffold		DRAFT_contig_70_122_len_27540_read_count_414059.20		
2558670445	DRAFT_01113	Coordinates		26922..27539(-)		
2558670445	DRAFT_01113	DNA_length		618bp		
2558670445	DRAFT_01113	Protein_length		205aa		
2558670445	DRAFT_01113	GC			0.61	
2558670445	DRAFT_01113	Transmembrane		Yes		
2558670446	DRAFT_01114	Locus_type		CDS		
2558670446	DRAFT_01114	Product_name		hypothetical protein		
2558670446	DRAFT_01114	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670446	DRAFT_01114	Coordinates		549..995(+)		
2558670446	DRAFT_01114	DNA_length		447bp		

2558670446	DRAFT_01114	Protein_length		148aa		
2558670446	DRAFT_01114	GC			0.57	
2558670447	DRAFT_01115	pfam13847	Methyltransf_31			5.90E-15
2558670447	DRAFT_01115	TIGR01444	methyltransferase, FkbM family			4.20E-11
2558670447	DRAFT_01115	Locus_type		CDS		
2558670447	DRAFT_01115	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2558670447	DRAFT_01115	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670447	DRAFT_01115	Coordinates		1100..1627(+)		
2558670447	DRAFT_01115	DNA_length		528bp		
2558670447	DRAFT_01115	Protein_length		175aa		
2558670447	DRAFT_01115	GC			0.57	
2558670448	DRAFT_01116	Locus_type		CDS		
2558670448	DRAFT_01116	Product_name		hypothetical protein		
2558670448	DRAFT_01116	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670448	DRAFT_01116	Coordinates		1781..2680(+)		
2558670448	DRAFT_01116	DNA_length		900bp		
2558670448	DRAFT_01116	Protein_length		299aa		
2558670448	DRAFT_01116	GC			0.54	
2558670448	DRAFT_01116	Transmembrane		Yes		
2558670449	DRAFT_01117	Locus_type		tRNA		
2558670449	DRAFT_01117	Product_name		tRNA_Pseudo_GTG		
2558670449	DRAFT_01117	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670449	DRAFT_01117	Coordinates		2867..2953(+)		
2558670449	DRAFT_01117	DNA_length		75bp		
2558670449	DRAFT_01117	GC			0.59	
2558670450	DRAFT_01118	Locus_type		CDS		
2558670450	DRAFT_01118	Product_name		hypothetical protein		
2558670450	DRAFT_01118	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670450	DRAFT_01118	Coordinates		3091..3453(+)		
2558670450	DRAFT_01118	DNA_length		363bp		

2558670450	DRAFT_01118	Protein_length	120aa
2558670450	DRAFT_01118	GC	0.51
2558670450	DRAFT_01118	Transmembrane	Yes
2558670451	DRAFT_01119	Locus_type	CDS
2558670451	DRAFT_01119	Product_name	hypothetical protein
2558670451	DRAFT_01119	Scaffold	DRAFT_contig_70_133_len_26431_read_count_520883.21
2558670451	DRAFT_01119	Coordinates	3434..3751(-)
2558670451	DRAFT_01119	DNA_length	318bp
2558670451	DRAFT_01119	Protein_length	105aa
2558670451	DRAFT_01119	GC	0.5
2558670452	DRAFT_01120	Locus_type	CDS
2558670452	DRAFT_01120	Product_name	hypothetical protein
2558670452	DRAFT_01120	Scaffold	DRAFT_contig_70_133_len_26431_read_count_520883.21
2558670452	DRAFT_01120	Coordinates	3954..4205(+)
2558670452	DRAFT_01120	DNA_length	252bp
2558670452	DRAFT_01120	Protein_length	83aa
2558670452	DRAFT_01120	GC	0.46
2558670453	DRAFT_01121	Locus_type	CDS
2558670453	DRAFT_01121	Product_name	hypothetical protein
2558670453	DRAFT_01121	Scaffold	DRAFT_contig_70_133_len_26431_read_count_520883.21
2558670453	DRAFT_01121	Coordinates	4233..4550(+)
2558670453	DRAFT_01121	DNA_length	318bp
2558670453	DRAFT_01121	Protein_length	105aa
2558670453	DRAFT_01121	GC	0.47
2558670454	DRAFT_01122	Locus_type	CDS
2558670454	DRAFT_01122	Product_name	hypothetical protein
2558670454	DRAFT_01122	Scaffold	DRAFT_contig_70_133_len_26431_read_count_520883.21
2558670454	DRAFT_01122	Coordinates	4615..5127(+)
2558670454	DRAFT_01122	DNA_length	513bp
2558670454	DRAFT_01122	Protein_length	170aa

2558670454	DRAFT_01122	GC		0.48	
2558670454	DRAFT_01122	Transmembrane		Yes	
2558670455	DRAFT_01123	Locus_type		CDS	
2558670455	DRAFT_01123	Product_name		hypothetical protein	
2558670455	DRAFT_01123	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670455	DRAFT_01123	Coordinates		5273..5392(+)	
2558670455	DRAFT_01123	DNA_length		120bp	
2558670455	DRAFT_01123	Protein_length		39aa	
2558670455	DRAFT_01123	GC		0.45	
2558670456	DRAFT_01124	Locus_type		CDS	
2558670456	DRAFT_01124	Product_name		hypothetical protein	
2558670456	DRAFT_01124	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670456	DRAFT_01124	Coordinates		5376..6149(+)	
2558670456	DRAFT_01124	DNA_length		774bp	
2558670456	DRAFT_01124	Protein_length		257aa	
2558670456	DRAFT_01124	GC		0.51	
2558670457	DRAFT_01125	Locus_type		CDS	
2558670457	DRAFT_01125	Product_name		hypothetical protein	
2558670457	DRAFT_01125	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670457	DRAFT_01125	Coordinates		6489..6650(-)	
2558670457	DRAFT_01125	DNA_length		162bp	
2558670457	DRAFT_01125	Protein_length		53aa	
2558670457	DRAFT_01125	GC		0.54	
2558670458	DRAFT_01126	COG_category	[E] Amino acid transport and metabolism		
2558670458	DRAFT_01126	COG0520	Selenocysteine lyase		2.00E-63
2558670458	DRAFT_01126	pfam00266	Aminotran_5		1.90E-62
2558670458	DRAFT_01126	Locus_type		CDS	
2558670458	DRAFT_01126	Product_name		Selenocysteine lyase	
2558670458	DRAFT_01126	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670458	DRAFT_01126	Coordinates		6801..7952(-)	

2558670458	DRAFT_01126	DNA_length		1152bp		
2558670458	DRAFT_01126	Protein_length		383aa		
2558670458	DRAFT_01126	GC			0.53	
2558670459	DRAFT_01127	Locus_type		CDS		
2558670459	DRAFT_01127	Product_name		hypothetical protein		
2558670459	DRAFT_01127	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670459	DRAFT_01127	Coordinates		8341..8583(-)		
2558670459	DRAFT_01127	DNA_length		243bp		
2558670459	DRAFT_01127	Protein_length		80aa		
2558670459	DRAFT_01127	GC			0.53	
2558670460	DRAFT_01128	COG_category	[S] Function unknown			
2558670460	DRAFT_01128	COG1833	Uncharacterized conserved protein			2.00E-16
2558670460	DRAFT_01128	pfam01986	DUF123			1.20E-18
2558670460	DRAFT_01128	Locus_type		CDS		
2558670460	DRAFT_01128	Product_name		Uncharacterized conserved protein		
2558670460	DRAFT_01128	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670460	DRAFT_01128	Coordinates		8614..8943(-)		
2558670460	DRAFT_01128	DNA_length		330bp		
2558670460	DRAFT_01128	Protein_length		109aa		
2558670460	DRAFT_01128	GC			0.57	
2558670461	DRAFT_01129	pfam00096	zf-C2H2			1.40E-03
2558670461	DRAFT_01129	Locus_type		CDS		
2558670461	DRAFT_01129	Product_name		Zinc finger, C2H2 type		
2558670461	DRAFT_01129	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670461	DRAFT_01129	Coordinates		9649..9963(-)		
2558670461	DRAFT_01129	DNA_length		315bp		
2558670461	DRAFT_01129	Protein_length		104aa		
2558670461	DRAFT_01129	GC			0.58	
2558670462	DRAFT_01130	KEGG_module	M00018: Threonine biosynthesis, aspartate => homoserine => threonine			
2558670462	DRAFT_01130	Metacyc	HOMOSER-THRESYN-PWY: threonine biosynthesis from homoserine			

2558670462	DRAFT_01130	IMG_pathway	133: L-threonine synthesis from L-homoserine			
2558670462	DRAFT_01130	COG_category	[E] Amino acid transport and metabolism			
2558670462	DRAFT_01130	COG0498	Threonine synthase			8.00E-53
2558670462	DRAFT_01130	pfam00291	PALP			4.90E-50
2558670462	DRAFT_01130	EC:4.2.3.1	Threonine synthase.			
2558670462	DRAFT_01130	TIGR00260	threonine synthase			3.40E-44
2558670462	DRAFT_01130	KO:K01733	threonine synthase [EC:4.2.3.1]			0.00E+00
2558670462	DRAFT_01130	ITERM:00220	L-threonine synthase (EC 4.2.3.1)			
2558670462	DRAFT_01130	Locus_type		CDS		
2558670462	DRAFT_01130	Product_name		L-threonine synthase (EC 4.2.3.1)		
2558670462	DRAFT_01130	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670462	DRAFT_01130	Coordinates		10216..11274(+)		
2558670462	DRAFT_01130	DNA_length		1059bp		
2558670462	DRAFT_01130	Protein_length		352aa		
2558670462	DRAFT_01130	GC			0.53	

2558670463	DRAFT_01131	Locus_type		CDS		
2558670463	DRAFT_01131	Product_name		hypothetical protein		
2558670463	DRAFT_01131	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670463	DRAFT_01131	Coordinates		11366..11560(+)		
2558670463	DRAFT_01131	DNA_length		195bp		
2558670463	DRAFT_01131	Protein_length		64aa		
2558670463	DRAFT_01131	GC			0.53	

2558670464	DRAFT_01132	Locus_type		CDS		
2558670464	DRAFT_01132	Product_name		hypothetical protein		
2558670464	DRAFT_01132	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670464	DRAFT_01132	Coordinates		11657..12007(+)		
2558670464	DRAFT_01132	DNA_length		351bp		
2558670464	DRAFT_01132	Protein_length		116aa		
2558670464	DRAFT_01132	GC			0.54	

2558670465	DRAFT_01133	Locus_type		CDS		
2558670465	DRAFT_01133	Product_name		hypothetical protein		

2558670465	DRAFT_01133	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670465	DRAFT_01133	Coordinates		11994..12311(+)	
2558670465	DRAFT_01133	DNA_length		318bp	
2558670465	DRAFT_01133	Protein_length		105aa	
2558670465	DRAFT_01133	GC		0.52	
2558670466	DRAFT_01134	Locus_type		CDS	
2558670466	DRAFT_01134	Product_name		hypothetical protein	
2558670466	DRAFT_01134	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670466	DRAFT_01134	Coordinates		12318..12836(+)	
2558670466	DRAFT_01134	DNA_length		519bp	
2558670466	DRAFT_01134	Protein_length		172aa	
2558670466	DRAFT_01134	GC		0.56	
2558670467	DRAFT_01135	COG_category	[R] General function prediction only		
2558670467	DRAFT_01135	COG0535	Predicted Fe-S oxidoreductases		1.00E-21
2558670467	DRAFT_01135	pfam04055	Radical_SAM		2.40E-09
2558670467	DRAFT_01135	pfam13353	Fer4_12		5.70E-06
2558670467	DRAFT_01135	TIGR04085	radical SAM additional 4Fe4S-binding SPASM domain		1.20E-10
2558670467	DRAFT_01135	TIGR04084	putative peptide-modifying radical SAM enzyme, AF0577 family		4.40E-101
2558670467	DRAFT_01135	Locus_type		CDS	
2558670467	DRAFT_01135	Product_name		putative peptide-modifying radical SAM enzyme, AF0577 family	
2558670467	DRAFT_01135	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670467	DRAFT_01135	Coordinates		12978..14060(-)	
2558670467	DRAFT_01135	DNA_length		1083bp	
2558670467	DRAFT_01135	Protein_length		360aa	
2558670467	DRAFT_01135	GC		0.53	
2558670468	DRAFT_01136	pfam13463	HTH_27		4.20E-06
2558670468	DRAFT_01136	Locus_type		CDS	
2558670468	DRAFT_01136	Product_name		Winged helix DNA-binding domain	
2558670468	DRAFT_01136	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670468	DRAFT_01136	Coordinates		14218..14490(+)	
2558670468	DRAFT_01136	DNA_length		273bp	

2558670468	DRAFT_01136	Protein_length		90aa		
2558670468	DRAFT_01136	GC			0.54	
2558670469	DRAFT_01137	Locus_type		CDS		
2558670469	DRAFT_01137	Product_name		hypothetical protein		
2558670469	DRAFT_01137	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670469	DRAFT_01137	Coordinates		14451..14582(-)		
2558670469	DRAFT_01137	DNA_length		132bp		
2558670469	DRAFT_01137	Protein_length		43aa		
2558670469	DRAFT_01137	GC			0.57	
2558670470	DRAFT_01138	COG_category	[K] Transcription			
2558670470	DRAFT_01138	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatic			1.00E-68
2558670470	DRAFT_01138	pfam00382	TFIIB			2.50E-19
2558670470	DRAFT_01138	pfam08271	TF_Zn_Ribbon			7.20E-11
2558670470	DRAFT_01138	pfam00382	TFIIB			2.70E-14
2558670470	DRAFT_01138	KO:K03124	transcription initiation factor TFIIB			0.00E+00
2558670470	DRAFT_01138	Locus_type		CDS		
2558670470	DRAFT_01138	Product_name		Transcription initiation factor IIB (TFIIB)		
2558670470	DRAFT_01138	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670470	DRAFT_01138	Coordinates		15175..16113(-)		
2558670470	DRAFT_01138	DNA_length		939bp		
2558670470	DRAFT_01138	Protein_length		312aa		
2558670470	DRAFT_01138	GC			0.6	
2558670471	DRAFT_01139	COG_category	[L] Replication, recombination and repair			
2558670471	DRAFT_01139	COG3316	Transposase and inactivated derivatives			2.00E-09
2558670471	DRAFT_01139	pfam13610	DDE_Tnp_IS240			4.20E-19
2558670471	DRAFT_01139	Locus_type		CDS		
2558670471	DRAFT_01139	Product_name		Transposase and inactivated derivatives		
2558670471	DRAFT_01139	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21		
2558670471	DRAFT_01139	Coordinates		16209..17363(-)		
2558670471	DRAFT_01139	DNA_length		1155bp		
2558670471	DRAFT_01139	Protein_length		384aa		

2558670471	DRAFT_01139	GC			0.54
2558670472	DRAFT_01140	Locus_type		CDS	
2558670472	DRAFT_01140	Product_name		hypothetical protein	
2558670472	DRAFT_01140	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670472	DRAFT_01140	Coordinates		17501..17764(+)	
2558670472	DRAFT_01140	DNA_length		264bp	
2558670472	DRAFT_01140	Protein_length		87aa	
2558670472	DRAFT_01140	GC			0.52
2558670473	DRAFT_01141	Locus_type		CDS	
2558670473	DRAFT_01141	Product_name		hypothetical protein	
2558670473	DRAFT_01141	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670473	DRAFT_01141	Coordinates		17757..18410(+)	
2558670473	DRAFT_01141	DNA_length		654bp	
2558670473	DRAFT_01141	Protein_length		217aa	
2558670473	DRAFT_01141	GC			0.53
2558670474	DRAFT_01142	Locus_type		CDS	
2558670474	DRAFT_01142	Product_name		hypothetical protein	
2558670474	DRAFT_01142	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670474	DRAFT_01142	Coordinates		18416..18775(+)	
2558670474	DRAFT_01142	DNA_length		360bp	
2558670474	DRAFT_01142	Protein_length		119aa	
2558670474	DRAFT_01142	GC			0.53
2558670475	DRAFT_01143	COG_category	[H] Coenzyme transport and metabolism		
2558670475	DRAFT_01143	COG0476	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine		2.00E-68
2558670475	DRAFT_01143	pfam05237	MoeZ_MoeB		2.20E-29
2558670475	DRAFT_01143	pfam00899	ThiF		9.00E-43
2558670475	DRAFT_01143	pfam00581	Rhodanese		6.90E-19
2558670475	DRAFT_01143	KO:K11996	adenylyltransferase and sulfurtransferase		0.00E+00
2558670475	DRAFT_01143	Locus_type		CDS	
2558670475	DRAFT_01143	Product_name		Dinucleotide-utilizing enzymes involved in molybdopterin and thiamin	

2558670475	DRAFT_01143	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670475	DRAFT_01143	Coordinates		19290..20438(-)	
2558670475	DRAFT_01143	DNA_length		1149bp	
2558670475	DRAFT_01143	Protein_length		382aa	
2558670475	DRAFT_01143	GC		0.62	
2558670475	DRAFT_01143	Fused_gene		Yes	
2558670476	DRAFT_01144	KEGG_module	M00254: ABC-2 type transport system		
2558670476	DRAFT_01144	COG_category	[V] Defense mechanisms		
2558670476	DRAFT_01144	COG1131	ABC-type multidrug transport system, ATPase component		6.00E-59
2558670476	DRAFT_01144	pfam00005	ABC_tran		5.80E-24
2558670476	DRAFT_01144	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2558670476	DRAFT_01144	Locus_type		CDS	
2558670476	DRAFT_01144	Product_name		ABC-type multidrug transport system, ATPase component	
2558670476	DRAFT_01144	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670476	DRAFT_01144	Coordinates		20548..21516(+)	
2558670476	DRAFT_01144	DNA_length		969bp	
2558670476	DRAFT_01144	Protein_length		322aa	
2558670476	DRAFT_01144	GC		0.61	
2558670477	DRAFT_01145	KEGG_module	M00248: Putative antibiotic transport system		
2558670477	DRAFT_01145	COG_category	[V] Defense mechanisms		
2558670477	DRAFT_01145	COG0842	ABC-type multidrug transport system, permease component		1.00E-06
2558670477	DRAFT_01145	pfam01061	ABC2_membrane		1.50E-13
2558670477	DRAFT_01145	KO:K09686	antibiotic transport system permease protein		8.80E-32
2558670477	DRAFT_01145	Locus_type		CDS	
2558670477	DRAFT_01145	Product_name		ABC-type multidrug transport system, permease component	
2558670477	DRAFT_01145	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670477	DRAFT_01145	Coordinates		21513..22277(+)	
2558670477	DRAFT_01145	DNA_length		765bp	
2558670477	DRAFT_01145	Protein_length		254aa	
2558670477	DRAFT_01145	GC		0.6	
2558670477	DRAFT_01145	Transmembrane		Yes	

2558670478	DRAFT_01146	Locus_type		CDS	
2558670478	DRAFT_01146	Product_name		hypothetical protein	
2558670478	DRAFT_01146	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670478	DRAFT_01146	Coordinates		22274..22468(+)	
2558670478	DRAFT_01146	DNA_length		195bp	
2558670478	DRAFT_01146	Protein_length		64aa	
2558670478	DRAFT_01146	GC			0.67

2558670479	DRAFT_01147	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558670479	DRAFT_01147	COG1225	Peroxiredoxin		1.00E-35
2558670479	DRAFT_01147	pfam00578	AhpC-TSA		3.80E-33
2558670479	DRAFT_01147	Locus_type		CDS	
2558670479	DRAFT_01147	Product_name		Peroxiredoxin	
2558670479	DRAFT_01147	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670479	DRAFT_01147	Coordinates		22504..22971(+)	
2558670479	DRAFT_01147	DNA_length		468bp	
2558670479	DRAFT_01147	Protein_length		155aa	
2558670479	DRAFT_01147	GC			0.59

2558670480	DRAFT_01148	pfam10604	Polyketide_cyc2		4.70E-12
2558670480	DRAFT_01148	Locus_type		CDS	
2558670480	DRAFT_01148	Product_name		Polyketide cyclase / dehydrase and lipid transport	
2558670480	DRAFT_01148	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670480	DRAFT_01148	Coordinates		23278..23706(-)	
2558670480	DRAFT_01148	DNA_length		429bp	
2558670480	DRAFT_01148	Protein_length		142aa	
2558670480	DRAFT_01148	GC			0.6

2558670481	DRAFT_01149	Locus_type		CDS	
2558670481	DRAFT_01149	Product_name		hypothetical protein	
2558670481	DRAFT_01149	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670481	DRAFT_01149	Coordinates		23766..24773(-)	
2558670481	DRAFT_01149	DNA_length		1008bp	
2558670481	DRAFT_01149	Protein_length		335aa	

2558670481	DRAFT_01149	GC		0.58	
2558670481	DRAFT_01149	Transmembrane		Yes	
2558670482	DRAFT_01150	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism		
2558670482	DRAFT_01150	COG0179	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydra		6.00E-73
2558670482	DRAFT_01150	pfam01557	FAA_hydrolase		3.60E-67
2558670482	DRAFT_01150	Locus_type		CDS	
2558670482	DRAFT_01150	Product_name		2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydr	
2558670482	DRAFT_01150	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670482	DRAFT_01150	Coordinates		24838..25707(-)	
2558670482	DRAFT_01150	DNA_length		870bp	
2558670482	DRAFT_01150	Protein_length		289aa	
2558670482	DRAFT_01150	GC		0.56	
2558670483	DRAFT_01151	ITERM:02472	TspO and MBR related proteins		
2558670483	DRAFT_01151	Locus_type		CDS	
2558670483	DRAFT_01151	Product_name		TspO and MBR related proteins	
2558670483	DRAFT_01151	Scaffold		DRAFT_contig_70_133_len_26431_read_count_520883.21	
2558670483	DRAFT_01151	Coordinates		25747..26430(-)	
2558670483	DRAFT_01151	DNA_length		684bp	
2558670483	DRAFT_01151	Protein_length		227aa	
2558670483	DRAFT_01151	GC		0.51	
2558670483	DRAFT_01151	Transmembrane		Yes	
2558670484	DRAFT_01152	KEGG_module	M00248: Putative antibiotic transport system		
2558670484	DRAFT_01152	pfam01061	ABC2_membrane		2.90E-26
2558670484	DRAFT_01152	KO:K09686	antibiotic transport system permease protein		7.40E-27
2558670484	DRAFT_01152	Locus_type		CDS	
2558670484	DRAFT_01152	Product_name		Predicted membrane protein	
2558670484	DRAFT_01152	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670484	DRAFT_01152	Coordinates		9..671(-)	
2558670484	DRAFT_01152	DNA_length		663bp	
2558670484	DRAFT_01152	Protein_length		220aa	
2558670484	DRAFT_01152	GC		0.6	

2558670484	DRAFT_01152	Transmembrane		Yes	
2558670485	DRAFT_01153	KEGG_module	M00248: Putative antibiotic transport system		
2558670485	DRAFT_01153	COG_category	[V] Defense mechanisms		
2558670485	DRAFT_01153	COG1131	ABC-type multidrug transport system, ATPase component		1.00E-59
2558670485	DRAFT_01153	pfam00005	ABC_tran		2.90E-24
2558670485	DRAFT_01153	KO:K09687	antibiotic transport system ATP-binding protein		0.00E+00
2558670485	DRAFT_01153	Locus_type		CDS	
2558670485	DRAFT_01153	Product_name		ABC-type multidrug transport system, ATPase component	
2558670485	DRAFT_01153	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670485	DRAFT_01153	Coordinates		752..1681(-)	
2558670485	DRAFT_01153	DNA_length		930bp	
2558670485	DRAFT_01153	Protein_length		309aa	
2558670485	DRAFT_01153	GC		0.56	
2558670486	DRAFT_01154	pfam00571	CBS		2.90E-09
2558670486	DRAFT_01154	pfam00571	CBS		7.30E-18
2558670486	DRAFT_01154	Locus_type		CDS	
2558670486	DRAFT_01154	Product_name		Predicted signal-transduction protein containing cAMP-binding and C	
2558670486	DRAFT_01154	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670486	DRAFT_01154	Coordinates		1736..2200(+)	
2558670486	DRAFT_01154	DNA_length		465bp	
2558670486	DRAFT_01154	Protein_length		154aa	
2558670486	DRAFT_01154	GC		0.55	
2558670487	DRAFT_01155	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558670487	DRAFT_01155	COG0071	Molecular chaperone (small heat shock protein)		6.00E-14
2558670487	DRAFT_01155	pfam00011	HSP20		9.70E-08
2558670487	DRAFT_01155	KO:K13993	HSP20 family protein		8.70E-43
2558670487	DRAFT_01155	Locus_type		CDS	
2558670487	DRAFT_01155	Product_name		Molecular chaperone (small heat shock protein)	
2558670487	DRAFT_01155	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670487	DRAFT_01155	Coordinates		2202..2798(-)	
2558670487	DRAFT_01155	DNA_length		597bp	

2558670487	DRAFT_01155	Protein_length		198aa	
2558670487	DRAFT_01155	GC		0.56	
2558670488	DRAFT_01156	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558670488	DRAFT_01156	COG0501	Zn-dependent protease with chaperone function		7.00E-40
2558670488	DRAFT_01156	pfam01435	Peptidase_M48		1.90E-39
2558670488	DRAFT_01156	EC:3.4.24.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Metalloendopeptidases.		
2558670488	DRAFT_01156	KO:K03799	heat shock protein HtpX [EC:3.4.24.-]		0.00E+00
2558670488	DRAFT_01156	Locus_type		CDS	
2558670488	DRAFT_01156	Product_name		Zn-dependent protease with chaperone function	
2558670488	DRAFT_01156	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670488	DRAFT_01156	Coordinates		2903..3802(+)	
2558670488	DRAFT_01156	DNA_length		900bp	
2558670488	DRAFT_01156	Protein_length		299aa	
2558670488	DRAFT_01156	GC		0.57	
2558670488	DRAFT_01156	Transmembrane		Yes	
2558670489	DRAFT_01157	Locus_type		CDS	
2558670489	DRAFT_01157	Product_name		hypothetical protein	
2558670489	DRAFT_01157	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670489	DRAFT_01157	Coordinates		3799..4296(-)	
2558670489	DRAFT_01157	DNA_length		498bp	
2558670489	DRAFT_01157	Protein_length		165aa	
2558670489	DRAFT_01157	GC		0.57	
2558670489	DRAFT_01157	Transmembrane		Yes	
2558670490	DRAFT_01158	COG_category	[L] Replication, recombination and repair		
2558670490	DRAFT_01158	COG4912	Predicted DNA alkylation repair enzyme		1.00E-08
2558670490	DRAFT_01158	pfam08713	DNA_alkylation		1.40E-37
2558670490	DRAFT_01158	Locus_type		CDS	
2558670490	DRAFT_01158	Product_name		Predicted DNA alkylation repair enzyme	
2558670490	DRAFT_01158	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670490	DRAFT_01158	Coordinates		4550..5263(-)	
2558670490	DRAFT_01158	DNA_length		714bp	

2558670490	DRAFT_01158	Protein_length		237aa		
2558670490	DRAFT_01158	GC			0.54	
2558670491	DRAFT_01159	pfam02589	DUF162			5.70E-18
2558670491	DRAFT_01159	Locus_type		CDS		
2558670491	DRAFT_01159	Product_name		Uncharacterised ACR, YkgG family COG1556		
2558670491	DRAFT_01159	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670491	DRAFT_01159	Coordinates		5413..6090(-)		
2558670491	DRAFT_01159	DNA_length		678bp		
2558670491	DRAFT_01159	Protein_length		225aa		
2558670491	DRAFT_01159	GC			0.61	
2558670492	DRAFT_01160	COG_category	[G] Carbohydrate transport and metabolism			
2558670492	DRAFT_01160	COG0662	Mannose-6-phosphate isomerase			7.00E-17
2558670492	DRAFT_01160	pfam07883	Cupin_2			3.90E-18
2558670492	DRAFT_01160	Locus_type		CDS		
2558670492	DRAFT_01160	Product_name		Mannose-6-phosphate isomerase		
2558670492	DRAFT_01160	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670492	DRAFT_01160	Coordinates		6353..6745(-)		
2558670492	DRAFT_01160	DNA_length		393bp		
2558670492	DRAFT_01160	Protein_length		130aa		
2558670492	DRAFT_01160	GC			0.54	
2558670493	DRAFT_01161	pfam07366	SnoaL			1.20E-27
2558670493	DRAFT_01161	Locus_type		CDS		
2558670493	DRAFT_01161	Product_name		SnoaL-like polyketide cyclase		
2558670493	DRAFT_01161	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670493	DRAFT_01161	Coordinates		6803..7258(+)		
2558670493	DRAFT_01161	DNA_length		456bp		
2558670493	DRAFT_01161	Protein_length		151aa		
2558670493	DRAFT_01161	GC			0.53	
2558670494	DRAFT_01162	COG_category	[R] General function prediction only			
2558670494	DRAFT_01162	COG0517	FOG: CBS domain			1.00E-11

2558670494	DRAFT_01162	pfam00571	CBS			2.40E-09
2558670494	DRAFT_01162	pfam00571	CBS			2.60E-11
2558670494	DRAFT_01162	Locus_type		CDS		
2558670494	DRAFT_01162	Product_name		FOG: CBS domain		
2558670494	DRAFT_01162	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670494	DRAFT_01162	Coordinates		7584..8186(-)		
2558670494	DRAFT_01162	DNA_length		603bp		
2558670494	DRAFT_01162	Protein_length		200aa		
2558670494	DRAFT_01162	GC			0.57	
2558670495	DRAFT_01163	Locus_type		CDS		
2558670495	DRAFT_01163	Product_name		hypothetical protein		
2558670495	DRAFT_01163	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670495	DRAFT_01163	Coordinates		8282..8536(+)		
2558670495	DRAFT_01163	DNA_length		255bp		
2558670495	DRAFT_01163	Protein_length		84aa		
2558670495	DRAFT_01163	GC			0.53	
2558670495	DRAFT_01163	Transmembrane		Yes		
2558670496	DRAFT_01164	Locus_type		CDS		
2558670496	DRAFT_01164	Product_name		hypothetical protein		
2558670496	DRAFT_01164	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670496	DRAFT_01164	Coordinates		8686..8892(-)		
2558670496	DRAFT_01164	DNA_length		207bp		
2558670496	DRAFT_01164	Protein_length		68aa		
2558670496	DRAFT_01164	GC			0.43	
2558670496	DRAFT_01164	Transmembrane		Yes		
2558670497	DRAFT_01165	COG_category	[S] Function unknown			
2558670497	DRAFT_01165	COG1814	Uncharacterized membrane protein			2.00E-11
2558670497	DRAFT_01165	pfam01988	VIT1			3.50E-41
2558670497	DRAFT_01165	Locus_type		CDS		
2558670497	DRAFT_01165	Product_name		Uncharacterized membrane protein		
2558670497	DRAFT_01165	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		

2558670497	DRAFT_01165	Coordinates		9021..9737(+)	
2558670497	DRAFT_01165	DNA_length		717bp	
2558670497	DRAFT_01165	Protein_length		238aa	
2558670497	DRAFT_01165	GC		0.56	
2558670497	DRAFT_01165	Transmembrane		Yes	
2558670498	DRAFT_01166	pfam08241	Methyltransf_11		4.80E-20
2558670498	DRAFT_01166	Locus_type		CDS	
2558670498	DRAFT_01166	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	
2558670498	DRAFT_01166	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670498	DRAFT_01166	Coordinates		9825..10424(+)	
2558670498	DRAFT_01166	DNA_length		600bp	
2558670498	DRAFT_01166	Protein_length		199aa	
2558670498	DRAFT_01166	GC		0.57	
2558670499	DRAFT_01167	pfam06053	DUF929		1.70E-24
2558670499	DRAFT_01167	Locus_type		CDS	
2558670499	DRAFT_01167	Product_name		Domain of unknown function (DUF929)	
2558670499	DRAFT_01167	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670499	DRAFT_01167	Coordinates		10663..11559(+)	
2558670499	DRAFT_01167	DNA_length		897bp	
2558670499	DRAFT_01167	Protein_length		298aa	
2558670499	DRAFT_01167	GC		0.56	
2558670499	DRAFT_01167	Transmembrane		Yes	
2558670500	DRAFT_01168	KEGG_module	M00021: Cysteine biosynthesis, serine => cysteine		
2558670500	DRAFT_01168	Metacyc	PWY-6936: seleno-amino acid biosynthesis		
2558670500	DRAFT_01168	Metacyc	CYSTSYN-PWY: cysteine biosynthesis I		
2558670500	DRAFT_01168	COG_category	[E] Amino acid transport and metabolism		
2558670500	DRAFT_01168	COG0031	Cysteine synthase		8.00E-78
2558670500	DRAFT_01168	pfam00291	PALP		1.80E-55
2558670500	DRAFT_01168	EC:2.5.1.47	Cysteine synthase.		
2558670500	DRAFT_01168	KO:K01738	cysteine synthase A [EC:2.5.1.47]		0.00E+00
2558670500	DRAFT_01168	Locus_type		CDS	

2558670500	DRAFT_01168	Product_name		Cysteine synthase	
2558670500	DRAFT_01168	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670500	DRAFT_01168	Coordinates		11560..12549(+)	
2558670500	DRAFT_01168	DNA_length		990bp	
2558670500	DRAFT_01168	Protein_length		329aa	
2558670500	DRAFT_01168	GC		0.52	
2558670501	DRAFT_01169	Locus_type		tRNA	
2558670501	DRAFT_01169	Product_name		tRNA_Val_GAC	
2558670501	DRAFT_01169	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670501	DRAFT_01169	Coordinates		12674..12773(-)	
2558670501	DRAFT_01169	DNA_length		77bp	
2558670501	DRAFT_01169	GC		0.64	
2558670502	DRAFT_01170	Metacyc	PWY-5074: mevalonate degradation		
2558670502	DRAFT_01170	IMG_pathway	178: Mevalonate pathway for isopentenyl pyrophopsphate synthesis		
2558670502	DRAFT_01170	IMG_pathway	591: Archaeal mevalonate pathway for isopentenyl pyrophosphate synthesis		
2558670502	DRAFT_01170	COG_category	[I] Lipid transport and metabolism		
2558670502	DRAFT_01170	COG1257	Hydroxymethylglutaryl-CoA reductase		2.00E-104
2558670502	DRAFT_01170	pfam00368	HMG-CoA_red		6.50E-92
2558670502	DRAFT_01170	EC:1.1.1.88	Hydroxymethylglutaryl-CoA reductase.		
2558670502	DRAFT_01170	TIGR00532	hydroxymethylglutaryl-CoA reductase, degradative		0.00E+00
2558670502	DRAFT_01170	KO:K00054	hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]		0.00E+00
2558670502	DRAFT_01170	ITERM:00463	3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34)		
2558670502	DRAFT_01170	Locus_type		CDS	
2558670502	DRAFT_01170	Product_name		3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34)	
2558670502	DRAFT_01170	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670502	DRAFT_01170	Coordinates		12903..14192(+)	
2558670502	DRAFT_01170	DNA_length		1290bp	
2558670502	DRAFT_01170	Protein_length		429aa	
2558670502	DRAFT_01170	GC		0.58	
2558670503	DRAFT_01171	KEGG_module	M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate		
2558670503	DRAFT_01171	Metacyc	HISDEG-PWY: histidine degradation I		

2558670503	DRAFT_01171	Metacyc	PWY-5028: histidine degradation II		
2558670503	DRAFT_01171	Metacyc	PWY-5030: histidine degradation III		
2558670503	DRAFT_01171	Metacyc	HISHP-PWY: histidine degradation VI		
2558670503	DRAFT_01171	IMG_pathway	189: L-histidine degradation to L-glutamate and formamide		
2558670503	DRAFT_01171	IMG_pathway	190: L-histidine degradation to L-glutamate and formiminotetrahydrofolate		
2558670503	DRAFT_01171	COG_category	[E] Amino acid transport and metabolism		
2558670503	DRAFT_01171	COG2987	Urocanate hydratase		0.00E+00
2558670503	DRAFT_01171	pfam01175	Urocanase		0.00E+00
2558670503	DRAFT_01171	EC:4.2.1.49	Urocanate hydratase.		
2558670503	DRAFT_01171	TIGR01228	urocanate hydratase		0.00E+00
2558670503	DRAFT_01171	KO:K01712	urocanate hydratase [EC:4.2.1.49]		0.00E+00
2558670503	DRAFT_01171	ITERM:00501	urocanate hydratase (EC 4.2.1.49)		
2558670503	DRAFT_01171	Locus_type		CDS	
2558670503	DRAFT_01171	Product_name		urocanate hydratase (EC 4.2.1.49)	
2558670503	DRAFT_01171	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670503	DRAFT_01171	Coordinates		14341..16044(-)	
2558670503	DRAFT_01171	DNA_length		1704bp	
2558670503	DRAFT_01171	Protein_length		567aa	
2558670503	DRAFT_01171	GC		0.62	
2558670504	DRAFT_01172	KEGG_module	M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine		
2558670504	DRAFT_01172	Metacyc	DAPLYSINESYN-PWY: lysine biosynthesis I		
2558670504	DRAFT_01172	COG_category	[E] Amino acid transport and metabolism		
2558670504	DRAFT_01172	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase a		7.00E-46
2558670504	DRAFT_01172	pfam07687	M20_dimer		3.40E-16
2558670504	DRAFT_01172	pfam01546	Peptidase_M20		1.40E-19
2558670504	DRAFT_01172	EC:3.5.1.18	Succinyl-diaminopimelate desuccinylase.		
2558670504	DRAFT_01172	KO:K01439	succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]		0.00E+00
2558670504	DRAFT_01172	Locus_type		CDS	
2558670504	DRAFT_01172	Product_name		Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase	
2558670504	DRAFT_01172	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670504	DRAFT_01172	Coordinates		16163..17059(+)	
2558670504	DRAFT_01172	DNA_length		897bp	
2558670504	DRAFT_01172	Protein_length		298aa	

2558670504	DRAFT_01172	GC			0.51	
2558670505	DRAFT_01173	Locus_type		CDS		
2558670505	DRAFT_01173	Product_name		hypothetical protein		
2558670505	DRAFT_01173	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670505	DRAFT_01173	Coordinates		17084..17410(+)		
2558670505	DRAFT_01173	DNA_length		327bp		
2558670505	DRAFT_01173	Protein_length		108aa		
2558670505	DRAFT_01173	GC			0.57	
2558670506	DRAFT_01174	Metacyc	GLNSYN-PWY: glutamine biosynthesis I			
2558670506	DRAFT_01174	Metacyc	PWY490-3: nitrate reduction VI (assimilatory)			
2558670506	DRAFT_01174	Metacyc	PWY-6964: ammonia assimilation cycle II			
2558670506	DRAFT_01174	Metacyc	PWY-381: nitrate reduction II (assimilatory)			
2558670506	DRAFT_01174	Metacyc	PWY-6549: glutamine biosynthesis III			
2558670506	DRAFT_01174	Metacyc	PWY-6963: ammonia assimilation cycle I			
2558670506	DRAFT_01174	Metacyc	PWY-5675: nitrate reduction V (assimilatory)			
2558670506	DRAFT_01174	COG_category	[E] Amino acid transport and metabolism			
2558670506	DRAFT_01174	COG0174	Glutamine synthetase			4.00E-114
2558670506	DRAFT_01174	pfam00120	Gln-synt_C			6.20E-78
2558670506	DRAFT_01174	pfam03951	Gln-synt_N			4.00E-16
2558670506	DRAFT_01174	EC:6.3.1.2	Glutamate--ammonia ligase.			
2558670506	DRAFT_01174	TIGR00653	glutamine synthetase, type I			0.00E+00
2558670506	DRAFT_01174	KO:K01915	glutamine synthetase [EC:6.3.1.2]			0.00E+00
2558670506	DRAFT_01174	Locus_type		CDS		
2558670506	DRAFT_01174	Product_name		Glutamine synthetase		
2558670506	DRAFT_01174	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670506	DRAFT_01174	Coordinates		17613..18941(+)		
2558670506	DRAFT_01174	DNA_length		1329bp		
2558670506	DRAFT_01174	Protein_length		442aa		
2558670506	DRAFT_01174	GC			0.55	
2558670507	DRAFT_01175	KEGG_module	M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate			
2558670507	DRAFT_01175	Metacyc	PWY-5030: histidine degradation III			

2558670507	DRAFT_01175	Metacyc	HISDEG-PWY: histidine degradation I			
2558670507	DRAFT_01175	Metacyc	PWY-5028: histidine degradation II			
2558670507	DRAFT_01175	Metacyc	HISHP-PWY: histidine degradation VI			
2558670507	DRAFT_01175	IMG_pathway	189: L-histidine degradation to L-glutamate and formamide			
2558670507	DRAFT_01175	IMG_pathway	190: L-histidine degradation to L-glutamate and formiminotetrahydrofolate			
2558670507	DRAFT_01175	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2558670507	DRAFT_01175	COG1228	Imidazolonepropionase and related amidohydrolases			3.00E-77
2558670507	DRAFT_01175	pfam01979	Amidohydro_1			1.20E-10
2558670507	DRAFT_01175	pfam13594	Amidohydro_5			2.20E-14
2558670507	DRAFT_01175	EC:3.5.2.7	Imidazolonepropionase.			
2558670507	DRAFT_01175	TIGR01224	imidazolonepropionase			2.10E-127
2558670507	DRAFT_01175	KO:K01468	imidazolonepropionase [EC:3.5.2.7]			0.00E+00
2558670507	DRAFT_01175	ITERM:00502	imidazolonepropionase (EC 3.5.2.7)			
2558670507	DRAFT_01175	Locus_type		CDS		
2558670507	DRAFT_01175	Product_name		imidazolonepropionase (EC 3.5.2.7)		
2558670507	DRAFT_01175	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670507	DRAFT_01175	Coordinates		18962..20233(+)		
2558670507	DRAFT_01175	DNA_length		1272bp		
2558670507	DRAFT_01175	Protein_length		423aa		
2558670507	DRAFT_01175	GC			0.56	

2558670508	DRAFT_01176	COG_category	[B] Chromatin structure and dynamics			
2558670508	DRAFT_01176	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2558670508	DRAFT_01176	COG0123	Deacetylases, including yeast histone deacetylase and acetoin utilizatio			1.00E-74
2558670508	DRAFT_01176	pfam00850	Hist_deacetyl			1.10E-71
2558670508	DRAFT_01176	KO:K04768	acetoin utilization protein AcuC			0.00E+00
2558670508	DRAFT_01176	Locus_type		CDS		
2558670508	DRAFT_01176	Product_name		Deacetylases, including yeast histone deacetylase and acetoin utilizati		
2558670508	DRAFT_01176	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22		
2558670508	DRAFT_01176	Coordinates		20358..21341(+)		
2558670508	DRAFT_01176	DNA_length		984bp		
2558670508	DRAFT_01176	Protein_length		327aa		
2558670508	DRAFT_01176	GC			0.57	

2558670509	DRAFT_01177	KEGG_module	M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate		
2558670509	DRAFT_01177	Metacyc	PWY-5030: histidine degradation III		
2558670509	DRAFT_01177	Metacyc	PWY-5028: histidine degradation II		
2558670509	DRAFT_01177	Metacyc	HISDEG-PWY: histidine degradation I		
2558670509	DRAFT_01177	Metacyc	HISHP-PWY: histidine degradation VI		
2558670509	DRAFT_01177	IMG_pathway	189: L-histidine degradation to L-glutamate and formamide		
2558670509	DRAFT_01177	IMG_pathway	190: L-histidine degradation to L-glutamate and formiminotetrahydrofolate		
2558670509	DRAFT_01177	COG_category	[E] Amino acid transport and metabolism		
2558670509	DRAFT_01177	COG2986	Histidine ammonia-lyase		0.00E+00
2558670509	DRAFT_01177	pfam00221	Lyase_aromatic		0.00E+00
2558670509	DRAFT_01177	EC:4.3.1.3	Histidine ammonia-lyase.		
2558670509	DRAFT_01177	TIGR01225	histidine ammonia-lyase		0.00E+00
2558670509	DRAFT_01177	KO:K01745	histidine ammonia-lyase [EC:4.3.1.3]		0.00E+00
2558670509	DRAFT_01177	ITERM:00500	histidine ammonia-lyase (EC 4.3.1.3)		
2558670509	DRAFT_01177	Locus_type		CDS	
2558670509	DRAFT_01177	Product_name		histidine ammonia-lyase (EC 4.3.1.3)	
2558670509	DRAFT_01177	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670509	DRAFT_01177	Coordinates		21463..23004(+)	
2558670509	DRAFT_01177	DNA_length		1542bp	
2558670509	DRAFT_01177	Protein_length		513aa	
2558670509	DRAFT_01177	GC		0.54	
2558670510	DRAFT_01178	pfam13385	Laminin_G_3		5.60E-10
2558670510	DRAFT_01178	Locus_type		CDS	
2558670510	DRAFT_01178	Product_name		Concanavalin A-like lectin/glucanases superfamily	
2558670510	DRAFT_01178	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670510	DRAFT_01178	Coordinates		23469..24881(-)	
2558670510	DRAFT_01178	DNA_length		1413bp	
2558670510	DRAFT_01178	Protein_length		470aa	
2558670510	DRAFT_01178	GC		0.55	
2558670510	DRAFT_01178	Transmembrane		Yes	
2558670511	DRAFT_01179	COG_category	[S] Function unknown		
2558670511	DRAFT_01179	COG0393	Uncharacterized conserved protein		2.00E-27

2558670511	DRAFT_01179	pfam01906	YbjQ_1		3.20E-31
2558670511	DRAFT_01179	Locus_type		CDS	
2558670511	DRAFT_01179	Product_name		Uncharacterized conserved protein	
2558670511	DRAFT_01179	Scaffold		DRAFT_contig_70_136_len_25737_read_count_476203.22	
2558670511	DRAFT_01179	Coordinates		25104..25499(-)	
2558670511	DRAFT_01179	DNA_length		396bp	
2558670511	DRAFT_01179	Protein_length		131aa	
2558670511	DRAFT_01179	GC		0.61	
2558670512	DRAFT_01180	Locus_type		CDS	
2558670512	DRAFT_01180	Product_name		hypothetical protein	
2558670512	DRAFT_01180	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670512	DRAFT_01180	Coordinates		158..295(+)	
2558670512	DRAFT_01180	DNA_length		138bp	
2558670512	DRAFT_01180	Protein_length		45aa	
2558670512	DRAFT_01180	GC		0.6	
2558670513	DRAFT_01181	COG_category	[L] Replication, recombination and repair		
2558670513	DRAFT_01181	COG0468	RecA/RadA recombinase		1.00E-64
2558670513	DRAFT_01181	pfam08423	Rad51		8.50E-95
2558670513	DRAFT_01181	TIGR02236	DNA repair and recombination protein RadA		1.40E-128
2558670513	DRAFT_01181	KO:K04483	DNA repair protein RadA		0.00E+00
2558670513	DRAFT_01181	Locus_type		CDS	
2558670513	DRAFT_01181	Product_name		DNA repair and recombination protein RadA	
2558670513	DRAFT_01181	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670513	DRAFT_01181	Coordinates		329..1321(-)	
2558670513	DRAFT_01181	DNA_length		993bp	
2558670513	DRAFT_01181	Protein_length		330aa	
2558670513	DRAFT_01181	GC		0.6	
2558670514	DRAFT_01182	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558670514	DRAFT_01182	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558670514	DRAFT_01182	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558670514	DRAFT_01182	IMG_pathway	499: L-asparagine ligation to tRNA(Asn)		

2558670514	DRAFT_01182	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670514	DRAFT_01182	COG0017	Aspartyl/asparaginyl-tRNA synthetases		0.00E+00
2558670514	DRAFT_01182	pfam01336	tRNA_anti-codon		3.30E-10
2558670514	DRAFT_01182	pfam00152	tRNA-synt_2		4.70E-73
2558670514	DRAFT_01182	EC:6.1.1.22	Asparagine--tRNA ligase.		
2558670514	DRAFT_01182	TIGR00457	asparaginyl-tRNA synthetase		4.70E-115
2558670514	DRAFT_01182	KO:K01893	asparaginyl-tRNA synthetase [EC:6.1.1.22]		0.00E+00
2558670514	DRAFT_01182	ITERM:00392	asparaginyl-tRNA synthetase (EC 6.1.1.22)		
2558670514	DRAFT_01182	Locus_type		CDS	
2558670514	DRAFT_01182	Product_name		asparaginyl-tRNA synthetase (EC 6.1.1.22)	
2558670514	DRAFT_01182	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670514	DRAFT_01182	Coordinates		1359..2651(-)	
2558670514	DRAFT_01182	DNA_length		1293bp	
2558670514	DRAFT_01182	Protein_length		430aa	
2558670514	DRAFT_01182	GC		0.6	
2558670515	DRAFT_01183	COG_category	[S] Function unknown		
2558670515	DRAFT_01183	COG2078	Uncharacterized conserved protein		3.00E-58
2558670515	DRAFT_01183	pfam01871	AMMECR1		4.40E-53
2558670515	DRAFT_01183	TIGR04335	AmmeMemoRadiSam system protein A		1.00E-53
2558670515	DRAFT_01183	TIGR00296	uncharacterized protein, PH0010 family		1.60E-64
2558670515	DRAFT_01183	KO:K09141	hypothetical protein		0.00E+00
2558670515	DRAFT_01183	Locus_type		CDS	
2558670515	DRAFT_01183	Product_name		uncharacterized protein, PH0010 family/AmmeMemoRadiSam systen	
2558670515	DRAFT_01183	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670515	DRAFT_01183	Coordinates		2837..3451(-)	
2558670515	DRAFT_01183	DNA_length		615bp	
2558670515	DRAFT_01183	Protein_length		204aa	
2558670515	DRAFT_01183	GC		0.61	
2558670516	DRAFT_01184	COG_category	[S] Function unknown		
2558670516	DRAFT_01184	COG1656	Uncharacterized conserved protein		1.00E-26
2558670516	DRAFT_01184	pfam01927	Mut7-C		1.50E-30
2558670516	DRAFT_01184	KO:K09122	hypothetical protein		6.60E-22

2558670516	DRAFT_01184	Locus_type		CDS	
2558670516	DRAFT_01184	Product_name		Uncharacterized conserved protein	
2558670516	DRAFT_01184	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670516	DRAFT_01184	Coordinates		3435..3899(-)	
2558670516	DRAFT_01184	DNA_length		465bp	
2558670516	DRAFT_01184	Protein_length		154aa	
2558670516	DRAFT_01184	GC		0.61	
2558670517	DRAFT_01185	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558670517	DRAFT_01185	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558670517	DRAFT_01185	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558670517	DRAFT_01185	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670517	DRAFT_01185	COG0162	Tyrosyl-tRNA synthetase		2.00E-45
2558670517	DRAFT_01185	pfam00579	tRNA-synt_1b		2.00E-08
2558670517	DRAFT_01185	pfam00579	tRNA-synt_1b		2.40E-26
2558670517	DRAFT_01185	EC:6.1.1.1	Tyrosine--tRNA ligase.		
2558670517	DRAFT_01185	KO:K01866	tyrosyl-tRNA synthetase [EC:6.1.1.1]		0.00E+00
2558670517	DRAFT_01185	Locus_type		CDS	
2558670517	DRAFT_01185	Product_name		Tyrosyl-tRNA synthetase	
2558670517	DRAFT_01185	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670517	DRAFT_01185	Coordinates		3967..5055(-)	
2558670517	DRAFT_01185	DNA_length		1089bp	
2558670517	DRAFT_01185	Protein_length		362aa	
2558670517	DRAFT_01185	GC		0.58	
2558670518	DRAFT_01186	IMG_pathway	964: DsbC-DsbD disulfide-isomerizing reductive system		
2558670518	DRAFT_01186	pfam00085	Thioredoxin		3.60E-31
2558670518	DRAFT_01186	TIGR01068	thioredoxin		7.00E-40
2558670518	DRAFT_01186	KO:K03671	thioredoxin 1		1.50E-28
2558670518	DRAFT_01186	ITERM:01894	thioredoxin		
2558670518	DRAFT_01186	Locus_type		CDS	
2558670518	DRAFT_01186	Product_name		thioredoxin	
2558670518	DRAFT_01186	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670518	DRAFT_01186	Coordinates		5177..5512(-)	

2558670518	DRAFT_01186	DNA_length		336bp		
2558670518	DRAFT_01186	Protein_length		111aa		
2558670518	DRAFT_01186	GC			0.57	
2558670519	DRAFT_01187	COG_category	[H] Coenzyme transport and metabolism			
2558670519	DRAFT_01187	COG0301	Thiamine biosynthesis ATP pyrophosphatase			3.00E-87
2558670519	DRAFT_01187	pfam02926	THUMP			4.60E-14
2558670519	DRAFT_01187	pfam02568	ThiI			1.30E-53
2558670519	DRAFT_01187	TIGR00342	tRNA sulfurtransferase ThiI			2.40E-94
2558670519	DRAFT_01187	KO:K03151	thiamine biosynthesis protein ThiI			0.00E+00
2558670519	DRAFT_01187	Locus_type		CDS		
2558670519	DRAFT_01187	Product_name		Thiamine biosynthesis ATP pyrophosphatase		
2558670519	DRAFT_01187	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670519	DRAFT_01187	Coordinates		5580..6773(-)		
2558670519	DRAFT_01187	DNA_length		1194bp		
2558670519	DRAFT_01187	Protein_length		397aa		
2558670519	DRAFT_01187	GC			0.61	
2558670520	DRAFT_01188	Metacyc	PWY-2681: <i>trans</i>-zeatin biosynthesis			
2558670520	DRAFT_01188	Metacyc	PWY-5381: pyridine nucleotide cycling (plants)			
2558670520	DRAFT_01188	Metacyc	PWY-6793: demethylmenaquinol-8 biosynthesis III			
2558670520	DRAFT_01188	Metacyc	PWY-5316: nicotine biosynthesis			
2558670520	DRAFT_01188	COG_category	[L] Replication, recombination and repair			
2558670520	DRAFT_01188	COG0122	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase			1.00E-33
2558670520	DRAFT_01188	pfam07934	OGG_N			2.00E-23
2558670520	DRAFT_01188	pfam00730	HhH-GPD			7.70E-09
2558670520	DRAFT_01188	EC:4.2.99.18	DNA-(apurinic or apyrimidinic site) lyase.			
2558670520	DRAFT_01188	EC:3.2.2.-	Hydrolases. Glycosylases. Hydrolyzing N-glycosyl compounds.			
2558670520	DRAFT_01188	TIGR00588	8-oxoguanine DNA-glycosylase (ogg)			5.80E-64
2558670520	DRAFT_01188	KO:K03660	N-glycosylase/DNA lyase [EC:3.2.2.- 4.2.99.18]			0.00E+00
2558670520	DRAFT_01188	Locus_type		CDS		
2558670520	DRAFT_01188	Product_name		3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase		
2558670520	DRAFT_01188	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670520	DRAFT_01188	Coordinates		7330..8244(-)		

2558670520	DRAFT_01188	DNA_length		915bp		
2558670520	DRAFT_01188	Protein_length		304aa		
2558670520	DRAFT_01188	GC			0.57	

2558670521	DRAFT_01189	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme			
2558670521	DRAFT_01189	Metacyc	PWY-5188: tetrapyrrole biosynthesis I (from glutamate)			
2558670521	DRAFT_01189	COG_category	[H] Coenzyme transport and metabolism			
2558670521	DRAFT_01189	COG0001	Glutamate-1-semialdehyde aminotransferase			2.00E-109
2558670521	DRAFT_01189	pfam00202	Aminotran_3			9.70E-48
2558670521	DRAFT_01189	EC:5.4.3.8	Glutamate-1-semialdehyde 2,1-aminomutase.			
2558670521	DRAFT_01189	TIGR00713	glutamate-1-semialdehyde-2,1-aminomutase			3.70E-105
2558670521	DRAFT_01189	KO:K01845	glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]			0.00E+00
2558670521	DRAFT_01189	Locus_type		CDS		
2558670521	DRAFT_01189	Product_name		Glutamate-1-semialdehyde aminotransferase		
2558670521	DRAFT_01189	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670521	DRAFT_01189	Coordinates		8332..9642(+)		
2558670521	DRAFT_01189	DNA_length		1311bp		
2558670521	DRAFT_01189	Protein_length		436aa		
2558670521	DRAFT_01189	GC			0.59	

2558670522	DRAFT_01190	Metacyc	DETOX1-PWY: superoxide radicals degradation			
2558670522	DRAFT_01190	Metacyc	PWY-6854: ethylene biosynthesis III (microbes)			
2558670522	DRAFT_01190	COG_category	[P] Inorganic ion transport and metabolism			
2558670522	DRAFT_01190	COG0605	Superoxide dismutase			2.00E-57
2558670522	DRAFT_01190	pfam02777	Sod_Fe_C			6.80E-33
2558670522	DRAFT_01190	pfam00081	Sod_Fe_N			2.80E-26
2558670522	DRAFT_01190	EC:1.15.1.1	Superoxide dismutase.			
2558670522	DRAFT_01190	KO:K04564	superoxide dismutase, Fe-Mn family [EC:1.15.1.1]			0.00E+00
2558670522	DRAFT_01190	Locus_type		CDS		
2558670522	DRAFT_01190	Product_name		Superoxide dismutase		
2558670522	DRAFT_01190	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670522	DRAFT_01190	Coordinates		9654..10262(-)		
2558670522	DRAFT_01190	DNA_length		609bp		
2558670522	DRAFT_01190	Protein_length		202aa		

2558670522	DRAFT_01190	GC		0.56	
2558670523	DRAFT_01191	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)		
2558670523	DRAFT_01191	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P		
2558670523	DRAFT_01191	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)		
2558670523	DRAFT_01191	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)		
2558670523	DRAFT_01191	Metacyc	PWY-5723: Rubisco shunt		
2558670523	DRAFT_01191	Metacyc	P124-PWY: Bifidobacterium shunt		
2558670523	DRAFT_01191	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)		
2558670523	DRAFT_01191	COG_category	[G] Carbohydrate transport and metabolism		
2558670523	DRAFT_01191	COG0176	Transaldolase		1.00E-60
2558670523	DRAFT_01191	pfam00923	Transaldolase		7.40E-55
2558670523	DRAFT_01191	EC:2.2.1.2	Transaldolase.		
2558670523	DRAFT_01191	TIGR00875	fructose-6-phosphate aldolase, TalC/MipB family		9.60E-95
2558670523	DRAFT_01191	KO:K00616	transaldolase [EC:2.2.1.2]		0.00E+00
2558670523	DRAFT_01191	Locus_type		CDS	
2558670523	DRAFT_01191	Product_name		fructose-6-phosphate aldolase, TalC/MipB family	
2558670523	DRAFT_01191	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670523	DRAFT_01191	Coordinates		10305..10970(-)	
2558670523	DRAFT_01191	DNA_length		666bp	
2558670523	DRAFT_01191	Protein_length		221aa	
2558670523	DRAFT_01191	GC		0.6	
2558670524	DRAFT_01192	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)		
2558670524	DRAFT_01192	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P		
2558670524	DRAFT_01192	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)		
2558670524	DRAFT_01192	KEGG_module	M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP		
2558670524	DRAFT_01192	Metacyc	PWY-5723: Rubisco shunt		
2558670524	DRAFT_01192	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)		
2558670524	DRAFT_01192	Metacyc	P21-PWY: pentose phosphate pathway (partial)		
2558670524	DRAFT_01192	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)		
2558670524	DRAFT_01192	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)		
2558670524	DRAFT_01192	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle		
2558670524	DRAFT_01192	Metacyc	P124-PWY: Bifidobacterium shunt		

2558670524	DRAFT_01192	Metacyc	PWY-6901: xylose degradation IV		
2558670524	DRAFT_01192	COG_category	[G] Carbohydrate transport and metabolism		
2558670524	DRAFT_01192	COG3958	Transketolase, C-terminal subunit		8.00E-105
2558670524	DRAFT_01192	pfam02780	Transketolase_C		3.70E-30
2558670524	DRAFT_01192	pfam02779	Transket_pyr		5.40E-39
2558670524	DRAFT_01192	EC:2.2.1.1	Transketolase.		
2558670524	DRAFT_01192	KO:K00615	transketolase [EC:2.2.1.1]		0.00E+00
2558670524	DRAFT_01192	Locus_type		CDS	
2558670524	DRAFT_01192	Product_name		Transketolase, C-terminal subunit	
2558670524	DRAFT_01192	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670524	DRAFT_01192	Coordinates		11005..11952(-)	
2558670524	DRAFT_01192	DNA_length		948bp	
2558670524	DRAFT_01192	Protein_length		315aa	
2558670524	DRAFT_01192	GC		0.59	
2558670525	DRAFT_01193	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)		
2558670525	DRAFT_01193	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P		
2558670525	DRAFT_01193	Metacyc	P21-PWY: pentose phosphate pathway (partial)		
2558670525	DRAFT_01193	Metacyc	P124-PWY: Bifidobacterium shunt		
2558670525	DRAFT_01193	Metacyc	RIBITOLUTIL-PWY: ribitol degradation		
2558670525	DRAFT_01193	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)		
2558670525	DRAFT_01193	Metacyc	DARABCAT-PWY: D-arabinose degradation II		
2558670525	DRAFT_01193	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)		
2558670525	DRAFT_01193	Metacyc	P122-PWY: heterolactic fermentation		
2558670525	DRAFT_01193	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)		
2558670525	DRAFT_01193	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle		
2558670525	DRAFT_01193	Metacyc	PWY-5723: Rubisco shunt		
2558670525	DRAFT_01193	COG_category	[G] Carbohydrate transport and metabolism		
2558670525	DRAFT_01193	COG0036	Pentose-5-phosphate-3-epimerase		2.00E-53
2558670525	DRAFT_01193	pfam00834	Ribul_P_3_epim		4.60E-54
2558670525	DRAFT_01193	EC:5.1.3.1	Ribulose-phosphate 3-epimerase.		
2558670525	DRAFT_01193	TIGR01163	ribulose-phosphate 3-epimerase		9.90E-60
2558670525	DRAFT_01193	KO:K01783	ribulose-phosphate 3-epimerase [EC:5.1.3.1]		2.80E-45
2558670525	DRAFT_01193	Locus_type		CDS	

2558670525	DRAFT_01193	Product_name		Pentose-5-phosphate-3-epimerase	
2558670525	DRAFT_01193	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670525	DRAFT_01193	Coordinates		11949..12635(-)	
2558670525	DRAFT_01193	DNA_length		687bp	
2558670525	DRAFT_01193	Protein_length		228aa	
2558670525	DRAFT_01193	GC		0.6	
2558670526	DRAFT_01194	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)		
2558670526	DRAFT_01194	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)		
2558670526	DRAFT_01194	KEGG_module	M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP		
2558670526	DRAFT_01194	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P		
2558670526	DRAFT_01194	Metacyc	P124-PWY: Bifidobacterium shunt		
2558670526	DRAFT_01194	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)		
2558670526	DRAFT_01194	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)		
2558670526	DRAFT_01194	Metacyc	PWY-6901: xylose degradation IV		
2558670526	DRAFT_01194	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle		
2558670526	DRAFT_01194	Metacyc	P21-PWY: pentose phosphate pathway (partial)		
2558670526	DRAFT_01194	Metacyc	PWY-5723: Rubisco shunt		
2558670526	DRAFT_01194	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)		
2558670526	DRAFT_01194	COG_category	[G] Carbohydrate transport and metabolism		
2558670526	DRAFT_01194	COG3959	Transketolase, N-terminal subunit		2.00E-88
2558670526	DRAFT_01194	pfam00456	Transketolase_N		9.00E-64
2558670526	DRAFT_01194	EC:2.2.1.1	Transketolase.		
2558670526	DRAFT_01194	KO:K00615	transketolase [EC:2.2.1.1]		0.00E+00
2558670526	DRAFT_01194	Locus_type		CDS	
2558670526	DRAFT_01194	Product_name		transketolase subunit A (EC 2.2.1.1)	
2558670526	DRAFT_01194	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670526	DRAFT_01194	Coordinates		12640..13458(-)	
2558670526	DRAFT_01194	DNA_length		819bp	
2558670526	DRAFT_01194	Protein_length		272aa	
2558670526	DRAFT_01194	GC		0.6	
2558670527	DRAFT_01195	pfam00294	PfkB		5.30E-21
2558670527	DRAFT_01195	TIGR02198	rfaE bifunctional protein, domain I		1.10E-67

2558670527	DRAFT_01195	Locus_type		CDS	
2558670527	DRAFT_01195	Product_name		ADP-heptose synthase, bifunctional sugar kinase/adenylyltransferase	
2558670527	DRAFT_01195	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670527	DRAFT_01195	Coordinates		13458..14498(-)	
2558670527	DRAFT_01195	DNA_length		1041bp	
2558670527	DRAFT_01195	Protein_length		346aa	
2558670527	DRAFT_01195	GC		0.6	
2558670528	DRAFT_01196	Locus_type		CDS	
2558670528	DRAFT_01196	Product_name		hypothetical protein	
2558670528	DRAFT_01196	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670528	DRAFT_01196	Coordinates		14528..15049(-)	
2558670528	DRAFT_01196	DNA_length		522bp	
2558670528	DRAFT_01196	Protein_length		173aa	
2558670528	DRAFT_01196	GC		0.58	
2558670529	DRAFT_01197	pfam03176	MMPL		2.80E-44
2558670529	DRAFT_01197	pfam03176	MMPL		3.40E-44
2558670529	DRAFT_01197	Locus_type		CDS	
2558670529	DRAFT_01197	Product_name		Predicted drug exporters of the RND superfamily	
2558670529	DRAFT_01197	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670529	DRAFT_01197	Coordinates		15084..18026(-)	
2558670529	DRAFT_01197	DNA_length		2943bp	
2558670529	DRAFT_01197	Protein_length		980aa	
2558670529	DRAFT_01197	GC		0.59	
2558670529	DRAFT_01197	Transmembrane		Yes	
2558670530	DRAFT_01198	KEGG_module	M00545: Trans-cinnamate degradation, trans-cinnamate => 2-oxopent-4-enoate + fumarate		
2558670530	DRAFT_01198	KEGG_module	M00543: Biphenyl degradation, biphenyl => 2-oxopent-4-enoate + benzoate		
2558670530	DRAFT_01198	KEGG_module	M00539: Cumate degradation, p-cumate => 2-oxopent-4-enoate + 2-methylpropanoate		
2558670530	DRAFT_01198	KEGG_module	M00547: Benzene/toluene degradation, benzene => catechol / toluene => 3-methylcatechol		
2558670530	DRAFT_01198	COG_category	[P] Inorganic ion transport and metabolism		
2558670530	DRAFT_01198	COG_category	[R] General function prediction only		
2558670530	DRAFT_01198	COG2146	Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxyge		3.00E-16

2558670530	DRAFT_01198	pfam00355	Rieske		1.70E-13
2558670530	DRAFT_01198	KO:K05710	dioxygenase ferredoxin subunit		1.30E-14
2558670530	DRAFT_01198	Locus_type		CDS	
2558670530	DRAFT_01198	Product_name		Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxyg	
2558670530	DRAFT_01198	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670530	DRAFT_01198	Coordinates		18089..18400(-)	
2558670530	DRAFT_01198	DNA_length		312bp	
2558670530	DRAFT_01198	Protein_length		103aa	
2558670530	DRAFT_01198	GC		0.57	
2558670531	DRAFT_01199	pfam00483	NTP_transferase		6.70E-31
2558670531	DRAFT_01199	Locus_type		CDS	
2558670531	DRAFT_01199	Product_name		Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopol	
2558670531	DRAFT_01199	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670531	DRAFT_01199	Coordinates		18439..19134(-)	
2558670531	DRAFT_01199	DNA_length		696bp	
2558670531	DRAFT_01199	Protein_length		231aa	
2558670531	DRAFT_01199	GC		0.57	
2558670532	DRAFT_01200	Locus_type		CDS	
2558670532	DRAFT_01200	Product_name		hypothetical protein	
2558670532	DRAFT_01200	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670532	DRAFT_01200	Coordinates		19364..19798(-)	
2558670532	DRAFT_01200	DNA_length		435bp	
2558670532	DRAFT_01200	Protein_length		144aa	
2558670532	DRAFT_01200	GC		0.53	
2558670532	DRAFT_01200	Transmembrane		Yes	
2558670533	DRAFT_01201	Locus_type		CDS	
2558670533	DRAFT_01201	Product_name		hypothetical protein	
2558670533	DRAFT_01201	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23	
2558670533	DRAFT_01201	Coordinates		19937..20350(-)	
2558670533	DRAFT_01201	DNA_length		414bp	
2558670533	DRAFT_01201	Protein_length		137aa	

2558670533	DRAFT_01201	GC			0.5	
2558670533	DRAFT_01201	Transmembrane		Yes		
2558670534	DRAFT_01202	Locus_type		CDS		
2558670534	DRAFT_01202	Product_name		hypothetical protein		
2558670534	DRAFT_01202	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670534	DRAFT_01202	Coordinates		20355..20486(-)		
2558670534	DRAFT_01202	DNA_length		132bp		
2558670534	DRAFT_01202	Protein_length		43aa		
2558670534	DRAFT_01202	GC			0.52	
2558670535	DRAFT_01203	COG_category	[L] Replication, recombination and repair			
2558670535	DRAFT_01203	COG3316	Transposase and inactivated derivatives			6.00E-17
2558670535	DRAFT_01203	pfam13610	DDE_Tnp_IS240			7.30E-24
2558670535	DRAFT_01203	Locus_type		CDS		
2558670535	DRAFT_01203	Product_name		Transposase and inactivated derivatives		
2558670535	DRAFT_01203	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670535	DRAFT_01203	Coordinates		20555..21778(+)		
2558670535	DRAFT_01203	DNA_length		1224bp		
2558670535	DRAFT_01203	Protein_length		407aa		
2558670535	DRAFT_01203	GC			0.55	
2558670536	DRAFT_01204	Locus_type		CDS		
2558670536	DRAFT_01204	Product_name		hypothetical protein		
2558670536	DRAFT_01204	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670536	DRAFT_01204	Coordinates		21750..21959(-)		
2558670536	DRAFT_01204	DNA_length		210bp		
2558670536	DRAFT_01204	Protein_length		69aa		
2558670536	DRAFT_01204	GC			0.52	
2558670537	DRAFT_01205	Locus_type		CDS		
2558670537	DRAFT_01205	Product_name		hypothetical protein		
2558670537	DRAFT_01205	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670537	DRAFT_01205	Coordinates		22024..22290(-)		

2558670537	DRAFT_01205	DNA_length		267bp		
2558670537	DRAFT_01205	Protein_length		88aa		
2558670537	DRAFT_01205	GC			0.57	
2558670537	DRAFT_01205	Transmembrane		Yes		
2558670538	DRAFT_01206	Locus_type		CDS		
2558670538	DRAFT_01206	Product_name		hypothetical protein		
2558670538	DRAFT_01206	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670538	DRAFT_01206	Coordinates		22343..24739(-)		
2558670538	DRAFT_01206	DNA_length		2397bp		
2558670538	DRAFT_01206	Protein_length		798aa		
2558670538	DRAFT_01206	GC			0.52	
2558670538	DRAFT_01206	Transmembrane		Yes		
2558670539	DRAFT_01207	Locus_type		CDS		
2558670539	DRAFT_01207	Product_name		hypothetical protein		
2558670539	DRAFT_01207	Scaffold		DRAFT_contig_70_139_len_25505_read_count_420782.23		
2558670539	DRAFT_01207	Coordinates		25277..25420(+)		
2558670539	DRAFT_01207	DNA_length		144bp		
2558670539	DRAFT_01207	Protein_length		47aa		
2558670539	DRAFT_01207	GC			0.59	
2558670540	DRAFT_01208	Locus_type		CDS		
2558670540	DRAFT_01208	Product_name		hypothetical protein		
2558670540	DRAFT_01208	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670540	DRAFT_01208	Coordinates		100..774(-)		
2558670540	DRAFT_01208	DNA_length		675bp		
2558670540	DRAFT_01208	Protein_length		224aa		
2558670540	DRAFT_01208	GC			0.57	
2558670540	DRAFT_01208	Transmembrane		Yes		
2558670541	DRAFT_01209	COG_category	[S] Function unknown			
2558670541	DRAFT_01209	COG1814	Uncharacterized membrane protein			2.00E-14
2558670541	DRAFT_01209	pfam01988	VIT1			9.70E-11

2558670541	DRAFT_01209	Locus_type		CDS	
2558670541	DRAFT_01209	Product_name		Uncharacterized membrane protein	
2558670541	DRAFT_01209	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670541	DRAFT_01209	Coordinates		946..1839(-)	
2558670541	DRAFT_01209	DNA_length		894bp	
2558670541	DRAFT_01209	Protein_length		297aa	
2558670541	DRAFT_01209	GC			0.56
2558670541	DRAFT_01209	Transmembrane		Yes	

2558670542	DRAFT_01210	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558670542	DRAFT_01210	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558670542	DRAFT_01210	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2558670542	DRAFT_01210	IMG_pathway	495: L-leucine ligation to tRNA(Leu)		
2558670542	DRAFT_01210	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670542	DRAFT_01210	COG0495	Leucyl-tRNA synthetase		0.00E+00
2558670542	DRAFT_01210	pfam00133	tRNA-synt_1		8.80E-06
2558670542	DRAFT_01210	pfam00133	tRNA-synt_1		4.60E-35
2558670542	DRAFT_01210	pfam09334	tRNA-synt_1g		3.70E-08
2558670542	DRAFT_01210	pfam08264	Anticodon_1		4.90E-21
2558670542	DRAFT_01210	EC:6.1.1.4	Leucine--tRNA ligase.		
2558670542	DRAFT_01210	TIGR00395	leucyl-tRNA synthetase, archaeal and cytosolic family		0.00E+00
2558670542	DRAFT_01210	KO:K01869	leucyl-tRNA synthetase [EC:6.1.1.4]		0.00E+00
2558670542	DRAFT_01210	ITERM:00405	leucyl-tRNA synthetase (EC 6.1.1.4)		
2558670542	DRAFT_01210	Locus_type		CDS	
2558670542	DRAFT_01210	Product_name		leucyl-tRNA synthetase (EC 6.1.1.4)	
2558670542	DRAFT_01210	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670542	DRAFT_01210	Coordinates		1939..4770(-)	
2558670542	DRAFT_01210	DNA_length		2832bp	
2558670542	DRAFT_01210	Protein_length		943aa	
2558670542	DRAFT_01210	GC			0.6

2558670543	DRAFT_01211	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2558670543	DRAFT_01211	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558670543	DRAFT_01211	Metacyc	TRNA-CHARGING-PWY: tRNA charging		

2558670543	DRAFT_01211	IMG_pathway	487: L-alanine ligation to tRNA(Ala)			
2558670543	DRAFT_01211	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670543	DRAFT_01211	COG0013	Alanyl-tRNA synthetase			0.00E+00
2558670543	DRAFT_01211	pfam02272	DHHA1			1.30E-04
2558670543	DRAFT_01211	pfam07973	tRNA_SAD			5.50E-14
2558670543	DRAFT_01211	pfam01411	tRNA-synt_2c			2.70E-79
2558670543	DRAFT_01211	EC:6.1.1.7	Alanine--tRNA ligase.			
2558670543	DRAFT_01211	TIGR00344	alanine--tRNA ligase			0.00E+00
2558670543	DRAFT_01211	TIGR03683	alanyl-tRNA synthetase			0.00E+00
2558670543	DRAFT_01211	KO:K01872	alanyl-tRNA synthetase [EC:6.1.1.7]			0.00E+00
2558670543	DRAFT_01211	ITERM:00391	alanyl-tRNA synthetase (EC 6.1.1.7)			
2558670543	DRAFT_01211	Locus_type		CDS		
2558670543	DRAFT_01211	Product_name		alanyl-tRNA synthetase (EC 6.1.1.7)		
2558670543	DRAFT_01211	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670543	DRAFT_01211	Coordinates		4767..7598(-)		
2558670543	DRAFT_01211	DNA_length		2832bp		
2558670543	DRAFT_01211	Protein_length		943aa		
2558670543	DRAFT_01211	GC			0.57	
2558670544	DRAFT_01212	KEGG_module	M00179: Ribosome, archaea			
2558670544	DRAFT_01212	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670544	DRAFT_01212	COG2058	Ribosomal protein L12E/L44/L45/RPP1/RPP2			1.00E-10
2558670544	DRAFT_01212	pfam00428	Ribosomal_60s			1.80E-15
2558670544	DRAFT_01212	TIGR03685	50S ribosomal protein L12P			5.90E-37
2558670544	DRAFT_01212	KO:K02869	large subunit ribosomal protein L12			2.80E-28
2558670544	DRAFT_01212	Locus_type		CDS		
2558670544	DRAFT_01212	Product_name		50S ribosomal protein L12P		
2558670544	DRAFT_01212	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670544	DRAFT_01212	Coordinates		7733..8098(+)		
2558670544	DRAFT_01212	DNA_length		366bp		
2558670544	DRAFT_01212	Protein_length		121aa		
2558670544	DRAFT_01212	GC			0.59	
2558670545	DRAFT_01213	KEGG_module	M00178: Ribosome, bacteria			

2558670545	DRAFT_01213	KEGG_module	M00179: Ribosome, archaea			
2558670545	DRAFT_01213	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670545	DRAFT_01213	COG0244	Ribosomal protein L10			1.00E-19
2558670545	DRAFT_01213	pfam00466	Ribosomal_L10			1.80E-20
2558670545	DRAFT_01213	KO:K02864	large subunit ribosomal protein L10			0.00E+00
2558670545	DRAFT_01213	ITERM:00276	LSU ribosomal protein L10P			
2558670545	DRAFT_01213	Locus_type		CDS		
2558670545	DRAFT_01213	Product_name		LSU ribosomal protein L10P		
2558670545	DRAFT_01213	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670545	DRAFT_01213	Coordinates		8117..8989(-)		
2558670545	DRAFT_01213	DNA_length		873bp		
2558670545	DRAFT_01213	Protein_length		290aa		
2558670545	DRAFT_01213	GC			0.6	
2558670546	DRAFT_01214	KEGG_module	M00178: Ribosome, bacteria			
2558670546	DRAFT_01214	KEGG_module	M00179: Ribosome, archaea			
2558670546	DRAFT_01214	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670546	DRAFT_01214	COG0081	Ribosomal protein L1			1.00E-32
2558670546	DRAFT_01214	pfam00687	Ribosomal_L1			3.70E-42
2558670546	DRAFT_01214	KO:K02863	large subunit ribosomal protein L1			0.00E+00
2558670546	DRAFT_01214	Locus_type		CDS		
2558670546	DRAFT_01214	Product_name		Ribosomal protein L1		
2558670546	DRAFT_01214	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670546	DRAFT_01214	Coordinates		8991..9641(-)		
2558670546	DRAFT_01214	DNA_length		651bp		
2558670546	DRAFT_01214	Protein_length		216aa		
2558670546	DRAFT_01214	GC			0.6	
2558670547	DRAFT_01215	KEGG_module	M00179: Ribosome, archaea			
2558670547	DRAFT_01215	KEGG_module	M00178: Ribosome, bacteria			
2558670547	DRAFT_01215	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670547	DRAFT_01215	COG0080	Ribosomal protein L11			3.00E-36
2558670547	DRAFT_01215	pfam00298	Ribosomal_L11			4.50E-19
2558670547	DRAFT_01215	pfam03946	Ribosomal_L11_N			9.80E-22

2558670547	DRAFT_01215	KO:K02867	large subunit ribosomal protein L11		0.00E+00
2558670547	DRAFT_01215	Locus_type		CDS	
2558670547	DRAFT_01215	Product_name		LSU ribosomal protein L11P	
2558670547	DRAFT_01215	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670547	DRAFT_01215	Coordinates		9710..10192(-)	
2558670547	DRAFT_01215	DNA_length		483bp	
2558670547	DRAFT_01215	Protein_length		160aa	
2558670547	DRAFT_01215	GC		0.59	

2558670548	DRAFT_01216	COG_category	[K] Transcription		
2558670548	DRAFT_01216	COG0250	Transcription antiterminator		1.00E-11
2558670548	DRAFT_01216	pfam00467	KOW		2.40E-07
2558670548	DRAFT_01216	pfam03439	Spt5-NGN		4.10E-20
2558670548	DRAFT_01216	TIGR00405	ribosomal protein L24p/L26e, archaeal		2.00E-41
2558670548	DRAFT_01216	KO:K02601	transcriptional antiterminator NusG		1.90E-32
2558670548	DRAFT_01216	Locus_type		CDS	
2558670548	DRAFT_01216	Product_name		ribosomal protein L24p/L26e, archaeal	
2558670548	DRAFT_01216	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670548	DRAFT_01216	Coordinates		10389..10880(-)	
2558670548	DRAFT_01216	DNA_length		492bp	
2558670548	DRAFT_01216	Protein_length		163aa	
2558670548	DRAFT_01216	GC		0.58	

2558670549	DRAFT_01217	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport		
2558670549	DRAFT_01217	COG2443	Preprotein translocase subunit Sss1		4.00E-06
2558670549	DRAFT_01217	TIGR00327	protein translocase SEC61 complex gamma subunit, archaeal and euka		5.20E-15
2558670549	DRAFT_01217	Locus_type		CDS	
2558670549	DRAFT_01217	Product_name		protein translocase SEC61 complex gamma subunit, archaeal and euk	
2558670549	DRAFT_01217	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670549	DRAFT_01217	Coordinates		10942..11109(-)	
2558670549	DRAFT_01217	DNA_length		168bp	
2558670549	DRAFT_01217	Protein_length		55aa	
2558670549	DRAFT_01217	GC		0.5	
2558670549	DRAFT_01217	Transmembrane		Yes	

2558670550	DRAFT_01218	COG_category	[S] Function unknown			
2558670550	DRAFT_01218	COG1650	Uncharacterized protein conserved in archaea			3.00E-53
2558670550	DRAFT_01218	pfam04414	tRNA_deacylase			3.00E-61
2558670550	DRAFT_01218	KO:K09716	hypothetical protein			0.00E+00
2558670550	DRAFT_01218	Locus_type		CDS		
2558670550	DRAFT_01218	Product_name		Uncharacterized protein conserved in archaea		
2558670550	DRAFT_01218	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670550	DRAFT_01218	Coordinates		11215..12042(+)		
2558670550	DRAFT_01218	DNA_length		828bp		
2558670550	DRAFT_01218	Protein_length		275aa		
2558670550	DRAFT_01218	GC			0.59	
2558670551	DRAFT_01219	KEGG_module	M00335: Sec (secretion) system			
2558670551	DRAFT_01219	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2558670551	DRAFT_01219	COG0552	Signal recognition particle GTPase			8.00E-80
2558670551	DRAFT_01219	pfam00448	SRP54			5.20E-69
2558670551	DRAFT_01219	pfam02881	SRP54_N			1.00E-05
2558670551	DRAFT_01219	TIGR00064	signal recognition particle-docking protein FtsY			3.60E-93
2558670551	DRAFT_01219	KO:K03110	fused signal recognition particle receptor			0.00E+00
2558670551	DRAFT_01219	Locus_type		CDS		
2558670551	DRAFT_01219	Product_name		signal recognition particle-docking protein FtsY		
2558670551	DRAFT_01219	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670551	DRAFT_01219	Coordinates		12119..13030(-)		
2558670551	DRAFT_01219	DNA_length		912bp		
2558670551	DRAFT_01219	Protein_length		303aa		
2558670551	DRAFT_01219	GC			0.6	
2558670552	DRAFT_01220	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670552	DRAFT_01220	COG1730	Predicted prefoldin, molecular chaperone implicated in de novo protei			2.00E-08
2558670552	DRAFT_01220	pfam02996	Prefoldin			1.60E-14
2558670552	DRAFT_01220	TIGR00293	prefoldin, archaeal alpha subunit/eukaryotic subunit 5			2.00E-19
2558670552	DRAFT_01220	KO:K04797	prefoldin alpha subunit			2.80E-11
2558670552	DRAFT_01220	Locus_type		CDS		

2558670552	DRAFT_01220	Product_name		prefoldin, archaeal alpha subunit/eukaryotic subunit 5		
2558670552	DRAFT_01220	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670552	DRAFT_01220	Coordinates		13038..13469(-)		
2558670552	DRAFT_01220	DNA_length		432bp		
2558670552	DRAFT_01220	Protein_length		143aa		
2558670552	DRAFT_01220	GC			0.63	

2558670553	DRAFT_01221	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670553	DRAFT_01221	COG1976	Translation initiation factor 6 (eIF-6)			7.00E-51
2558670553	DRAFT_01221	pfam01912	eIF-6			5.00E-62
2558670553	DRAFT_01221	TIGR00323	translation initiation factor eIF-6, putative			5.40E-59
2558670553	DRAFT_01221	KO:K03264	translation initiation factor 6			0.00E+00
2558670553	DRAFT_01221	ITERM:01949	translation initiation factor 6 (aeIF-6)			
2558670553	DRAFT_01221	Locus_type		CDS		
2558670553	DRAFT_01221	Product_name		translation initiation factor 6 (aeIF-6)		
2558670553	DRAFT_01221	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670553	DRAFT_01221	Coordinates		13489..14154(-)		
2558670553	DRAFT_01221	DNA_length		666bp		
2558670553	DRAFT_01221	Protein_length		221aa		
2558670553	DRAFT_01221	GC			0.6	

2558670554	DRAFT_01222	KEGG_module	M00179: Ribosome, archaea			
2558670554	DRAFT_01222	KEGG_module	M00177: Ribosome, eukaryotes			
2558670554	DRAFT_01222	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670554	DRAFT_01222	COG2097	Ribosomal protein L31E			6.00E-14
2558670554	DRAFT_01222	pfam01198	Ribosomal_L31e			4.10E-22
2558670554	DRAFT_01222	KO:K02910	large subunit ribosomal protein L31e			7.80E-13
2558670554	DRAFT_01222	Locus_type		CDS		
2558670554	DRAFT_01222	Product_name		Ribosomal protein L31E		
2558670554	DRAFT_01222	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670554	DRAFT_01222	Coordinates		14158..14451(-)		
2558670554	DRAFT_01222	DNA_length		294bp		
2558670554	DRAFT_01222	Protein_length		97aa		
2558670554	DRAFT_01222	GC			0.56	

2558670555	DRAFT_01223	KEGG_module	M00177: Ribosome, eukaryotes			
2558670555	DRAFT_01223	KEGG_module	M00179: Ribosome, archaea			
2558670555	DRAFT_01223	pfam00832	Ribosomal_L39			2.50E-14
2558670555	DRAFT_01223	KO:K02924	large subunit ribosomal protein L39e			2.40E-08
2558670555	DRAFT_01223	ITERM:00272	LSU ribosomal protein L39E			
2558670555	DRAFT_01223	Locus_type		CDS		
2558670555	DRAFT_01223	Product_name		LSU ribosomal protein L39E		
2558670555	DRAFT_01223	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670555	DRAFT_01223	Coordinates		14458..14616(-)		
2558670555	DRAFT_01223	DNA_length		159bp		
2558670555	DRAFT_01223	Protein_length		52aa		
2558670555	DRAFT_01223	GC			0.55	

2558670556	DRAFT_01224	pfam01984	dsDNA_bind			5.90E-22
2558670556	DRAFT_01224	KO:K06875	programmed cell death protein 5			2.20E-17
2558670556	DRAFT_01224	ITERM:01948	DNA-binding TFAR19-related protein			
2558670556	DRAFT_01224	Locus_type		CDS		
2558670556	DRAFT_01224	Product_name		DNA-binding TFAR19-related protein		
2558670556	DRAFT_01224	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670556	DRAFT_01224	Coordinates		14618..14893(-)		
2558670556	DRAFT_01224	DNA_length		276bp		
2558670556	DRAFT_01224	Protein_length		91aa		
2558670556	DRAFT_01224	GC			0.59	

2558670557	DRAFT_01225	KEGG_module	M00177: Ribosome, eukaryotes			
2558670557	DRAFT_01225	KEGG_module	M00179: Ribosome, archaea			
2558670557	DRAFT_01225	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670557	DRAFT_01225	COG2238	Ribosomal protein S19E (S16A)			2.00E-45
2558670557	DRAFT_01225	pfam01090	Ribosomal_S19e			8.40E-49
2558670557	DRAFT_01225	KO:K02966	small subunit ribosomal protein S19e			2.30E-40
2558670557	DRAFT_01225	Locus_type		CDS		
2558670557	DRAFT_01225	Product_name		Ribosomal protein S19E (S16A)		
2558670557	DRAFT_01225	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		

2558670557	DRAFT_01225	Coordinates		14896..15348(-)		
2558670557	DRAFT_01225	DNA_length		453bp		
2558670557	DRAFT_01225	Protein_length		150aa		
2558670557	DRAFT_01225	GC			0.61	
2558670558	DRAFT_01226	Metacyc	PWY0-1479: tRNA processing			
2558670558	DRAFT_01226	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670558	DRAFT_01226	COG2023	RNase P subunit RPR2			9.00E-10
2558670558	DRAFT_01226	pfam04032	Rpr2			3.40E-13
2558670558	DRAFT_01226	EC:3.1.26.5	Ribonuclease P.			
2558670558	DRAFT_01226	KO:K03540	ribonuclease P protein subunit RPR2 [EC:3.1.26.5]			1.00E-12
2558670558	DRAFT_01226	Locus_type		CDS		
2558670558	DRAFT_01226	Product_name		RNase P subunit RPR2		
2558670558	DRAFT_01226	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670558	DRAFT_01226	Coordinates		15355..15735(-)		
2558670558	DRAFT_01226	DNA_length		381bp		
2558670558	DRAFT_01226	Protein_length		126aa		
2558670558	DRAFT_01226	GC			0.61	
2558670559	DRAFT_01227	COG_category	[S] Function unknown			
2558670559	DRAFT_01227	COG1756	Uncharacterized conserved protein			3.00E-44
2558670559	DRAFT_01227	pfam03587	EMG1			1.90E-38
2558670559	DRAFT_01227	KO:K14568	essential for mitotic growth 1			4.20E-45
2558670559	DRAFT_01227	Locus_type		CDS		
2558670559	DRAFT_01227	Product_name		Uncharacterized conserved protein		
2558670559	DRAFT_01227	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670559	DRAFT_01227	Coordinates		15769..16434(+)		
2558670559	DRAFT_01227	DNA_length		666bp		
2558670559	DRAFT_01227	Protein_length		221aa		
2558670559	DRAFT_01227	GC			0.64	
2558670560	DRAFT_01228	Locus_type		CDS		
2558670560	DRAFT_01228	Product_name		hypothetical protein		
2558670560	DRAFT_01228	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		

2558670560	DRAFT_01228	Coordinates		16742..17083(+)		
2558670560	DRAFT_01228	DNA_length		342bp		
2558670560	DRAFT_01228	Protein_length		113aa		
2558670560	DRAFT_01228	GC			0.52	
2558670561	DRAFT_01229	pfam12847	Methyltransf_18			2.80E-15
2558670561	DRAFT_01229	Locus_type		CDS		
2558670561	DRAFT_01229	Product_name		Methyltransferase domain		
2558670561	DRAFT_01229	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670561	DRAFT_01229	Coordinates		17416..18276(+)		
2558670561	DRAFT_01229	DNA_length		861bp		
2558670561	DRAFT_01229	Protein_length		286aa		
2558670561	DRAFT_01229	GC			0.51	
2558670562	DRAFT_01230	Metacyc	PWY-6575: juvenile hormone III biosynthesis I			
2558670562	DRAFT_01230	Metacyc	PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I			
2558670562	DRAFT_01230	Metacyc	PWY-7206: pyrimidine deoxyribonucleotides dephosphorylation			
2558670562	DRAFT_01230	Metacyc	PWY-6502: oxidized GTP and dGTP detoxification			
2558670562	DRAFT_01230	Metacyc	PWY-6797: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (archaea)			
2558670562	DRAFT_01230	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis			
2558670562	DRAFT_01230	COG_category	[F] Nucleotide transport and metabolism			
2558670562	DRAFT_01230	COG1051	ADP-ribose pyrophosphatase			1.00E-10
2558670562	DRAFT_01230	pfam00293	NUDIX			5.80E-22
2558670562	DRAFT_01230	EC:3.6.1.-	Hydrolases. Acting on acid anhydrides. In phosphorous-containing anhydrides.			
2558670562	DRAFT_01230	KO:K03574	7,8-dihydro-8-oxoguanine triphosphatase [EC:3.6.1.-]			2.80E-11
2558670562	DRAFT_01230	Locus_type		CDS		
2558670562	DRAFT_01230	Product_name		ADP-ribose pyrophosphatase		
2558670562	DRAFT_01230	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670562	DRAFT_01230	Coordinates		18284..18709(+)		
2558670562	DRAFT_01230	DNA_length		426bp		
2558670562	DRAFT_01230	Protein_length		141aa		
2558670562	DRAFT_01230	GC			0.56	
2558670563	DRAFT_01231	Metacyc	NAD-BIOSYNTHESIS-III: NAD biosynthesis III			

2558670563	DRAFT_01231	Metacyc	PWY3O-4106: NAD salvage pathway III		
2558670563	DRAFT_01231	COG_category	[H] Coenzyme transport and metabolism		
2558670563	DRAFT_01231	COG1056	Nicotinamide mononucleotide adenylyltransferase		1.00E-19
2558670563	DRAFT_01231	pfam01467	CTP_transf_2		6.60E-13
2558670563	DRAFT_01231	EC:2.7.7.1	Nicotinamide-nucleotide adenylyltransferase.		
2558670563	DRAFT_01231	TIGR00125	cytidyltransferase-like domain		5.10E-18
2558670563	DRAFT_01231	TIGR01527	nicotinamide-nucleotide adenylyltransferase		3.20E-32
2558670563	DRAFT_01231	KO:K00952	nicotinamide-nucleotide adenylyltransferase [EC:2.7.7.1]		3.00E-20
2558670563	DRAFT_01231	Locus_type		CDS	
2558670563	DRAFT_01231	Product_name		cytidyltransferase-like domain	
2558670563	DRAFT_01231	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670563	DRAFT_01231	Coordinates		18787..19296(-)	
2558670563	DRAFT_01231	DNA_length		510bp	
2558670563	DRAFT_01231	Protein_length		169aa	
2558670563	DRAFT_01231	GC		0.48	

2558670564	DRAFT_01232	COG_category	[I] Lipid transport and metabolism		
2558670564	DRAFT_01232	COG1443	Isopentenyldiphosphate isomerase		2.00E-16
2558670564	DRAFT_01232	pfam00293	NUDIX		2.40E-16
2558670564	DRAFT_01232	Locus_type		CDS	
2558670564	DRAFT_01232	Product_name		Isopentenyldiphosphate isomerase	
2558670564	DRAFT_01232	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670564	DRAFT_01232	Coordinates		19361..19852(-)	
2558670564	DRAFT_01232	DNA_length		492bp	
2558670564	DRAFT_01232	Protein_length		163aa	
2558670564	DRAFT_01232	GC		0.56	

2558670565	DRAFT_01233	pfam08241	Methyltransf_11		1.10E-12
2558670565	DRAFT_01233	Locus_type		CDS	
2558670565	DRAFT_01233	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	
2558670565	DRAFT_01233	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670565	DRAFT_01233	Coordinates		19990..20811(-)	
2558670565	DRAFT_01233	DNA_length		822bp	
2558670565	DRAFT_01233	Protein_length		273aa	

2558670565	DRAFT_01233	GC			0.54	
2558670566	DRAFT_01234	COG_category	[R] General function prediction only			
2558670566	DRAFT_01234	COG0456	Acetyltransferases			6.00E-09
2558670566	DRAFT_01234	pfam00583	Acetyltransf_1			1.00E-14
2558670566	DRAFT_01234	Locus_type		CDS		
2558670566	DRAFT_01234	Product_name		Acetyltransferases		
2558670566	DRAFT_01234	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670566	DRAFT_01234	Coordinates		20911..21375(-)		
2558670566	DRAFT_01234	DNA_length		465bp		
2558670566	DRAFT_01234	Protein_length		154aa		
2558670566	DRAFT_01234	GC			0.57	
2558670567	DRAFT_01235	Locus_type		CDS		
2558670567	DRAFT_01235	Product_name		hypothetical protein		
2558670567	DRAFT_01235	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670567	DRAFT_01235	Coordinates		21569..21961(-)		
2558670567	DRAFT_01235	DNA_length		393bp		
2558670567	DRAFT_01235	Protein_length		130aa		
2558670567	DRAFT_01235	GC			0.5	
2558670567	DRAFT_01235	Transmembrane		Yes		
2558670568	DRAFT_01236	pfam08241	Methyltransf_11			5.40E-13
2558670568	DRAFT_01236	Locus_type		CDS		
2558670568	DRAFT_01236	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2558670568	DRAFT_01236	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24		
2558670568	DRAFT_01236	Coordinates		22327..23103(+)		
2558670568	DRAFT_01236	DNA_length		777bp		
2558670568	DRAFT_01236	Protein_length		258aa		
2558670568	DRAFT_01236	GC			0.59	
2558670569	DRAFT_01237	pfam00583	Acetyltransf_1			1.20E-12
2558670569	DRAFT_01237	Locus_type		CDS		
2558670569	DRAFT_01237	Product_name		Acetyltransferases		

2558670569	DRAFT_01237	Scaffold		DRAFT_contig_70_158_len_24011_read_count_400064.24	
2558670569	DRAFT_01237	Coordinates		23272..23745(+)	
2558670569	DRAFT_01237	DNA_length		474bp	
2558670569	DRAFT_01237	Protein_length		157aa	
2558670569	DRAFT_01237	GC		0.55	
2558670570	DRAFT_01238	pfam12697	Abhydrolase_6		6.70E-19
2558670570	DRAFT_01238	Locus_type		CDS	
2558670570	DRAFT_01238	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super	
2558670570	DRAFT_01238	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670570	DRAFT_01238	Coordinates		2..439(-)	
2558670570	DRAFT_01238	DNA_length		438bp	
2558670570	DRAFT_01238	Protein_length		146aa	
2558670570	DRAFT_01238	GC		0.6	
2558670571	DRAFT_01239	COG_category	[E] Amino acid transport and metabolism		
2558670571	DRAFT_01239	COG1703	Putative periplasmic protein kinase ArgK and related GTPases of G3E fa		8.00E-70
2558670571	DRAFT_01239	pfam03308	ArgK		6.10E-84
2558670571	DRAFT_01239	EC:2.7.-	Transferases. Transferring phosphorous-containing groups.		
2558670571	DRAFT_01239	TIGR00750	LAO/AO transport system ATPase		9.80E-93
2558670571	DRAFT_01239	KO:K07588	LAO/AO transport system kinase [EC:2.7.-.-]		0.00E+00
2558670571	DRAFT_01239	Locus_type		CDS	
2558670571	DRAFT_01239	Product_name		LAO/AO transport system ATPase	
2558670571	DRAFT_01239	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670571	DRAFT_01239	Coordinates		507..1442(-)	
2558670571	DRAFT_01239	DNA_length		936bp	
2558670571	DRAFT_01239	Protein_length		311aa	
2558670571	DRAFT_01239	GC		0.61	
2558670572	DRAFT_01240	KEGG_module	M00376: 3-Hydroxypropionate bicycle		
2558670572	DRAFT_01240	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle		
2558670572	DRAFT_01240	Metacyc	PWY0-43: conversion of succinate to propionate		
2558670572	DRAFT_01240	Metacyc	P108-PWY: pyruvate fermentation to propionate I		
2558670572	DRAFT_01240	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle		

2558670572	DRAFT_01240	Metacyc	PROPIONMET-PWY: methylmalonyl pathway		
2558670572	DRAFT_01240	Metacyc	PWY-6728: methylaspartate cycle		
2558670572	DRAFT_01240	Metacyc	PWY-5743: 3-hydroxypropionate cycle		
2558670572	DRAFT_01240	IMG_pathway	370: Oxaloacetate conversion to propionate via methylmalonyl-CoA		
2558670572	DRAFT_01240	IMG_pathway	525: Hydroxypropionate cycle		
2558670572	DRAFT_01240	IMG_pathway	596: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2558670572	DRAFT_01240	IMG_pathway	837: Propionyl-CoA conversion to succinyl-CoA via methylmalonyl pathway		
2558670572	DRAFT_01240	IMG_pathway	962: Glyoxylate from acetyl-CoA via ethylmalonyl-CoA pathway		
2558670572	DRAFT_01240	COG_category	[I] Lipid transport and metabolism		
2558670572	DRAFT_01240	COG1884	Methylmalonyl-CoA mutase, N-terminal domain/subunit		0.00E+00
2558670572	DRAFT_01240	pfam01642	MM_CoA_mutase		0.00E+00
2558670572	DRAFT_01240	EC:5.4.99.2	Methylmalonyl-CoA mutase.		
2558670572	DRAFT_01240	TIGR00641	methylmalonyl-CoA mutase N-terminal domain		0.00E+00
2558670572	DRAFT_01240	KO:K01848	methylmalonyl-CoA mutase, N-terminal domain [EC:5.4.99.2]		0.00E+00
2558670572	DRAFT_01240	ITERM:01588	methylmalonyl-CoA mutase (EC 5.4.99.2)		
2558670572	DRAFT_01240	Locus_type		CDS	
2558670572	DRAFT_01240	Product_name		methylmalonyl-CoA mutase (EC 5.4.99.2)	
2558670572	DRAFT_01240	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670572	DRAFT_01240	Coordinates		1487..3262(+)	
2558670572	DRAFT_01240	DNA_length		1776bp	
2558670572	DRAFT_01240	Protein_length		591aa	
2558670572	DRAFT_01240	GC		0.58	
2558670573	DRAFT_01241	KEGG_module	M00376: 3-Hydroxypropionate bicycle		
2558670573	DRAFT_01241	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle		
2558670573	DRAFT_01241	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2558670573	DRAFT_01241	Metacyc	PWY-5743: 3-hydroxypropionate cycle		
2558670573	DRAFT_01241	Metacyc	P108-PWY: pyruvate fermentation to propionate I		
2558670573	DRAFT_01241	Metacyc	PROPIONMET-PWY: methylmalonyl pathway		
2558670573	DRAFT_01241	Metacyc	PWY-6728: methylaspartate cycle		
2558670573	DRAFT_01241	Metacyc	PWY0-43: conversion of succinate to propionate		
2558670573	DRAFT_01241	COG_category	[I] Lipid transport and metabolism		
2558670573	DRAFT_01241	COG2185	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-bi		6.00E-36
2558670573	DRAFT_01241	pfam02310	B12-binding		1.10E-18

2558670573	DRAFT_01241	EC:5.4.99.2	Methylmalonyl-CoA mutase.			
2558670573	DRAFT_01241	TIGR00640	methylmalonyl-CoA mutase C-terminal domain			3.90E-52
2558670573	DRAFT_01241	KO:K01849	methylmalonyl-CoA mutase, C-terminal domain [EC:5.4.99.2]			6.60E-44
2558670573	DRAFT_01241	Locus_type		CDS		
2558670573	DRAFT_01241	Product_name		methylmalonyl-CoA mutase C-terminal domain		
2558670573	DRAFT_01241	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670573	DRAFT_01241	Coordinates		3238..3738(+)		
2558670573	DRAFT_01241	DNA_length		501bp		
2558670573	DRAFT_01241	Protein_length		166aa		
2558670573	DRAFT_01241	GC			0.59	
2558670574	DRAFT_01242	COG_category	[I] Lipid transport and metabolism			
2558670574	DRAFT_01242	COG1960	Acyl-CoA dehydrogenases			1.00E-69
2558670574	DRAFT_01242	pfam02771	Acyl-CoA_dh_N			8.90E-20
2558670574	DRAFT_01242	pfam00441	Acyl-CoA_dh_1			4.30E-37
2558670574	DRAFT_01242	pfam02770	Acyl-CoA_dh_M			8.00E-14
2558670574	DRAFT_01242	EC:1.3.99.32	Glutaryl-CoA dehydrogenase (non-decarboxylating).			
2558670574	DRAFT_01242	KO:K16173	glutaryl-CoA dehydrogenase (non-decarboxylating) [EC:1.3.99.32]			0.00E+00
2558670574	DRAFT_01242	Locus_type		CDS		
2558670574	DRAFT_01242	Product_name		Acyl-CoA dehydrogenases		
2558670574	DRAFT_01242	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670574	DRAFT_01242	Coordinates		3743..4963(+)		
2558670574	DRAFT_01242	DNA_length		1221bp		
2558670574	DRAFT_01242	Protein_length		406aa		
2558670574	DRAFT_01242	GC			0.58	
2558670575	DRAFT_01243	Locus_type		CDS		
2558670575	DRAFT_01243	Product_name		hypothetical protein		
2558670575	DRAFT_01243	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670575	DRAFT_01243	Coordinates		5060..5290(+)		
2558670575	DRAFT_01243	DNA_length		231bp		
2558670575	DRAFT_01243	Protein_length		76aa		
2558670575	DRAFT_01243	GC			0.62	

2558670576	DRAFT_01244	COG_category	[C] Energy production and conversion			
2558670576	DRAFT_01244	COG0644	Dehydrogenases (flavoproteins)			2.00E-55
2558670576	DRAFT_01244	pfam01266	DAO			6.30E-15
2558670576	DRAFT_01244	EC:1.5.5.-	Oxidoreductases. Acting on the CH-NH group of donors. With a quinone or similar compound			
2558670576	DRAFT_01244	KO:K00313	electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]			0.00E+00
2558670576	DRAFT_01244	Locus_type		CDS		
2558670576	DRAFT_01244	Product_name		Dehydrogenases (flavoproteins)		
2558670576	DRAFT_01244	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670576	DRAFT_01244	Coordinates		5251..6612(+)		
2558670576	DRAFT_01244	DNA_length		1362bp		
2558670576	DRAFT_01244	Protein_length		453aa		
2558670576	DRAFT_01244	GC			0.58	

2558670577	DRAFT_01245	COG_category	[C] Energy production and conversion			
2558670577	DRAFT_01245	COG2440	Ferredoxin-like protein			2.00E-20
2558670577	DRAFT_01245	KO:K03855	ferredoxin like protein			3.40E-20
2558670577	DRAFT_01245	Locus_type		CDS		
2558670577	DRAFT_01245	Product_name		Ferredoxin-like protein		
2558670577	DRAFT_01245	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670577	DRAFT_01245	Coordinates		6609..6893(+)		
2558670577	DRAFT_01245	DNA_length		285bp		
2558670577	DRAFT_01245	Protein_length		94aa		
2558670577	DRAFT_01245	GC			0.6	

2558670578	DRAFT_01246	COG_category	[C] Energy production and conversion			
2558670578	DRAFT_01246	COG2086	Electron transfer flavoprotein, beta subunit			6.00E-54
2558670578	DRAFT_01246	pfam01012	ETF			2.30E-40
2558670578	DRAFT_01246	KO:K03521	electron transfer flavoprotein beta subunit			0.00E+00
2558670578	DRAFT_01246	ITERM:01639	electron transfer flavoprotein beta subunit			
2558670578	DRAFT_01246	Locus_type		CDS		
2558670578	DRAFT_01246	Product_name		electron transfer flavoprotein beta subunit		
2558670578	DRAFT_01246	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670578	DRAFT_01246	Coordinates		6931..7704(+)		
2558670578	DRAFT_01246	DNA_length		774bp		

2558670578	DRAFT_01246	Protein_length		257aa		
2558670578	DRAFT_01246	GC			0.61	
2558670579	DRAFT_01247	COG_category	[C] Energy production and conversion			
2558670579	DRAFT_01247	COG2025	Electron transfer flavoprotein, alpha subunit			1.00E-81
2558670579	DRAFT_01247	pfam01012	ETF			3.80E-40
2558670579	DRAFT_01247	pfam00766	ETF_alpha			5.20E-30
2558670579	DRAFT_01247	KO:K03522	electron transfer flavoprotein alpha subunit			0.00E+00
2558670579	DRAFT_01247	ITERM:01638	electron transfer flavoprotein alpha subunit apoprotein			
2558670579	DRAFT_01247	Locus_type		CDS		
2558670579	DRAFT_01247	Product_name		electron transfer flavoprotein alpha subunit apoprotein		
2558670579	DRAFT_01247	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670579	DRAFT_01247	Coordinates		7709..8692(+)		
2558670579	DRAFT_01247	DNA_length		984bp		
2558670579	DRAFT_01247	Protein_length		327aa		
2558670579	DRAFT_01247	GC			0.6	
2558670580	DRAFT_01248	KEGG_module	M00013: Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA			
2558670580	DRAFT_01248	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA			
2558670580	DRAFT_01248	KEGG_module	M00087: beta-Oxidation			
2558670580	DRAFT_01248	Metacyc	PWY-7094: fatty acid salvage			
2558670580	DRAFT_01248	COG_category	[I] Lipid transport and metabolism			
2558670580	DRAFT_01248	COG1960	Acyl-CoA dehydrogenases			4.00E-57
2558670580	DRAFT_01248	pfam00441	Acyl-CoA_dh_1			2.30E-31
2558670580	DRAFT_01248	pfam02770	Acyl-CoA_dh_M			1.80E-10
2558670580	DRAFT_01248	pfam02771	Acyl-CoA_dh_N			2.80E-27
2558670580	DRAFT_01248	EC:1.3.8.7	Medium-chain acyl-CoA dehydrogenase.			
2558670580	DRAFT_01248	KO:K00249	acyl-CoA dehydrogenase [EC:1.3.8.7]			0.00E+00
2558670580	DRAFT_01248	Locus_type		CDS		
2558670580	DRAFT_01248	Product_name		Acyl-CoA dehydrogenases		
2558670580	DRAFT_01248	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670580	DRAFT_01248	Coordinates		8762..10003(+)		
2558670580	DRAFT_01248	DNA_length		1242bp		
2558670580	DRAFT_01248	Protein_length		413aa		

2558670580	DRAFT_01248	GC			0.59	

2558670581	DRAFT_01249	Metacyc	ASPARAGINESYN-PWY: asparagine biosynthesis II			
2558670581	DRAFT_01249	IMG_pathway	107: Asparagine synthesis using NH3			
2558670581	DRAFT_01249	COG_category	[E] Amino acid transport and metabolism			
2558670581	DRAFT_01249	COG2502	Asparagine synthetase A			8.00E-92
2558670581	DRAFT_01249	pfam03590	AsnA			5.00E-69
2558670581	DRAFT_01249	EC:6.3.1.1	Aspartate--ammonia ligase.			
2558670581	DRAFT_01249	TIGR00669	aspartate--ammonia ligase, AsnA-type			9.20E-99
2558670581	DRAFT_01249	KO:K01914	aspartate--ammonia ligase [EC:6.3.1.1]			0.00E+00
2558670581	DRAFT_01249	ITERM:00175	aspartate-ammonia ligase (EC 6.3.1.1)			
2558670581	DRAFT_01249	Locus_type		CDS		
2558670581	DRAFT_01249	Product_name		aspartate-ammonia ligase (EC 6.3.1.1)		
2558670581	DRAFT_01249	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670581	DRAFT_01249	Coordinates		10155..11279(+)		
2558670581	DRAFT_01249	DNA_length		1125bp		
2558670581	DRAFT_01249	Protein_length		374aa		
2558670581	DRAFT_01249	GC			0.56	

2558670582	DRAFT_01250	Metacyc	PWY-7018: paromomycin biosynthesis			
2558670582	DRAFT_01250	Metacyc	PWY-5706: alliin degradation			
2558670582	DRAFT_01250	Metacyc	PWY-5707: isoalliin degradation			
2558670582	DRAFT_01250	Metacyc	PWY-7000: kanamycin biosynthesis			
2558670582	DRAFT_01250	Metacyc	PWY-181: photorespiration			
2558670582	DRAFT_01250	Metacyc	P421-PWY: 4-nitrotoluene degradation I			
2558670582	DRAFT_01250	COG_category	[R] General function prediction only			
2558670582	DRAFT_01250	COG0579	Predicted dehydrogenase			1.00E-48
2558670582	DRAFT_01250	pfam01266	DAO			6.40E-38
2558670582	DRAFT_01250	EC:1.1.3.-	Oxidoreductases. Acting on the CH-OH group of donors. With oxygen as acceptor.			
2558670582	DRAFT_01250	KO:K15736	L-2-hydroxyglutarate oxidase [EC:1.1.3.-]			0.00E+00
2558670582	DRAFT_01250	Locus_type		CDS		
2558670582	DRAFT_01250	Product_name		Predicted dehydrogenase		
2558670582	DRAFT_01250	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670582	DRAFT_01250	Coordinates		11340..12668(-)		

2558670582	DRAFT_01250	DNA_length		1329bp	
2558670582	DRAFT_01250	Protein_length		442aa	
2558670582	DRAFT_01250	GC		0.59	
2558670582	DRAFT_01250	Transmembrane		Yes	

2558670583	DRAFT_01251	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670583	DRAFT_01251	COG0361	Translation initiation factor 1 (IF-1)		2.00E-15
2558670583	DRAFT_01251	pfam01176	eIF-1a		2.10E-22
2558670583	DRAFT_01251	TIGR00523	eukaryotic/archaeal initiation factor 1A		6.50E-35
2558670583	DRAFT_01251	KO:K03236	translation initiation factor 1A		2.30E-31
2558670583	DRAFT_01251	Locus_type		CDS	
2558670583	DRAFT_01251	Product_name		translation initiation factor 1A (aeIF-1A)	
2558670583	DRAFT_01251	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670583	DRAFT_01251	Coordinates		12764..13069(-)	
2558670583	DRAFT_01251	DNA_length		306bp	
2558670583	DRAFT_01251	Protein_length		101aa	
2558670583	DRAFT_01251	GC		0.55	

2558670584	DRAFT_01252	COG_category	[K] Transcription		
2558670584	DRAFT_01252	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670584	DRAFT_01252	COG_category	[L] Replication, recombination and repair		
2558670584	DRAFT_01252	COG0513	Superfamily II DNA and RNA helicases		2.00E-108
2558670584	DRAFT_01252	pfam00270	DEAD		2.40E-46
2558670584	DRAFT_01252	pfam00271	Helicase_C		2.60E-24
2558670584	DRAFT_01252	EC:3.6.4.13	RNA helicase.		
2558670584	DRAFT_01252	KO:K05592	ATP-dependent RNA helicase DeaD [EC:3.6.4.13]		0.00E+00
2558670584	DRAFT_01252	Locus_type		CDS	
2558670584	DRAFT_01252	Product_name		Superfamily II DNA and RNA helicases	
2558670584	DRAFT_01252	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670584	DRAFT_01252	Coordinates		13126..14334(-)	
2558670584	DRAFT_01252	DNA_length		1209bp	
2558670584	DRAFT_01252	Protein_length		402aa	
2558670584	DRAFT_01252	GC		0.6	

2558670585	DRAFT_01253	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670585	DRAFT_01253	COG1970	Large-conductance mechanosensitive channel		1.00E-15
2558670585	DRAFT_01253	pfam01741	MscL		1.80E-16
2558670585	DRAFT_01253	TIGR00220	large conductance mechanosensitive channel protein		1.30E-19
2558670585	DRAFT_01253	KO:K03282	large conductance mechanosensitive channel		2.80E-14
2558670585	DRAFT_01253	Locus_type		CDS	
2558670585	DRAFT_01253	Product_name		Large-conductance mechanosensitive channel	
2558670585	DRAFT_01253	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670585	DRAFT_01253	Coordinates		14653..15039(-)	
2558670585	DRAFT_01253	DNA_length		387bp	
2558670585	DRAFT_01253	Protein_length		128aa	
2558670585	DRAFT_01253	GC		0.54	
2558670585	DRAFT_01253	Transmembrane		Yes	
2558670586	DRAFT_01254	Locus_type		CDS	
2558670586	DRAFT_01254	Product_name		hypothetical protein	
2558670586	DRAFT_01254	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670586	DRAFT_01254	Coordinates		15370..15699(-)	
2558670586	DRAFT_01254	DNA_length		330bp	
2558670586	DRAFT_01254	Protein_length		109aa	
2558670586	DRAFT_01254	GC		0.55	
2558670587	DRAFT_01255	Locus_type		CDS	
2558670587	DRAFT_01255	Product_name		hypothetical protein	
2558670587	DRAFT_01255	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670587	DRAFT_01255	Coordinates		15748..16485(-)	
2558670587	DRAFT_01255	DNA_length		738bp	
2558670587	DRAFT_01255	Protein_length		245aa	
2558670587	DRAFT_01255	GC		0.56	
2558670587	DRAFT_01255	Transmembrane		Yes	
2558670588	DRAFT_01256	Locus_type		tRNA	
2558670588	DRAFT_01256	Product_name		tRNA_Asp_GTC	
2558670588	DRAFT_01256	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	

2558670588	DRAFT_01256	Coordinates		16795..16863(-)		
2558670588	DRAFT_01256	DNA_length		69bp		
2558670588	DRAFT_01256	GC			0.57	

2558670589	DRAFT_01257	pfam12847	Methyltransf_18			1.00E-08
2558670589	DRAFT_01257	Locus_type		CDS		
2558670589	DRAFT_01257	Product_name		Methyltransferase domain		
2558670589	DRAFT_01257	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670589	DRAFT_01257	Coordinates		17323..17913(-)		
2558670589	DRAFT_01257	DNA_length		591bp		
2558670589	DRAFT_01257	Protein_length		196aa		
2558670589	DRAFT_01257	GC			0.55	

2558670590	DRAFT_01258	pfam02353	CMAS			1.70E-09
2558670590	DRAFT_01258	Locus_type		CDS		
2558670590	DRAFT_01258	Product_name		Mycolic acid cyclopropane synthetase		
2558670590	DRAFT_01258	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670590	DRAFT_01258	Coordinates		18020..18490(-)		
2558670590	DRAFT_01258	DNA_length		471bp		
2558670590	DRAFT_01258	Protein_length		156aa		
2558670590	DRAFT_01258	GC			0.55	

2558670591	DRAFT_01259	KEGG_module	M00178: Ribosome, bacteria			
2558670591	DRAFT_01259	KEGG_module	M00179: Ribosome, archaea			
2558670591	DRAFT_01259	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670591	DRAFT_01259	COG0051	Ribosomal protein S10			2.00E-23
2558670591	DRAFT_01259	pfam00338	Ribosomal_S10			7.40E-29
2558670591	DRAFT_01259	TIGR01046	ribosomal protein S10(archaeal)/S20(eukaryotic)			2.90E-47
2558670591	DRAFT_01259	KO:K02946	small subunit ribosomal protein S10			1.40E-31
2558670591	DRAFT_01259	ITERM:00293	SSU ribosomal protein S10P			
2558670591	DRAFT_01259	Locus_type		CDS		
2558670591	DRAFT_01259	Product_name		SSU ribosomal protein S10P		
2558670591	DRAFT_01259	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25		
2558670591	DRAFT_01259	Coordinates		18649..18960(+)		

2558670591	DRAFT_01259	DNA_length		312bp	
2558670591	DRAFT_01259	Protein_length		103aa	
2558670591	DRAFT_01259	GC		0.54	
2558670592	DRAFT_01260	Locus_type		CDS	
2558670592	DRAFT_01260	Product_name		hypothetical protein	
2558670592	DRAFT_01260	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670592	DRAFT_01260	Coordinates		19130..19309(-)	
2558670592	DRAFT_01260	DNA_length		180bp	
2558670592	DRAFT_01260	Protein_length		59aa	
2558670592	DRAFT_01260	GC		0.48	
2558670593	DRAFT_01261	Locus_type		CDS	
2558670593	DRAFT_01261	Product_name		hypothetical protein	
2558670593	DRAFT_01261	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	
2558670593	DRAFT_01261	Coordinates		19374..19553(+)	
2558670593	DRAFT_01261	DNA_length		180bp	
2558670593	DRAFT_01261	Protein_length		59aa	
2558670593	DRAFT_01261	GC		0.54	
2558670594	DRAFT_01262	KEGG_module	M00403: HRD1/SEL1 ERAD complex		
2558670594	DRAFT_01262	KEGG_module	M00400: p97-Ufd1-Npl4 complex		
2558670594	DRAFT_01262	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558670594	DRAFT_01262	COG0464	ATPases of the AAA+ class		0.00E+00
2558670594	DRAFT_01262	pfam00004	AAA		2.70E-48
2558670594	DRAFT_01262	pfam00004	AAA		2.20E-45
2558670594	DRAFT_01262	pfam02933	CDC48_2		1.00E-08
2558670594	DRAFT_01262	pfam02359	CDC48_N		3.90E-28
2558670594	DRAFT_01262	TIGR01243	AAA family ATPase, CDC48 subfamily		0.00E+00
2558670594	DRAFT_01262	TIGR01242	26S proteasome subunit P45 family		3.00E-96
2558670594	DRAFT_01262	KO:K13525	transitional endoplasmic reticulum ATPase		0.00E+00
2558670594	DRAFT_01262	Locus_type		CDS	
2558670594	DRAFT_01262	Product_name		AAA family ATPase, CDC48 subfamily	
2558670594	DRAFT_01262	Scaffold		DRAFT_contig_70_169_len_23014_read_count_390000.25	

2558670594	DRAFT_01262	Coordinates	19689..21878(-)
2558670594	DRAFT_01262	DNA_length	2190bp
2558670594	DRAFT_01262	Protein_length	729aa
2558670594	DRAFT_01262	GC	0.55
2558670595	DRAFT_01263	Locus_type	CDS
2558670595	DRAFT_01263	Product_name	hypothetical protein
2558670595	DRAFT_01263	Scaffold	DRAFT_contig_70_169_len_23014_read_count_390000.25
2558670595	DRAFT_01263	Coordinates	22849..23013(+)
2558670595	DRAFT_01263	DNA_length	165bp
2558670595	DRAFT_01263	Protein_length	55aa
2558670595	DRAFT_01263	GC	0.45
2558670596	DRAFT_01264	Locus_type	tRNA
2558670596	DRAFT_01264	Product_name	tRNA_Arg_CCG
2558670596	DRAFT_01264	Scaffold	DRAFT_contig_70_192_len_21347_read_count_357287.26
2558670596	DRAFT_01264	Coordinates	50..124(-)
2558670596	DRAFT_01264	DNA_length	75bp
2558670596	DRAFT_01264	GC	0.67
2558670597	DRAFT_01265	Locus_type	CDS
2558670597	DRAFT_01265	Product_name	hypothetical protein
2558670597	DRAFT_01265	Scaffold	DRAFT_contig_70_192_len_21347_read_count_357287.26
2558670597	DRAFT_01265	Coordinates	618..929(-)
2558670597	DRAFT_01265	DNA_length	312bp
2558670597	DRAFT_01265	Protein_length	103aa
2558670597	DRAFT_01265	GC	0.54
2558670597	DRAFT_01265	Transmembrane	Yes
2558670598	DRAFT_01266	Locus_type	CDS
2558670598	DRAFT_01266	Product_name	Uncharacterized protein, possibly involved in aromatic compounds ca
2558670598	DRAFT_01266	Scaffold	DRAFT_contig_70_192_len_21347_read_count_357287.26
2558670598	DRAFT_01266	Coordinates	1221..1703(-)
2558670598	DRAFT_01266	DNA_length	483bp

2558670598	DRAFT_01266	Protein_length		160aa		
2558670598	DRAFT_01266	GC			0.58	
2558670599	DRAFT_01267	pfam13474	SnoaL_3			7.20E-10
2558670599	DRAFT_01267	Locus_type		CDS		
2558670599	DRAFT_01267	Product_name		SnoaL-like domain		
2558670599	DRAFT_01267	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670599	DRAFT_01267	Coordinates		2101..2484(-)		
2558670599	DRAFT_01267	DNA_length		384bp		
2558670599	DRAFT_01267	Protein_length		127aa		
2558670599	DRAFT_01267	GC			0.52	
2558670600	DRAFT_01268	Locus_type		CDS		
2558670600	DRAFT_01268	Product_name		hypothetical protein		
2558670600	DRAFT_01268	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670600	DRAFT_01268	Coordinates		2952..3242(+)		
2558670600	DRAFT_01268	DNA_length		291bp		
2558670600	DRAFT_01268	Protein_length		96aa		
2558670600	DRAFT_01268	GC			0.56	
2558670600	DRAFT_01268	Transmembrane		Yes		
2558670601	DRAFT_01269	COG_category	[C] Energy production and conversion			
2558670601	DRAFT_01269	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopte			8.00E-52
2558670601	DRAFT_01269	pfam00296	Bac_luciferase			2.20E-73
2558670601	DRAFT_01269	TIGR03560	probable F420-dependent oxidoreductase, Rv1855c family			1.20E-75
2558670601	DRAFT_01269	TIGR03619	probable F420-dependent oxidoreductase, Rv2161c family			6.00E-56
2558670601	DRAFT_01269	TIGR03621	probable F420-dependent oxidoreductase, MSMEG_2516 family			1.50E-52
2558670601	DRAFT_01269	Locus_type		CDS		
2558670601	DRAFT_01269	Product_name		probable F420-dependent oxidoreductase, Rv1855c family		
2558670601	DRAFT_01269	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670601	DRAFT_01269	Coordinates		3346..4290(-)		
2558670601	DRAFT_01269	DNA_length		945bp		
2558670601	DRAFT_01269	Protein_length		314aa		
2558670601	DRAFT_01269	GC			0.49	

2558670602	DRAFT_01270	Locus_type		CDS		
2558670602	DRAFT_01270	Product_name		hypothetical protein		
2558670602	DRAFT_01270	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670602	DRAFT_01270	Coordinates		4562..5221(-)		
2558670602	DRAFT_01270	DNA_length		660bp		
2558670602	DRAFT_01270	Protein_length		219aa		
2558670602	DRAFT_01270	GC			0.55	
2558670602	DRAFT_01270	Transmembrane		Yes		

2558670603	DRAFT_01271	COG_category	[S] Function unknown			
2558670603	DRAFT_01271	COG5616	Predicted integral membrane protein			1.00E-36
2558670603	DRAFT_01271	pfam13414	TPR_11			7.30E-09
2558670603	DRAFT_01271	pfam00211	Guanylate_cyc			2.80E-21
2558670603	DRAFT_01271	EC:4.6.1.1	Adenylate cyclase.			
2558670603	DRAFT_01271	KO:K01768	adenylate cyclase [EC:4.6.1.1]			0.00E+00
2558670603	DRAFT_01271	Locus_type		CDS		
2558670603	DRAFT_01271	Product_name		Predicted integral membrane protein		
2558670603	DRAFT_01271	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670603	DRAFT_01271	Coordinates		5428..7365(-)		
2558670603	DRAFT_01271	DNA_length		1938bp		
2558670603	DRAFT_01271	Protein_length		645aa		
2558670603	DRAFT_01271	GC			0.58	
2558670603	DRAFT_01271	Fused_gene		Yes		

2558670604	DRAFT_01272	COG_category	[R] General function prediction only			
2558670604	DRAFT_01272	COG5485	Predicted ester cyclase			1.00E-12
2558670604	DRAFT_01272	pfam07366	SnoaL			4.90E-32
2558670604	DRAFT_01272	Locus_type		CDS		
2558670604	DRAFT_01272	Product_name		Predicted ester cyclase		
2558670604	DRAFT_01272	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670604	DRAFT_01272	Coordinates		7560..7970(+)		
2558670604	DRAFT_01272	DNA_length		411bp		
2558670604	DRAFT_01272	Protein_length		136aa		

2558670604	DRAFT_01272	GC			0.54	
2558670605	DRAFT_01273	Locus_type		CDS		
2558670605	DRAFT_01273	Product_name		hypothetical protein		
2558670605	DRAFT_01273	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670605	DRAFT_01273	Coordinates		8019..8360(-)		
2558670605	DRAFT_01273	DNA_length		342bp		
2558670605	DRAFT_01273	Protein_length		113aa		
2558670605	DRAFT_01273	GC			0.43	
2558670605	DRAFT_01273	Transmembrane		Yes		
2558670606	DRAFT_01274	COG_category	[S] Function unknown			
2558670606	DRAFT_01274	COG5616	Predicted integral membrane protein			5.00E-36
2558670606	DRAFT_01274	pfam00211	Guanylate_cyc			4.80E-22
2558670606	DRAFT_01274	pfam13414	TPR_11			1.30E-12
2558670606	DRAFT_01274	pfam13414	TPR_11			1.80E-06
2558670606	DRAFT_01274	EC:4.6.1.1	Adenylate cyclase.			
2558670606	DRAFT_01274	KO:K01768	adenylate cyclase [EC:4.6.1.1]			0.00E+00
2558670606	DRAFT_01274	Locus_type		CDS		
2558670606	DRAFT_01274	Product_name		Predicted integral membrane protein		
2558670606	DRAFT_01274	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670606	DRAFT_01274	Coordinates		8516..10444(-)		
2558670606	DRAFT_01274	DNA_length		1929bp		
2558670606	DRAFT_01274	Protein_length		642aa		
2558670606	DRAFT_01274	GC			0.56	
2558670607	DRAFT_01275	KEGG_module	M00114: Ascorbate biosynthesis, plants, glucose-6P => ascorbate			
2558670607	DRAFT_01275	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2558670607	DRAFT_01275	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2558670607	DRAFT_01275	Metacyc	PWY-5659: GDP-mannose biosynthesis			
2558670607	DRAFT_01275	Metacyc	PWY-6082: alginate biosynthesis II			
2558670607	DRAFT_01275	Metacyc	PWY-6073: alginate biosynthesis I			
2558670607	DRAFT_01275	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)			
2558670607	DRAFT_01275	pfam00483	NTP_transferase			1.60E-27

2558670607	DRAFT_01275	EC:2.7.7.13	Mannose-1-phosphate guanylyltransferase.			
2558670607	DRAFT_01275	KO:K00966	mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]			3.00E-40
2558670607	DRAFT_01275	Locus_type		CDS		
2558670607	DRAFT_01275	Product_name		Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopol		
2558670607	DRAFT_01275	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670607	DRAFT_01275	Coordinates		10920..11681(+)		
2558670607	DRAFT_01275	DNA_length		762bp		
2558670607	DRAFT_01275	Protein_length		253aa		
2558670607	DRAFT_01275	GC			0.58	
2558670608	DRAFT_01276	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2558670608	DRAFT_01276	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558670608	DRAFT_01276	IMG_pathway	497: L-lysine ligation to tRNA(Lys)			
2558670608	DRAFT_01276	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670608	DRAFT_01276	COG1384	Lysyl-tRNA synthetase (class I)			1.00E-92
2558670608	DRAFT_01276	pfam01921	tRNA-synt_1f			6.80E-101
2558670608	DRAFT_01276	EC:6.1.1.6	Lysine--tRNA ligase.			
2558670608	DRAFT_01276	TIGR00467	lysyl-tRNA synthetase, archaeal and spirochete			3.20E-76
2558670608	DRAFT_01276	KO:K04566	lysyl-tRNA synthetase, class I [EC:6.1.1.6]			0.00E+00
2558670608	DRAFT_01276	ITERM:00395	lysyl-tRNA synthetase, class I (EC 6.1.1.6)			
2558670608	DRAFT_01276	Locus_type		CDS		
2558670608	DRAFT_01276	Product_name		lysyl-tRNA synthetase, class I (EC 6.1.1.6)		
2558670608	DRAFT_01276	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26		
2558670608	DRAFT_01276	Coordinates		11728..13326(-)		
2558670608	DRAFT_01276	DNA_length		1599bp		
2558670608	DRAFT_01276	Protein_length		532aa		
2558670608	DRAFT_01276	GC			0.58	
2558670609	DRAFT_01277	KEGG_module	M00400: p97-Ufd1-Npl4 complex			
2558670609	DRAFT_01277	KEGG_module	M00403: HRD1/SEL1 ERAD complex			
2558670609	DRAFT_01277	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670609	DRAFT_01277	COG0464	ATPases of the AAA+ class			4.00E-130
2558670609	DRAFT_01277	pfam00004	AAA			1.30E-49
2558670609	DRAFT_01277	pfam02359	CDC48_N			2.30E-29

2558670609	DRAFT_01277	pfam00004	AAA		1.30E-44
2558670609	DRAFT_01277	pfam02933	CDC48_2		1.10E-08
2558670609	DRAFT_01277	TIGR01243	AAA family ATPase, CDC48 subfamily		0.00E+00
2558670609	DRAFT_01277	KO:K13525	transitional endoplasmic reticulum ATPase		0.00E+00
2558670609	DRAFT_01277	Locus_type		CDS	
2558670609	DRAFT_01277	Product_name		AAA family ATPase, CDC48 subfamily	
2558670609	DRAFT_01277	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26	
2558670609	DRAFT_01277	Coordinates		13487..15688(-)	
2558670609	DRAFT_01277	DNA_length		2202bp	
2558670609	DRAFT_01277	Protein_length		733aa	
2558670609	DRAFT_01277	GC		0.58	
2558670609	DRAFT_01277	Fused_gene		Yes	

2558670610	DRAFT_01278	pfam00011	HSP20		7.60E-06
2558670610	DRAFT_01278	KO:K13993	HSP20 family protein		1.60E-21
2558670610	DRAFT_01278	Locus_type		CDS	
2558670610	DRAFT_01278	Product_name		Molecular chaperone (small heat shock protein)	
2558670610	DRAFT_01278	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26	
2558670610	DRAFT_01278	Coordinates		15702..16208(-)	
2558670610	DRAFT_01278	DNA_length		507bp	
2558670610	DRAFT_01278	Protein_length		168aa	
2558670610	DRAFT_01278	GC		0.55	

2558670611	DRAFT_01279	COG_category	[K] Transcription		
2558670611	DRAFT_01279	COG1777	Predicted transcriptional regulators		7.00E-05
2558670611	DRAFT_01279	pfam12840	HTH_20		1.10E-08
2558670611	DRAFT_01279	Locus_type		CDS	
2558670611	DRAFT_01279	Product_name		Predicted transcriptional regulators	
2558670611	DRAFT_01279	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26	
2558670611	DRAFT_01279	Coordinates		16220..16900(+)	
2558670611	DRAFT_01279	DNA_length		681bp	
2558670611	DRAFT_01279	Protein_length		226aa	
2558670611	DRAFT_01279	GC		0.57	

2558670612	DRAFT_01280	Locus_type		CDS	
2558670612	DRAFT_01280	Product_name		hypothetical protein	
2558670612	DRAFT_01280	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26	
2558670612	DRAFT_01280	Coordinates		17004..17507(+)	
2558670612	DRAFT_01280	DNA_length		504bp	
2558670612	DRAFT_01280	Protein_length		167aa	
2558670612	DRAFT_01280	GC		0.59	
2558670612	DRAFT_01280	Transmembrane		Yes	
2558670613	DRAFT_01281	COG_category	[R] General function prediction only		
2558670613	DRAFT_01281	COG1245	Predicted ATPase, RNase L inhibitor (RLI) homolog		0.00E+00
2558670613	DRAFT_01281	pfam04068	RLI		2.00E-08
2558670613	DRAFT_01281	pfam00037	Fer4		1.10E-08
2558670613	DRAFT_01281	pfam00005	ABC_tran		7.50E-19
2558670613	DRAFT_01281	pfam00005	ABC_tran		8.90E-16
2558670613	DRAFT_01281	KO:K06174	ATP-binding cassette, sub-family E, member 1		0.00E+00
2558670613	DRAFT_01281	Locus_type		CDS	
2558670613	DRAFT_01281	Product_name		Predicted ATPase, RNase L inhibitor (RLI) homolog	
2558670613	DRAFT_01281	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26	
2558670613	DRAFT_01281	Coordinates		17518..19344(+)	
2558670613	DRAFT_01281	DNA_length		1827bp	
2558670613	DRAFT_01281	Protein_length		608aa	
2558670613	DRAFT_01281	GC		0.59	
2558670614	DRAFT_01282	Locus_type		CDS	
2558670614	DRAFT_01282	Product_name		hypothetical protein	
2558670614	DRAFT_01282	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26	
2558670614	DRAFT_01282	Coordinates		19452..19964(+)	
2558670614	DRAFT_01282	DNA_length		513bp	
2558670614	DRAFT_01282	Protein_length		170aa	
2558670614	DRAFT_01282	GC		0.59	
2558670614	DRAFT_01282	Transmembrane		Yes	
2558670615	DRAFT_01283	Locus_type		CDS	

2558670615	DRAFT_01283	Product_name		hypothetical protein	
2558670615	DRAFT_01283	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26	
2558670615	DRAFT_01283	Coordinates		19961..20125(+)	
2558670615	DRAFT_01283	DNA_length		165bp	
2558670615	DRAFT_01283	Protein_length		54aa	
2558670615	DRAFT_01283	GC		0.6	
2558670616	DRAFT_01284	KEGG_module	M00239: Peptides/nickel transport system		
2558670616	DRAFT_01284	COG_category	[E] Amino acid transport and metabolism		
2558670616	DRAFT_01284	COG4608	ABC-type oligopeptide transport system, ATPase component		2.00E-93
2558670616	DRAFT_01284	pfam08352	oligo_HPY		5.40E-20
2558670616	DRAFT_01284	pfam00005	ABC_tran		2.10E-29
2558670616	DRAFT_01284	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termin		2.10E-31
2558670616	DRAFT_01284	KO:K02032	peptide/nickel transport system ATP-binding protein		0.00E+00
2558670616	DRAFT_01284	Locus_type		CDS	
2558670616	DRAFT_01284	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termi	
2558670616	DRAFT_01284	Scaffold		DRAFT_contig_70_192_len_21347_read_count_357287.26	
2558670616	DRAFT_01284	Coordinates		20198..21274(-)	
2558670616	DRAFT_01284	DNA_length		1077bp	
2558670616	DRAFT_01284	Protein_length		358aa	
2558670616	DRAFT_01284	GC		0.6	
2558670617	DRAFT_01285	pfam12849	PBP_like_2		1.60E-31
2558670617	DRAFT_01285	Locus_type		CDS	
2558670617	DRAFT_01285	Product_name		ABC-type phosphate transport system, periplasmic component	
2558670617	DRAFT_01285	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670617	DRAFT_01285	Coordinates		3..752(-)	
2558670617	DRAFT_01285	DNA_length		750bp	
2558670617	DRAFT_01285	Protein_length		250aa	
2558670617	DRAFT_01285	GC		0.57	
2558670617	DRAFT_01285	Signal_peptide		Yes	
2558670617	DRAFT_01285	Transmembrane		Yes	
2558670618	DRAFT_01286	Locus_type		CDS	

2558670618	DRAFT_01286	Product_name		hypothetical protein		
2558670618	DRAFT_01286	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670618	DRAFT_01286	Coordinates		1617..1952(-)		
2558670618	DRAFT_01286	DNA_length		336bp		
2558670618	DRAFT_01286	Protein_length		111aa		
2558670618	DRAFT_01286	GC			0.54	
2558670619	DRAFT_01287	Locus_type		CDS		
2558670619	DRAFT_01287	Product_name		hypothetical protein		
2558670619	DRAFT_01287	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670619	DRAFT_01287	Coordinates		2031..2495(-)		
2558670619	DRAFT_01287	DNA_length		465bp		
2558670619	DRAFT_01287	Protein_length		154aa		
2558670619	DRAFT_01287	GC			0.56	
2558670620	DRAFT_01288	Locus_type		CDS		
2558670620	DRAFT_01288	Product_name		hypothetical protein		
2558670620	DRAFT_01288	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670620	DRAFT_01288	Coordinates		3008..3427(-)		
2558670620	DRAFT_01288	DNA_length		420bp		
2558670620	DRAFT_01288	Protein_length		139aa		
2558670620	DRAFT_01288	GC			0.53	
2558670621	DRAFT_01289	COG_category	[K] Transcription			
2558670621	DRAFT_01289	COG1378	Predicted transcriptional regulators			2.00E-28
2558670621	DRAFT_01289	pfam11495	Regulator_TrmB			2.60E-08
2558670621	DRAFT_01289	pfam01978	TrmB			4.10E-24
2558670621	DRAFT_01289	Locus_type		CDS		
2558670621	DRAFT_01289	Product_name		Predicted transcriptional regulators		
2558670621	DRAFT_01289	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670621	DRAFT_01289	Coordinates		3672..4472(-)		
2558670621	DRAFT_01289	DNA_length		801bp		
2558670621	DRAFT_01289	Protein_length		266aa		
2558670621	DRAFT_01289	GC			0.57	

2558670622	DRAFT_01290	COG_category	[R] General function prediction only		
2558670622	DRAFT_01290	COG1964	Predicted Fe-S oxidoreductases		0.00E+00
2558670622	DRAFT_01290	pfam04055	Radical_SAM		2.60E-19
2558670622	DRAFT_01290	pfam13394	Fer4_14		9.80E-07
2558670622	DRAFT_01290	Locus_type		CDS	
2558670622	DRAFT_01290	Product_name		Predicted Fe-S oxidoreductases	
2558670622	DRAFT_01290	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670622	DRAFT_01290	Coordinates		4818..6491(+)	
2558670622	DRAFT_01290	DNA_length		1674bp	
2558670622	DRAFT_01290	Protein_length		557aa	
2558670622	DRAFT_01290	GC		0.55	
2558670623	DRAFT_01291	Locus_type		CDS	
2558670623	DRAFT_01291	Product_name		hypothetical protein	
2558670623	DRAFT_01291	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670623	DRAFT_01291	Coordinates		6642..7394(-)	
2558670623	DRAFT_01291	DNA_length		753bp	
2558670623	DRAFT_01291	Protein_length		250aa	
2558670623	DRAFT_01291	GC		0.56	
2558670624	DRAFT_01292	COG_category	[R] General function prediction only		
2558670624	DRAFT_01292	COG2047	Uncharacterized protein (ATP-grasp superfamily)		5.00E-17
2558670624	DRAFT_01292	pfam09754	PAC2		1.60E-11
2558670624	DRAFT_01292	Locus_type		CDS	
2558670624	DRAFT_01292	Product_name		Uncharacterized protein (ATP-grasp superfamily)	
2558670624	DRAFT_01292	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670624	DRAFT_01292	Coordinates		7666..8391(-)	
2558670624	DRAFT_01292	DNA_length		726bp	
2558670624	DRAFT_01292	Protein_length		241aa	
2558670624	DRAFT_01292	GC		0.6	
2558670625	DRAFT_01293	COG_category	[L] Replication, recombination and repair		
2558670625	DRAFT_01293	COG3569	Topoisomerase IB		2.00E-14

2558670625	DRAFT_01293	pfam14370	Topo_C_assoc			2.50E-18
2558670625	DRAFT_01293	pfam02919	Topoisom_I_N			2.20E-60
2558670625	DRAFT_01293	pfam01028	Topoisom_I			7.70E-62
2558670625	DRAFT_01293	EC:5.99.1.2	DNA topoisomerase.			
2558670625	DRAFT_01293	KO:K03163	DNA topoisomerase I [EC:5.99.1.2]			0.00E+00
2558670625	DRAFT_01293	Locus_type		CDS		
2558670625	DRAFT_01293	Product_name		Topoisomerase IB		
2558670625	DRAFT_01293	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670625	DRAFT_01293	Coordinates		8516..10093(+)		
2558670625	DRAFT_01293	DNA_length		1578bp		
2558670625	DRAFT_01293	Protein_length		525aa		
2558670625	DRAFT_01293	GC			0.57	
2558670626	DRAFT_01294	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670626	DRAFT_01294	COG0309	Hydrogenase maturation factor			5.00E-62
2558670626	DRAFT_01294	pfam00586	AIRS			3.70E-06
2558670626	DRAFT_01294	pfam02769	AIRS_C			7.20E-22
2558670626	DRAFT_01294	Locus_type		CDS		
2558670626	DRAFT_01294	Product_name		Hydrogenase maturation factor		
2558670626	DRAFT_01294	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670626	DRAFT_01294	Coordinates		10064..11059(-)		
2558670626	DRAFT_01294	DNA_length		996bp		
2558670626	DRAFT_01294	Protein_length		331aa		
2558670626	DRAFT_01294	GC			0.61	
2558670627	DRAFT_01295	COG_category	[S] Function unknown			
2558670627	DRAFT_01295	COG4720	Predicted membrane protein			8.00E-12
2558670627	DRAFT_01295	pfam07155	ECF-ribofla_trS			1.60E-26
2558670627	DRAFT_01295	pfam07155	ECF-ribofla_trS			3.80E-06
2558670627	DRAFT_01295	Locus_type		CDS		
2558670627	DRAFT_01295	Product_name		Predicted membrane protein		
2558670627	DRAFT_01295	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670627	DRAFT_01295	Coordinates		11056..11889(-)		
2558670627	DRAFT_01295	DNA_length		834bp		

2558670627	DRAFT_01295	Protein_length		277aa		
2558670627	DRAFT_01295	GC			0.55	
2558670627	DRAFT_01295	Transmembrane		Yes		

2558670628	DRAFT_01296	KEGG_module	M00018: Threonine biosynthesis, aspartate => homoserine => threonine			
2558670628	DRAFT_01296	Metacyc	HOMOSER-THRESYN-PWY: threonine biosynthesis from homoserine			
2558670628	DRAFT_01296	IMG_pathway	133: L-threonine synthesis from L-homoserine			
2558670628	DRAFT_01296	COG_category	[E] Amino acid transport and metabolism			
2558670628	DRAFT_01296	COG0498	Threonine synthase			2.00E-65
2558670628	DRAFT_01296	pfam03551	PadR			1.50E-09
2558670628	DRAFT_01296	pfam00291	PALP			2.20E-55
2558670628	DRAFT_01296	EC:4.2.3.1	Threonine synthase.			
2558670628	DRAFT_01296	TIGR00260	threonine synthase			3.90E-46
2558670628	DRAFT_01296	KO:K01733	threonine synthase [EC:4.2.3.1]			0.00E+00
2558670628	DRAFT_01296	ITERM:00220	L-threonine synthase (EC 4.2.3.1)			
2558670628	DRAFT_01296	Locus_type		CDS		
2558670628	DRAFT_01296	Product_name		L-threonine synthase (EC 4.2.3.1)		
2558670628	DRAFT_01296	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670628	DRAFT_01296	Coordinates		12005..13435(+)		
2558670628	DRAFT_01296	DNA_length		1431bp		
2558670628	DRAFT_01296	Protein_length		476aa		
2558670628	DRAFT_01296	GC			0.59	

2558670629	DRAFT_01297	pfam01944	DUF95			1.10E-07
2558670629	DRAFT_01297	Locus_type		CDS		
2558670629	DRAFT_01297	Product_name		Integral membrane protein DUF95		
2558670629	DRAFT_01297	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670629	DRAFT_01297	Coordinates		13476..14159(-)		
2558670629	DRAFT_01297	DNA_length		684bp		
2558670629	DRAFT_01297	Protein_length		227aa		
2558670629	DRAFT_01297	GC			0.58	
2558670629	DRAFT_01297	Transmembrane		Yes		

2558670630	DRAFT_01298	COG_category	[S] Function unknown			

2558670630	DRAFT_01298	COG1814	Uncharacterized membrane protein		2.00E-08
2558670630	DRAFT_01298	pfam01988	VIT1		1.50E-31
2558670630	DRAFT_01298	Locus_type		CDS	
2558670630	DRAFT_01298	Product_name		Uncharacterized membrane protein	
2558670630	DRAFT_01298	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670630	DRAFT_01298	Coordinates		14204..14806(-)	
2558670630	DRAFT_01298	DNA_length		603bp	
2558670630	DRAFT_01298	Protein_length		200aa	
2558670630	DRAFT_01298	GC		0.56	
2558670630	DRAFT_01298	Transmembrane		Yes	
2558670631	DRAFT_01299	Locus_type		CDS	
2558670631	DRAFT_01299	Product_name		hypothetical protein	
2558670631	DRAFT_01299	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670631	DRAFT_01299	Coordinates		15084..15206(+)	
2558670631	DRAFT_01299	DNA_length		123bp	
2558670631	DRAFT_01299	Protein_length		40aa	
2558670631	DRAFT_01299	GC		0.54	
2558670631	DRAFT_01299	Transmembrane		Yes	
2558670632	DRAFT_01300	Locus_type		CDS	
2558670632	DRAFT_01300	Product_name		hypothetical protein	
2558670632	DRAFT_01300	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670632	DRAFT_01300	Coordinates		15213..16355(-)	
2558670632	DRAFT_01300	DNA_length		1143bp	
2558670632	DRAFT_01300	Protein_length		380aa	
2558670632	DRAFT_01300	GC		0.53	
2558670633	DRAFT_01301	Locus_type		CDS	
2558670633	DRAFT_01301	Product_name		hypothetical protein	
2558670633	DRAFT_01301	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670633	DRAFT_01301	Coordinates		16798..17361(+)	
2558670633	DRAFT_01301	DNA_length		564bp	
2558670633	DRAFT_01301	Protein_length		187aa	

2558670633	DRAFT_01301	GC		0.56	
2558670634	DRAFT_01302	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558670634	DRAFT_01302	COG1765	Predicted redox protein, regulator of disulfide bond formation		1.00E-17
2558670634	DRAFT_01302	pfam02566	OsmC		1.50E-14
2558670634	DRAFT_01302	KO:K07397	putative redox protein		2.40E-19
2558670634	DRAFT_01302	Locus_type		CDS	
2558670634	DRAFT_01302	Product_name		Predicted redox protein, regulator of disulfide bond formation	
2558670634	DRAFT_01302	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670634	DRAFT_01302	Coordinates		17462..17776(+)	
2558670634	DRAFT_01302	DNA_length		315bp	
2558670634	DRAFT_01302	Protein_length		104aa	
2558670634	DRAFT_01302	GC		0.57	
2558670634	DRAFT_01302	Transmembrane		Yes	
2558670635	DRAFT_01303	COG_category	[C] Energy production and conversion		
2558670635	DRAFT_01303	COG_category	[R] General function prediction only		
2558670635	DRAFT_01303	COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases		2.00E-77
2558670635	DRAFT_01303	pfam08240	ADH_N		4.10E-26
2558670635	DRAFT_01303	pfam00107	ADH_zinc_N		3.00E-38
2558670635	DRAFT_01303	Locus_type		CDS	
2558670635	DRAFT_01303	Product_name		NADPH:quinone reductase and related Zn-dependent oxidoreductase	
2558670635	DRAFT_01303	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670635	DRAFT_01303	Coordinates		17773..18801(-)	
2558670635	DRAFT_01303	DNA_length		1029bp	
2558670635	DRAFT_01303	Protein_length		342aa	
2558670635	DRAFT_01303	GC		0.6	
2558670636	DRAFT_01304	Locus_type		CDS	
2558670636	DRAFT_01304	Product_name		hypothetical protein	
2558670636	DRAFT_01304	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27	
2558670636	DRAFT_01304	Coordinates		19286..19510(+)	
2558670636	DRAFT_01304	DNA_length		225bp	
2558670636	DRAFT_01304	Protein_length		74aa	

2558670636	DRAFT_01304	GC			0.49	
2558670637	DRAFT_01305	Locus_type		CDS		
2558670637	DRAFT_01305	Product_name		hypothetical protein		
2558670637	DRAFT_01305	Scaffold		DRAFT_contig_70_197_len_20500_read_count_357023.27		
2558670637	DRAFT_01305	Coordinates		19631..20497(+)		
2558670637	DRAFT_01305	DNA_length		867bp		
2558670637	DRAFT_01305	Protein_length		289aa		
2558670637	DRAFT_01305	GC			0.54	
2558670638	DRAFT_01306	Locus_type		CDS		
2558670638	DRAFT_01306	Product_name		hypothetical protein		
2558670638	DRAFT_01306	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670638	DRAFT_01306	Coordinates		53..973(+)		
2558670638	DRAFT_01306	DNA_length		921bp		
2558670638	DRAFT_01306	Protein_length		306aa		
2558670638	DRAFT_01306	GC			0.55	
2558670638	DRAFT_01306	Transmembrane		Yes		
2558670639	DRAFT_01307	Locus_type		CDS		
2558670639	DRAFT_01307	Product_name		hypothetical protein		
2558670639	DRAFT_01307	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670639	DRAFT_01307	Coordinates		1159..3102(-)		
2558670639	DRAFT_01307	DNA_length		1944bp		
2558670639	DRAFT_01307	Protein_length		647aa		
2558670639	DRAFT_01307	GC			0.58	
2558670639	DRAFT_01307	Transmembrane		Yes		
2558670640	DRAFT_01308	pfam05048	NosD			5.90E-23
2558670640	DRAFT_01308	TIGR03804	parallel beta-helix repeat (two copies)			2.30E-13
2558670640	DRAFT_01308	Locus_type		CDS		
2558670640	DRAFT_01308	Product_name		parallel beta-helix repeat (two copies)		
2558670640	DRAFT_01308	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670640	DRAFT_01308	Coordinates		3422..4417(+)		

2558670640	DRAFT_01308	DNA_length		996bp		
2558670640	DRAFT_01308	Protein_length		331aa		
2558670640	DRAFT_01308	GC			0.54	
2558670640	DRAFT_01308	Transmembrane		Yes		

2558670641	DRAFT_01309	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2558670641	DRAFT_01309	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2558670641	DRAFT_01309	Metacyc	PWY-3821: galactose degradation III			
2558670641	DRAFT_01309	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			
2558670641	DRAFT_01309	Metacyc	PWY-6397: mycolyl-arabinogalactan-peptidoglycan complex biosynthesis			
2558670641	DRAFT_01309	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2558670641	DRAFT_01309	Metacyc	PWY-6527: stachyose degradation			
2558670641	DRAFT_01309	COG_category	[G] Carbohydrate transport and metabolism			
2558670641	DRAFT_01309	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558670641	DRAFT_01309	COG0451	Nucleoside-diphosphate-sugar epimerases			2.00E-58
2558670641	DRAFT_01309	pfam01370	Epimerase			1.00E-63
2558670641	DRAFT_01309	EC:5.1.3.2	UDP-glucose 4-epimerase.			
2558670641	DRAFT_01309	KO:K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]			0.00E+00
2558670641	DRAFT_01309	Locus_type		CDS		
2558670641	DRAFT_01309	Product_name		Nucleoside-diphosphate-sugar epimerases		
2558670641	DRAFT_01309	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670641	DRAFT_01309	Coordinates		4803..5726(+)		
2558670641	DRAFT_01309	DNA_length		924bp		
2558670641	DRAFT_01309	Protein_length		307aa		
2558670641	DRAFT_01309	GC			0.55	

2558670642	DRAFT_01310	pfam00535	Glycos_transf_2			1.80E-23
2558670642	DRAFT_01310	Locus_type		CDS		
2558670642	DRAFT_01310	Product_name		Glycosyltransferases involved in cell wall biogenesis		
2558670642	DRAFT_01310	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670642	DRAFT_01310	Coordinates		5737..6585(+)		
2558670642	DRAFT_01310	DNA_length		849bp		
2558670642	DRAFT_01310	Protein_length		282aa		
2558670642	DRAFT_01310	GC			0.54	

2558670642	DRAFT_01310	Transmembrane		Yes		
2558670643	DRAFT_01311	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558670643	DRAFT_01311	COG0438	Glycosyltransferase			9.00E-30
2558670643	DRAFT_01311	pfam00534	Glycos_transf_1			1.90E-22
2558670643	DRAFT_01311	Locus_type		CDS		
2558670643	DRAFT_01311	Product_name		Glycosyltransferase		
2558670643	DRAFT_01311	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670643	DRAFT_01311	Coordinates		6552..7871(+)		
2558670643	DRAFT_01311	DNA_length		1320bp		
2558670643	DRAFT_01311	Protein_length		439aa		
2558670643	DRAFT_01311	GC			0.54	
2558670643	DRAFT_01311	Transmembrane		Yes		
2558670644	DRAFT_01312	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558670644	DRAFT_01312	COG0438	Glycosyltransferase			3.00E-15
2558670644	DRAFT_01312	pfam13579	Glyco_trans_4_4			5.00E-10
2558670644	DRAFT_01312	pfam13692	Glyco_trans_1_4			6.10E-09
2558670644	DRAFT_01312	Locus_type		CDS		
2558670644	DRAFT_01312	Product_name		Glycosyltransferase		
2558670644	DRAFT_01312	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670644	DRAFT_01312	Coordinates		7950..9062(+)		
2558670644	DRAFT_01312	DNA_length		1113bp		
2558670644	DRAFT_01312	Protein_length		370aa		
2558670644	DRAFT_01312	GC			0.52	
2558670644	DRAFT_01312	Transmembrane		Yes		
2558670645	DRAFT_01313	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2558670645	DRAFT_01313	Metacyc	ECASYN-PWY: enterobacterial common antigen biosynthesis			
2558670645	DRAFT_01313	Metacyc	TEICHOICACID-PWY: teichoic acid (poly-glycerol) biosynthesis			
2558670645	DRAFT_01313	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558670645	DRAFT_01313	COG0381	UDP-N-acetylglucosamine 2-epimerase			1.00E-85
2558670645	DRAFT_01313	pfam02350	Epimerase_2			3.00E-99
2558670645	DRAFT_01313	EC:5.1.3.14	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing).			

2558670645	DRAFT_01313	TIGR00236	UDP-N-acetylglucosamine 2-epimerase			1.30E-105
2558670645	DRAFT_01313	KO:K01791	UDP-N-acetylglucosamine 2-epimerase [EC:5.1.3.14]			0.00E+00
2558670645	DRAFT_01313	Locus_type		CDS		
2558670645	DRAFT_01313	Product_name		UDP-N-acetylglucosamine 2-epimerase		
2558670645	DRAFT_01313	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670645	DRAFT_01313	Coordinates		9126..10229(+)		
2558670645	DRAFT_01313	DNA_length		1104bp		
2558670645	DRAFT_01313	Protein_length		367aa		
2558670645	DRAFT_01313	GC			0.51	
2558670646	DRAFT_01314	COG_category	[R] General function prediction only			
2558670646	DRAFT_01314	COG2244	Membrane protein involved in the export of O-antigen and teichoic aci			8.00E-12
2558670646	DRAFT_01314	pfam01943	Polysacc_synt			2.40E-20
2558670646	DRAFT_01314	Locus_type		CDS		
2558670646	DRAFT_01314	Product_name		Membrane protein involved in the export of O-antigen and teichoic a		
2558670646	DRAFT_01314	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670646	DRAFT_01314	Coordinates		10390..11967(+)		
2558670646	DRAFT_01314	DNA_length		1578bp		
2558670646	DRAFT_01314	Protein_length		525aa		
2558670646	DRAFT_01314	GC			0.57	
2558670646	DRAFT_01314	Transmembrane		Yes		
2558670647	DRAFT_01315	pfam05159	Capsule_synth			1.20E-08
2558670647	DRAFT_01315	Locus_type		CDS		
2558670647	DRAFT_01315	Product_name		Putative glycosyl/glycerophosphate transferases involved in teichoic		
2558670647	DRAFT_01315	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		
2558670647	DRAFT_01315	Coordinates		12017..13696(+)		
2558670647	DRAFT_01315	DNA_length		1680bp		
2558670647	DRAFT_01315	Protein_length		559aa		
2558670647	DRAFT_01315	GC			0.52	
2558670648	DRAFT_01316	Locus_type		CDS		
2558670648	DRAFT_01316	Product_name		hypothetical protein		
2558670648	DRAFT_01316	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28		

2558670648	DRAFT_01316	Coordinates		13708..15921(+)	
2558670648	DRAFT_01316	DNA_length		2214bp	
2558670648	DRAFT_01316	Protein_length		737aa	
2558670648	DRAFT_01316	GC		0.52	
2558670648	DRAFT_01316	Transmembrane		Yes	
2558670649	DRAFT_01317	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670649	DRAFT_01317	COG1083	CMP-N-acetylneuraminic acid synthetase		1.00E-33
2558670649	DRAFT_01317	pfam02348	CTP_transf_3		2.20E-21
2558670649	DRAFT_01317	Locus_type		CDS	
2558670649	DRAFT_01317	Product_name		CMP-N-acetylneuraminic acid synthetase	
2558670649	DRAFT_01317	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28	
2558670649	DRAFT_01317	Coordinates		16106..17785(+)	
2558670649	DRAFT_01317	DNA_length		1680bp	
2558670649	DRAFT_01317	Protein_length		559aa	
2558670649	DRAFT_01317	GC		0.53	
2558670649	DRAFT_01317	Fused_gene		Yes	
2558670650	DRAFT_01318	Metacyc	PWY-6139: CMP-<i>N</i>-acetylneuraminate biosynthesis II (bacteria)		
2558670650	DRAFT_01318	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670650	DRAFT_01318	COG2089	Sialic acid synthase		3.00E-69
2558670650	DRAFT_01318	pfam03102	NeuB		1.30E-67
2558670650	DRAFT_01318	pfam08666	SAF		8.10E-06
2558670650	DRAFT_01318	EC:2.5.1.56	N-acetylneuraminate synthase.		
2558670650	DRAFT_01318	KO:K01654	N-acetylneuraminate synthase [EC:2.5.1.56]		0.00E+00
2558670650	DRAFT_01318	Locus_type		CDS	
2558670650	DRAFT_01318	Product_name		N-acetylneuraminate synthase (EC 2.5.1.56)	
2558670650	DRAFT_01318	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28	
2558670650	DRAFT_01318	Coordinates		17778..18863(+)	
2558670650	DRAFT_01318	DNA_length		1086bp	
2558670650	DRAFT_01318	Protein_length		361aa	
2558670650	DRAFT_01318	GC		0.52	
2558670651	DRAFT_01319	pfam01436	NHL		4.70E-06

2558670651	DRAFT_01319	Locus_type		CDS	
2558670651	DRAFT_01319	Product_name		NHL repeat	
2558670651	DRAFT_01319	Scaffold		DRAFT_contig_70_219_len_19329_read_count_354966.28	
2558670651	DRAFT_01319	Coordinates		19008..19328(+)	
2558670651	DRAFT_01319	DNA_length		321bp	
2558670651	DRAFT_01319	Protein_length		107aa	
2558670651	DRAFT_01319	GC		0.52	
2558670651	DRAFT_01319	Transmembrane		Yes	
2558670652	DRAFT_01320	Locus_type		CDS	
2558670652	DRAFT_01320	Product_name		hypothetical protein	
2558670652	DRAFT_01320	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670652	DRAFT_01320	Coordinates		1..315(+)	
2558670652	DRAFT_01320	DNA_length		315bp	
2558670652	DRAFT_01320	Protein_length		104aa	
2558670652	DRAFT_01320	GC		0.53	
2558670652	DRAFT_01320	Transmembrane		Yes	
2558670653	DRAFT_01321	COG_category	[S] Function unknown		
2558670653	DRAFT_01321	COG1872	Uncharacterized conserved protein		8.00E-11
2558670653	DRAFT_01321	pfam02594	DUF167		4.60E-22
2558670653	DRAFT_01321	TIGR00251	TIGR00251 family protein		5.10E-16
2558670653	DRAFT_01321	KO:K09131	hypothetical protein		2.20E-11
2558670653	DRAFT_01321	Locus_type		CDS	
2558670653	DRAFT_01321	Product_name		Uncharacterized conserved protein	
2558670653	DRAFT_01321	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670653	DRAFT_01321	Coordinates		721..942(+)	
2558670653	DRAFT_01321	DNA_length		222bp	
2558670653	DRAFT_01321	Protein_length		73aa	
2558670653	DRAFT_01321	GC		0.51	
2558670654	DRAFT_01322	Locus_type		CDS	
2558670654	DRAFT_01322	Product_name		hypothetical protein	
2558670654	DRAFT_01322	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	

2558670654	DRAFT_01322	Coordinates		1257..1691(-)		
2558670654	DRAFT_01322	DNA_length		435bp		
2558670654	DRAFT_01322	Protein_length		144aa		
2558670654	DRAFT_01322	GC			0.57	
2558670654	DRAFT_01322	Transmembrane		Yes		

2558670655	DRAFT_01323	Locus_type		CDS		
2558670655	DRAFT_01323	Product_name		hypothetical protein		
2558670655	DRAFT_01323	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670655	DRAFT_01323	Coordinates		1688..1894(-)		
2558670655	DRAFT_01323	DNA_length		207bp		
2558670655	DRAFT_01323	Protein_length		68aa		
2558670655	DRAFT_01323	GC			0.54	

2558670656	DRAFT_01324	Locus_type		CDS		
2558670656	DRAFT_01324	Product_name		hypothetical protein		
2558670656	DRAFT_01324	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670656	DRAFT_01324	Coordinates		1934..3055(+)		
2558670656	DRAFT_01324	DNA_length		1122bp		
2558670656	DRAFT_01324	Protein_length		373aa		
2558670656	DRAFT_01324	GC			0.57	
2558670656	DRAFT_01324	Transmembrane		Yes		

2558670657	DRAFT_01325	COG_category	[R] General function prediction only			
2558670657	DRAFT_01325	COG1011	Predicted hydrolase (HAD superfamily)			4.00E-16
2558670657	DRAFT_01325	pfam13419	HAD_2			5.80E-13
2558670657	DRAFT_01325	Locus_type		CDS		
2558670657	DRAFT_01325	Product_name		Predicted hydrolase (HAD superfamily)		
2558670657	DRAFT_01325	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670657	DRAFT_01325	Coordinates		3338..4093(-)		
2558670657	DRAFT_01325	DNA_length		756bp		
2558670657	DRAFT_01325	Protein_length		251aa		
2558670657	DRAFT_01325	GC			0.59	

2558670658	DRAFT_01326	pfam00583	Acetyltransf_1		7.30E-17
2558670658	DRAFT_01326	Locus_type		CDS	
2558670658	DRAFT_01326	Product_name		Acetyltransferases	
2558670658	DRAFT_01326	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670658	DRAFT_01326	Coordinates		4181..4669(-)	
2558670658	DRAFT_01326	DNA_length		489bp	
2558670658	DRAFT_01326	Protein_length		162aa	
2558670658	DRAFT_01326	GC		0.53	
2558670659	DRAFT_01327	COG_category	[K] Transcription		
2558670659	DRAFT_01327	COG1321	Mn-dependent transcriptional regulator		7.00E-25
2558670659	DRAFT_01327	pfam01325	Fe_dep_repress		1.40E-19
2558670659	DRAFT_01327	pfam02742	Fe_dep_repr_C		4.50E-14
2558670659	DRAFT_01327	ITERM:02272	iron (metal) dependent repressor, DtxR family		
2558670659	DRAFT_01327	Locus_type		CDS	
2558670659	DRAFT_01327	Product_name		iron (metal) dependent repressor, DtxR family	
2558670659	DRAFT_01327	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670659	DRAFT_01327	Coordinates		5230..5700(-)	
2558670659	DRAFT_01327	DNA_length		471bp	
2558670659	DRAFT_01327	Protein_length		156aa	
2558670659	DRAFT_01327	GC		0.53	
2558670660	DRAFT_01328	pfam01566	Nramp		4.90E-19
2558670660	DRAFT_01328	TIGR01197	NRAMP (natural resistance-associated macrophage protein) metal ion		4.50E-20
2558670660	DRAFT_01328	Locus_type		CDS	
2558670660	DRAFT_01328	Product_name		Mn2+ and Fe2+ transporters of the NRAMP family	
2558670660	DRAFT_01328	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670660	DRAFT_01328	Coordinates		6042..6383(+)	
2558670660	DRAFT_01328	DNA_length		342bp	
2558670660	DRAFT_01328	Protein_length		113aa	
2558670660	DRAFT_01328	GC		0.6	
2558670661	DRAFT_01329	pfam00383	dCMP_cyt_deam_1		5.70E-15
2558670661	DRAFT_01329	Locus_type		CDS	

2558670661	DRAFT_01329	Product_name		Deoxycytidylate deaminase	
2558670661	DRAFT_01329	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670661	DRAFT_01329	Coordinates		6265..6516(-)	
2558670661	DRAFT_01329	DNA_length		252bp	
2558670661	DRAFT_01329	Protein_length		83aa	
2558670661	DRAFT_01329	GC		0.5	
2558670662	DRAFT_01330	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670662	DRAFT_01330	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins		2.00E-11
2558670662	DRAFT_01330	pfam00583	Acetyltransf_1		1.50E-15
2558670662	DRAFT_01330	Locus_type		CDS	
2558670662	DRAFT_01330	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins	
2558670662	DRAFT_01330	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670662	DRAFT_01330	Coordinates		6937..7545(+)	
2558670662	DRAFT_01330	DNA_length		609bp	
2558670662	DRAFT_01330	Protein_length		202aa	
2558670662	DRAFT_01330	GC		0.57	
2558670663	DRAFT_01331	Locus_type		CDS	
2558670663	DRAFT_01331	Product_name		hypothetical protein	
2558670663	DRAFT_01331	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670663	DRAFT_01331	Coordinates		7655..8347(-)	
2558670663	DRAFT_01331	DNA_length		693bp	
2558670663	DRAFT_01331	Protein_length		230aa	
2558670663	DRAFT_01331	GC		0.52	
2558670664	DRAFT_01332	COG_category	[E] Amino acid transport and metabolism		
2558670664	DRAFT_01332	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases		5.00E-89
2558670664	DRAFT_01332	pfam00326	Peptidase_S9		8.30E-56
2558670664	DRAFT_01332	pfam07676	PD40		3.60E-09
2558670664	DRAFT_01332	Locus_type		CDS	
2558670664	DRAFT_01332	Product_name		Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	
2558670664	DRAFT_01332	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670664	DRAFT_01332	Coordinates		8589..10631(-)	

2558670664	DRAFT_01332	DNA_length		2043bp		
2558670664	DRAFT_01332	Protein_length		680aa		
2558670664	DRAFT_01332	GC			0.62	

2558670665	DRAFT_01333	IMG_pathway	217: N-3-alkylpurine repair via base excision			
2558670665	DRAFT_01333	COG_category	[L] Replication, recombination and repair			
2558670665	DRAFT_01333	COG2231	Uncharacterized protein related to Endonuclease III			4.00E-34
2558670665	DRAFT_01333	pfam00633	HHH			1.80E-05
2558670665	DRAFT_01333	pfam00730	HhH-GPD			2.40E-07
2558670665	DRAFT_01333	KO:K07457	endonuclease III related protein			0.00E+00
2558670665	DRAFT_01333	ITERM:00576	DNA-3-methyladenine glycosylase III (EC 3.2.2.-)			
2558670665	DRAFT_01333	Locus_type		CDS		
2558670665	DRAFT_01333	Product_name		DNA-3-methyladenine glycosylase III (EC 3.2.2.-)		
2558670665	DRAFT_01333	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670665	DRAFT_01333	Coordinates		10736..11437(-)		
2558670665	DRAFT_01333	DNA_length		702bp		
2558670665	DRAFT_01333	Protein_length		233aa		
2558670665	DRAFT_01333	GC			0.54	

2558670666	DRAFT_01334	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670666	DRAFT_01334	COG4870	Cysteine protease			2.00E-19
2558670666	DRAFT_01334	pfam00112	Peptidase_C1			4.60E-11
2558670666	DRAFT_01334	Locus_type		CDS		
2558670666	DRAFT_01334	Product_name		Cysteine protease		
2558670666	DRAFT_01334	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670666	DRAFT_01334	Coordinates		11675..12367(+)		
2558670666	DRAFT_01334	DNA_length		693bp		
2558670666	DRAFT_01334	Protein_length		230aa		
2558670666	DRAFT_01334	GC			0.58	

2558670667	DRAFT_01335	COG_category	[K] Transcription			
2558670667	DRAFT_01335	COG1846	Transcriptional regulators			3.00E-11
2558670667	DRAFT_01335	pfam01047	MarR			2.40E-16
2558670667	DRAFT_01335	Locus_type		CDS		

2558670667	DRAFT_01335	Product_name		Transcriptional regulators		
2558670667	DRAFT_01335	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670667	DRAFT_01335	Coordinates		12464..12910(+)		
2558670667	DRAFT_01335	DNA_length		447bp		
2558670667	DRAFT_01335	Protein_length		148aa		
2558670667	DRAFT_01335	GC			0.57	
2558670668	DRAFT_01336	pfam07690	MFS_1			3.80E-44
2558670668	DRAFT_01336	TIGR00711	drug resistance transporter, EmrB/QacA subfamily			7.70E-63
2558670668	DRAFT_01336	Locus_type		CDS		
2558670668	DRAFT_01336	Product_name		Arabinose efflux permease		
2558670668	DRAFT_01336	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670668	DRAFT_01336	Coordinates		12920..14386(+)		
2558670668	DRAFT_01336	DNA_length		1467bp		
2558670668	DRAFT_01336	Protein_length		488aa		
2558670668	DRAFT_01336	GC			0.6	
2558670668	DRAFT_01336	Transmembrane		Yes		
2558670669	DRAFT_01337	pfam00924	MS_channel			2.20E-22
2558670669	DRAFT_01337	Locus_type		CDS		
2558670669	DRAFT_01337	Product_name		Small-conductance mechanosensitive channel		
2558670669	DRAFT_01337	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670669	DRAFT_01337	Coordinates		14541..15086(-)		
2558670669	DRAFT_01337	DNA_length		546bp		
2558670669	DRAFT_01337	Protein_length		181aa		
2558670669	DRAFT_01337	GC			0.64	
2558670669	DRAFT_01337	Transmembrane		Yes		
2558670670	DRAFT_01338	pfam00230	MIP			4.10E-14
2558670670	DRAFT_01338	Locus_type		CDS		
2558670670	DRAFT_01338	Product_name		Glycerol uptake facilitator and related permeases (Major Intrinsic Pro		
2558670670	DRAFT_01338	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29		
2558670670	DRAFT_01338	Coordinates		15287..15784(+)		
2558670670	DRAFT_01338	DNA_length		498bp		

2558670670	DRAFT_01338	Protein_length		165aa	
2558670670	DRAFT_01338	GC		0.55	
2558670670	DRAFT_01338	Transmembrane		Yes	
2558670671	DRAFT_01339	TIGR02276	40-residue YVTN family beta-propeller repeat		1.70E-11
2558670671	DRAFT_01339	Locus_type		CDS	
2558670671	DRAFT_01339	Product_name		40-residue YVTN family beta-propeller repeat	
2558670671	DRAFT_01339	Scaffold		DRAFT_contig_70_220_len_19073_read_count_329530.29	
2558670671	DRAFT_01339	Coordinates		15757..19071(+)	
2558670671	DRAFT_01339	DNA_length		3315bp	
2558670671	DRAFT_01339	Protein_length		1105aa	
2558670671	DRAFT_01339	GC		0.58	
2558670671	DRAFT_01339	Transmembrane		Yes	
2558670672	DRAFT_01340	Metacyc	3-HYDROXYPHENYLACETATE-DEGRADATION-PWY: 4-hydroxyphenylacetate degradation		
2558670672	DRAFT_01340	Metacyc	PWY-7153: grixazone biosynthesis		
2558670672	DRAFT_01340	Metacyc	PWY-7046: 4-coumarate degradation (anaerobic)		
2558670672	DRAFT_01340	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)		
2558670672	DRAFT_01340	Metacyc	PWY-6713: L-rhamnose degradation II		
2558670672	DRAFT_01340	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle		
2558670672	DRAFT_01340	Metacyc	PWY-7085: triethylamine degradation		
2558670672	DRAFT_01340	Metacyc	PWY0-1517: sedoheptulose bisphosphate bypass		
2558670672	DRAFT_01340	COG_category	[G] Carbohydrate transport and metabolism		
2558670672	DRAFT_01340	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes		2.00E-63
2558670672	DRAFT_01340	pfam01791	DeoC		3.10E-22
2558670672	DRAFT_01340	EC:4.1.2.-	Lyases. Carbon-carbon lyases. Aldehyde-lyases.		
2558670672	DRAFT_01340	KO:K08321	putative autoinducer-2 (AI-2) aldolase [EC:4.1.2.-]		0.00E+00
2558670672	DRAFT_01340	Locus_type		CDS	
2558670672	DRAFT_01340	Product_name		DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	
2558670672	DRAFT_01340	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670672	DRAFT_01340	Coordinates		226..1002(-)	
2558670672	DRAFT_01340	DNA_length		777bp	
2558670672	DRAFT_01340	Protein_length		258aa	
2558670672	DRAFT_01340	GC		0.57	

2558670673	DRAFT_01341	Metacyc	PWY-4101: sorbitol degradation I		
2558670673	DRAFT_01341	Metacyc	PWY-6693: galactose degradation IV		
2558670673	DRAFT_01341	COG_category	[R] General function prediction only		
2558670673	DRAFT_01341	COG_category	[E] Amino acid transport and metabolism		
2558670673	DRAFT_01341	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases		5.00E-55
2558670673	DRAFT_01341	pfam08240	ADH_N		8.20E-26
2558670673	DRAFT_01341	pfam00107	ADH_zinc_N		5.90E-19
2558670673	DRAFT_01341	EC:1.1.1.14	L-iditol 2-dehydrogenase.		
2558670673	DRAFT_01341	KO:K00008	L-iditol 2-dehydrogenase [EC:1.1.1.14]		0.00E+00
2558670673	DRAFT_01341	Locus_type		CDS	
2558670673	DRAFT_01341	Product_name		Threonine dehydrogenase and related Zn-dependent dehydrogenases	
2558670673	DRAFT_01341	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670673	DRAFT_01341	Coordinates		1073..2095(-)	
2558670673	DRAFT_01341	DNA_length		1023bp	
2558670673	DRAFT_01341	Protein_length		340aa	
2558670673	DRAFT_01341	GC		0.57	

2558670674	DRAFT_01342	Locus_type		CDS	
2558670674	DRAFT_01342	Product_name		hypothetical protein	
2558670674	DRAFT_01342	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670674	DRAFT_01342	Coordinates		2512..2760(-)	
2558670674	DRAFT_01342	DNA_length		249bp	
2558670674	DRAFT_01342	Protein_length		82aa	
2558670674	DRAFT_01342	GC		0.51	
2558670674	DRAFT_01342	Transmembrane		Yes	

2558670675	DRAFT_01343	COG_category	[R] General function prediction only		
2558670675	DRAFT_01343	COG1163	Predicted GTPase		5.00E-123
2558670675	DRAFT_01343	pfam01926	MMR_HSR1		2.50E-21
2558670675	DRAFT_01343	pfam02824	TGS		1.90E-15
2558670675	DRAFT_01343	TIGR00231	small GTP-binding protein domain		3.80E-23
2558670675	DRAFT_01343	Locus_type		CDS	
2558670675	DRAFT_01343	Product_name		small GTP-binding protein domain	

2558670675	DRAFT_01343	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30		
2558670675	DRAFT_01343	Coordinates		2881..3978(+)		
2558670675	DRAFT_01343	DNA_length		1098bp		
2558670675	DRAFT_01343	Protein_length		365aa		
2558670675	DRAFT_01343	GC			0.55	
2558670676	DRAFT_01344	KEGG_module	M00003: Gluconeogenesis, oxaloacetate => fructose-6P			
2558670676	DRAFT_01344	COG_category	[C] Energy production and conversion			
2558670676	DRAFT_01344	COG1274	Phosphoenolpyruvate carboxykinase (GTP)			0.00E+00
2558670676	DRAFT_01344	pfam00821	PEPCK			0.00E+00
2558670676	DRAFT_01344	EC:4.1.1.32	Phosphoenolpyruvate carboxykinase (GTP).			
2558670676	DRAFT_01344	KO:K01596	phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]			0.00E+00
2558670676	DRAFT_01344	Locus_type		CDS		
2558670676	DRAFT_01344	Product_name		Phosphoenolpyruvate carboxykinase (GTP)		
2558670676	DRAFT_01344	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30		
2558670676	DRAFT_01344	Coordinates		4012..5853(-)		
2558670676	DRAFT_01344	DNA_length		1842bp		
2558670676	DRAFT_01344	Protein_length		613aa		
2558670676	DRAFT_01344	GC			0.58	
2558670677	DRAFT_01345	Locus_type		CDS		
2558670677	DRAFT_01345	Product_name		hypothetical protein		
2558670677	DRAFT_01345	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30		
2558670677	DRAFT_01345	Coordinates		6006..6704(+)		
2558670677	DRAFT_01345	DNA_length		699bp		
2558670677	DRAFT_01345	Protein_length		232aa		
2558670677	DRAFT_01345	GC			0.52	
2558670677	DRAFT_01345	Transmembrane		Yes		
2558670678	DRAFT_01346	COG_category	[K] Transcription			
2558670678	DRAFT_01346	COG3432	Predicted transcriptional regulator			6.00E-08
2558670678	DRAFT_01346	pfam14947	HTH_45			4.10E-11
2558670678	DRAFT_01346	Locus_type		CDS		
2558670678	DRAFT_01346	Product_name		Predicted transcriptional regulator		

2558670678	DRAFT_01346	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670678	DRAFT_01346	Coordinates		6691..6978(+)	
2558670678	DRAFT_01346	DNA_length		288bp	
2558670678	DRAFT_01346	Protein_length		95aa	
2558670678	DRAFT_01346	GC		0.53	
2558670679	DRAFT_01347	KEGG_module	M00171: C4-dicarboxylic acid cycle, NAD+ -malic enzyme type		
2558670679	DRAFT_01347	KEGG_module	M00168: CAM (Crassulacean acid metabolism), dark		
2558670679	DRAFT_01347	KEGG_module	M00012: Glyoxylate cycle		
2558670679	DRAFT_01347	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2558670679	DRAFT_01347	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670679	DRAFT_01347	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2558670679	DRAFT_01347	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)		
2558670679	DRAFT_01347	KEGG_module	M00346: Formaldehyde assimilation, serine pathway		
2558670679	DRAFT_01347	Metacyc	PWY-7115: C4 photosynthetic carbon assimilation cycle, NAD-ME type		
2558670679	DRAFT_01347	Metacyc	GLYOXYLATE-BYPASS: glyoxylate cycle		
2558670679	DRAFT_01347	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558670679	DRAFT_01347	Metacyc	GLUCONEO-PWY: gluconeogenesis I		
2558670679	DRAFT_01347	Metacyc	FERMENTATION-PWY: mixed acid fermentation		
2558670679	DRAFT_01347	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558670679	DRAFT_01347	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)		
2558670679	DRAFT_01347	Metacyc	P108-PWY: pyruvate fermentation to propionate I		
2558670679	DRAFT_01347	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)		
2558670679	DRAFT_01347	Metacyc	TCA: TCA cycle I (prokaryotic)		
2558670679	DRAFT_01347	Metacyc	P23-PWY: reductive TCA cycle I		
2558670679	DRAFT_01347	Metacyc	PWY-6728: methylaspartate cycle		
2558670679	DRAFT_01347	Metacyc	PWY-5690: TCA cycle II (eukaryotic)		
2558670679	DRAFT_01347	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)		
2558670679	DRAFT_01347	Metacyc	ANARESP1-PWY: respiration (anaerobic)		
2558670679	DRAFT_01347	Metacyc	MALATE-ASPARTATE-SHUTTLE-PWY: aspartate degradation II		
2558670679	DRAFT_01347	Metacyc	PWY-561: superpathway of glyoxylate cycle and fatty acid degradation		
2558670679	DRAFT_01347	Metacyc	PWY-5392: reductive TCA cycle II		
2558670679	DRAFT_01347	COG_category	[C] Energy production and conversion		
2558670679	DRAFT_01347	COG0039	Malate/lactate dehydrogenases		5.00E-81

2558670679	DRAFT_01347	pfam00056	Ldh_1_N			6.90E-32
2558670679	DRAFT_01347	pfam02866	Ldh_1_C			1.10E-28
2558670679	DRAFT_01347	EC:1.1.1.37	Malate dehydrogenase.			
2558670679	DRAFT_01347	TIGR01763	malate dehydrogenase, NAD-dependent			4.10E-91
2558670679	DRAFT_01347	KO:K00024	malate dehydrogenase [EC:1.1.1.37]			0.00E+00
2558670679	DRAFT_01347	Locus_type		CDS		
2558670679	DRAFT_01347	Product_name		Malate/lactate dehydrogenases		
2558670679	DRAFT_01347	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30		
2558670679	DRAFT_01347	Coordinates		7056..7967(+)		
2558670679	DRAFT_01347	DNA_length		912bp		
2558670679	DRAFT_01347	Protein_length		303aa		
2558670679	DRAFT_01347	GC			0.59	
2558670680	DRAFT_01348	Locus_type		CDS		
2558670680	DRAFT_01348	Product_name		hypothetical protein		
2558670680	DRAFT_01348	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30		
2558670680	DRAFT_01348	Coordinates		7877..8098(-)		
2558670680	DRAFT_01348	DNA_length		222bp		
2558670680	DRAFT_01348	Protein_length		73aa		
2558670680	DRAFT_01348	GC			0.47	
2558670680	DRAFT_01348	Transmembrane		Yes		
2558670681	DRAFT_01349	pfam01012	ETF			5.20E-12
2558670681	DRAFT_01349	ITERM:01639	electron transfer flavoprotein beta subunit			
2558670681	DRAFT_01349	Locus_type		CDS		
2558670681	DRAFT_01349	Product_name		electron transfer flavoprotein beta subunit		
2558670681	DRAFT_01349	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30		
2558670681	DRAFT_01349	Coordinates		8222..9400(+)		
2558670681	DRAFT_01349	DNA_length		1179bp		
2558670681	DRAFT_01349	Protein_length		392aa		
2558670681	DRAFT_01349	GC			0.59	
2558670682	DRAFT_01350	COG_category	[C] Energy production and conversion			
2558670682	DRAFT_01350	COG2025	Electron transfer flavoprotein, alpha subunit			6.00E-67

2558670682	DRAFT_01350	pfam01012	ETF		1.40E-31
2558670682	DRAFT_01350	pfam00766	ETF_alpha		7.40E-18
2558670682	DRAFT_01350	KO:K03522	electron transfer flavoprotein alpha subunit		0.00E+00
2558670682	DRAFT_01350	Locus_type		CDS	
2558670682	DRAFT_01350	Product_name		Electron transfer flavoprotein, alpha subunit	
2558670682	DRAFT_01350	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670682	DRAFT_01350	Coordinates		9397..10482(+)	
2558670682	DRAFT_01350	DNA_length		1086bp	
2558670682	DRAFT_01350	Protein_length		361aa	
2558670682	DRAFT_01350	GC		0.6	
2558670683	DRAFT_01351	COG_category	[C] Energy production and conversion		
2558670683	DRAFT_01351	COG0644	Dehydrogenases (flavoproteins)		2.00E-41
2558670683	DRAFT_01351	pfam01266	DAO		1.10E-17
2558670683	DRAFT_01351	EC:1.5.5.-	Oxidoreductases. Acting on the CH-NH group of donors. With a quinone or similar compound		
2558670683	DRAFT_01351	KO:K00313	electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]		0.00E+00
2558670683	DRAFT_01351	Locus_type		CDS	
2558670683	DRAFT_01351	Product_name		Dehydrogenases (flavoproteins)	
2558670683	DRAFT_01351	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670683	DRAFT_01351	Coordinates		10472..12166(+)	
2558670683	DRAFT_01351	DNA_length		1695bp	
2558670683	DRAFT_01351	Protein_length		564aa	
2558670683	DRAFT_01351	GC		0.59	
2558670684	DRAFT_01352	KEGG_module	M00141: C1-unit interconversion, eukaryotes		
2558670684	DRAFT_01352	KEGG_module	M00532: Photorespiration		
2558670684	DRAFT_01352	KEGG_module	M00346: Formaldehyde assimilation, serine pathway		
2558670684	DRAFT_01352	KEGG_module	M00140: C1-unit interconversion, prokaryotes		
2558670684	DRAFT_01352	Metacyc	1CMET2-PWY: formylTHF biosynthesis I		
2558670684	DRAFT_01352	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)		
2558670684	DRAFT_01352	Metacyc	PWY-2161: folate polyglutamylation		
2558670684	DRAFT_01352	Metacyc	PWY-3661: glycine betaine degradation		
2558670684	DRAFT_01352	Metacyc	PWY-3841: folate transformations II		
2558670684	DRAFT_01352	Metacyc	PWY-181: photorespiration		

2558670684	DRAFT_01352	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2558670684	DRAFT_01352	Metacyc	GLYSYN-PWY: glycine biosynthesis I		
2558670684	DRAFT_01352	Metacyc	PWY-2201: folate transformations I		
2558670684	DRAFT_01352	COG_category	[E] Amino acid transport and metabolism		
2558670684	DRAFT_01352	COG0112	Glycine/serine hydroxymethyltransferase		3.00E-82
2558670684	DRAFT_01352	pfam00464	SHMT		2.10E-33
2558670684	DRAFT_01352	EC:2.1.2.1	Glycine hydroxymethyltransferase.		
2558670684	DRAFT_01352	KO:K00600	glycine hydroxymethyltransferase [EC:2.1.2.1]		0.00E+00
2558670684	DRAFT_01352	Locus_type		CDS	
2558670684	DRAFT_01352	Product_name		Glycine/serine hydroxymethyltransferase	
2558670684	DRAFT_01352	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670684	DRAFT_01352	Coordinates		12227..13429(+)	
2558670684	DRAFT_01352	DNA_length		1203bp	
2558670684	DRAFT_01352	Protein_length		400aa	
2558670684	DRAFT_01352	GC		0.58	
2558670685	DRAFT_01353	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds		
2558670685	DRAFT_01353	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate		
2558670685	DRAFT_01353	KEGG_module	M00166: Reductive pentose phosphate cycle, RuBP + CO2 => glyceraldehyde-3P		
2558670685	DRAFT_01353	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)		
2558670685	DRAFT_01353	IMG_pathway	336: Standard Embden-Meyerhof pathway		
2558670685	DRAFT_01353	IMG_pathway	359: Conversion of glyceraldehyde-3-phosphate to pyruvate		
2558670685	DRAFT_01353	IMG_pathway	527: Calvin cycle		
2558670685	DRAFT_01353	COG_category	[G] Carbohydrate transport and metabolism		
2558670685	DRAFT_01353	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate d		9.00E-62
2558670685	DRAFT_01353	pfam00044	Gp_dh_N		4.50E-19
2558670685	DRAFT_01353	pfam02800	Gp_dh_C		3.90E-21
2558670685	DRAFT_01353	EC:1.2.1.59	Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)(+)) (phosphorylating).		
2558670685	DRAFT_01353	TIGR01546	glyceraldehyde-3-phosphate dehydrogenase, type II		0.00E+00
2558670685	DRAFT_01353	KO:K00150	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]		0.00E+00
2558670685	DRAFT_01353	ITERM:07087	glyceraldehyde 3-phosphate dehydrogenase (NAD(P)+) (EC 1.2.1.59)		
2558670685	DRAFT_01353	Locus_type		CDS	
2558670685	DRAFT_01353	Product_name		glyceraldehyde 3-phosphate dehydrogenase (NAD(P)+) (EC 1.2.1.59)	
2558670685	DRAFT_01353	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	

2558670685	DRAFT_01353	Coordinates		13430..14446(-)		
2558670685	DRAFT_01353	DNA_length		1017bp		
2558670685	DRAFT_01353	Protein_length		338aa		
2558670685	DRAFT_01353	GC			0.6	
2558670686	DRAFT_01354	KEGG_module	M00166: Reductive pentose phosphate cycle, RuBP + CO2 => glyceraldehyde-3P			
2558670686	DRAFT_01354	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)			
2558670686	DRAFT_01354	KEGG_module	M00003: Gluconeogenesis, oxaloacetate => fructose-6P			
2558670686	DRAFT_01354	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds			
2558670686	DRAFT_01354	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2558670686	DRAFT_01354	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2558670686	DRAFT_01354	Metacyc	SUCSYN-PWY: sucrose biosynthesis			
2558670686	DRAFT_01354	Metacyc	GLYCOLYSIS: glycolysis I			
2558670686	DRAFT_01354	Metacyc	PWY-1042: glycolysis IV (plant cytosol)			
2558670686	DRAFT_01354	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis			
2558670686	DRAFT_01354	Metacyc	PWY-6901: xylose degradation IV			
2558670686	DRAFT_01354	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2558670686	DRAFT_01354	Metacyc	PWY-7003: glycerol degradation to butanol			
2558670686	DRAFT_01354	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2558670686	DRAFT_01354	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			
2558670686	DRAFT_01354	Metacyc	P124-PWY: Bifidobacterium shunt			
2558670686	DRAFT_01354	Metacyc	P122-PWY: heterolactic fermentation			
2558670686	DRAFT_01354	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2558670686	DRAFT_01354	IMG_pathway	336: Standard Embden-Meyerhof pathway			
2558670686	DRAFT_01354	IMG_pathway	359: Conversion of glyceraldehyde-3-phosphate to pyruvate			
2558670686	DRAFT_01354	IMG_pathway	527: Calvin cycle			
2558670686	DRAFT_01354	COG_category	[G] Carbohydrate transport and metabolism			
2558670686	DRAFT_01354	COG0126	3-phosphoglycerate kinase			2.00E-97
2558670686	DRAFT_01354	pfam00162	PGK			4.40E-105
2558670686	DRAFT_01354	EC:2.7.2.3	Phosphoglycerate kinase.			
2558670686	DRAFT_01354	KO:K00927	phosphoglycerate kinase [EC:2.7.2.3]			0.00E+00
2558670686	DRAFT_01354	ITERM:01477	phosphoglycerate kinase (EC 2.7.2.3)			
2558670686	DRAFT_01354	Locus_type		CDS		
2558670686	DRAFT_01354	Product_name		phosphoglycerate kinase (EC 2.7.2.3)		

2558670686	DRAFT_01354	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670686	DRAFT_01354	Coordinates		14471..15700(-)	
2558670686	DRAFT_01354	DNA_length		1230bp	
2558670686	DRAFT_01354	Protein_length		409aa	
2558670686	DRAFT_01354	GC		0.58	
2558670687	DRAFT_01355	Locus_type		CDS	
2558670687	DRAFT_01355	Product_name		hypothetical protein	
2558670687	DRAFT_01355	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670687	DRAFT_01355	Coordinates		15979..16101(-)	
2558670687	DRAFT_01355	DNA_length		123bp	
2558670687	DRAFT_01355	Protein_length		40aa	
2558670687	DRAFT_01355	GC		0.51	
2558670687	DRAFT_01355	Transmembrane		Yes	
2558670688	DRAFT_01356	COG_category	[V] Defense mechanisms		
2558670688	DRAFT_01356	COG1968	Uncharacterized bacitracin resistance protein		2.00E-31
2558670688	DRAFT_01356	pfam02673	BacA		6.30E-49
2558670688	DRAFT_01356	EC:3.6.1.27	Undecaprenyl-diphosphate phosphatase.		
2558670688	DRAFT_01356	TIGR00753	undecaprenyl-diphosphatase UppP		3.00E-40
2558670688	DRAFT_01356	KO:K06153	undecaprenyl-diphosphatase [EC:3.6.1.27]		0.00E+00
2558670688	DRAFT_01356	Locus_type		CDS	
2558670688	DRAFT_01356	Product_name		Uncharacterized bacitracin resistance protein	
2558670688	DRAFT_01356	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670688	DRAFT_01356	Coordinates		16747..17565(-)	
2558670688	DRAFT_01356	DNA_length		819bp	
2558670688	DRAFT_01356	Protein_length		272aa	
2558670688	DRAFT_01356	GC		0.58	
2558670688	DRAFT_01356	Transmembrane		Yes	
2558670688	DRAFT_01356	Fused_gene		Yes	
2558670689	DRAFT_01357	Locus_type		CDS	
2558670689	DRAFT_01357	Product_name		hypothetical protein	
2558670689	DRAFT_01357	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	

2558670689	DRAFT_01357	Coordinates		17686..18069(+)	
2558670689	DRAFT_01357	DNA_length		384bp	
2558670689	DRAFT_01357	Protein_length		127aa	
2558670689	DRAFT_01357	GC			0.53
2558670689	DRAFT_01357	Transmembrane		Yes	

2558670690	DRAFT_01358	Locus_type		CDS	
2558670690	DRAFT_01358	Product_name		hypothetical protein	
2558670690	DRAFT_01358	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670690	DRAFT_01358	Coordinates		18117..18515(-)	
2558670690	DRAFT_01358	DNA_length		399bp	
2558670690	DRAFT_01358	Protein_length		132aa	
2558670690	DRAFT_01358	GC			0.57

2558670691	DRAFT_01359	Locus_type		CDS	
2558670691	DRAFT_01359	Product_name		hypothetical protein	
2558670691	DRAFT_01359	Scaffold		DRAFT_contig_70_226_len_18807_read_count_299628.30	
2558670691	DRAFT_01359	Coordinates		18512..18739(-)	
2558670691	DRAFT_01359	DNA_length		228bp	
2558670691	DRAFT_01359	Protein_length		75aa	
2558670691	DRAFT_01359	GC			0.57

2558670692	DRAFT_01360	COG_category	[C] Energy production and conversion		
2558670692	DRAFT_01360	COG2025	Electron transfer flavoprotein, alpha subunit		9.00E-34
2558670692	DRAFT_01360	pfam01012	ETF		5.50E-34
2558670692	DRAFT_01360	KO:K03522	electron transfer flavoprotein alpha subunit		4.10E-44
2558670692	DRAFT_01360	ITERM:01638	electron transfer flavoprotein alpha subunit apoprotein		
2558670692	DRAFT_01360	Locus_type		CDS	
2558670692	DRAFT_01360	Product_name		electron transfer flavoprotein alpha subunit apoprotein	
2558670692	DRAFT_01360	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670692	DRAFT_01360	Coordinates		3..761(-)	
2558670692	DRAFT_01360	DNA_length		759bp	
2558670692	DRAFT_01360	Protein_length		253aa	
2558670692	DRAFT_01360	GC			0.61

2558670693	DRAFT_01361	COG_category	[C] Energy production and conversion			
2558670693	DRAFT_01361	COG0247	Fe-S oxidoreductase			8.00E-58
2558670693	DRAFT_01361	pfam02754	CCG			9.50E-18
2558670693	DRAFT_01361	pfam02754	CCG			5.70E-16
2558670693	DRAFT_01361	pfam13183	Fer4_8			1.00E-09
2558670693	DRAFT_01361	Locus_type		CDS		
2558670693	DRAFT_01361	Product_name		Fe-S oxidoreductase		
2558670693	DRAFT_01361	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31		
2558670693	DRAFT_01361	Coordinates		745..1881(-)		
2558670693	DRAFT_01361	DNA_length		1137bp		
2558670693	DRAFT_01361	Protein_length		378aa		
2558670693	DRAFT_01361	GC			0.63	

2558670694	DRAFT_01362	KEGG_module	M00563: Methanogenesis, methylamine => methane		
2558670694	DRAFT_01362	KEGG_module	M00562: Methanogenesis, dimethylamine => methane		
2558670694	DRAFT_01362	KEGG_module	M00561: Methanogenesis, trimethylamine => methane		
2558670694	DRAFT_01362	KEGG_module	M00567: Methanogenesis, CO2 => methane		
2558670694	DRAFT_01362	KEGG_module	M00356: Methanogenesis, methanol => methane		
2558670694	DRAFT_01362	KEGG_module	M00357: Methanogenesis, acetate => methane		
2558670694	DRAFT_01362	KEGG_module	M00347: Methanogenesis, formate => methane		
2558670694	DRAFT_01362	Metacyc	PWY-5207: coenzyme B/coenzyme M regeneration		
2558670694	DRAFT_01362	pfam07992	Pyr_redox_2		1.40E-08
2558670694	DRAFT_01362	pfam02662	FlpD		8.10E-42
2558670694	DRAFT_01362	pfam12838	Fer4_7		3.10E-08
2558670694	DRAFT_01362	pfam07992	Pyr_redox_2		6.10E-10
2558670694	DRAFT_01362	EC:1.8.98.1	CoB--CoM heterodisulfide reductase.		
2558670694	DRAFT_01362	KO:K03388	heterodisulfide reductase subunit A [EC:1.8.98.1]		0.00E+00
2558670694	DRAFT_01362	Locus_type		CDS	
2558670694	DRAFT_01362	Product_name		Pyridine nucleotide-disulphide oxidoreductase/Methyl-viologen-redu	
2558670694	DRAFT_01362	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670694	DRAFT_01362	Coordinates		1878..5297(-)	
2558670694	DRAFT_01362	DNA_length		3420bp	
2558670694	DRAFT_01362	Protein_length		1139aa	

2558670694	DRAFT_01362	GC		0.62	
2558670694	DRAFT_01362	Fused_gene		Yes	
2558670695	DRAFT_01363	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558670695	DRAFT_01363	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670695	DRAFT_01363	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558670695	DRAFT_01363	Metacyc	P23-PWY: reductive TCA cycle I		
2558670695	DRAFT_01363	Metacyc	PWY-5392: reductive TCA cycle II		
2558670695	DRAFT_01363	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558670695	DRAFT_01363	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558670695	DRAFT_01363	COG_category	[C] Energy production and conversion		
2558670695	DRAFT_01363	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		4.00E-16
2558670695	DRAFT_01363	pfam01558	POR		2.10E-26
2558670695	DRAFT_01363	EC:1.2.7.3	2-oxoglutarate synthase.		
2558670695	DRAFT_01363	KO:K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]		3.30E-28
2558670695	DRAFT_01363	Locus_type		CDS	
2558670695	DRAFT_01363	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin	
2558670695	DRAFT_01363	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670695	DRAFT_01363	Coordinates		5290..5844(-)	
2558670695	DRAFT_01363	DNA_length		555bp	
2558670695	DRAFT_01363	Protein_length		184aa	
2558670695	DRAFT_01363	GC		0.62	
2558670696	DRAFT_01364	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670696	DRAFT_01364	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558670696	DRAFT_01364	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558670696	DRAFT_01364	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558670696	DRAFT_01364	Metacyc	P23-PWY: reductive TCA cycle I		
2558670696	DRAFT_01364	Metacyc	PWY-5392: reductive TCA cycle II		
2558670696	DRAFT_01364	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558670696	DRAFT_01364	COG_category	[C] Energy production and conversion		
2558670696	DRAFT_01364	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		5.00E-64
2558670696	DRAFT_01364	pfam02775	TPP_enzyme_C		1.80E-33
2558670696	DRAFT_01364	EC:1.2.7.3	2-oxoglutarate synthase.		

2558670696	DRAFT_01364	KO:K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]		0.00E+00
2558670696	DRAFT_01364	Locus_type		CDS	
2558670696	DRAFT_01364	Product_name		2-oxoglutarate ferredoxin oxidoreductase, beta subunit (EC 1.2.7.3)	
2558670696	DRAFT_01364	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670696	DRAFT_01364	Coordinates		5841..6719(-)	
2558670696	DRAFT_01364	DNA_length		879bp	
2558670696	DRAFT_01364	Protein_length		292aa	
2558670696	DRAFT_01364	GC		0.62	
2558670697	DRAFT_01365	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558670697	DRAFT_01365	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2558670697	DRAFT_01365	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670697	DRAFT_01365	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558670697	DRAFT_01365	Metacyc	PWY-5392: reductive TCA cycle II		
2558670697	DRAFT_01365	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558670697	DRAFT_01365	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558670697	DRAFT_01365	Metacyc	P23-PWY: reductive TCA cycle I		
2558670697	DRAFT_01365	COG_category	[C] Energy production and conversion		
2558670697	DRAFT_01365	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		9.00E-72
2558670697	DRAFT_01365	pfam01855	POR_N		3.20E-63
2558670697	DRAFT_01365	pfam02780	Transketolase_C		1.30E-08
2558670697	DRAFT_01365	EC:1.2.7.3	2-oxoglutarate synthase.		
2558670697	DRAFT_01365	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]		0.00E+00
2558670697	DRAFT_01365	Locus_type		CDS	
2558670697	DRAFT_01365	Product_name		2-oxoglutarate ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.3)	
2558670697	DRAFT_01365	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670697	DRAFT_01365	Coordinates		6719..7873(-)	
2558670697	DRAFT_01365	DNA_length		1155bp	
2558670697	DRAFT_01365	Protein_length		384aa	
2558670697	DRAFT_01365	GC		0.61	
2558670698	DRAFT_01366	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558670698	DRAFT_01366	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670698	DRAFT_01366	Metacyc	PWY-5392: reductive TCA cycle II		

2558670698	DRAFT_01366	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2558670698	DRAFT_01366	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2558670698	DRAFT_01366	Metacyc	P23-PWY: reductive TCA cycle I			
2558670698	DRAFT_01366	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2558670698	DRAFT_01366	COG_category	[C] Energy production and conversion			
2558670698	DRAFT_01366	COG1146	Ferredoxin			2.00E-04
2558670698	DRAFT_01366	pfam12838	Fer4_7			7.30E-08
2558670698	DRAFT_01366	EC:1.2.7.3	2-oxoglutarate synthase.			
2558670698	DRAFT_01366	KO:K00176	2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7.3]			6.80E-17
2558670698	DRAFT_01366	Locus_type		CDS		
2558670698	DRAFT_01366	Product_name		Ferredoxin		
2558670698	DRAFT_01366	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31		
2558670698	DRAFT_01366	Coordinates		7876..8199(-)		
2558670698	DRAFT_01366	DNA_length		324bp		
2558670698	DRAFT_01366	Protein_length		107aa		
2558670698	DRAFT_01366	GC			0.54	

2558670699	DRAFT_01367	Locus_type		tRNA		
2558670699	DRAFT_01367	Product_name		tRNA_Leu_CAA		
2558670699	DRAFT_01367	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31		
2558670699	DRAFT_01367	Coordinates		8422..8530(+)		
2558670699	DRAFT_01367	DNA_length		87bp		
2558670699	DRAFT_01367	GC			0.61	

2558670700	DRAFT_01368	KEGG_module	M00357: Methanogenesis, acetate => methane			
2558670700	DRAFT_01368	Metacyc	PWY0-1313: acetate conversion to acetyl-CoA			
2558670700	DRAFT_01368	Metacyc	PWY66-161: oxidative ethanol degradation III			
2558670700	DRAFT_01368	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)			
2558670700	DRAFT_01368	Metacyc	PWY-6672: <i>cis</i>-genanyl-CoA degradation			
2558670700	DRAFT_01368	Metacyc	PWY66-21: ethanol degradation II			
2558670700	DRAFT_01368	Metacyc	PWY66-162: ethanol degradation IV			
2558670700	DRAFT_01368	COG_category	[I] Lipid transport and metabolism			
2558670700	DRAFT_01368	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases			0.00E+00
2558670700	DRAFT_01368	pfam13193	AMP-binding_C			1.60E-18

2558670700	DRAFT_01368	pfam00501	AMP-binding			1.00E-76
2558670700	DRAFT_01368	EC:6.2.1.1	Acetate--CoA ligase.			
2558670700	DRAFT_01368	TIGR02188	acetate--CoA ligase			0.00E+00
2558670700	DRAFT_01368	KO:K01895	acetyl-CoA synthetase [EC:6.2.1.1]			0.00E+00
2558670700	DRAFT_01368	Locus_type		CDS		
2558670700	DRAFT_01368	Product_name		Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases		
2558670700	DRAFT_01368	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31		
2558670700	DRAFT_01368	Coordinates		8797..10728(-)		
2558670700	DRAFT_01368	DNA_length		1932bp		
2558670700	DRAFT_01368	Protein_length		643aa		
2558670700	DRAFT_01368	GC			0.58	
2558670701	DRAFT_01369	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			
2558670701	DRAFT_01369	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2558670701	DRAFT_01369	Metacyc	PWY-5392: reductive TCA cycle II			
2558670701	DRAFT_01369	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2558670701	DRAFT_01369	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2558670701	DRAFT_01369	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2558670701	DRAFT_01369	Metacyc	P23-PWY: reductive TCA cycle I			
2558670701	DRAFT_01369	COG_category	[C] Energy production and conversion			
2558670701	DRAFT_01369	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin c			6.00E-26
2558670701	DRAFT_01369	pfam01558	POR			4.80E-38
2558670701	DRAFT_01369	EC:1.2.7.3	2-oxoglutarate synthase.			
2558670701	DRAFT_01369	TIGR02175	2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-ketois			1.90E-33
2558670701	DRAFT_01369	KO:K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]			1.50E-37
2558670701	DRAFT_01369	Locus_type		CDS		
2558670701	DRAFT_01369	Product_name		2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-keto		
2558670701	DRAFT_01369	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31		
2558670701	DRAFT_01369	Coordinates		10949..11488(-)		
2558670701	DRAFT_01369	DNA_length		540bp		
2558670701	DRAFT_01369	Protein_length		179aa		
2558670701	DRAFT_01369	GC			0.58	
2558670702	DRAFT_01370	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			

2558670702	DRAFT_01370	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558670702	DRAFT_01370	Metacyc	P23-PWY: reductive TCA cycle I		
2558670702	DRAFT_01370	Metacyc	PWY-5392: reductive TCA cycle II		
2558670702	DRAFT_01370	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558670702	DRAFT_01370	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558670702	DRAFT_01370	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558670702	DRAFT_01370	COG_category	[C] Energy production and conversion		
2558670702	DRAFT_01370	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		2.00E-64
2558670702	DRAFT_01370	pfam02775	TPP_enzyme_C		4.40E-36
2558670702	DRAFT_01370	EC:1.2.7.3	2-oxoglutarate synthase.		
2558670702	DRAFT_01370	KO:K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]		0.00E+00
2558670702	DRAFT_01370	Locus_type		CDS	
2558670702	DRAFT_01370	Product_name		2-oxoglutarate ferredoxin oxidoreductase, beta subunit (EC 1.2.7.3)	
2558670702	DRAFT_01370	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670702	DRAFT_01370	Coordinates		11472..12305(-)	
2558670702	DRAFT_01370	DNA_length		834bp	
2558670702	DRAFT_01370	Protein_length		277aa	
2558670702	DRAFT_01370	GC		0.59	
2558670703	DRAFT_01371	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2558670703	DRAFT_01371	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670703	DRAFT_01371	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558670703	DRAFT_01371	Metacyc	PWY-5392: reductive TCA cycle II		
2558670703	DRAFT_01371	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558670703	DRAFT_01371	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558670703	DRAFT_01371	Metacyc	P23-PWY: reductive TCA cycle I		
2558670703	DRAFT_01371	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558670703	DRAFT_01371	COG_category	[C] Energy production and conversion		
2558670703	DRAFT_01371	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin		2.00E-70
2558670703	DRAFT_01371	pfam01855	POR_N		2.90E-70
2558670703	DRAFT_01371	pfam02780	Transketolase_C		5.80E-07
2558670703	DRAFT_01371	EC:1.2.7.3	2-oxoglutarate synthase.		
2558670703	DRAFT_01371	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]		0.00E+00
2558670703	DRAFT_01371	ITERM:01389	2-oxoglutarate ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.3)		

2558670703	DRAFT_01371	Locus_type		CDS	
2558670703	DRAFT_01371	Product_name		2-oxoglutarate ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.3)	
2558670703	DRAFT_01371	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670703	DRAFT_01371	Coordinates		12307..13443(-)	
2558670703	DRAFT_01371	DNA_length		1137bp	
2558670703	DRAFT_01371	Protein_length		378aa	
2558670703	DRAFT_01371	GC		0.55	
2558670704	DRAFT_01372	COG_category	[F] Nucleotide transport and metabolism		
2558670704	DRAFT_01372	COG0528	Uridylate kinase		6.00E-36
2558670704	DRAFT_01372	pfam00696	AA_kinase		1.60E-29
2558670704	DRAFT_01372	EC:2.7.4.22	UMP kinase.		
2558670704	DRAFT_01372	TIGR02076	uridylate kinase, putative		9.70E-60
2558670704	DRAFT_01372	KO:K09903	uridylate kinase [EC:2.7.4.22]		1.40E-38
2558670704	DRAFT_01372	Locus_type		CDS	
2558670704	DRAFT_01372	Product_name		uridylate kinase, putative	
2558670704	DRAFT_01372	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670704	DRAFT_01372	Coordinates		13600..14265(-)	
2558670704	DRAFT_01372	DNA_length		666bp	
2558670704	DRAFT_01372	Protein_length		221aa	
2558670704	DRAFT_01372	GC		0.6	
2558670705	DRAFT_01373	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670705	DRAFT_01373	COG1503	Peptide chain release factor 1 (eRF1)		2.00E-106
2558670705	DRAFT_01373	pfam03464	eRF1_2		1.20E-31
2558670705	DRAFT_01373	pfam03465	eRF1_3		7.70E-24
2558670705	DRAFT_01373	pfam03463	eRF1_1		1.50E-19
2558670705	DRAFT_01373	TIGR03676	peptide chain release factor 1, archaeal and eukaryotic forms		0.00E+00
2558670705	DRAFT_01373	KO:K03265	peptide chain release factor subunit 1		0.00E+00
2558670705	DRAFT_01373	Locus_type		CDS	
2558670705	DRAFT_01373	Product_name		peptide chain release factor 1, archaeal and eukaryotic forms	
2558670705	DRAFT_01373	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31	
2558670705	DRAFT_01373	Coordinates		14403..15653(+)	
2558670705	DRAFT_01373	DNA_length		1251bp	

2558670705	DRAFT_01373	Protein_length		416aa		
2558670705	DRAFT_01373	GC			0.57	
2558670706	DRAFT_01374	Locus_type		CDS		
2558670706	DRAFT_01374	Product_name		hypothetical protein		
2558670706	DRAFT_01374	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31		
2558670706	DRAFT_01374	Coordinates		15810..16235(+)		
2558670706	DRAFT_01374	DNA_length		426bp		
2558670706	DRAFT_01374	Protein_length		141aa		
2558670706	DRAFT_01374	GC			0.55	
2558670706	DRAFT_01374	Transmembrane		Yes		
2558670707	DRAFT_01375	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670707	DRAFT_01375	COG0012	Predicted GTPase, probable translation factor			1.00E-69
2558670707	DRAFT_01375	pfam01926	MMR_HSR1			6.10E-17
2558670707	DRAFT_01375	pfam08438	MMR_HSR1_C			2.10E-31
2558670707	DRAFT_01375	pfam02824	TGS			4.30E-08
2558670707	DRAFT_01375	Locus_type		CDS		
2558670707	DRAFT_01375	Product_name		GTP-binding conserved hypothetical protein TIGR00650		
2558670707	DRAFT_01375	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31		
2558670707	DRAFT_01375	Coordinates		16308..17522(+)		
2558670707	DRAFT_01375	DNA_length		1215bp		
2558670707	DRAFT_01375	Protein_length		404aa		
2558670707	DRAFT_01375	GC			0.58	
2558670708	DRAFT_01376	Locus_type		CDS		
2558670708	DRAFT_01376	Product_name		hypothetical protein		
2558670708	DRAFT_01376	Scaffold		DRAFT_contig_70_236_len_18515_read_count_318899.31		
2558670708	DRAFT_01376	Coordinates		17536..18513(+)		
2558670708	DRAFT_01376	DNA_length		978bp		
2558670708	DRAFT_01376	Protein_length		326aa		
2558670708	DRAFT_01376	GC			0.58	
2558670709	DRAFT_01377	Locus_type		CDS		

2558670709	DRAFT_01377	Product_name		hypothetical protein		
2558670709	DRAFT_01377	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670709	DRAFT_01377	Coordinates		152..661(-)		
2558670709	DRAFT_01377	DNA_length		510bp		
2558670709	DRAFT_01377	Protein_length		169aa		
2558670709	DRAFT_01377	GC			0.53	
2558670709	DRAFT_01377	Signal_peptide		Yes		
2558670709	DRAFT_01377	Transmembrane		Yes		
2558670710	DRAFT_01378	pfam07760	DUF1616			1.80E-19
2558670710	DRAFT_01378	Locus_type		CDS		
2558670710	DRAFT_01378	Product_name		Protein of unknown function (DUF1616)		
2558670710	DRAFT_01378	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670710	DRAFT_01378	Coordinates		866..1456(-)		
2558670710	DRAFT_01378	DNA_length		591bp		
2558670710	DRAFT_01378	Protein_length		196aa		
2558670710	DRAFT_01378	GC			0.54	
2558670710	DRAFT_01378	Transmembrane		Yes		
2558670711	DRAFT_01379	pfam07760	DUF1616			1.90E-15
2558670711	DRAFT_01379	Locus_type		CDS		
2558670711	DRAFT_01379	Product_name		Protein of unknown function (DUF1616)		
2558670711	DRAFT_01379	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670711	DRAFT_01379	Coordinates		1469..1954(-)		
2558670711	DRAFT_01379	DNA_length		486bp		
2558670711	DRAFT_01379	Protein_length		161aa		
2558670711	DRAFT_01379	GC			0.55	
2558670711	DRAFT_01379	Transmembrane		Yes		
2558670712	DRAFT_01380	Locus_type		CDS		
2558670712	DRAFT_01380	Product_name		hypothetical protein		
2558670712	DRAFT_01380	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670712	DRAFT_01380	Coordinates		1951..2442(-)		
2558670712	DRAFT_01380	DNA_length		492bp		

2558670712	DRAFT_01380	Protein_length		163aa		
2558670712	DRAFT_01380	GC			0.55	
2558670712	DRAFT_01380	Signal_peptide		Yes		
2558670712	DRAFT_01380	Transmembrane		Yes		
2558670713	DRAFT_01381	Locus_type		CDS		
2558670713	DRAFT_01381	Product_name		hypothetical protein		
2558670713	DRAFT_01381	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670713	DRAFT_01381	Coordinates		2575..2976(-)		
2558670713	DRAFT_01381	DNA_length		402bp		
2558670713	DRAFT_01381	Protein_length		133aa		
2558670713	DRAFT_01381	GC			0.53	
2558670714	DRAFT_01382	Locus_type		CDS		
2558670714	DRAFT_01382	Product_name		hypothetical protein		
2558670714	DRAFT_01382	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670714	DRAFT_01382	Coordinates		3104..3334(+)		
2558670714	DRAFT_01382	DNA_length		231bp		
2558670714	DRAFT_01382	Protein_length		76aa		
2558670714	DRAFT_01382	GC			0.55	
2558670715	DRAFT_01383	COG_category	[K] Transcription			
2558670715	DRAFT_01383	COG3432	Predicted transcriptional regulator			4.00E-08
2558670715	DRAFT_01383	pfam14947	HTH_45			2.30E-18
2558670715	DRAFT_01383	Locus_type		CDS		
2558670715	DRAFT_01383	Product_name		Predicted transcriptional regulator		
2558670715	DRAFT_01383	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670715	DRAFT_01383	Coordinates		3515..3835(-)		
2558670715	DRAFT_01383	DNA_length		321bp		
2558670715	DRAFT_01383	Protein_length		106aa		
2558670715	DRAFT_01383	GC			0.54	
2558670716	DRAFT_01384	Locus_type		CDS		
2558670716	DRAFT_01384	Product_name		hypothetical protein		

2558670716	DRAFT_01384	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670716	DRAFT_01384	Coordinates		3863..4150(-)		
2558670716	DRAFT_01384	DNA_length		288bp		
2558670716	DRAFT_01384	Protein_length		95aa		
2558670716	DRAFT_01384	GC			0.54	
2558670717	DRAFT_01385	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2558670717	DRAFT_01385	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2558670717	DRAFT_01385	Metacyc	PWY-6527: stachyose degradation			
2558670717	DRAFT_01385	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			
2558670717	DRAFT_01385	Metacyc	PWY-3821: galactose degradation III			
2558670717	DRAFT_01385	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2558670717	DRAFT_01385	Metacyc	PWY-6397: mycolyl-arabinogalactan-peptidoglycan complex biosynthesis			
2558670717	DRAFT_01385	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558670717	DRAFT_01385	COG_category	[G] Carbohydrate transport and metabolism			
2558670717	DRAFT_01385	COG0451	Nucleoside-diphosphate-sugar epimerases			1.00E-47
2558670717	DRAFT_01385	pfam01370	Epimerase			1.40E-41
2558670717	DRAFT_01385	EC:5.1.3.2	UDP-glucose 4-epimerase.			
2558670717	DRAFT_01385	KO:K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]			0.00E+00
2558670717	DRAFT_01385	Locus_type		CDS		
2558670717	DRAFT_01385	Product_name		Nucleoside-diphosphate-sugar epimerases		
2558670717	DRAFT_01385	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670717	DRAFT_01385	Coordinates		4482..5453(-)		
2558670717	DRAFT_01385	DNA_length		972bp		
2558670717	DRAFT_01385	Protein_length		323aa		
2558670717	DRAFT_01385	GC			0.53	
2558670718	DRAFT_01386	Locus_type		CDS		
2558670718	DRAFT_01386	Product_name		hypothetical protein		
2558670718	DRAFT_01386	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670718	DRAFT_01386	Coordinates		5922..6341(+)		
2558670718	DRAFT_01386	DNA_length		420bp		
2558670718	DRAFT_01386	Protein_length		139aa		
2558670718	DRAFT_01386	GC			0.56	

2558670718	DRAFT_01386	Transmembrane		Yes	
2558670719	DRAFT_01387	Locus_type		CDS	
2558670719	DRAFT_01387	Product_name		hypothetical protein	
2558670719	DRAFT_01387	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32	
2558670719	DRAFT_01387	Coordinates		6427..6951(+)	
2558670719	DRAFT_01387	DNA_length		525bp	
2558670719	DRAFT_01387	Protein_length		174aa	
2558670719	DRAFT_01387	GC		0.57	
2558670719	DRAFT_01387	Transmembrane		Yes	
2558670720	DRAFT_01388	Locus_type		CDS	
2558670720	DRAFT_01388	Product_name		hypothetical protein	
2558670720	DRAFT_01388	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32	
2558670720	DRAFT_01388	Coordinates		7094..7498(+)	
2558670720	DRAFT_01388	DNA_length		405bp	
2558670720	DRAFT_01388	Protein_length		134aa	
2558670720	DRAFT_01388	GC		0.58	
2558670721	DRAFT_01389	COG_category	[K] Transcription		
2558670721	DRAFT_01389	COG3432	Predicted transcriptional regulator		2.00E-11
2558670721	DRAFT_01389	pfam14947	HTH_45		1.60E-16
2558670721	DRAFT_01389	Locus_type		CDS	
2558670721	DRAFT_01389	Product_name		Predicted transcriptional regulator	
2558670721	DRAFT_01389	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32	
2558670721	DRAFT_01389	Coordinates		7588..7902(-)	
2558670721	DRAFT_01389	DNA_length		315bp	
2558670721	DRAFT_01389	Protein_length		104aa	
2558670721	DRAFT_01389	GC		0.59	
2558670722	DRAFT_01390	Locus_type		CDS	
2558670722	DRAFT_01390	Product_name		hypothetical protein	
2558670722	DRAFT_01390	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32	
2558670722	DRAFT_01390	Coordinates		8307..8930(+)	

2558670722	DRAFT_01390	DNA_length		624bp		
2558670722	DRAFT_01390	Protein_length		207aa		
2558670722	DRAFT_01390	GC			0.57	
2558670723	DRAFT_01391	Locus_type		CDS		
2558670723	DRAFT_01391	Product_name		hypothetical protein		
2558670723	DRAFT_01391	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670723	DRAFT_01391	Coordinates		8989..9438(+)		
2558670723	DRAFT_01391	DNA_length		450bp		
2558670723	DRAFT_01391	Protein_length		149aa		
2558670723	DRAFT_01391	GC			0.56	
2558670723	DRAFT_01391	Transmembrane		Yes		
2558670724	DRAFT_01392	Locus_type		CDS		
2558670724	DRAFT_01392	Product_name		hypothetical protein		
2558670724	DRAFT_01392	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670724	DRAFT_01392	Coordinates		9489..9950(+)		
2558670724	DRAFT_01392	DNA_length		462bp		
2558670724	DRAFT_01392	Protein_length		153aa		
2558670724	DRAFT_01392	GC			0.57	
2558670725	DRAFT_01393	Locus_type		CDS		
2558670725	DRAFT_01393	Product_name		hypothetical protein		
2558670725	DRAFT_01393	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670725	DRAFT_01393	Coordinates		10056..10442(+)		
2558670725	DRAFT_01393	DNA_length		387bp		
2558670725	DRAFT_01393	Protein_length		128aa		
2558670725	DRAFT_01393	GC			0.56	
2558670726	DRAFT_01394	COG_category	[K] Transcription			
2558670726	DRAFT_01394	COG3432	Predicted transcriptional regulator			8.00E-17
2558670726	DRAFT_01394	pfam14947	HTH_45			2.60E-19
2558670726	DRAFT_01394	Locus_type		CDS		
2558670726	DRAFT_01394	Product_name		Predicted transcriptional regulator		

2558670726	DRAFT_01394	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670726	DRAFT_01394	Coordinates		10612..11010(+)		
2558670726	DRAFT_01394	DNA_length		399bp		
2558670726	DRAFT_01394	Protein_length		132aa		
2558670726	DRAFT_01394	GC			0.56	
2558670727	DRAFT_01395	COG_category	[K] Transcription			
2558670727	DRAFT_01395	COG3432	Predicted transcriptional regulator			3.00E-09
2558670727	DRAFT_01395	pfam14947	HTH_45			1.50E-17
2558670727	DRAFT_01395	Locus_type		CDS		
2558670727	DRAFT_01395	Product_name		Predicted transcriptional regulator		
2558670727	DRAFT_01395	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670727	DRAFT_01395	Coordinates		10970..11296(-)		
2558670727	DRAFT_01395	DNA_length		327bp		
2558670727	DRAFT_01395	Protein_length		108aa		
2558670727	DRAFT_01395	GC			0.55	
2558670728	DRAFT_01396	COG_category	[R] General function prediction only			
2558670728	DRAFT_01396	COG1719	Predicted hydrocarbon binding protein (contains V4R domain)			3.00E-10
2558670728	DRAFT_01396	pfam02830	V4R			5.90E-13
2558670728	DRAFT_01396	Locus_type		CDS		
2558670728	DRAFT_01396	Product_name		Predicted hydrocarbon binding protein (contains V4R domain)		
2558670728	DRAFT_01396	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670728	DRAFT_01396	Coordinates		11436..11963(-)		
2558670728	DRAFT_01396	DNA_length		528bp		
2558670728	DRAFT_01396	Protein_length		175aa		
2558670728	DRAFT_01396	GC			0.6	
2558670729	DRAFT_01397	pfam08241	Methyltransf_11			7.40E-17
2558670729	DRAFT_01397	Locus_type		CDS		
2558670729	DRAFT_01397	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2558670729	DRAFT_01397	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670729	DRAFT_01397	Coordinates		12042..12842(-)		
2558670729	DRAFT_01397	DNA_length		801bp		

2558670729	DRAFT_01397	Protein_length		266aa		
2558670729	DRAFT_01397	GC			0.61	
2558670729	DRAFT_01397	Transmembrane		Yes		
2558670730	DRAFT_01398	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2558670730	DRAFT_01398	COG_category	[N] Cell motility			
2558670730	DRAFT_01398	COG1955	Archaeal flagella assembly protein J			3.00E-23
2558670730	DRAFT_01398	pfam00482	T2SF			4.80E-06
2558670730	DRAFT_01398	pfam00482	T2SF			1.70E-09
2558670730	DRAFT_01398	KO:K07333	archaeal flagellar protein FlaJ			0.00E+00
2558670730	DRAFT_01398	Locus_type		CDS		
2558670730	DRAFT_01398	Product_name		Archaeal flagella assembly protein J		
2558670730	DRAFT_01398	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670730	DRAFT_01398	Coordinates		12900..14645(-)		
2558670730	DRAFT_01398	DNA_length		1746bp		
2558670730	DRAFT_01398	Protein_length		581aa		
2558670730	DRAFT_01398	GC			0.56	
2558670730	DRAFT_01398	Transmembrane		Yes		
2558670730	DRAFT_01398	Fused_gene		Yes		
2558670731	DRAFT_01399	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2558670731	DRAFT_01399	COG_category	[N] Cell motility			
2558670731	DRAFT_01399	COG0630	Type IV secretory pathway, VirB11 components, and related ATPases ir			3.00E-77
2558670731	DRAFT_01399	pfam00437	T2SE			1.90E-47
2558670731	DRAFT_01399	KO:K07332	archaeal flagellar protein FlaI			0.00E+00
2558670731	DRAFT_01399	Locus_type		CDS		
2558670731	DRAFT_01399	Product_name		Type IV secretory pathway, VirB11 components, and related ATPases		
2558670731	DRAFT_01399	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32		
2558670731	DRAFT_01399	Coordinates		14642..16267(-)		
2558670731	DRAFT_01399	DNA_length		1626bp		
2558670731	DRAFT_01399	Protein_length		541aa		
2558670731	DRAFT_01399	GC			0.57	
2558670732	DRAFT_01400	Locus_type		CDS		

2558670732	DRAFT_01400	Product_name		hypothetical protein	
2558670732	DRAFT_01400	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32	
2558670732	DRAFT_01400	Coordinates		16736..16957(-)	
2558670732	DRAFT_01400	DNA_length		222bp	
2558670732	DRAFT_01400	Protein_length		73aa	
2558670732	DRAFT_01400	GC		0.52	
2558670733	DRAFT_01401	Locus_type		CDS	
2558670733	DRAFT_01401	Product_name		hypothetical protein	
2558670733	DRAFT_01401	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32	
2558670733	DRAFT_01401	Coordinates		17005..17436(+)	
2558670733	DRAFT_01401	DNA_length		432bp	
2558670733	DRAFT_01401	Protein_length		143aa	
2558670733	DRAFT_01401	GC		0.57	
2558670734	DRAFT_01402	Locus_type		CDS	
2558670734	DRAFT_01402	Product_name		hypothetical protein	
2558670734	DRAFT_01402	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32	
2558670734	DRAFT_01402	Coordinates		17455..18000(+)	
2558670734	DRAFT_01402	DNA_length		546bp	
2558670734	DRAFT_01402	Protein_length		181aa	
2558670734	DRAFT_01402	GC		0.6	
2558670735	DRAFT_01403	Locus_type		CDS	
2558670735	DRAFT_01403	Product_name		hypothetical protein	
2558670735	DRAFT_01403	Scaffold		DRAFT_contig_70_243_len_18171_read_count_294079.32	
2558670735	DRAFT_01403	Coordinates		18019..18168(+)	
2558670735	DRAFT_01403	DNA_length		150bp	
2558670735	DRAFT_01403	Protein_length		50aa	
2558670735	DRAFT_01403	GC		0.55	
2558670736	DRAFT_01404	COG_category	[R] General function prediction only		
2558670736	DRAFT_01404	COG1201	Lhr-like helicases		0.00E+00
2558670736	DRAFT_01404	pfam00271	Helicase_C		5.00E-13

2558670736	DRAFT_01404	pfam08494	DEAD_assoc			4.40E-11
2558670736	DRAFT_01404	pfam00270	DEAD			9.90E-31
2558670736	DRAFT_01404	EC:3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; involved in cellular and subc			
2558670736	DRAFT_01404	KO:K03724	ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.4.-]			0.00E+00
2558670736	DRAFT_01404	ITERM:05263	ATP dependent helicase, Lhr family			
2558670736	DRAFT_01404	Locus_type		CDS		
2558670736	DRAFT_01404	Product_name		ATP dependent helicase, Lhr family		
2558670736	DRAFT_01404	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670736	DRAFT_01404	Coordinates		3..2051(-)		
2558670736	DRAFT_01404	DNA_length		2049bp		
2558670736	DRAFT_01404	Protein_length		683aa		
2558670736	DRAFT_01404	GC			0.59	

2558670737	DRAFT_01405	COG_category	[R] General function prediction only			
2558670737	DRAFT_01405	COG2522	Predicted transcriptional regulator			4.00E-12
2558670737	DRAFT_01405	Locus_type		CDS		
2558670737	DRAFT_01405	Product_name		Predicted transcriptional regulator		
2558670737	DRAFT_01405	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670737	DRAFT_01405	Coordinates		2240..2665(+)		
2558670737	DRAFT_01405	DNA_length		426bp		
2558670737	DRAFT_01405	Protein_length		141aa		
2558670737	DRAFT_01405	GC			0.58	

2558670738	DRAFT_01406	Metacyc	PWY-6987: lipoate biosynthesis and incorporation III (Bacillus)			
2558670738	DRAFT_01406	Metacyc	PWY0-1275: lipoate biosynthesis and incorporation II			
2558670738	DRAFT_01406	Metacyc	PWY0-501: lipoate biosynthesis and incorporation I			
2558670738	DRAFT_01406	COG_category	[H] Coenzyme transport and metabolism			
2558670738	DRAFT_01406	COG0320	Lipoate synthase			3.00E-114
2558670738	DRAFT_01406	pfam04055	Radical_SAM			3.30E-09
2558670738	DRAFT_01406	EC:2.8.1.8	Lipoyl synthase.			
2558670738	DRAFT_01406	TIGR00510	lipoate synthase			2.40E-113
2558670738	DRAFT_01406	KO:K03644	lipoic acid synthetase [EC:2.8.1.8]			0.00E+00
2558670738	DRAFT_01406	Locus_type		CDS		
2558670738	DRAFT_01406	Product_name		lipoate synthase		

2558670738	DRAFT_01406	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33	
2558670738	DRAFT_01406	Coordinates		2667..3581(+)	
2558670738	DRAFT_01406	DNA_length		915bp	
2558670738	DRAFT_01406	Protein_length		304aa	
2558670738	DRAFT_01406	GC		0.6	
2558670739	DRAFT_01407	pfam00364	Biotin_lipoyl		1.20E-24
2558670739	DRAFT_01407	Locus_type		CDS	
2558670739	DRAFT_01407	Product_name		Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide	
2558670739	DRAFT_01407	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33	
2558670739	DRAFT_01407	Coordinates		3646..3930(+)	
2558670739	DRAFT_01407	DNA_length		285bp	
2558670739	DRAFT_01407	Protein_length		94aa	
2558670739	DRAFT_01407	GC		0.56	
2558670740	DRAFT_01408	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA		
2558670740	DRAFT_01408	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)		
2558670740	DRAFT_01408	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670740	DRAFT_01408	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA		
2558670740	DRAFT_01408	Metacyc	PWY-5084: 2-oxoglutarate decarboxylation to succinyl-CoA		
2558670740	DRAFT_01408	Metacyc	PWY-5046: 2-oxoisovalerate decarboxylation to isobutanoyl-CoA		
2558670740	DRAFT_01408	Metacyc	PYRUVDEHYD-PWY: pyruvate decarboxylation to acetyl CoA		
2558670740	DRAFT_01408	Metacyc	GLYCLEAV-PWY: glycine cleavage		
2558670740	DRAFT_01408	COG_category	[C] Energy production and conversion		
2558670740	DRAFT_01408	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide d		0.00E+00
2558670740	DRAFT_01408	pfam00070	Pyr_redox		1.80E-21
2558670740	DRAFT_01408	pfam02852	Pyr_redox_dim		7.40E-37
2558670740	DRAFT_01408	pfam07992	Pyr_redox_2		8.30E-38
2558670740	DRAFT_01408	EC:1.8.1.4	Dihydrolipoyl dehydrogenase.		
2558670740	DRAFT_01408	TIGR01350	dihydrolipoamide dehydrogenase		0.00E+00
2558670740	DRAFT_01408	KO:K00382	dihydrolipoamide dehydrogenase [EC:1.8.1.4]		0.00E+00
2558670740	DRAFT_01408	Locus_type		CDS	
2558670740	DRAFT_01408	Product_name		dihydrolipoamide dehydrogenase	
2558670740	DRAFT_01408	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33	

2558670740	DRAFT_01408	Coordinates		3992..5389(+)	
2558670740	DRAFT_01408	DNA_length		1398bp	
2558670740	DRAFT_01408	Protein_length		465aa	
2558670740	DRAFT_01408	GC		0.6	
2558670741	DRAFT_01409	Metacyc	PWY-6987: lipoate biosynthesis and incorporation III (Bacillus)		
2558670741	DRAFT_01409	Metacyc	PWY0-501: lipoate biosynthesis and incorporation I		
2558670741	DRAFT_01409	COG_category	[H] Coenzyme transport and metabolism		
2558670741	DRAFT_01409	COG0321	Lipoate-protein ligase B		2.00E-54
2558670741	DRAFT_01409	pfam03099	BPL_LplA_LipB		1.10E-17
2558670741	DRAFT_01409	EC:2.3.1.181	Lipoyl(octanoyl) transferase.		
2558670741	DRAFT_01409	TIGR00214	lipoate-protein ligase B		9.50E-49
2558670741	DRAFT_01409	KO:K03801	lipoyl(octanoyl) transferase [EC:2.3.1.181]		2.80E-45
2558670741	DRAFT_01409	Locus_type		CDS	
2558670741	DRAFT_01409	Product_name		lipoate-protein ligase B	
2558670741	DRAFT_01409	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33	
2558670741	DRAFT_01409	Coordinates		5386..6042(+)	
2558670741	DRAFT_01409	DNA_length		657bp	
2558670741	DRAFT_01409	Protein_length		218aa	
2558670741	DRAFT_01409	GC		0.61	
2558670742	DRAFT_01410	Metacyc	HYDROXYPRODEG-PWY: 4-hydroxyproline degradation I		
2558670742	DRAFT_01410	COG_category	[C] Energy production and conversion		
2558670742	DRAFT_01410	COG1012	NAD-dependent aldehyde dehydrogenases		4.00E-104
2558670742	DRAFT_01410	pfam00171	Aldedh		0.00E+00
2558670742	DRAFT_01410	EC:1.5.1.12	1-pyrroline-5-carboxylate dehydrogenase.		
2558670742	DRAFT_01410	KO:K00294	1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]		0.00E+00
2558670742	DRAFT_01410	Locus_type		CDS	
2558670742	DRAFT_01410	Product_name		NAD-dependent aldehyde dehydrogenases	
2558670742	DRAFT_01410	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33	
2558670742	DRAFT_01410	Coordinates		6066..7646(+)	
2558670742	DRAFT_01410	DNA_length		1581bp	
2558670742	DRAFT_01410	Protein_length		526aa	
2558670742	DRAFT_01410	GC		0.61	

2558670743	DRAFT_01411	KEGG_module	M00178: Ribosome, bacteria			
2558670743	DRAFT_01411	KEGG_module	M00179: Ribosome, archaea			
2558670743	DRAFT_01411	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670743	DRAFT_01411	COG0185	Ribosomal protein S19			2.00E-26
2558670743	DRAFT_01411	pfam00203	Ribosomal_S19			2.00E-25
2558670743	DRAFT_01411	TIGR01025	ribosomal protein S19(archaeal)/S15(eukaryotic)			1.90E-56
2558670743	DRAFT_01411	KO:K02965	small subunit ribosomal protein S19			4.10E-41
2558670743	DRAFT_01411	Locus_type		CDS		
2558670743	DRAFT_01411	Product_name		SSU ribosomal protein S19P		
2558670743	DRAFT_01411	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670743	DRAFT_01411	Coordinates		7819..8214(-)		
2558670743	DRAFT_01411	DNA_length		396bp		
2558670743	DRAFT_01411	Protein_length		131aa		
2558670743	DRAFT_01411	GC			0.58	
2558670744	DRAFT_01412	KEGG_module	M00179: Ribosome, archaea			
2558670744	DRAFT_01412	KEGG_module	M00178: Ribosome, bacteria			
2558670744	DRAFT_01412	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670744	DRAFT_01412	COG0090	Ribosomal protein L2			1.00E-51
2558670744	DRAFT_01412	pfam03947	Ribosomal_L2_C			2.20E-38
2558670744	DRAFT_01412	KO:K02886	large subunit ribosomal protein L2			0.00E+00
2558670744	DRAFT_01412	Locus_type		CDS		
2558670744	DRAFT_01412	Product_name		Ribosomal protein L2		
2558670744	DRAFT_01412	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670744	DRAFT_01412	Coordinates		8215..8958(-)		
2558670744	DRAFT_01412	DNA_length		744bp		
2558670744	DRAFT_01412	Protein_length		247aa		
2558670744	DRAFT_01412	GC			0.6	
2558670745	DRAFT_01413	KEGG_module	M00178: Ribosome, bacteria			
2558670745	DRAFT_01413	KEGG_module	M00179: Ribosome, archaea			
2558670745	DRAFT_01413	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670745	DRAFT_01413	COG0089	Ribosomal protein L23			6.00E-13

2558670745	DRAFT_01413	pfam00276	Ribosomal_L23			7.10E-15
2558670745	DRAFT_01413	TIGR03636	archaeal ribosomal protein L23			4.30E-31
2558670745	DRAFT_01413	KO:K02892	large subunit ribosomal protein L23			7.10E-21
2558670745	DRAFT_01413	Locus_type		CDS		
2558670745	DRAFT_01413	Product_name		Ribosomal protein L23		
2558670745	DRAFT_01413	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670745	DRAFT_01413	Coordinates		8962..9228(-)		
2558670745	DRAFT_01413	DNA_length		267bp		
2558670745	DRAFT_01413	Protein_length		88aa		
2558670745	DRAFT_01413	GC			0.56	

2558670746	DRAFT_01414	KEGG_module	M00177: Ribosome, eukaryotes			
2558670746	DRAFT_01414	KEGG_module	M00179: Ribosome, archaea			
2558670746	DRAFT_01414	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670746	DRAFT_01414	COG0088	Ribosomal protein L4			4.00E-20
2558670746	DRAFT_01414	pfam00573	Ribosomal_L4			2.40E-28
2558670746	DRAFT_01414	KO:K02930	large subunit ribosomal protein L4e			4.00E-41
2558670746	DRAFT_01414	Locus_type		CDS		
2558670746	DRAFT_01414	Product_name		Ribosomal protein L4		
2558670746	DRAFT_01414	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670746	DRAFT_01414	Coordinates		9218..9874(-)		
2558670746	DRAFT_01414	DNA_length		657bp		
2558670746	DRAFT_01414	Protein_length		218aa		
2558670746	DRAFT_01414	GC			0.61	

2558670747	DRAFT_01415	KEGG_module	M00178: Ribosome, bacteria			
2558670747	DRAFT_01415	KEGG_module	M00179: Ribosome, archaea			
2558670747	DRAFT_01415	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670747	DRAFT_01415	COG0087	Ribosomal protein L3			3.00E-28
2558670747	DRAFT_01415	pfam00297	Ribosomal_L3			2.50E-48
2558670747	DRAFT_01415	KO:K02906	large subunit ribosomal protein L3			0.00E+00
2558670747	DRAFT_01415	Locus_type		CDS		
2558670747	DRAFT_01415	Product_name		Ribosomal protein L3		
2558670747	DRAFT_01415	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		

2558670747	DRAFT_01415	Coordinates		10030..10977(-)	
2558670747	DRAFT_01415	DNA_length		948bp	
2558670747	DRAFT_01415	Protein_length		315aa	
2558670747	DRAFT_01415	GC		0.6	
2558670748	DRAFT_01416	COG_category	[S] Function unknown		
2558670748	DRAFT_01416	COG2106	Uncharacterized conserved protein		3.00E-45
2558670748	DRAFT_01416	pfam02598	Methyltrn_RNA_3		9.40E-47
2558670748	DRAFT_01416	KO:K09142	hypothetical protein		1.80E-43
2558670748	DRAFT_01416	Locus_type		CDS	
2558670748	DRAFT_01416	Product_name		Uncharacterized conserved protein	
2558670748	DRAFT_01416	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33	
2558670748	DRAFT_01416	Coordinates		11029..11844(-)	
2558670748	DRAFT_01416	DNA_length		816bp	
2558670748	DRAFT_01416	Protein_length		271aa	
2558670748	DRAFT_01416	GC		0.59	
2558670749	DRAFT_01417	Locus_type		CDS	
2558670749	DRAFT_01417	Product_name		hypothetical protein	
2558670749	DRAFT_01417	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33	
2558670749	DRAFT_01417	Coordinates		11928..13247(+)	
2558670749	DRAFT_01417	DNA_length		1320bp	
2558670749	DRAFT_01417	Protein_length		439aa	
2558670749	DRAFT_01417	GC		0.6	
2558670749	DRAFT_01417	Transmembrane		Yes	
2558670750	DRAFT_01418	Locus_type		CDS	
2558670750	DRAFT_01418	Product_name		hypothetical protein	
2558670750	DRAFT_01418	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33	
2558670750	DRAFT_01418	Coordinates		13300..13602(+)	
2558670750	DRAFT_01418	DNA_length		303bp	
2558670750	DRAFT_01418	Protein_length		100aa	
2558670750	DRAFT_01418	GC		0.55	

2558670751	DRAFT_01419	COG_category	[G] Carbohydrate transport and metabolism			
2558670751	DRAFT_01419	COG2814	Arabinose efflux permease			8.00E-11
2558670751	DRAFT_01419	pfam07690	MFS_1			6.10E-53
2558670751	DRAFT_01419	TIGR00711	drug resistance transporter, EmrB/QacA subfamily			2.20E-59
2558670751	DRAFT_01419	Locus_type		CDS		
2558670751	DRAFT_01419	Product_name		Arabinose efflux permease		
2558670751	DRAFT_01419	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670751	DRAFT_01419	Coordinates		13614..15101(+)		
2558670751	DRAFT_01419	DNA_length		1488bp		
2558670751	DRAFT_01419	Protein_length		495aa		
2558670751	DRAFT_01419	GC			0.58	
2558670751	DRAFT_01419	Transmembrane		Yes		
2558670752	DRAFT_01420	COG_category	[S] Function unknown			
2558670752	DRAFT_01420	COG3372	Uncharacterized conserved protein			3.00E-86
2558670752	DRAFT_01420	pfam05626	DUF790			1.70E-117
2558670752	DRAFT_01420	KO:K09744	hypothetical protein			0.00E+00
2558670752	DRAFT_01420	Locus_type		CDS		
2558670752	DRAFT_01420	Product_name		Uncharacterized conserved protein		
2558670752	DRAFT_01420	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670752	DRAFT_01420	Coordinates		15232..16818(-)		
2558670752	DRAFT_01420	DNA_length		1587bp		
2558670752	DRAFT_01420	Protein_length		528aa		
2558670752	DRAFT_01420	GC			0.57	
2558670753	DRAFT_01421	pfam00271	Helicase_C			1.40E-14
2558670753	DRAFT_01421	Locus_type		CDS		
2558670753	DRAFT_01421	Product_name		DNA or RNA helicases of superfamily II		
2558670753	DRAFT_01421	Scaffold		DRAFT_contig_70_262_len_17398_read_count_287202.33		
2558670753	DRAFT_01421	Coordinates		16818..17396(-)		
2558670753	DRAFT_01421	DNA_length		579bp		
2558670753	DRAFT_01421	Protein_length		192aa		
2558670753	DRAFT_01421	GC			0.59	

2558670754	DRAFT_01422	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670754	DRAFT_01422	COG1236	Predicted exonuclease of the beta-lactamase fold involved in RNA proc		3.00E-78
2558670754	DRAFT_01422	pfam10996	Beta-Casp		2.90E-17
2558670754	DRAFT_01422	pfam00753	Lactamase_B		9.50E-15
2558670754	DRAFT_01422	pfam07521	RMMBL		3.20E-05
2558670754	DRAFT_01422	KO:K07577	putative mRNA 3-end processing factor		0.00E+00
2558670754	DRAFT_01422	Locus_type		CDS	
2558670754	DRAFT_01422	Product_name		Predicted exonuclease of the beta-lactamase fold involved in RNA prc	
2558670754	DRAFT_01422	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670754	DRAFT_01422	Coordinates		2..1276(+)	
2558670754	DRAFT_01422	DNA_length		1275bp	
2558670754	DRAFT_01422	Protein_length		424aa	
2558670754	DRAFT_01422	GC		0.58	
2558670755	DRAFT_01423	Locus_type		CDS	
2558670755	DRAFT_01423	Product_name		hypothetical protein	
2558670755	DRAFT_01423	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670755	DRAFT_01423	Coordinates		1273..2151(+)	
2558670755	DRAFT_01423	DNA_length		879bp	
2558670755	DRAFT_01423	Protein_length		292aa	
2558670755	DRAFT_01423	GC		0.6	
2558670755	DRAFT_01423	Transmembrane		Yes	
2558670756	DRAFT_01424	pfam01781	Ribosomal_L38e		3.40E-05
2558670756	DRAFT_01424	Locus_type		CDS	
2558670756	DRAFT_01424	Product_name		Ribosomal L38e protein family	
2558670756	DRAFT_01424	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670756	DRAFT_01424	Coordinates		2139..2345(-)	
2558670756	DRAFT_01424	DNA_length		207bp	
2558670756	DRAFT_01424	Protein_length		68aa	
2558670756	DRAFT_01424	GC		0.56	
2558670757	DRAFT_01425	COG_category	[R] General function prediction only		
2558670757	DRAFT_01425	COG3269	Predicted RNA-binding protein, contains TRAM domain		9.00E-13

2558670757	DRAFT_01425	pfam01938	TRAM			1.00E-11
2558670757	DRAFT_01425	Locus_type		CDS		
2558670757	DRAFT_01425	Product_name		Predicted RNA-binding protein, contains TRAM domain		
2558670757	DRAFT_01425	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34		
2558670757	DRAFT_01425	Coordinates		2620..2928(+)		
2558670757	DRAFT_01425	DNA_length		309bp		
2558670757	DRAFT_01425	Protein_length		102aa		
2558670757	DRAFT_01425	GC			0.58	
2558670758	DRAFT_01426	COG_category	[L] Replication, recombination and repair			
2558670758	DRAFT_01426	COG0328	Ribonuclease HI			7.00E-16
2558670758	DRAFT_01426	pfam13456	RVT_3			9.00E-18
2558670758	DRAFT_01426	EC:3.1.26.4	Ribonuclease H.			
2558670758	DRAFT_01426	KO:K03469	ribonuclease HI [EC:3.1.26.4]			1.70E-26
2558670758	DRAFT_01426	Locus_type		CDS		
2558670758	DRAFT_01426	Product_name		Ribonuclease HI		
2558670758	DRAFT_01426	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34		
2558670758	DRAFT_01426	Coordinates		3236..3646(+)		
2558670758	DRAFT_01426	DNA_length		411bp		
2558670758	DRAFT_01426	Protein_length		136aa		
2558670758	DRAFT_01426	GC			0.54	
2558670759	DRAFT_01427	pfam13508	Acetyltransf_7			6.30E-12
2558670759	DRAFT_01427	Locus_type		CDS		
2558670759	DRAFT_01427	Product_name		Acetyltransferases		
2558670759	DRAFT_01427	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34		
2558670759	DRAFT_01427	Coordinates		4395..4832(+)		
2558670759	DRAFT_01427	DNA_length		438bp		
2558670759	DRAFT_01427	Protein_length		145aa		
2558670759	DRAFT_01427	GC			0.5	
2558670760	DRAFT_01428	KEGG_module	M00258: Putative ABC transport system			
2558670760	DRAFT_01428	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558670760	DRAFT_01428	COG4591	ABC-type transport system, involved in lipoprotein release, permease c			2.00E-36

2558670760	DRAFT_01428	pfam12704	MacB_PCD		4.20E-33
2558670760	DRAFT_01428	pfam02687	FtsX		3.10E-25
2558670760	DRAFT_01428	KO:K02004	putative ABC transport system permease protein		0.00E+00
2558670760	DRAFT_01428	Locus_type		CDS	
2558670760	DRAFT_01428	Product_name		ABC-type transport system, involved in lipoprotein release, permease	
2558670760	DRAFT_01428	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670760	DRAFT_01428	Coordinates		5428..6687(+)	
2558670760	DRAFT_01428	DNA_length		1260bp	
2558670760	DRAFT_01428	Protein_length		419aa	
2558670760	DRAFT_01428	GC		0.59	
2558670760	DRAFT_01428	Transmembrane		Yes	

2558670761	DRAFT_01429	KEGG_module	M00258: Putative ABC transport system		
2558670761	DRAFT_01429	COG_category	[V] Defense mechanisms		
2558670761	DRAFT_01429	COG1136	ABC-type antimicrobial peptide transport system, ATPase component		3.00E-79
2558670761	DRAFT_01429	pfam00005	ABC_tran		3.20E-34
2558670761	DRAFT_01429	KO:K02003	putative ABC transport system ATP-binding protein		0.00E+00
2558670761	DRAFT_01429	Locus_type		CDS	
2558670761	DRAFT_01429	Product_name		ABC-type antimicrobial peptide transport system, ATPase component	
2558670761	DRAFT_01429	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670761	DRAFT_01429	Coordinates		6680..7423(+)	
2558670761	DRAFT_01429	DNA_length		744bp	
2558670761	DRAFT_01429	Protein_length		247aa	
2558670761	DRAFT_01429	GC		0.59	

2558670762	DRAFT_01430	Locus_type		CDS	
2558670762	DRAFT_01430	Product_name		hypothetical protein	
2558670762	DRAFT_01430	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670762	DRAFT_01430	Coordinates		7566..8072(-)	
2558670762	DRAFT_01430	DNA_length		507bp	
2558670762	DRAFT_01430	Protein_length		168aa	
2558670762	DRAFT_01430	GC		0.54	

2558670763	DRAFT_01431	pfam13659	Methyltransf_26		1.70E-06

2558670763	DRAFT_01431	Locus_type		CDS		
2558670763	DRAFT_01431	Product_name		Methyltransferase domain		
2558670763	DRAFT_01431	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34		
2558670763	DRAFT_01431	Coordinates		8294..8722(-)		
2558670763	DRAFT_01431	DNA_length		429bp		
2558670763	DRAFT_01431	Protein_length		142aa		
2558670763	DRAFT_01431	GC			0.57	
2558670763	DRAFT_01431	Transmembrane		Yes		
2558670764	DRAFT_01432	COG_category	[C] Energy production and conversion			
2558670764	DRAFT_01432	COG0778	Nitroreductase			5.00E-18
2558670764	DRAFT_01432	pfam00881	Nitroreductase			2.00E-30
2558670764	DRAFT_01432	Locus_type		CDS		
2558670764	DRAFT_01432	Product_name		Nitroreductase		
2558670764	DRAFT_01432	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34		
2558670764	DRAFT_01432	Coordinates		8949..9668(+)		
2558670764	DRAFT_01432	DNA_length		720bp		
2558670764	DRAFT_01432	Protein_length		239aa		
2558670764	DRAFT_01432	GC			0.57	
2558670765	DRAFT_01433	COG_category	[R] General function prediction only			
2558670765	DRAFT_01433	COG0300	Short-chain dehydrogenases of various substrate specificities			2.00E-40
2558670765	DRAFT_01433	pfam00106	adh_short			4.10E-26
2558670765	DRAFT_01433	Locus_type		CDS		
2558670765	DRAFT_01433	Product_name		Short-chain dehydrogenases of various substrate specificities		
2558670765	DRAFT_01433	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34		
2558670765	DRAFT_01433	Coordinates		9722..10513(+)		
2558670765	DRAFT_01433	DNA_length		792bp		
2558670765	DRAFT_01433	Protein_length		263aa		
2558670765	DRAFT_01433	GC			0.59	
2558670766	DRAFT_01434	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670766	DRAFT_01434	COG1180	Pyruvate-formate lyase-activating enzyme			1.00E-38
2558670766	DRAFT_01434	pfam04055	Radical_SAM			2.80E-26

2558670766	DRAFT_01434	pfam13353	Fer4_12		7.00E-12
2558670766	DRAFT_01434	EC:1.97.1.4	[Formate-C-acetyltransferase]-activating enzyme.		
2558670766	DRAFT_01434	TIGR02494	glycyl-radical enzyme activating protein family		5.90E-105
2558670766	DRAFT_01434	KO:K04069	pyruvate formate lyase activating enzyme [EC:1.97.1.4]		0.00E+00
2558670766	DRAFT_01434	Locus_type		CDS	
2558670766	DRAFT_01434	Product_name		glycyl-radical enzyme activating protein family	
2558670766	DRAFT_01434	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670766	DRAFT_01434	Coordinates		10660..11649(-)	
2558670766	DRAFT_01434	DNA_length		990bp	
2558670766	DRAFT_01434	Protein_length		329aa	
2558670766	DRAFT_01434	GC		0.55	
2558670767	DRAFT_01435	Metacyc	PWY-5493: reductive monocarboxylic acid cycle		
2558670767	DRAFT_01435	Metacyc	PWY4LZ-257: superpathway of fermentation (<i>Chlamydomonas reinhardtii</i>)		
2558670767	DRAFT_01435	Metacyc	ANARESP1-PWY: respiration (anaerobic)		
2558670767	DRAFT_01435	Metacyc	FERMENTATION-PWY: mixed acid fermentation		
2558670767	DRAFT_01435	Metacyc	PWY-5480: pyruvate fermentation to ethanol I		
2558670767	DRAFT_01435	Metacyc	PWY-5485: pyruvate fermentation to acetate IV		
2558670767	DRAFT_01435	COG_category	[C] Energy production and conversion		
2558670767	DRAFT_01435	COG1882	Pyruvate-formate lyase		4.00E-113
2558670767	DRAFT_01435	pfam02901	PFL		0.00E+00
2558670767	DRAFT_01435	pfam01228	Gly_radical		1.20E-25
2558670767	DRAFT_01435	EC:2.3.1.54	Formate C-acetyltransferase.		
2558670767	DRAFT_01435	TIGR01774	glycyl radical enzyme, PFL2/glycerol dehydratase family		0.00E+00
2558670767	DRAFT_01435	KO:K00656	formate C-acetyltransferase [EC:2.3.1.54]		0.00E+00
2558670767	DRAFT_01435	Locus_type		CDS	
2558670767	DRAFT_01435	Product_name		Pyruvate-formate lyase	
2558670767	DRAFT_01435	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670767	DRAFT_01435	Coordinates		11621..14017(-)	
2558670767	DRAFT_01435	DNA_length		2397bp	
2558670767	DRAFT_01435	Protein_length		798aa	
2558670767	DRAFT_01435	GC		0.55	
2558670768	DRAFT_01436	COG_category	[E] Amino acid transport and metabolism		

2558670768	DRAFT_01436	COG2317	Zn-dependent carboxypeptidase		0.00E+00
2558670768	DRAFT_01436	pfam02074	Peptidase_M32		0.00E+00
2558670768	DRAFT_01436	EC:3.4.17.19	Carboxypeptidase Taq.		
2558670768	DRAFT_01436	KO:K01299	carboxypeptidase Taq [EC:3.4.17.19]		0.00E+00
2558670768	DRAFT_01436	Locus_type		CDS	
2558670768	DRAFT_01436	Product_name		carboxypeptidase Pfu. Metallo peptidase. MEROPS family M32	
2558670768	DRAFT_01436	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670768	DRAFT_01436	Coordinates		14188..15858(+)	
2558670768	DRAFT_01436	DNA_length		1671bp	
2558670768	DRAFT_01436	Protein_length		556aa	
2558670768	DRAFT_01436	GC		0.6	
2558670769	DRAFT_01437	pfam00571	CBS		9.30E-15
2558670769	DRAFT_01437	pfam00571	CBS		1.10E-15
2558670769	DRAFT_01437	Locus_type		CDS	
2558670769	DRAFT_01437	Product_name		Predicted signal-transduction protein containing cAMP-binding and C	
2558670769	DRAFT_01437	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670769	DRAFT_01437	Coordinates		16052..16543(+)	
2558670769	DRAFT_01437	DNA_length		492bp	
2558670769	DRAFT_01437	Protein_length		163aa	
2558670769	DRAFT_01437	GC		0.53	
2558670770	DRAFT_01438	Locus_type		CDS	
2558670770	DRAFT_01438	Product_name		hypothetical protein	
2558670770	DRAFT_01438	Scaffold		DRAFT_contig_70_273_len_16991_read_count_274243.34	
2558670770	DRAFT_01438	Coordinates		16703..16990(+)	
2558670770	DRAFT_01438	DNA_length		288bp	
2558670770	DRAFT_01438	Protein_length		96aa	
2558670770	DRAFT_01438	GC		0.52	
2558670771	DRAFT_01439	pfam02239	Cytochrom_D1		4.00E-05
2558670771	DRAFT_01439	pfam05568	ASFV_J13L		3.40E-05
2558670771	DRAFT_01439	TIGR02276	40-residue YVTN family beta-propeller repeat		2.40E-13
2558670771	DRAFT_01439	Locus_type		CDS	

2558670771	DRAFT_01439	Product_name		40-residue YVTN family beta-propeller repeat		
2558670771	DRAFT_01439	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35		
2558670771	DRAFT_01439	Coordinates		1..510(+)		
2558670771	DRAFT_01439	DNA_length		510bp		
2558670771	DRAFT_01439	Protein_length		169aa		
2558670771	DRAFT_01439	GC			0.55	
2558670771	DRAFT_01439	Transmembrane		Yes		
2558670772	DRAFT_01440	pfam00801	PKD			1.50E-08
2558670772	DRAFT_01440	Locus_type		CDS		
2558670772	DRAFT_01440	Product_name		Uncharacterized protein involved in biosynthesis of c-type cytochrom		
2558670772	DRAFT_01440	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35		
2558670772	DRAFT_01440	Coordinates		709..1818(-)		
2558670772	DRAFT_01440	DNA_length		1110bp		
2558670772	DRAFT_01440	Protein_length		369aa		
2558670772	DRAFT_01440	GC			0.57	
2558670772	DRAFT_01440	Transmembrane		Yes		
2558670773	DRAFT_01441	Locus_type		CDS		
2558670773	DRAFT_01441	Product_name		hypothetical protein		
2558670773	DRAFT_01441	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35		
2558670773	DRAFT_01441	Coordinates		2084..2755(-)		
2558670773	DRAFT_01441	DNA_length		672bp		
2558670773	DRAFT_01441	Protein_length		223aa		
2558670773	DRAFT_01441	GC			0.53	
2558670773	DRAFT_01441	Transmembrane		Yes		
2558670774	DRAFT_01442	COG_category	[S] Function unknown			
2558670774	DRAFT_01442	COG3391	Uncharacterized conserved protein			2.00E-13
2558670774	DRAFT_01442	pfam10282	Lactonase			2.10E-04
2558670774	DRAFT_01442	pfam10282	Lactonase			2.90E-04
2558670774	DRAFT_01442	TIGR02276	40-residue YVTN family beta-propeller repeat			2.90E-09
2558670774	DRAFT_01442	Locus_type		CDS		
2558670774	DRAFT_01442	Product_name		Uncharacterized conserved protein		

2558670774	DRAFT_01442	Scaffold	DRAFT_contig_70_281_len_16680_read_count_284862.35
2558670774	DRAFT_01442	Coordinates	3044..4408(+)
2558670774	DRAFT_01442	DNA_length	1365bp
2558670774	DRAFT_01442	Protein_length	454aa
2558670774	DRAFT_01442	GC	0.56
2558670774	DRAFT_01442	Transmembrane	Yes
2558670775	DRAFT_01443	Locus_type	CDS
2558670775	DRAFT_01443	Product_name	hypothetical protein
2558670775	DRAFT_01443	Scaffold	DRAFT_contig_70_281_len_16680_read_count_284862.35
2558670775	DRAFT_01443	Coordinates	4834..7479(+)
2558670775	DRAFT_01443	DNA_length	2646bp
2558670775	DRAFT_01443	Protein_length	881aa
2558670775	DRAFT_01443	GC	0.56
2558670775	DRAFT_01443	Signal_peptide	Yes
2558670775	DRAFT_01443	Transmembrane	Yes
2558670776	DRAFT_01444	Locus_type	CDS
2558670776	DRAFT_01444	Product_name	hypothetical protein
2558670776	DRAFT_01444	Scaffold	DRAFT_contig_70_281_len_16680_read_count_284862.35
2558670776	DRAFT_01444	Coordinates	7611..8003(+)
2558670776	DRAFT_01444	DNA_length	393bp
2558670776	DRAFT_01444	Protein_length	130aa
2558670776	DRAFT_01444	GC	0.59
2558670777	DRAFT_01445	Locus_type	CDS
2558670777	DRAFT_01445	Product_name	hypothetical protein
2558670777	DRAFT_01445	Scaffold	DRAFT_contig_70_281_len_16680_read_count_284862.35
2558670777	DRAFT_01445	Coordinates	8109..8627(-)
2558670777	DRAFT_01445	DNA_length	519bp
2558670777	DRAFT_01445	Protein_length	172aa
2558670777	DRAFT_01445	GC	0.58
2558670777	DRAFT_01445	Transmembrane	Yes

2558670778	DRAFT_01446	Locus_type		CDS	
2558670778	DRAFT_01446	Product_name		hypothetical protein	
2558670778	DRAFT_01446	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35	
2558670778	DRAFT_01446	Coordinates		8658..9485(-)	
2558670778	DRAFT_01446	DNA_length		828bp	
2558670778	DRAFT_01446	Protein_length		275aa	
2558670778	DRAFT_01446	GC		0.55	
2558670778	DRAFT_01446	Transmembrane		Yes	
2558670779	DRAFT_01447	KEGG_module	M00239: Peptides/nickel transport system		
2558670779	DRAFT_01447	COG_category	[E] Amino acid transport and metabolism		
2558670779	DRAFT_01447	COG_category	[P] Inorganic ion transport and metabolism		
2558670779	DRAFT_01447	COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase com		1.00E-90
2558670779	DRAFT_01447	pfam00005	ABC_tran		1.20E-32
2558670779	DRAFT_01447	pfam08352	oligo_HPY		6.70E-18
2558670779	DRAFT_01447	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termin		5.00E-28
2558670779	DRAFT_01447	KO:K02032	peptide/nickel transport system ATP-binding protein		0.00E+00
2558670779	DRAFT_01447	Locus_type		CDS	
2558670779	DRAFT_01447	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termi	
2558670779	DRAFT_01447	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35	
2558670779	DRAFT_01447	Coordinates		9472..10527(-)	
2558670779	DRAFT_01447	DNA_length		1056bp	
2558670779	DRAFT_01447	Protein_length		351aa	
2558670779	DRAFT_01447	GC		0.58	
2558670780	DRAFT_01448	KEGG_module	M00239: Peptides/nickel transport system		
2558670780	DRAFT_01448	COG_category	[E] Amino acid transport and metabolism		
2558670780	DRAFT_01448	COG_category	[P] Inorganic ion transport and metabolism		
2558670780	DRAFT_01448	COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase com		8.00E-114
2558670780	DRAFT_01448	pfam00005	ABC_tran		6.90E-25
2558670780	DRAFT_01448	pfam08352	oligo_HPY		4.00E-19
2558670780	DRAFT_01448	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termin		4.50E-30
2558670780	DRAFT_01448	KO:K02031	peptide/nickel transport system ATP-binding protein		0.00E+00
2558670780	DRAFT_01448	Locus_type		CDS	

2558670780	DRAFT_01448	Product_name		ABC-type dipeptide/oligopeptide/nickel transport system, ATPase cor	
2558670780	DRAFT_01448	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35	
2558670780	DRAFT_01448	Coordinates		10527..11480(-)	
2558670780	DRAFT_01448	DNA_length		954bp	
2558670780	DRAFT_01448	Protein_length		317aa	
2558670780	DRAFT_01448	GC		0.58	

2558670781	DRAFT_01449	KEGG_module	M00239: Peptides/nickel transport system		
2558670781	DRAFT_01449	COG_category	[P] Inorganic ion transport and metabolism		
2558670781	DRAFT_01449	COG_category	[E] Amino acid transport and metabolism		
2558670781	DRAFT_01449	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c		9.00E-53
2558670781	DRAFT_01449	pfam00528	BPD_transp_1		1.30E-21
2558670781	DRAFT_01449	pfam12911	OppC_N		3.40E-08
2558670781	DRAFT_01449	KO:K02034	peptide/nickel transport system permease protein		0.00E+00
2558670781	DRAFT_01449	Locus_type		CDS	
2558670781	DRAFT_01449	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease	
2558670781	DRAFT_01449	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35	
2558670781	DRAFT_01449	Coordinates		11517..13088(-)	
2558670781	DRAFT_01449	DNA_length		1572bp	
2558670781	DRAFT_01449	Protein_length		523aa	
2558670781	DRAFT_01449	GC		0.57	
2558670781	DRAFT_01449	Transmembrane		Yes	

2558670782	DRAFT_01450	KEGG_module	M00239: Peptides/nickel transport system		
2558670782	DRAFT_01450	COG_category	[P] Inorganic ion transport and metabolism		
2558670782	DRAFT_01450	COG_category	[E] Amino acid transport and metabolism		
2558670782	DRAFT_01450	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c		5.00E-58
2558670782	DRAFT_01450	pfam00528	BPD_transp_1		3.60E-39
2558670782	DRAFT_01450	KO:K02033	peptide/nickel transport system permease protein		0.00E+00
2558670782	DRAFT_01450	Locus_type		CDS	
2558670782	DRAFT_01450	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease	
2558670782	DRAFT_01450	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35	
2558670782	DRAFT_01450	Coordinates		13090..14130(-)	
2558670782	DRAFT_01450	DNA_length		1041bp	

2558670782	DRAFT_01450	Protein_length		346aa		
2558670782	DRAFT_01450	GC			0.52	
2558670782	DRAFT_01450	Transmembrane		Yes		
2558670783	DRAFT_01451	COG_category	[S] Function unknown			
2558670783	DRAFT_01451	COG3391	Uncharacterized conserved protein			4.00E-14
2558670783	DRAFT_01451	pfam10282	Lactonase			3.30E-05
2558670783	DRAFT_01451	TIGR02276	40-residue YVTN family beta-propeller repeat			5.40E-15
2558670783	DRAFT_01451	Locus_type		CDS		
2558670783	DRAFT_01451	Product_name		40-residue YVTN family beta-propeller repeat		
2558670783	DRAFT_01451	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35		
2558670783	DRAFT_01451	Coordinates		14240..15475(+)		
2558670783	DRAFT_01451	DNA_length		1236bp		
2558670783	DRAFT_01451	Protein_length		411aa		
2558670783	DRAFT_01451	GC			0.53	
2558670783	DRAFT_01451	Transmembrane		Yes		
2558670784	DRAFT_01452	COG_category	[C] Energy production and conversion			
2558670784	DRAFT_01452	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558670784	DRAFT_01452	COG0526	Thiol-disulfide isomerase and thioredoxins			4.00E-07
2558670784	DRAFT_01452	pfam08534	Redoxin			1.40E-12
2558670784	DRAFT_01452	Locus_type		CDS		
2558670784	DRAFT_01452	Product_name		Thiol-disulfide isomerase and thioredoxins		
2558670784	DRAFT_01452	Scaffold		DRAFT_contig_70_281_len_16680_read_count_284862.35		
2558670784	DRAFT_01452	Coordinates		15620..16678(-)		
2558670784	DRAFT_01452	DNA_length		1059bp		
2558670784	DRAFT_01452	Protein_length		352aa		
2558670784	DRAFT_01452	GC			0.53	
2558670785	DRAFT_01453	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2558670785	DRAFT_01453	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2558670785	DRAFT_01453	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558670785	DRAFT_01453	IMG_pathway	505: L-valine ligation to tRNA(Val)			
2558670785	DRAFT_01453	COG_category	[J] Translation, ribosomal structure and biogenesis			

2558670785	DRAFT_01453	COG0525	Valyl-tRNA synthetase			0.00E+00
2558670785	DRAFT_01453	pfam08264	Anticodon_1			1.10E-29
2558670785	DRAFT_01453	pfam00133	tRNA-synt_1			2.70E-104
2558670785	DRAFT_01453	EC:6.1.1.9	Valine--tRNA ligase.			
2558670785	DRAFT_01453	TIGR00422	valyl-tRNA synthetase			0.00E+00
2558670785	DRAFT_01453	KO:K01873	valyl-tRNA synthetase [EC:6.1.1.9]			0.00E+00
2558670785	DRAFT_01453	ITERM:00407	valyl-tRNA synthetase (EC 6.1.1.9)			
2558670785	DRAFT_01453	Locus_type		CDS		
2558670785	DRAFT_01453	Product_name		valyl-tRNA synthetase (EC 6.1.1.9)		
2558670785	DRAFT_01453	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670785	DRAFT_01453	Coordinates		51..2390(+)		
2558670785	DRAFT_01453	DNA_length		2340bp		
2558670785	DRAFT_01453	Protein_length		779aa		
2558670785	DRAFT_01453	GC			0.56	
2558670786	DRAFT_01454	COG_category	[R] General function prediction only			
2558670786	DRAFT_01454	COG0656	Aldo/keto reductases, related to diketogulonate reductase			5.00E-64
2558670786	DRAFT_01454	pfam00248	Aldo_ket_red			1.30E-66
2558670786	DRAFT_01454	Locus_type		CDS		
2558670786	DRAFT_01454	Product_name		Aldo/keto reductases, related to diketogulonate reductase		
2558670786	DRAFT_01454	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670786	DRAFT_01454	Coordinates		2473..3279(-)		
2558670786	DRAFT_01454	DNA_length		807bp		
2558670786	DRAFT_01454	Protein_length		268aa		
2558670786	DRAFT_01454	GC			0.56	
2558670787	DRAFT_01455	COG_category	[R] General function prediction only			
2558670787	DRAFT_01455	COG1373	Predicted ATPase (AAA+ superfamily)			1.00E-39
2558670787	DRAFT_01455	pfam13173	AAA_14			1.30E-21
2558670787	DRAFT_01455	pfam13635	DUF4143			2.20E-08
2558670787	DRAFT_01455	Locus_type		CDS		
2558670787	DRAFT_01455	Product_name		Predicted ATPase (AAA+ superfamily)		
2558670787	DRAFT_01455	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670787	DRAFT_01455	Coordinates		3957..5459(-)		

2558670787	DRAFT_01455	DNA_length	1503bp
2558670787	DRAFT_01455	Protein_length	500aa
2558670787	DRAFT_01455	GC	0.46
2558670788	DRAFT_01456	Locus_type	CDS
2558670788	DRAFT_01456	Product_name	hypothetical protein
2558670788	DRAFT_01456	Scaffold	DRAFT_contig_70_288_len_16535_read_count_319708.36
2558670788	DRAFT_01456	Coordinates	5594..6580(-)
2558670788	DRAFT_01456	DNA_length	987bp
2558670788	DRAFT_01456	Protein_length	328aa
2558670788	DRAFT_01456	GC	0.46
2558670789	DRAFT_01457	Locus_type	CDS
2558670789	DRAFT_01457	Product_name	hypothetical protein
2558670789	DRAFT_01457	Scaffold	DRAFT_contig_70_288_len_16535_read_count_319708.36
2558670789	DRAFT_01457	Coordinates	6720..6857(+)
2558670789	DRAFT_01457	DNA_length	138bp
2558670789	DRAFT_01457	Protein_length	45aa
2558670789	DRAFT_01457	GC	0.45
2558670790	DRAFT_01458	Locus_type	CDS
2558670790	DRAFT_01458	Product_name	hypothetical protein
2558670790	DRAFT_01458	Scaffold	DRAFT_contig_70_288_len_16535_read_count_319708.36
2558670790	DRAFT_01458	Coordinates	7049..7330(+)
2558670790	DRAFT_01458	DNA_length	282bp
2558670790	DRAFT_01458	Protein_length	93aa
2558670790	DRAFT_01458	GC	0.49
2558670791	DRAFT_01459	Locus_type	CDS
2558670791	DRAFT_01459	Product_name	hypothetical protein
2558670791	DRAFT_01459	Scaffold	DRAFT_contig_70_288_len_16535_read_count_319708.36
2558670791	DRAFT_01459	Coordinates	7327..8043(+)
2558670791	DRAFT_01459	DNA_length	717bp
2558670791	DRAFT_01459	Protein_length	238aa

2558670791	DRAFT_01459	GC			0.48	
2558670791	DRAFT_01459	Transmembrane		Yes		
2558670792	DRAFT_01460	Locus_type		CDS		
2558670792	DRAFT_01460	Product_name		hypothetical protein		
2558670792	DRAFT_01460	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670792	DRAFT_01460	Coordinates		8206..8964(-)		
2558670792	DRAFT_01460	DNA_length		759bp		
2558670792	DRAFT_01460	Protein_length		252aa		
2558670792	DRAFT_01460	GC			0.48	
2558670792	DRAFT_01460	Transmembrane		Yes		
2558670793	DRAFT_01461	pfam09195	Endonuc-BglII			2.80E-06
2558670793	DRAFT_01461	Locus_type		CDS		
2558670793	DRAFT_01461	Product_name		Restriction endonuclease BglII		
2558670793	DRAFT_01461	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670793	DRAFT_01461	Coordinates		8984..9277(-)		
2558670793	DRAFT_01461	DNA_length		294bp		
2558670793	DRAFT_01461	Protein_length		97aa		
2558670793	DRAFT_01461	GC			0.47	
2558670794	DRAFT_01462	pfam04014	Antitoxin-MazE			1.20E-05
2558670794	DRAFT_01462	Locus_type		CDS		
2558670794	DRAFT_01462	Product_name		Antidote-toxin recognition MazE		
2558670794	DRAFT_01462	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670794	DRAFT_01462	Coordinates		9316..9486(-)		
2558670794	DRAFT_01462	DNA_length		171bp		
2558670794	DRAFT_01462	Protein_length		56aa		
2558670794	DRAFT_01462	GC			0.45	
2558670795	DRAFT_01463	Locus_type		CDS		
2558670795	DRAFT_01463	Product_name		hypothetical protein		
2558670795	DRAFT_01463	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670795	DRAFT_01463	Coordinates		9554..10261(+)		

2558670795	DRAFT_01463	DNA_length		708bp		
2558670795	DRAFT_01463	Protein_length		235aa		
2558670795	DRAFT_01463	GC			0.52	
2558670796	DRAFT_01464	Locus_type		CDS		
2558670796	DRAFT_01464	Product_name		hypothetical protein		
2558670796	DRAFT_01464	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670796	DRAFT_01464	Coordinates		10689..10832(+)		
2558670796	DRAFT_01464	DNA_length		144bp		
2558670796	DRAFT_01464	Protein_length		47aa		
2558670796	DRAFT_01464	GC			0.53	
2558670797	DRAFT_01465	Locus_type		CDS		
2558670797	DRAFT_01465	Product_name		hypothetical protein		
2558670797	DRAFT_01465	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670797	DRAFT_01465	Coordinates		10829..11290(+)		
2558670797	DRAFT_01465	DNA_length		462bp		
2558670797	DRAFT_01465	Protein_length		153aa		
2558670797	DRAFT_01465	GC			0.48	
2558670798	DRAFT_01466	Locus_type		CDS		
2558670798	DRAFT_01466	Product_name		hypothetical protein		
2558670798	DRAFT_01466	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670798	DRAFT_01466	Coordinates		11937..12617(+)		
2558670798	DRAFT_01466	DNA_length		681bp		
2558670798	DRAFT_01466	Protein_length		226aa		
2558670798	DRAFT_01466	GC			0.47	
2558670799	DRAFT_01467	pfam00589	Phage_integrase			9.20E-18
2558670799	DRAFT_01467	Locus_type		CDS		
2558670799	DRAFT_01467	Product_name		Site-specific recombinase XerD		
2558670799	DRAFT_01467	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36		
2558670799	DRAFT_01467	Coordinates		12827..13645(-)		
2558670799	DRAFT_01467	DNA_length		819bp		

2558670799	DRAFT_01467	Protein_length		272aa	
2558670799	DRAFT_01467	GC		0.51	
2558670800	DRAFT_01468	Locus_type		tRNA	
2558670800	DRAFT_01468	Product_name		tRNA_Thr_TGT	
2558670800	DRAFT_01468	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36	
2558670800	DRAFT_01468	Coordinates		13879..13952(-)	
2558670800	DRAFT_01468	DNA_length		74bp	
2558670800	DRAFT_01468	GC		0.62	
2558670801	DRAFT_01469	Locus_type		CDS	
2558670801	DRAFT_01469	Product_name		hypothetical protein	
2558670801	DRAFT_01469	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36	
2558670801	DRAFT_01469	Coordinates		13999..14379(-)	
2558670801	DRAFT_01469	DNA_length		381bp	
2558670801	DRAFT_01469	Protein_length		126aa	
2558670801	DRAFT_01469	GC		0.57	
2558670802	DRAFT_01470	COG_category	[L] Replication, recombination and repair		
2558670802	DRAFT_01470	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair		1.00E-58
2558670802	DRAFT_01470	pfam11798	IMS_HHH		1.00E-05
2558670802	DRAFT_01470	pfam00817	IMS		1.90E-35
2558670802	DRAFT_01470	pfam11799	IMS_C		9.30E-12
2558670802	DRAFT_01470	EC:2.7.7.7	DNA-directed DNA polymerase.		
2558670802	DRAFT_01470	KO:K04479	DNA polymerase IV (archaeal DinB-like DNA polymerase) [EC:2.7.7.7]		0.00E+00
2558670802	DRAFT_01470	Locus_type		CDS	
2558670802	DRAFT_01470	Product_name		Nucleotidyltransferase/DNA polymerase involved in DNA repair	
2558670802	DRAFT_01470	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36	
2558670802	DRAFT_01470	Coordinates		14384..15484(-)	
2558670802	DRAFT_01470	DNA_length		1101bp	
2558670802	DRAFT_01470	Protein_length		366aa	
2558670802	DRAFT_01470	GC		0.57	
2558670803	DRAFT_01471	Locus_type		CDS	

2558670803	DRAFT_01471	Product_name		hypothetical protein	
2558670803	DRAFT_01471	Scaffold		DRAFT_contig_70_288_len_16535_read_count_319708.36	
2558670803	DRAFT_01471	Coordinates		15592..16431(+)	
2558670803	DRAFT_01471	DNA_length		840bp	
2558670803	DRAFT_01471	Protein_length		279aa	
2558670803	DRAFT_01471	GC		0.57	
2558670803	DRAFT_01471	Transmembrane		Yes	
2558670804	DRAFT_01472	pfam01844	HNH		1.50E-08
2558670804	DRAFT_01472	Locus_type		CDS	
2558670804	DRAFT_01472	Product_name		HNH endonuclease	
2558670804	DRAFT_01472	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37	
2558670804	DRAFT_01472	Coordinates		339..659(-)	
2558670804	DRAFT_01472	DNA_length		321bp	
2558670804	DRAFT_01472	Protein_length		106aa	
2558670804	DRAFT_01472	GC		0.51	
2558670805	DRAFT_01473	Locus_type		CDS	
2558670805	DRAFT_01473	Product_name		hypothetical protein	
2558670805	DRAFT_01473	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37	
2558670805	DRAFT_01473	Coordinates		653..907(-)	
2558670805	DRAFT_01473	DNA_length		255bp	
2558670805	DRAFT_01473	Protein_length		84aa	
2558670805	DRAFT_01473	GC		0.51	
2558670805	DRAFT_01473	Transmembrane		Yes	
2558670806	DRAFT_01474	Locus_type		CDS	
2558670806	DRAFT_01474	Product_name		hypothetical protein	
2558670806	DRAFT_01474	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37	
2558670806	DRAFT_01474	Coordinates		888..1223(-)	
2558670806	DRAFT_01474	DNA_length		336bp	
2558670806	DRAFT_01474	Protein_length		111aa	
2558670806	DRAFT_01474	GC		0.51	
2558670806	DRAFT_01474	Transmembrane		Yes	

2558670807	DRAFT_01475	pfam01828	Peptidase_A4			9.50E-10
2558670807	DRAFT_01475	Locus_type		CDS		
2558670807	DRAFT_01475	Product_name		Peptidase A4 family		
2558670807	DRAFT_01475	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37		
2558670807	DRAFT_01475	Coordinates		1338..2489(+)		
2558670807	DRAFT_01475	DNA_length		1152bp		
2558670807	DRAFT_01475	Protein_length		383aa		
2558670807	DRAFT_01475	GC			0.51	
2558670807	DRAFT_01475	Transmembrane		Yes		
2558670808	DRAFT_01476	Locus_type		CDS		
2558670808	DRAFT_01476	Product_name		hypothetical protein		
2558670808	DRAFT_01476	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37		
2558670808	DRAFT_01476	Coordinates		2513..3040(-)		
2558670808	DRAFT_01476	DNA_length		528bp		
2558670808	DRAFT_01476	Protein_length		175aa		
2558670808	DRAFT_01476	GC			0.54	
2558670808	DRAFT_01476	Transmembrane		Yes		
2558670809	DRAFT_01477	Locus_type		CDS		
2558670809	DRAFT_01477	Product_name		hypothetical protein		
2558670809	DRAFT_01477	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37		
2558670809	DRAFT_01477	Coordinates		3129..3632(+)		
2558670809	DRAFT_01477	DNA_length		504bp		
2558670809	DRAFT_01477	Protein_length		167aa		
2558670809	DRAFT_01477	GC			0.54	
2558670809	DRAFT_01477	Transmembrane		Yes		
2558670810	DRAFT_01478	pfam04307	DUF457			5.60E-14
2558670810	DRAFT_01478	Locus_type		CDS		
2558670810	DRAFT_01478	Product_name		Predicted membrane-bound metal-dependent hydrolase (DUF457)		
2558670810	DRAFT_01478	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37		
2558670810	DRAFT_01478	Coordinates		4064..4993(+)		

2558670810	DRAFT_01478	DNA_length	930bp	
2558670810	DRAFT_01478	Protein_length	309aa	
2558670810	DRAFT_01478	GC		0.52
2558670810	DRAFT_01478	Transmembrane	Yes	
2558670811	DRAFT_01479	Locus_type	CDS	
2558670811	DRAFT_01479	Product_name	hypothetical protein	
2558670811	DRAFT_01479	Scaffold	DRAFT_contig_70_424_len_12921_read_count_259234.37	
2558670811	DRAFT_01479	Coordinates	5277..5402(+)	
2558670811	DRAFT_01479	DNA_length	126bp	
2558670811	DRAFT_01479	Protein_length	41aa	
2558670811	DRAFT_01479	GC		0.56
2558670811	DRAFT_01479	Transmembrane	Yes	
2558670812	DRAFT_01480	Locus_type	CDS	
2558670812	DRAFT_01480	Product_name	hypothetical protein	
2558670812	DRAFT_01480	Scaffold	DRAFT_contig_70_424_len_12921_read_count_259234.37	
2558670812	DRAFT_01480	Coordinates	5399..6523(-)	
2558670812	DRAFT_01480	DNA_length	1125bp	
2558670812	DRAFT_01480	Protein_length	374aa	
2558670812	DRAFT_01480	GC		0.53
2558670813	DRAFT_01481	Locus_type	CDS	
2558670813	DRAFT_01481	Product_name	hypothetical protein	
2558670813	DRAFT_01481	Scaffold	DRAFT_contig_70_424_len_12921_read_count_259234.37	
2558670813	DRAFT_01481	Coordinates	6726..8141(+)	
2558670813	DRAFT_01481	DNA_length	1416bp	
2558670813	DRAFT_01481	Protein_length	471aa	
2558670813	DRAFT_01481	GC		0.51
2558670813	DRAFT_01481	Transmembrane	Yes	
2558670814	DRAFT_01482	Locus_type	CDS	
2558670814	DRAFT_01482	Product_name	hypothetical protein	
2558670814	DRAFT_01482	Scaffold	DRAFT_contig_70_424_len_12921_read_count_259234.37	

2558670814	DRAFT_01482	Coordinates		8600..9202(+)		
2558670814	DRAFT_01482	DNA_length		603bp		
2558670814	DRAFT_01482	Protein_length		200aa		
2558670814	DRAFT_01482	GC			0.49	
2558670814	DRAFT_01482	Transmembrane		Yes		
2558670815	DRAFT_01483	COG_category	[R] General function prediction only			
2558670815	DRAFT_01483	COG0456	Acetyltransferases			9.00E-08
2558670815	DRAFT_01483	pfam00583	Acetyltransf_1			5.90E-15
2558670815	DRAFT_01483	pfam13673	Acetyltransf_10			7.00E-09
2558670815	DRAFT_01483	Locus_type		CDS		
2558670815	DRAFT_01483	Product_name		Acetyltransferases		
2558670815	DRAFT_01483	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37		
2558670815	DRAFT_01483	Coordinates		9278..10243(-)		
2558670815	DRAFT_01483	DNA_length		966bp		
2558670815	DRAFT_01483	Protein_length		321aa		
2558670815	DRAFT_01483	GC			0.5	
2558670816	DRAFT_01484	pfam05977	MFS_3			9.70E-21
2558670816	DRAFT_01484	Locus_type		CDS		
2558670816	DRAFT_01484	Product_name		Transmembrane secretion effector		
2558670816	DRAFT_01484	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37		
2558670816	DRAFT_01484	Coordinates		10364..11605(-)		
2558670816	DRAFT_01484	DNA_length		1242bp		
2558670816	DRAFT_01484	Protein_length		413aa		
2558670816	DRAFT_01484	GC			0.57	
2558670816	DRAFT_01484	Transmembrane		Yes		
2558670817	DRAFT_01485	Locus_type		CDS		
2558670817	DRAFT_01485	Product_name		hypothetical protein		
2558670817	DRAFT_01485	Scaffold		DRAFT_contig_70_424_len_12921_read_count_259234.37		
2558670817	DRAFT_01485	Coordinates		11936..12487(+)		
2558670817	DRAFT_01485	DNA_length		552bp		
2558670817	DRAFT_01485	Protein_length		183aa		

2558670817	DRAFT_01485	GC		0.51	
2558670818	DRAFT_01486	pfam00766	ETF_alpha		8.60E-15
2558670818	DRAFT_01486	Locus_type		CDS	
2558670818	DRAFT_01486	Product_name		Electron transfer flavoprotein, alpha subunit	
2558670818	DRAFT_01486	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38	
2558670818	DRAFT_01486	Coordinates		3..338(+)	
2558670818	DRAFT_01486	DNA_length		336bp	
2558670818	DRAFT_01486	Protein_length		111aa	
2558670818	DRAFT_01486	GC		0.64	
2558670819	DRAFT_01487	COG_category	[C] Energy production and conversion		
2558670819	DRAFT_01487	COG2086	Electron transfer flavoprotein, beta subunit		3.00E-53
2558670819	DRAFT_01487	pfam01012	ETF		3.00E-41
2558670819	DRAFT_01487	KO:K03521	electron transfer flavoprotein beta subunit		0.00E+00
2558670819	DRAFT_01487	ITERM:01639	electron transfer flavoprotein beta subunit		
2558670819	DRAFT_01487	Locus_type		CDS	
2558670819	DRAFT_01487	Product_name		electron transfer flavoprotein beta subunit	
2558670819	DRAFT_01487	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38	
2558670819	DRAFT_01487	Coordinates		335..1120(+)	
2558670819	DRAFT_01487	DNA_length		786bp	
2558670819	DRAFT_01487	Protein_length		261aa	
2558670819	DRAFT_01487	GC		0.62	
2558670820	DRAFT_01488	Locus_type		CDS	
2558670820	DRAFT_01488	Product_name		hypothetical protein	
2558670820	DRAFT_01488	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38	
2558670820	DRAFT_01488	Coordinates		1221..2273(+)	
2558670820	DRAFT_01488	DNA_length		1053bp	
2558670820	DRAFT_01488	Protein_length		350aa	
2558670820	DRAFT_01488	GC		0.6	
2558670821	DRAFT_01489	Locus_type		CDS	
2558670821	DRAFT_01489	Product_name		hypothetical protein	

2558670821	DRAFT_01489	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38		
2558670821	DRAFT_01489	Coordinates		2529..2768(+)		
2558670821	DRAFT_01489	DNA_length		240bp		
2558670821	DRAFT_01489	Protein_length		79aa		
2558670821	DRAFT_01489	GC			0.62	
2558670822	DRAFT_01490	COG_category	[P] Inorganic ion transport and metabolism			
2558670822	DRAFT_01490	COG0704	Phosphate uptake regulator			2.00E-13
2558670822	DRAFT_01490	pfam04014	Antitoxin-MazE			1.60E-08
2558670822	DRAFT_01490	pfam01895	PhoU			7.80E-07
2558670822	DRAFT_01490	Locus_type		CDS		
2558670822	DRAFT_01490	Product_name		Phosphate uptake regulator		
2558670822	DRAFT_01490	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38		
2558670822	DRAFT_01490	Coordinates		2782..3813(-)		
2558670822	DRAFT_01490	DNA_length		1032bp		
2558670822	DRAFT_01490	Protein_length		343aa		
2558670822	DRAFT_01490	GC			0.56	
2558670823	DRAFT_01491	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2558670823	DRAFT_01491	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			
2558670823	DRAFT_01491	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2558670823	DRAFT_01491	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2558670823	DRAFT_01491	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2558670823	DRAFT_01491	Metacyc	P23-PWY: reductive TCA cycle I			
2558670823	DRAFT_01491	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2558670823	DRAFT_01491	Metacyc	PWY-5392: reductive TCA cycle II			
2558670823	DRAFT_01491	COG_category	[C] Energy production and conversion			
2558670823	DRAFT_01491	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin c			5.00E-71
2558670823	DRAFT_01491	pfam01855	POR_N			1.10E-55
2558670823	DRAFT_01491	pfam02780	Transketolase_C			3.40E-08
2558670823	DRAFT_01491	pfam01558	POR			2.80E-38
2558670823	DRAFT_01491	EC:1.2.7.3	2-oxoglutarate synthase.			
2558670823	DRAFT_01491	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]			0.00E+00
2558670823	DRAFT_01491	Locus_type		CDS		

2558670823	DRAFT_01491	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin	
2558670823	DRAFT_01491	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38	
2558670823	DRAFT_01491	Coordinates		3899..5878(+)	
2558670823	DRAFT_01491	DNA_length		1980bp	
2558670823	DRAFT_01491	Protein_length		659aa	
2558670823	DRAFT_01491	GC		0.59	
2558670823	DRAFT_01491	Fused_gene		Yes	
2558670824	DRAFT_01492	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2558670824	DRAFT_01492	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670824	DRAFT_01492	Metacyc	PWY-5392: reductive TCA cycle II		
2558670824	DRAFT_01492	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558670824	DRAFT_01492	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558670824	DRAFT_01492	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558670824	DRAFT_01492	Metacyc	P23-PWY: reductive TCA cycle I		
2558670824	DRAFT_01492	COG_category	[C] Energy production and conversion		
2558670824	DRAFT_01492	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin c		8.00E-77
2558670824	DRAFT_01492	pfam02775	TPP_enzyme_C		4.10E-29
2558670824	DRAFT_01492	pfam12367	PFO_beta_C		2.30E-05
2558670824	DRAFT_01492	EC:1.2.7.3	2-oxoglutarate synthase.		
2558670824	DRAFT_01492	TIGR02177	2-oxoacid:acceptor oxidoreductase, beta subunit, pyruvate/2-ketoisova		8.20E-130
2558670824	DRAFT_01492	KO:K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]		0.00E+00
2558670824	DRAFT_01492	Locus_type		CDS	
2558670824	DRAFT_01492	Product_name		2-oxoacid:acceptor oxidoreductase, beta subunit, pyruvate/2-ketoiso	
2558670824	DRAFT_01492	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38	
2558670824	DRAFT_01492	Coordinates		5868..6833(+)	
2558670824	DRAFT_01492	DNA_length		966bp	
2558670824	DRAFT_01492	Protein_length		321aa	
2558670824	DRAFT_01492	GC		0.61	
2558670825	DRAFT_01493	Locus_type		rRNA	
2558670825	DRAFT_01493	Gene_symbol		16S	
2558670825	DRAFT_01493	Product_name		16S rRNA. Archaeal SSU	
2558670825	DRAFT_01493	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38	

2558670825	DRAFT_01493	Coordinates		7258..8612(+)	
2558670825	DRAFT_01493	DNA_length		1355bp	
2558670825	DRAFT_01493	GC			0.58
2558670826	DRAFT_01494	Locus_type		CDS	
2558670826	DRAFT_01494	Product_name		hypothetical protein	
2558670826	DRAFT_01494	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38	
2558670826	DRAFT_01494	Coordinates		8769..8969(-)	
2558670826	DRAFT_01494	DNA_length		201bp	
2558670826	DRAFT_01494	Protein_length		66aa	
2558670826	DRAFT_01494	GC			0.56
2558670827	DRAFT_01495	Locus_type		rRNA	
2558670827	DRAFT_01495	Gene_symbol		23S	
2558670827	DRAFT_01495	Product_name		23S rRNA. Archaeal LSU	
2558670827	DRAFT_01495	Scaffold		DRAFT_contig_70_444_len_12584_read_count_230646.38	
2558670827	DRAFT_01495	Coordinates		8970..12544(+)	
2558670827	DRAFT_01495	DNA_length		3060bp	
2558670827	DRAFT_01495	GC			0.57
2558670828	DRAFT_01496	COG_category	[S] Function unknown		
2558670828	DRAFT_01496	COG5616	Predicted integral membrane protein		4.00E-34
2558670828	DRAFT_01496	pfam13414	TPR_11		2.30E-07
2558670828	DRAFT_01496	pfam13414	TPR_11		3.00E-09
2558670828	DRAFT_01496	pfam13414	TPR_11		8.50E-07
2558670828	DRAFT_01496	Locus_type		CDS	
2558670828	DRAFT_01496	Product_name		Predicted integral membrane protein	
2558670828	DRAFT_01496	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39	
2558670828	DRAFT_01496	Coordinates		1..1587(+)	
2558670828	DRAFT_01496	DNA_length		1587bp	
2558670828	DRAFT_01496	Protein_length		528aa	
2558670828	DRAFT_01496	GC			0.57
2558670829	DRAFT_01497	Locus_type		CDS	

2558670829	DRAFT_01497	Product_name		hypothetical protein		
2558670829	DRAFT_01497	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39		
2558670829	DRAFT_01497	Coordinates		1913..2230(-)		
2558670829	DRAFT_01497	DNA_length		318bp		
2558670829	DRAFT_01497	Protein_length		105aa		
2558670829	DRAFT_01497	GC			0.49	

2558670830	DRAFT_01498	COG_category	[E] Amino acid transport and metabolism			
2558670830	DRAFT_01498	COG3579	Aminopeptidase C			0.00E+00
2558670830	DRAFT_01498	pfam03051	Peptidase_C1_2			0.00E+00
2558670830	DRAFT_01498	EC:3.4.22.40	Bleomycin hydrolase.			
2558670830	DRAFT_01498	KO:K01372	bleomycin hydrolase [EC:3.4.22.40]			0.00E+00
2558670830	DRAFT_01498	Locus_type		CDS		
2558670830	DRAFT_01498	Product_name		Aminopeptidase C		
2558670830	DRAFT_01498	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39		
2558670830	DRAFT_01498	Coordinates		2350..3693(-)		
2558670830	DRAFT_01498	DNA_length		1344bp		
2558670830	DRAFT_01498	Protein_length		447aa		
2558670830	DRAFT_01498	GC			0.49	

2558670831	DRAFT_01499	COG_category	[G] Carbohydrate transport and metabolism			
2558670831	DRAFT_01499	COG0383	Alpha-mannosidase			4.00E-127
2558670831	DRAFT_01499	pfam01074	Glyco_hydro_38			1.10E-74
2558670831	DRAFT_01499	pfam09261	Alpha-mann_mid			1.70E-24
2558670831	DRAFT_01499	pfam07748	Glyco_hydro_38C			2.10E-74
2558670831	DRAFT_01499	EC:3.2.1.24	Alpha-mannosidase.			
2558670831	DRAFT_01499	KO:K01191	alpha-mannosidase [EC:3.2.1.24]			0.00E+00
2558670831	DRAFT_01499	Locus_type		CDS		
2558670831	DRAFT_01499	Product_name		Alpha-mannosidase		
2558670831	DRAFT_01499	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39		
2558670831	DRAFT_01499	Coordinates		4087..6765(+)		
2558670831	DRAFT_01499	DNA_length		2679bp		
2558670831	DRAFT_01499	Protein_length		892aa		
2558670831	DRAFT_01499	GC			0.58	

2558670832	DRAFT_01500	Locus_type		CDS	
2558670832	DRAFT_01500	Product_name		hypothetical protein	
2558670832	DRAFT_01500	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39	
2558670832	DRAFT_01500	Coordinates		6762..6938(+)	
2558670832	DRAFT_01500	DNA_length		177bp	
2558670832	DRAFT_01500	Protein_length		58aa	
2558670832	DRAFT_01500	GC		0.58	
2558670833	DRAFT_01501	COG_category	[G] Carbohydrate transport and metabolism		
2558670833	DRAFT_01501	COG2814	Arabinose efflux permease		4.00E-05
2558670833	DRAFT_01501	pfam07690	MFS_1		2.30E-16
2558670833	DRAFT_01501	pfam07690	MFS_1		3.20E-13
2558670833	DRAFT_01501	Locus_type		CDS	
2558670833	DRAFT_01501	Product_name		Arabinose efflux permease	
2558670833	DRAFT_01501	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39	
2558670833	DRAFT_01501	Coordinates		7150..8520(-)	
2558670833	DRAFT_01501	DNA_length		1371bp	
2558670833	DRAFT_01501	Protein_length		456aa	
2558670833	DRAFT_01501	GC		0.62	
2558670833	DRAFT_01501	Transmembrane		Yes	
2558670834	DRAFT_01502	COG_category	[G] Carbohydrate transport and metabolism		
2558670834	DRAFT_01502	COG2814	Arabinose efflux permease		2.00E-05
2558670834	DRAFT_01502	pfam05977	MFS_3		2.00E-32
2558670834	DRAFT_01502	Locus_type		CDS	
2558670834	DRAFT_01502	Product_name		Arabinose efflux permease	
2558670834	DRAFT_01502	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39	
2558670834	DRAFT_01502	Coordinates		8943..10217(-)	
2558670834	DRAFT_01502	DNA_length		1275bp	
2558670834	DRAFT_01502	Protein_length		424aa	
2558670834	DRAFT_01502	GC		0.55	
2558670834	DRAFT_01502	Transmembrane		Yes	

2558670835	DRAFT_01503	pfam01037	AsnC_trans_reg			5.20E-08
2558670835	DRAFT_01503	Locus_type		CDS		
2558670835	DRAFT_01503	Product_name		Transcriptional regulators		
2558670835	DRAFT_01503	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39		
2558670835	DRAFT_01503	Coordinates		10735..11094(-)		
2558670835	DRAFT_01503	DNA_length		360bp		
2558670835	DRAFT_01503	Protein_length		119aa		
2558670835	DRAFT_01503	GC			0.53	
2558670836	DRAFT_01504	pfam01037	AsnC_trans_reg			6.40E-12
2558670836	DRAFT_01504	Locus_type		CDS		
2558670836	DRAFT_01504	Product_name		Transcriptional regulators		
2558670836	DRAFT_01504	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39		
2558670836	DRAFT_01504	Coordinates		11101..11349(-)		
2558670836	DRAFT_01504	DNA_length		249bp		
2558670836	DRAFT_01504	Protein_length		82aa		
2558670836	DRAFT_01504	GC			0.53	
2558670837	DRAFT_01505	COG_category	[R] General function prediction only			
2558670837	DRAFT_01505	COG0121	Predicted glutamine amidotransferase			4.00E-19
2558670837	DRAFT_01505	pfam13522	GATase_6			1.60E-08
2558670837	DRAFT_01505	KO:K07008	glutamine amidotransferase			1.10E-42
2558670837	DRAFT_01505	Locus_type		CDS		
2558670837	DRAFT_01505	Product_name		Predicted glutamine amidotransferase		
2558670837	DRAFT_01505	Scaffold		DRAFT_contig_70_456_len_12330_read_count_203941.39		
2558670837	DRAFT_01505	Coordinates		11412..12140(-)		
2558670837	DRAFT_01505	DNA_length		729bp		
2558670837	DRAFT_01505	Protein_length		242aa		
2558670837	DRAFT_01505	GC			0.54	
2558670838	DRAFT_01506	pfam04434	SWIM			7.30E-08
2558670838	DRAFT_01506	Locus_type		CDS		
2558670838	DRAFT_01506	Product_name		SWIM zinc finger		
2558670838	DRAFT_01506	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40		

2558670838	DRAFT_01506	Coordinates		2..316(-)	
2558670838	DRAFT_01506	DNA_length		315bp	
2558670838	DRAFT_01506	Protein_length		105aa	
2558670838	DRAFT_01506	GC			0.53
2558670839	DRAFT_01507	Locus_type		CDS	
2558670839	DRAFT_01507	Product_name		hypothetical protein	
2558670839	DRAFT_01507	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670839	DRAFT_01507	Coordinates		434..577(+)	
2558670839	DRAFT_01507	DNA_length		144bp	
2558670839	DRAFT_01507	Protein_length		47aa	
2558670839	DRAFT_01507	GC			0.53
2558670840	DRAFT_01508	Locus_type		CDS	
2558670840	DRAFT_01508	Product_name		hypothetical protein	
2558670840	DRAFT_01508	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670840	DRAFT_01508	Coordinates		579..1118(-)	
2558670840	DRAFT_01508	DNA_length		540bp	
2558670840	DRAFT_01508	Protein_length		179aa	
2558670840	DRAFT_01508	GC			0.5
2558670840	DRAFT_01508	Transmembrane		Yes	
2558670841	DRAFT_01509	Locus_type		CDS	
2558670841	DRAFT_01509	Product_name		hypothetical protein	
2558670841	DRAFT_01509	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670841	DRAFT_01509	Coordinates		1265..1918(-)	
2558670841	DRAFT_01509	DNA_length		654bp	
2558670841	DRAFT_01509	Protein_length		217aa	
2558670841	DRAFT_01509	GC			0.54
2558670841	DRAFT_01509	Transmembrane		Yes	
2558670842	DRAFT_01510	pfam13847	Methyltransf_31		5.80E-08
2558670842	DRAFT_01510	Locus_type		CDS	
2558670842	DRAFT_01510	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	

2558670842	DRAFT_01510	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670842	DRAFT_01510	Coordinates		2046..2474(+)	
2558670842	DRAFT_01510	DNA_length		429bp	
2558670842	DRAFT_01510	Protein_length		142aa	
2558670842	DRAFT_01510	GC		0.54	
2558670843	DRAFT_01511	Locus_type		tRNA	
2558670843	DRAFT_01511	Product_name		tRNA_Gln_TTG	
2558670843	DRAFT_01511	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670843	DRAFT_01511	Coordinates		2557..2629(-)	
2558670843	DRAFT_01511	DNA_length		73bp	
2558670843	DRAFT_01511	GC		0.64	
2558670844	DRAFT_01512	COG_category	[S] Function unknown		
2558670844	DRAFT_01512	COG1817	Uncharacterized protein conserved in archaea		3.00E-48
2558670844	DRAFT_01512	pfam04007	DUF354		1.10E-38
2558670844	DRAFT_01512	KO:K09726	hypothetical protein		0.00E+00
2558670844	DRAFT_01512	Locus_type		CDS	
2558670844	DRAFT_01512	Product_name		Uncharacterized protein conserved in archaea	
2558670844	DRAFT_01512	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670844	DRAFT_01512	Coordinates		2659..3720(-)	
2558670844	DRAFT_01512	DNA_length		1062bp	
2558670844	DRAFT_01512	Protein_length		353aa	
2558670844	DRAFT_01512	GC		0.6	
2558670845	DRAFT_01513	KEGG_module	M00126: Tetrahydrofolate biosynthesis, GTP => THF		
2558670845	DRAFT_01513	Metacyc	PWY-6614: tetrahydrofolate biosynthesis		
2558670845	DRAFT_01513	Metacyc	1CMET2-PWY: formylTHF biosynthesis I		
2558670845	DRAFT_01513	Metacyc	PWY-2161: folate polyglutamylation		
2558670845	DRAFT_01513	COG_category	[H] Coenzyme transport and metabolism		
2558670845	DRAFT_01513	COG0285	Folylpolyglutamate synthase		1.00E-90
2558670845	DRAFT_01513	pfam02875	Mur_ligase_C		8.10E-07
2558670845	DRAFT_01513	pfam08245	Mur_ligase_M		3.50E-15
2558670845	DRAFT_01513	EC:6.3.2.17	Tetrahydrofolate synthase.		

2558670845	DRAFT_01513	EC:6.3.2.12	Dihydrofolate synthase.			
2558670845	DRAFT_01513	TIGR01499	folylpolyglutamate synthase/dihydrofolate synthase			2.80E-96
2558670845	DRAFT_01513	KO:K11754	dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12 6.3.			0.00E+00
2558670845	DRAFT_01513	Locus_type		CDS		
2558670845	DRAFT_01513	Product_name		folylpolyglutamate synthase/dihydrofolate synthase		
2558670845	DRAFT_01513	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40		
2558670845	DRAFT_01513	Coordinates		4055..5407(+)		
2558670845	DRAFT_01513	DNA_length		1353bp		
2558670845	DRAFT_01513	Protein_length		450aa		
2558670845	DRAFT_01513	GC			0.6	
2558670846	DRAFT_01514	Locus_type		CDS		
2558670846	DRAFT_01514	Product_name		hypothetical protein		
2558670846	DRAFT_01514	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40		
2558670846	DRAFT_01514	Coordinates		5502..6632(+)		
2558670846	DRAFT_01514	DNA_length		1131bp		
2558670846	DRAFT_01514	Protein_length		376aa		
2558670846	DRAFT_01514	GC			0.58	
2558670847	DRAFT_01515	Locus_type		CDS		
2558670847	DRAFT_01515	Product_name		hypothetical protein		
2558670847	DRAFT_01515	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40		
2558670847	DRAFT_01515	Coordinates		6692..6955(+)		
2558670847	DRAFT_01515	DNA_length		264bp		
2558670847	DRAFT_01515	Protein_length		87aa		
2558670847	DRAFT_01515	GC			0.49	
2558670847	DRAFT_01515	Transmembrane		Yes		
2558670848	DRAFT_01516	COG_category	[R] General function prediction only			
2558670848	DRAFT_01516	COG0673	Predicted dehydrogenases and related proteins			8.00E-50
2558670848	DRAFT_01516	pfam01408	GFO_IDH_MocA			6.20E-28
2558670848	DRAFT_01516	pfam02894	GFO_IDH_MocA_C			1.10E-05
2558670848	DRAFT_01516	Locus_type		CDS		
2558670848	DRAFT_01516	Product_name		Predicted dehydrogenases and related proteins		

2558670848	DRAFT_01516	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670848	DRAFT_01516	Coordinates		7081..8019(+)	
2558670848	DRAFT_01516	DNA_length		939bp	
2558670848	DRAFT_01516	Protein_length		312aa	
2558670848	DRAFT_01516	GC		0.58	
2558670849	DRAFT_01517	pfam00132	Hexapep		1.90E-05
2558670849	DRAFT_01517	pfam00132	Hexapep		2.30E-08
2558670849	DRAFT_01517	pfam14602	Hexapep_2		2.00E-09
2558670849	DRAFT_01517	Locus_type		CDS	
2558670849	DRAFT_01517	Product_name		N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleot	
2558670849	DRAFT_01517	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670849	DRAFT_01517	Coordinates		8024..8509(+)	
2558670849	DRAFT_01517	DNA_length		486bp	
2558670849	DRAFT_01517	Protein_length		161aa	
2558670849	DRAFT_01517	GC		0.57	
2558670850	DRAFT_01518	Locus_type		CDS	
2558670850	DRAFT_01518	Product_name		hypothetical protein	
2558670850	DRAFT_01518	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670850	DRAFT_01518	Coordinates		8478..8732(-)	
2558670850	DRAFT_01518	DNA_length		255bp	
2558670850	DRAFT_01518	Protein_length		84aa	
2558670850	DRAFT_01518	GC		0.58	
2558670850	DRAFT_01518	Transmembrane		Yes	
2558670851	DRAFT_01519	KEGG_module	M00055: N-glycan precursor biosynthesis		
2558670851	DRAFT_01519	Metacyc	MANNOSYL-CHITO-DOLICHOL-BIOSYNTHESIS: dolichyl-diphosphooligosaccharide biosynthesis		
2558670851	DRAFT_01519	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670851	DRAFT_01519	COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acety		7.00E-19
2558670851	DRAFT_01519	pfam00953	Glycos_transf_4		1.10E-24
2558670851	DRAFT_01519	EC:2.7.8.15	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase.		
2558670851	DRAFT_01519	KO:K01001	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminepho		0.00E+00
2558670851	DRAFT_01519	Locus_type		CDS	

2558670851	DRAFT_01519	Product_name		UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acet	
2558670851	DRAFT_01519	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670851	DRAFT_01519	Coordinates		8734..9768(-)	
2558670851	DRAFT_01519	DNA_length		1035bp	
2558670851	DRAFT_01519	Protein_length		344aa	
2558670851	DRAFT_01519	GC		0.59	
2558670851	DRAFT_01519	Transmembrane		Yes	

2558670852	DRAFT_01520	KEGG_module	M00288: RPA complex		
2558670852	DRAFT_01520	pfam01336	tRNA_anti-codon		4.80E-09
2558670852	DRAFT_01520	KO:K07466	replication factor A1		3.00E-20
2558670852	DRAFT_01520	Locus_type		CDS	
2558670852	DRAFT_01520	Product_name		OB-fold nucleic acid binding domain	
2558670852	DRAFT_01520	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670852	DRAFT_01520	Coordinates		9865..10158(+)	
2558670852	DRAFT_01520	DNA_length		294bp	
2558670852	DRAFT_01520	Protein_length		97aa	
2558670852	DRAFT_01520	GC		0.59	

2558670853	DRAFT_01521	COG_category	[T] Signal transduction mechanisms		
2558670853	DRAFT_01521	COG2453	Predicted protein-tyrosine phosphatase		1.00E-16
2558670853	DRAFT_01521	pfam00782	DSPc		4.70E-19
2558670853	DRAFT_01521	EC:3.1.3.16	Phosphoprotein phosphatase.		
2558670853	DRAFT_01521	EC:3.1.3.48	Protein-tyrosine-phosphatase.		
2558670853	DRAFT_01521	KO:K14165	dual specificity phosphatase [EC:3.1.3.16 3.1.3.48]		2.60E-32
2558670853	DRAFT_01521	Locus_type		CDS	
2558670853	DRAFT_01521	Product_name		Predicted protein-tyrosine phosphatase	
2558670853	DRAFT_01521	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40	
2558670853	DRAFT_01521	Coordinates		10202..10699(+)	
2558670853	DRAFT_01521	DNA_length		498bp	
2558670853	DRAFT_01521	Protein_length		165aa	
2558670853	DRAFT_01521	GC		0.6	

2558670854	DRAFT_01522	COG_category	[T] Signal transduction mechanisms		

2558670854	DRAFT_01522	COG2114	Adenylate cyclase, family 3 (some proteins contain HAMP domain)			3.00E-27
2558670854	DRAFT_01522	pfam00211	Guanylate_cyc			4.70E-26
2558670854	DRAFT_01522	Locus_type		CDS		
2558670854	DRAFT_01522	Product_name		Adenylate cyclase, family 3 (some proteins contain HAMP domain)		
2558670854	DRAFT_01522	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40		
2558670854	DRAFT_01522	Coordinates		10850..11884(+)		
2558670854	DRAFT_01522	DNA_length		1035bp		
2558670854	DRAFT_01522	Protein_length		344aa		
2558670854	DRAFT_01522	GC			0.53	

2558670855	DRAFT_01523	Locus_type		tRNA		
2558670855	DRAFT_01523	Product_name		tRNA_Leu_GAG		
2558670855	DRAFT_01523	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40		
2558670855	DRAFT_01523	Coordinates		11944..12031(-)		
2558670855	DRAFT_01523	DNA_length		88bp		
2558670855	DRAFT_01523	GC			0.68	

2558670856	DRAFT_01524	Locus_type		tRNA		
2558670856	DRAFT_01524	Product_name		tRNA_Gly_TCC		
2558670856	DRAFT_01524	Scaffold		DRAFT_contig_70_462_len_12209_read_count_202887.40		
2558670856	DRAFT_01524	Coordinates		12119..12208(+)		
2558670856	DRAFT_01524	DNA_length		74bp		
2558670856	DRAFT_01524	GC			0.69	

2558670857	DRAFT_01525	pfam02771	Acyl-CoA_dh_N			8.10E-16
2558670857	DRAFT_01525	Locus_type		CDS		
2558670857	DRAFT_01525	Product_name		Acyl-CoA dehydrogenases		
2558670857	DRAFT_01525	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41		
2558670857	DRAFT_01525	Coordinates		2..226(-)		
2558670857	DRAFT_01525	DNA_length		225bp		
2558670857	DRAFT_01525	Protein_length		75aa		
2558670857	DRAFT_01525	GC			0.59	

2558670858	DRAFT_01526	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA			

2558670858	DRAFT_01526	KEGG_module	M00087: beta-Oxidation			
2558670858	DRAFT_01526	KEGG_module	M00013: Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA			
2558670858	DRAFT_01526	Metacyc	PWY-7094: fatty acid salvage			
2558670858	DRAFT_01526	COG_category	[I] Lipid transport and metabolism			
2558670858	DRAFT_01526	COG1960	Acyl-CoA dehydrogenases			5.00E-74
2558670858	DRAFT_01526	pfam00441	Acyl-CoA_dh_1			8.20E-37
2558670858	DRAFT_01526	pfam02770	Acyl-CoA_dh_M			1.10E-19
2558670858	DRAFT_01526	pfam02771	Acyl-CoA_dh_N			3.80E-14
2558670858	DRAFT_01526	EC:1.3.8.7	Medium-chain acyl-CoA dehydrogenase.			
2558670858	DRAFT_01526	KO:K00249	acyl-CoA dehydrogenase [EC:1.3.8.7]			0.00E+00
2558670858	DRAFT_01526	Locus_type		CDS		
2558670858	DRAFT_01526	Product_name		Acyl-CoA dehydrogenases		
2558670858	DRAFT_01526	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41		
2558670858	DRAFT_01526	Coordinates		231..1373(-)		
2558670858	DRAFT_01526	DNA_length		1143bp		
2558670858	DRAFT_01526	Protein_length		380aa		
2558670858	DRAFT_01526	GC			0.58	

2558670859	DRAFT_01527	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle
2558670859	DRAFT_01527	KEGG_module	M00373: Ethylmalonyl pathway
2558670859	DRAFT_01527	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle
2558670859	DRAFT_01527	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone
2558670859	DRAFT_01527	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway
2558670859	DRAFT_01527	Metacyc	PWY-922: mevalonate pathway I
2558670859	DRAFT_01527	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis
2558670859	DRAFT_01527	Metacyc	PWY-6583: pyruvate fermentation to butanol I
2558670859	DRAFT_01527	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate
2558670859	DRAFT_01527	Metacyc	PWY66-368: ketolysis
2558670859	DRAFT_01527	Metacyc	PWY66-367: ketogenesis
2558670859	DRAFT_01527	Metacyc	PWY-7003: glycerol degradation to butanol
2558670859	DRAFT_01527	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)
2558670859	DRAFT_01527	Metacyc	PWY-6174: mevalonate pathway II (archaea)
2558670859	DRAFT_01527	Metacyc	PWY-5741: ethylmalonyl pathway
2558670859	DRAFT_01527	Metacyc	PWY-5177: glutaryl-CoA degradation

2558670859	DRAFT_01527	Metacyc	PWY-6876: isopropanol biosynthesis			
2558670859	DRAFT_01527	Metacyc	PWY-6588: pyruvate fermentation to acetone			
2558670859	DRAFT_01527	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate			
2558670859	DRAFT_01527	Metacyc	ILEUDEG-PWY: isoleucine degradation I			
2558670859	DRAFT_01527	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			
2558670859	DRAFT_01527	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis			
2558670859	DRAFT_01527	Metacyc	PWY-6883: pyruvate fermentation to butanol II			
2558670859	DRAFT_01527	Metacyc	PWY-6863: pyruvate fermentation to hexanol			
2558670859	DRAFT_01527	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II			
2558670859	DRAFT_01527	COG_category	[I] Lipid transport and metabolism			
2558670859	DRAFT_01527	COG0183	Acetyl-CoA acetyltransferase			1.00E-85
2558670859	DRAFT_01527	pfam02803	Thiolase_C			4.30E-46
2558670859	DRAFT_01527	pfam00108	Thiolase_N			2.60E-63
2558670859	DRAFT_01527	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.			
2558670859	DRAFT_01527	TIGR01930	acetyl-CoA acetyltransferases			0.00E+00
2558670859	DRAFT_01527	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]			0.00E+00
2558670859	DRAFT_01527	Locus_type		CDS		
2558670859	DRAFT_01527	Product_name		acetyl-CoA acetyltransferases		
2558670859	DRAFT_01527	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41		
2558670859	DRAFT_01527	Coordinates		1465..2649(-)		
2558670859	DRAFT_01527	DNA_length		1185bp		
2558670859	DRAFT_01527	Protein_length		394aa		
2558670859	DRAFT_01527	GC			0.6	
2558670860	DRAFT_01528	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			
2558670860	DRAFT_01528	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle			
2558670860	DRAFT_01528	Metacyc	PWY-7007: methyl ketone biosynthesis			
2558670860	DRAFT_01528	Metacyc	PWY-6948: sitosterol degradation to androstenedione			
2558670860	DRAFT_01528	Metacyc	PWY-6945: cholesterol degradation to androstenedione I (cholesterol oxidase)			
2558670860	DRAFT_01528	Metacyc	PWY-735: jasmonic acid biosynthesis			
2558670860	DRAFT_01528	Metacyc	PWY-6863: pyruvate fermentation to hexanol			
2558670860	DRAFT_01528	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II			
2558670860	DRAFT_01528	Metacyc	PWY-1361: benzoyl-CoA degradation I (aerobic)			
2558670860	DRAFT_01528	Metacyc	PWY-7094: fatty acid salvage			

2558670860	DRAFT_01528	Metacyc	PWY-6883: pyruvate fermentation to butanol II		
2558670860	DRAFT_01528	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2558670860	DRAFT_01528	Metacyc	PWY0-321: phenylacetate degradation I (aerobic)		
2558670860	DRAFT_01528	Metacyc	PWY66-391: fatty acid β-oxidation VI (peroxisome)		
2558670860	DRAFT_01528	Metacyc	FAO-PWY: fatty acid β-oxidation I		
2558670860	DRAFT_01528	Metacyc	PWY-6944: androstenedione degradation		
2558670860	DRAFT_01528	Metacyc	PWY-5136: fatty acid β-oxidation II (peroxisome)		
2558670860	DRAFT_01528	Metacyc	PWY-6946: cholesterol degradation to androstenedione II (cholesterol dehydrogenase)		
2558670860	DRAFT_01528	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2558670860	DRAFT_01528	Metacyc	PWY-5741: ethylmalonyl pathway		
2558670860	DRAFT_01528	Metacyc	PWY-6583: pyruvate fermentation to butanol I		
2558670860	DRAFT_01528	Metacyc	PWY-6435: 4-hydroxybenzoate biosynthesis V		
2558670860	DRAFT_01528	Metacyc	PWY-5177: glutaryl-CoA degradation		
2558670860	DRAFT_01528	IMG_pathway	1014: Dicarboxylate/4-hydroxybutyrate cycle		
2558670860	DRAFT_01528	IMG_pathway	222: L-isoleucine degradation to propionyl-CoA and acetyl-CoA		
2558670860	DRAFT_01528	IMG_pathway	369: Pyruvate conversion to butyrate		
2558670860	DRAFT_01528	IMG_pathway	389: Crotonyl-CoA conversion to acetate		
2558670860	DRAFT_01528	IMG_pathway	596: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2558670860	DRAFT_01528	IMG_pathway	962: Glyoxylate from acetyl-CoA via ethylmalonyl-CoA pathway		
2558670860	DRAFT_01528	COG_category	[I] Lipid transport and metabolism		
2558670860	DRAFT_01528	COG1250	3-hydroxyacyl-CoA dehydrogenase		2.00E-79
2558670860	DRAFT_01528	pfam00725	3HCDH		2.80E-18
2558670860	DRAFT_01528	pfam00378	ECH		2.90E-55
2558670860	DRAFT_01528	pfam00725	3HCDH		2.20E-06
2558670860	DRAFT_01528	pfam02737	3HCDH_N		4.80E-64
2558670860	DRAFT_01528	EC:1.1.1.35	3-hydroxyacyl-CoA dehydrogenase.		
2558670860	DRAFT_01528	EC:4.2.1.55	3-hydroxybutyryl-CoA dehydratase.		
2558670860	DRAFT_01528	KO:K15016	3-hydroxybutyryl-CoA dehydratase / 3-hydroxyacyl-CoA dehydrogenas		0.00E+00
2558670860	DRAFT_01528	ITERM:00577	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)		
2558670860	DRAFT_01528	ITERM:00611	Enoyl-CoA hydratase (EC 4.2.1.17)		
2558670860	DRAFT_01528	Locus_type		CDS	
2558670860	DRAFT_01528	Product_name		3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)/Enoyl-CoA hydratase	
2558670860	DRAFT_01528	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41	
2558670860	DRAFT_01528	Coordinates		2671..4668(-)	

2558670860	DRAFT_01528	DNA_length		1998bp		
2558670860	DRAFT_01528	Protein_length		665aa		
2558670860	DRAFT_01528	GC			0.6	
2558670860	DRAFT_01528	Fused_gene		Yes		
2558670861	DRAFT_01529	Metacyc	PWY-7027: hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosynthesis			
2558670861	DRAFT_01529	Metacyc	PWY-5996: oleate biosynthesis II (animals and fungi)			
2558670861	DRAFT_01529	Metacyc	PWY-6039: chlorogenic acid biosynthesis I			
2558670861	DRAFT_01529	Metacyc	PWY-7007: methyl ketone biosynthesis			
2558670861	DRAFT_01529	Metacyc	PWY-981: salicylate biosynthesis II			
2558670861	DRAFT_01529	Metacyc	PWY-6320: phaselate biosynthesis			
2558670861	DRAFT_01529	Metacyc	PWY-361: phenylpropanoid biosynthesis			
2558670861	DRAFT_01529	Metacyc	PWY-6453: stigma estolide biosynthesis			
2558670861	DRAFT_01529	Metacyc	PWY-6944: androstenedione degradation			
2558670861	DRAFT_01529	Metacyc	PWY-6585: 2-tridecanone biosynthesis			
2558670861	DRAFT_01529	Metacyc	PWY-6673: caffeoylglucarate biosynthesis			
2558670861	DRAFT_01529	Metacyc	PWY-7053: docosahexanoate biosynthesis I			
2558670861	DRAFT_01529	Metacyc	PWY-6948: sitosterol degradation to androstenedione			
2558670861	DRAFT_01529	Metacyc	PWY-6951: docosahexanoate biosynthesis II			
2558670861	DRAFT_01529	Metacyc	PWY0-1337: oleate β-oxidation			
2558670861	DRAFT_01529	Metacyc	PWY-6048: methylthiopropionate degradation I (cleavage)			
2558670861	DRAFT_01529	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2558670861	DRAFT_01529	COG2050	Uncharacterized protein, possibly involved in aromatic compounds cat			1.00E-20
2558670861	DRAFT_01529	pfam03061	4HBT			5.10E-14
2558670861	DRAFT_01529	EC:3.1.2.-	Hydrolases. Acting on ester bonds. Thiolester hydrolases.			
2558670861	DRAFT_01529	TIGR00369	uncharacterized domain 1			2.20E-24
2558670861	DRAFT_01529	KO:K02614	acyl-CoA thioesterase [EC:3.1.2.-]			3.20E-32
2558670861	DRAFT_01529	Locus_type		CDS		
2558670861	DRAFT_01529	Product_name		uncharacterized domain 1		
2558670861	DRAFT_01529	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41		
2558670861	DRAFT_01529	Coordinates		4787..5260(-)		
2558670861	DRAFT_01529	DNA_length		474bp		
2558670861	DRAFT_01529	Protein_length		157aa		
2558670861	DRAFT_01529	GC			0.52	

2558670862	DRAFT_01530	pfam00571	CBS			1.20E-15
2558670862	DRAFT_01530	pfam00571	CBS			1.80E-07
2558670862	DRAFT_01530	Locus_type		CDS		
2558670862	DRAFT_01530	Product_name		Predicted signal-transduction protein containing cAMP-binding and C		
2558670862	DRAFT_01530	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41		
2558670862	DRAFT_01530	Coordinates		5458..6027(+)		
2558670862	DRAFT_01530	DNA_length		570bp		
2558670862	DRAFT_01530	Protein_length		189aa		
2558670862	DRAFT_01530	GC			0.56	
2558670863	DRAFT_01531	Locus_type		CDS		
2558670863	DRAFT_01531	Product_name		hypothetical protein		
2558670863	DRAFT_01531	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41		
2558670863	DRAFT_01531	Coordinates		6188..6433(+)		
2558670863	DRAFT_01531	DNA_length		246bp		
2558670863	DRAFT_01531	Protein_length		81aa		
2558670863	DRAFT_01531	GC			0.61	
2558670864	DRAFT_01532	pfam07690	MFS_1			1.90E-45
2558670864	DRAFT_01532	TIGR00711	drug resistance transporter, EmrB/QacA subfamily			1.00E-57
2558670864	DRAFT_01532	Locus_type		CDS		
2558670864	DRAFT_01532	Product_name		Arabinose efflux permease		
2558670864	DRAFT_01532	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41		
2558670864	DRAFT_01532	Coordinates		6589..7962(+)		
2558670864	DRAFT_01532	DNA_length		1374bp		
2558670864	DRAFT_01532	Protein_length		457aa		
2558670864	DRAFT_01532	GC			0.6	
2558670864	DRAFT_01532	Transmembrane		Yes		
2558670865	DRAFT_01533	COG_category	[S] Function unknown			
2558670865	DRAFT_01533	COG3189	Uncharacterized conserved protein			2.00E-19
2558670865	DRAFT_01533	pfam04343	DUF488			1.30E-20
2558670865	DRAFT_01533	Locus_type		CDS		

2558670865	DRAFT_01533	Product_name		Uncharacterized conserved protein	
2558670865	DRAFT_01533	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41	
2558670865	DRAFT_01533	Coordinates		8152..8496(+)	
2558670865	DRAFT_01533	DNA_length		345bp	
2558670865	DRAFT_01533	Protein_length		114aa	
2558670865	DRAFT_01533	GC		0.57	

2558670866	DRAFT_01534	COG_category	[S] Function unknown		
2558670866	DRAFT_01534	COG4832	Uncharacterized conserved protein		1.00E-54
2558670866	DRAFT_01534	pfam06445	GyrI-like		2.50E-21
2558670866	DRAFT_01534	Locus_type		CDS	
2558670866	DRAFT_01534	Product_name		Uncharacterized conserved protein	
2558670866	DRAFT_01534	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41	
2558670866	DRAFT_01534	Coordinates		8690..9310(+)	
2558670866	DRAFT_01534	DNA_length		621bp	
2558670866	DRAFT_01534	Protein_length		206aa	
2558670866	DRAFT_01534	GC		0.53	

2558670867	DRAFT_01535	Locus_type		CDS	
2558670867	DRAFT_01535	Product_name		hypothetical protein	
2558670867	DRAFT_01535	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41	
2558670867	DRAFT_01535	Coordinates		9378..10436(-)	
2558670867	DRAFT_01535	DNA_length		1059bp	
2558670867	DRAFT_01535	Protein_length		352aa	
2558670867	DRAFT_01535	GC		0.58	

2558670868	DRAFT_01536	COG_category	[E] Amino acid transport and metabolism		
2558670868	DRAFT_01536	COG1505	Serine proteases of the peptidase family S9A		2.00E-100
2558670868	DRAFT_01536	pfam00326	Peptidase_S9		5.20E-56
2558670868	DRAFT_01536	EC:3.4.21.26	Prolyl oligopeptidase.		
2558670868	DRAFT_01536	KO:K01322	prolyl oligopeptidase [EC:3.4.21.26]		0.00E+00
2558670868	DRAFT_01536	ITERM:04609	prolyl oligopeptidase. Serine peptidase. MEROPS family S09A		
2558670868	DRAFT_01536	Locus_type		CDS	
2558670868	DRAFT_01536	Product_name		prolyl oligopeptidase. Serine peptidase. MEROPS family S09A	

2558670868	DRAFT_01536	Scaffold		DRAFT_contig_70_472_len_12013_read_count_183073.41		
2558670868	DRAFT_01536	Coordinates		10532..12010(-)		
2558670868	DRAFT_01536	DNA_length		1479bp		
2558670868	DRAFT_01536	Protein_length		492aa		
2558670868	DRAFT_01536	GC			0.62	
2558670869	DRAFT_01537	Locus_type		CDS		
2558670869	DRAFT_01537	Product_name		hypothetical protein		
2558670869	DRAFT_01537	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670869	DRAFT_01537	Coordinates		183..608(-)		
2558670869	DRAFT_01537	DNA_length		426bp		
2558670869	DRAFT_01537	Protein_length		141aa		
2558670869	DRAFT_01537	GC			0.5	
2558670870	DRAFT_01538	pfam09721	Exosortase_EpsH			7.70E-16
2558670870	DRAFT_01538	TIGR04178	exosortase/archaeosortase family protein			1.60E-17
2558670870	DRAFT_01538	Locus_type		CDS		
2558670870	DRAFT_01538	Product_name		exosortase/archaeosortase family protein		
2558670870	DRAFT_01538	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670870	DRAFT_01538	Coordinates		741..1682(+)		
2558670870	DRAFT_01538	DNA_length		942bp		
2558670870	DRAFT_01538	Protein_length		313aa		
2558670870	DRAFT_01538	GC			0.5	
2558670870	DRAFT_01538	Transmembrane		Yes		
2558670871	DRAFT_01539	COG_category	[E] Amino acid transport and metabolism			
2558670871	DRAFT_01539	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases			2.00E-47
2558670871	DRAFT_01539	pfam00326	Peptidase_S9			6.00E-36
2558670871	DRAFT_01539	Locus_type		CDS		
2558670871	DRAFT_01539	Product_name		Dipeptidyl aminopeptidases/acylaminoacyl-peptidases		
2558670871	DRAFT_01539	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670871	DRAFT_01539	Coordinates		2074..3909(+)		
2558670871	DRAFT_01539	DNA_length		1836bp		
2558670871	DRAFT_01539	Protein_length		611aa		

2558670871	DRAFT_01539	GC			0.62	
2558670872	DRAFT_01540	COG_category	[R] General function prediction only			
2558670872	DRAFT_01540	COG0456	Acetyltransferases			9.00E-09
2558670872	DRAFT_01540	pfam00583	Acetyltransf_1			1.70E-13
2558670872	DRAFT_01540	Locus_type		CDS		
2558670872	DRAFT_01540	Product_name		Acetyltransferases		
2558670872	DRAFT_01540	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670872	DRAFT_01540	Coordinates		4044..4502(-)		
2558670872	DRAFT_01540	DNA_length		459bp		
2558670872	DRAFT_01540	Protein_length		152aa		
2558670872	DRAFT_01540	GC			0.51	
2558670873	DRAFT_01541	COG_category	[E] Amino acid transport and metabolism			
2558670873	DRAFT_01541	COG2309	Leucyl aminopeptidase (aminopeptidase T)			1.00E-21
2558670873	DRAFT_01541	pfam02073	Peptidase_M29			6.00E-17
2558670873	DRAFT_01541	Locus_type		CDS		
2558670873	DRAFT_01541	Product_name		Leucyl aminopeptidase (aminopeptidase T)		
2558670873	DRAFT_01541	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670873	DRAFT_01541	Coordinates		4644..5789(+)		
2558670873	DRAFT_01541	DNA_length		1146bp		
2558670873	DRAFT_01541	Protein_length		381aa		
2558670873	DRAFT_01541	GC			0.53	
2558670874	DRAFT_01542	Locus_type		CDS		
2558670874	DRAFT_01542	Product_name		hypothetical protein		
2558670874	DRAFT_01542	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670874	DRAFT_01542	Coordinates		5876..6070(+)		
2558670874	DRAFT_01542	DNA_length		195bp		
2558670874	DRAFT_01542	Protein_length		64aa		
2558670874	DRAFT_01542	GC			0.54	
2558670875	DRAFT_01543	Locus_type		CDS		
2558670875	DRAFT_01543	Product_name		hypothetical protein		

2558670875	DRAFT_01543	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42	
2558670875	DRAFT_01543	Coordinates		6083..6775(-)	
2558670875	DRAFT_01543	DNA_length		693bp	
2558670875	DRAFT_01543	Protein_length		230aa	
2558670875	DRAFT_01543	GC		0.5	
2558670875	DRAFT_01543	Transmembrane		Yes	
2558670876	DRAFT_01544	Locus_type		tRNA	
2558670876	DRAFT_01544	Product_name		tRNA_Pro_GGG	
2558670876	DRAFT_01544	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42	
2558670876	DRAFT_01544	Coordinates		7789..7864(+)	
2558670876	DRAFT_01544	DNA_length		76bp	
2558670876	DRAFT_01544	GC		0.64	
2558670877	DRAFT_01545	pfam01040	UbiA		1.10E-20
2558670877	DRAFT_01545	Locus_type		CDS	
2558670877	DRAFT_01545	Product_name		1,4-dihydroxy-2-naphthoate octaprenyltransferase	
2558670877	DRAFT_01545	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42	
2558670877	DRAFT_01545	Coordinates		7943..8581(-)	
2558670877	DRAFT_01545	DNA_length		639bp	
2558670877	DRAFT_01545	Protein_length		212aa	
2558670877	DRAFT_01545	GC		0.57	
2558670877	DRAFT_01545	Transmembrane		Yes	
2558670878	DRAFT_01546	pfam13426	PAS_9		5.70E-07
2558670878	DRAFT_01546	Locus_type		CDS	
2558670878	DRAFT_01546	Product_name		PAS domain	
2558670878	DRAFT_01546	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42	
2558670878	DRAFT_01546	Coordinates		8858..9202(-)	
2558670878	DRAFT_01546	DNA_length		345bp	
2558670878	DRAFT_01546	Protein_length		114aa	
2558670878	DRAFT_01546	GC		0.58	
2558670879	DRAFT_01547	COG_category	[R] General function prediction only		

2558670879	DRAFT_01547	COG3654	Prophage maintenance system killer protein			5.00E-09
2558670879	DRAFT_01547	pfam02661	Fic			1.00E-05
2558670879	DRAFT_01547	TIGR01550	death-on-curing family protein			5.00E-16
2558670879	DRAFT_01547	KO:K07341	death on curing protein			2.10E-06
2558670879	DRAFT_01547	Locus_type		CDS		
2558670879	DRAFT_01547	Product_name		death-on-curing family protein		
2558670879	DRAFT_01547	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670879	DRAFT_01547	Coordinates		9397..9888(+)		
2558670879	DRAFT_01547	DNA_length		492bp		
2558670879	DRAFT_01547	Protein_length		163aa		
2558670879	DRAFT_01547	GC			0.58	

2558670880	DRAFT_01548	COG_category	[R] General function prediction only			
2558670880	DRAFT_01548	COG0375	Zn finger protein HypA/HybF (possibly regulating hydrogenase expressi			8.00E-13
2558670880	DRAFT_01548	pfam01155	HypA			7.30E-19
2558670880	DRAFT_01548	KO:K04651	hydrogenase nickel incorporation protein HypA/HybF			8.70E-10
2558670880	DRAFT_01548	Locus_type		CDS		
2558670880	DRAFT_01548	Product_name		Zn finger protein HypA/HybF (possibly regulating hydrogenase expres		
2558670880	DRAFT_01548	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670880	DRAFT_01548	Coordinates		10080..10433(+)		
2558670880	DRAFT_01548	DNA_length		354bp		
2558670880	DRAFT_01548	Protein_length		117aa		
2558670880	DRAFT_01548	GC			0.61	

2558670881	DRAFT_01549	COG_category	[C] Energy production and conversion			
2558670881	DRAFT_01549	COG0680	Ni,Fe-hydrogenase maturation factor			5.00E-11
2558670881	DRAFT_01549	pfam01750	HycI			2.50E-08
2558670881	DRAFT_01549	TIGR00072	hydrogenase maturation protease			7.80E-30
2558670881	DRAFT_01549	Locus_type		CDS		
2558670881	DRAFT_01549	Product_name		hydrogenase maturation protease		
2558670881	DRAFT_01549	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42		
2558670881	DRAFT_01549	Coordinates		10472..10957(+)		
2558670881	DRAFT_01549	DNA_length		486bp		
2558670881	DRAFT_01549	Protein_length		161aa		

2558670881	DRAFT_01549	GC		0.56	

2558670882	DRAFT_01550	Locus_type		CDS	
2558670882	DRAFT_01550	Product_name		hypothetical protein	
2558670882	DRAFT_01550	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42	
2558670882	DRAFT_01550	Coordinates		10954..11298(+)	
2558670882	DRAFT_01550	DNA_length		345bp	
2558670882	DRAFT_01550	Protein_length		114aa	
2558670882	DRAFT_01550	GC		0.6	
2558670882	DRAFT_01550	Transmembrane		Yes	

2558670883	DRAFT_01551	COG_category	[C] Energy production and conversion		
2558670883	DRAFT_01551	COG3260	Ni,Fe-hydrogenase III small subunit		3.00E-47
2558670883	DRAFT_01551	pfam01058	Oxidored_q6		4.10E-26
2558670883	DRAFT_01551	EC:1.6.99.3	NADH dehydrogenase.		
2558670883	DRAFT_01551	TIGR01957	NADH-quinone oxidoreductase, B subunit		3.10E-47
2558670883	DRAFT_01551	KO:K00356	NADH dehydrogenase [EC:1.6.99.3]		4.60E-44
2558670883	DRAFT_01551	Locus_type		CDS	
2558670883	DRAFT_01551	Product_name		Membrane bound hydrogenase subunit mbhJ	
2558670883	DRAFT_01551	Scaffold		DRAFT_contig_70_494_len_11744_read_count_211670.42	
2558670883	DRAFT_01551	Coordinates		11285..11743(+)	
2558670883	DRAFT_01551	DNA_length		459bp	
2558670883	DRAFT_01551	Protein_length		153aa	
2558670883	DRAFT_01551	GC		0.6	

2558670884	DRAFT_01552	pfam00188	CAP		1.30E-07
2558670884	DRAFT_01552	Locus_type		CDS	
2558670884	DRAFT_01552	Product_name		Cysteine-rich secretory protein family	
2558670884	DRAFT_01552	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670884	DRAFT_01552	Coordinates		297..1418(+)	
2558670884	DRAFT_01552	DNA_length		1122bp	
2558670884	DRAFT_01552	Protein_length		373aa	
2558670884	DRAFT_01552	GC		0.57	
2558670884	DRAFT_01552	Transmembrane		Yes	

2558670885	DRAFT_01553	COG_category	[R] General function prediction only		
2558670885	DRAFT_01553	COG_category	[G] Carbohydrate transport and metabolism		
2558670885	DRAFT_01553	COG_category	[F] Nucleotide transport and metabolism		
2558670885	DRAFT_01553	COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hy		3.00E-31
2558670885	DRAFT_01553	pfam01230	HIT		1.20E-24
2558670885	DRAFT_01553	KO:K02503	Hit-like protein involved in cell-cycle regulation		2.30E-24
2558670885	DRAFT_01553	Locus_type		CDS	
2558670885	DRAFT_01553	Product_name		Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hy	
2558670885	DRAFT_01553	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670885	DRAFT_01553	Coordinates		1428..1880(-)	
2558670885	DRAFT_01553	DNA_length		453bp	
2558670885	DRAFT_01553	Protein_length		150aa	
2558670885	DRAFT_01553	GC		0.57	
2558670886	DRAFT_01554	Locus_type		CDS	
2558670886	DRAFT_01554	Product_name		hypothetical protein	
2558670886	DRAFT_01554	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670886	DRAFT_01554	Coordinates		1971..2129(+)	
2558670886	DRAFT_01554	DNA_length		159bp	
2558670886	DRAFT_01554	Protein_length		52aa	
2558670886	DRAFT_01554	GC		0.57	
2558670887	DRAFT_01555	Locus_type		CDS	
2558670887	DRAFT_01555	Product_name		hypothetical protein	
2558670887	DRAFT_01555	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670887	DRAFT_01555	Coordinates		2152..2520(-)	
2558670887	DRAFT_01555	DNA_length		369bp	
2558670887	DRAFT_01555	Protein_length		122aa	
2558670887	DRAFT_01555	GC		0.56	
2558670888	DRAFT_01556	Locus_type		CDS	
2558670888	DRAFT_01556	Product_name		hypothetical protein	
2558670888	DRAFT_01556	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	

2558670888	DRAFT_01556	Coordinates		2825..3508(-)		
2558670888	DRAFT_01556	DNA_length		684bp		
2558670888	DRAFT_01556	Protein_length		227aa		
2558670888	DRAFT_01556	GC			0.58	
2558670888	DRAFT_01556	Transmembrane		Yes		

2558670889	DRAFT_01557	Locus_type		CDS		
2558670889	DRAFT_01557	Product_name		hypothetical protein		
2558670889	DRAFT_01557	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43		
2558670889	DRAFT_01557	Coordinates		3495..4079(-)		
2558670889	DRAFT_01557	DNA_length		585bp		
2558670889	DRAFT_01557	Protein_length		194aa		
2558670889	DRAFT_01557	GC			0.6	
2558670889	DRAFT_01557	Transmembrane		Yes		

2558670890	DRAFT_01558	Locus_type		CDS		
2558670890	DRAFT_01558	Product_name		hypothetical protein		
2558670890	DRAFT_01558	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43		
2558670890	DRAFT_01558	Coordinates		4159..4779(+)		
2558670890	DRAFT_01558	DNA_length		621bp		
2558670890	DRAFT_01558	Protein_length		206aa		
2558670890	DRAFT_01558	GC			0.62	

2558670891	DRAFT_01559	COG_category	[R] General function prediction only			
2558670891	DRAFT_01559	COG2151	Predicted metal-sulfur cluster biosynthetic enzyme			6.00E-07
2558670891	DRAFT_01559	pfam01883	DUF59			2.30E-11
2558670891	DRAFT_01559	Locus_type		CDS		
2558670891	DRAFT_01559	Product_name		Predicted metal-sulfur cluster biosynthetic enzyme		
2558670891	DRAFT_01559	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43		
2558670891	DRAFT_01559	Coordinates		4780..5124(-)		
2558670891	DRAFT_01559	DNA_length		345bp		
2558670891	DRAFT_01559	Protein_length		114aa		
2558670891	DRAFT_01559	GC			0.52	

2558670892	DRAFT_01560	COG_category	[C] Energy production and conversion		
2558670892	DRAFT_01560	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopte		1.00E-25
2558670892	DRAFT_01560	pfam00296	Bac_luciferase		1.30E-54
2558670892	DRAFT_01560	TIGR03617	probable F420-dependent oxidoreductase, MSMEG_2256 family		1.60E-127
2558670892	DRAFT_01560	Locus_type		CDS	
2558670892	DRAFT_01560	Product_name		probable F420-dependent oxidoreductase, MSMEG_2256 family	
2558670892	DRAFT_01560	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670892	DRAFT_01560	Coordinates		5259..6266(-)	
2558670892	DRAFT_01560	DNA_length		1008bp	
2558670892	DRAFT_01560	Protein_length		335aa	
2558670892	DRAFT_01560	GC		0.61	
2558670893	DRAFT_01561	pfam13463	HTH_27		7.80E-05
2558670893	DRAFT_01561	Locus_type		CDS	
2558670893	DRAFT_01561	Product_name		Winged helix DNA-binding domain	
2558670893	DRAFT_01561	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670893	DRAFT_01561	Coordinates		6867..7091(+)	
2558670893	DRAFT_01561	DNA_length		225bp	
2558670893	DRAFT_01561	Protein_length		74aa	
2558670893	DRAFT_01561	GC		0.54	
2558670894	DRAFT_01562	Locus_type		CDS	
2558670894	DRAFT_01562	Product_name		hypothetical protein	
2558670894	DRAFT_01562	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670894	DRAFT_01562	Coordinates		7045..7179(+)	
2558670894	DRAFT_01562	DNA_length		135bp	
2558670894	DRAFT_01562	Protein_length		44aa	
2558670894	DRAFT_01562	GC		0.53	
2558670895	DRAFT_01563	COG_category	[R] General function prediction only		
2558670895	DRAFT_01563	COG2872	Predicted metal-dependent hydrolases related to alanyl-tRNA syntheta		3.00E-56
2558670895	DRAFT_01563	pfam01411	tRNA-synt_2c		3.80E-07
2558670895	DRAFT_01563	pfam07973	tRNA_SAD		6.70E-12
2558670895	DRAFT_01563	Locus_type		CDS	

2558670895	DRAFT_01563	Product_name		Predicted metal-dependent hydrolases related to alanyl-tRNA synthet	
2558670895	DRAFT_01563	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670895	DRAFT_01563	Coordinates		7262..7930(-)	
2558670895	DRAFT_01563	DNA_length		669bp	
2558670895	DRAFT_01563	Protein_length		222aa	
2558670895	DRAFT_01563	GC		0.57	
2558670896	DRAFT_01564	COG_category	[S] Function unknown		
2558670896	DRAFT_01564	COG1602	Uncharacterized conserved protein		2.00E-119
2558670896	DRAFT_01564	pfam04894	DUF650		4.60E-100
2558670896	DRAFT_01564	pfam04895	DUF651		4.10E-33
2558670896	DRAFT_01564	Locus_type		CDS	
2558670896	DRAFT_01564	Product_name		Uncharacterized conserved protein	
2558670896	DRAFT_01564	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670896	DRAFT_01564	Coordinates		8000..9316(-)	
2558670896	DRAFT_01564	DNA_length		1317bp	
2558670896	DRAFT_01564	Protein_length		438aa	
2558670896	DRAFT_01564	GC		0.62	
2558670897	DRAFT_01565	COG_category	[L] Replication, recombination and repair		
2558670897	DRAFT_01565	COG0420	DNA repair exonuclease		2.00E-30
2558670897	DRAFT_01565	pfam12850	Metallophos_2		1.60E-14
2558670897	DRAFT_01565	Locus_type		CDS	
2558670897	DRAFT_01565	Product_name		DNA repair exonuclease	
2558670897	DRAFT_01565	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	
2558670897	DRAFT_01565	Coordinates		9425..10675(+)	
2558670897	DRAFT_01565	DNA_length		1251bp	
2558670897	DRAFT_01565	Protein_length		416aa	
2558670897	DRAFT_01565	GC		0.58	
2558670898	DRAFT_01566	pfam13476	AAA_23		1.40E-15
2558670898	DRAFT_01566	Locus_type		CDS	
2558670898	DRAFT_01566	Product_name		AAA domain	
2558670898	DRAFT_01566	Scaffold		DRAFT_contig_70_498_len_11660_read_count_202600.43	

2558670898	DRAFT_01566	Coordinates		10696..11658(+)		
2558670898	DRAFT_01566	DNA_length		963bp		
2558670898	DRAFT_01566	Protein_length		321aa		
2558670898	DRAFT_01566	GC			0.6	
2558670899	DRAFT_01567	pfam01269	Fibrillarin			8.20E-53
2558670899	DRAFT_01567	Locus_type		CDS		
2558670899	DRAFT_01567	Product_name		Fibrillarin-like rRNA methylase		
2558670899	DRAFT_01567	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44		
2558670899	DRAFT_01567	Coordinates		2..439(-)		
2558670899	DRAFT_01567	DNA_length		438bp		
2558670899	DRAFT_01567	Protein_length		146aa		
2558670899	DRAFT_01567	GC			0.6	
2558670900	DRAFT_01568	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670900	DRAFT_01568	COG1498	Protein implicated in ribosomal biogenesis, Nop56p homolog			9.00E-76
2558670900	DRAFT_01568	pfam08060	NOSIC			1.30E-15
2558670900	DRAFT_01568	pfam01798	Nop			1.20E-50
2558670900	DRAFT_01568	KO:K14564	nucleolar protein 56			0.00E+00
2558670900	DRAFT_01568	ITERM:02514	rRNA biogenesis protein Nop56/Nop58			
2558670900	DRAFT_01568	Locus_type		CDS		
2558670900	DRAFT_01568	Product_name		rRNA biogenesis protein Nop56/Nop58		
2558670900	DRAFT_01568	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44		
2558670900	DRAFT_01568	Coordinates		436..1392(-)		
2558670900	DRAFT_01568	DNA_length		957bp		
2558670900	DRAFT_01568	Protein_length		318aa		
2558670900	DRAFT_01568	GC			0.6	
2558670901	DRAFT_01569	COG_category	[B] Chromatin structure and dynamics			
2558670901	DRAFT_01569	COG_category	[K] Transcription			
2558670901	DRAFT_01569	COG1243	Histone acetyltransferase			0.00E+00
2558670901	DRAFT_01569	pfam04055	Radical_SAM			5.10E-15
2558670901	DRAFT_01569	pfam00583	Acetyltransf_1			2.80E-06
2558670901	DRAFT_01569	EC:2.3.1.48	Histone acetyltransferase.			

2558670901	DRAFT_01569	TIGR01211	histone acetyltransferase, ELP3 family			0.00E+00
2558670901	DRAFT_01569	KO:K07739	elongator complex protein 3 [EC:2.3.1.48]			0.00E+00
2558670901	DRAFT_01569	Locus_type		CDS		
2558670901	DRAFT_01569	Product_name		histone acetyltransferase, ELP3 family		
2558670901	DRAFT_01569	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44		
2558670901	DRAFT_01569	Coordinates		1784..3379(+)		
2558670901	DRAFT_01569	DNA_length		1596bp		
2558670901	DRAFT_01569	Protein_length		531aa		
2558670901	DRAFT_01569	GC			0.62	
2558670902	DRAFT_01570	Locus_type		CDS		
2558670902	DRAFT_01570	Product_name		hypothetical protein		
2558670902	DRAFT_01570	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44		
2558670902	DRAFT_01570	Coordinates		3399..4244(-)		
2558670902	DRAFT_01570	DNA_length		846bp		
2558670902	DRAFT_01570	Protein_length		281aa		
2558670902	DRAFT_01570	GC			0.63	
2558670902	DRAFT_01570	Transmembrane		Yes		
2558670903	DRAFT_01571	KEGG_module	M00248: Putative antibiotic transport system			
2558670903	DRAFT_01571	COG_category	[V] Defense mechanisms			
2558670903	DRAFT_01571	COG0842	ABC-type multidrug transport system, permease component			1.00E-06
2558670903	DRAFT_01571	pfam01061	ABC2_membrane			9.00E-10
2558670903	DRAFT_01571	KO:K09686	antibiotic transport system permease protein			9.70E-44
2558670903	DRAFT_01571	Locus_type		CDS		
2558670903	DRAFT_01571	Product_name		ABC-type multidrug transport system, permease component		
2558670903	DRAFT_01571	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44		
2558670903	DRAFT_01571	Coordinates		4241..5050(-)		
2558670903	DRAFT_01571	DNA_length		810bp		
2558670903	DRAFT_01571	Protein_length		269aa		
2558670903	DRAFT_01571	GC			0.59	
2558670903	DRAFT_01571	Transmembrane		Yes		
2558670904	DRAFT_01572	KEGG_module	M00248: Putative antibiotic transport system			

2558670904	DRAFT_01572	COG_category	[V] Defense mechanisms		
2558670904	DRAFT_01572	COG1131	ABC-type multidrug transport system, ATPase component		1.00E-65
2558670904	DRAFT_01572	pfam00005	ABC_tran		1.20E-23
2558670904	DRAFT_01572	KO:K09687	antibiotic transport system ATP-binding protein		0.00E+00
2558670904	DRAFT_01572	Locus_type		CDS	
2558670904	DRAFT_01572	Product_name		ABC-type multidrug transport system, ATPase component	
2558670904	DRAFT_01572	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44	
2558670904	DRAFT_01572	Coordinates		5040..6038(-)	
2558670904	DRAFT_01572	DNA_length		999bp	
2558670904	DRAFT_01572	Protein_length		332aa	
2558670904	DRAFT_01572	GC		0.59	
2558670905	DRAFT_01573	Metacyc	PWY-5921: L-glutamine biosynthesis II (tRNA-dependent)		
2558670905	DRAFT_01573	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670905	DRAFT_01573	COG_category	[E] Amino acid transport and metabolism		
2558670905	DRAFT_01573	COG0252	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D		2.00E-81
2558670905	DRAFT_01573	pfam00710	Asparaginase		2.40E-87
2558670905	DRAFT_01573	EC:6.3.5.7	Glutaminyl-tRNA synthase (glutamine-hydrolyzing).		
2558670905	DRAFT_01573	TIGR00519	L-asparaginase, type I		8.40E-107
2558670905	DRAFT_01573	TIGR02153	glutamyl-tRNA(Gln) amidotransferase, subunit D		0.00E+00
2558670905	DRAFT_01573	KO:K09482	glutamyl-tRNA(Gln) amidotransferase subunit D [EC:6.3.5.7]		0.00E+00
2558670905	DRAFT_01573	ITERM:01532	glutamyl-tRNA(Gln) amidotransferase subunit D (EC 6.3.5.7)		
2558670905	DRAFT_01573	Locus_type		CDS	
2558670905	DRAFT_01573	Product_name		glutamyl-tRNA(Gln) amidotransferase subunit D (EC 6.3.5.7)	
2558670905	DRAFT_01573	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44	
2558670905	DRAFT_01573	Coordinates		6147..7469(+)	
2558670905	DRAFT_01573	DNA_length		1323bp	
2558670905	DRAFT_01573	Protein_length		440aa	
2558670905	DRAFT_01573	GC		0.63	
2558670906	DRAFT_01574	Metacyc	PWY-5921: L-glutamine biosynthesis II (tRNA-dependent)		
2558670906	DRAFT_01574	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558670906	DRAFT_01574	COG2511	Archaeal Glu-tRNAGln amidotransferase subunit E (contains GAD doma		0.00E+00
2558670906	DRAFT_01574	pfam02938	GAD		3.60E-05

2558670906	DRAFT_01574	pfam02637	GatB_Yqey			2.40E-21
2558670906	DRAFT_01574	pfam02934	GatB_N			5.20E-67
2558670906	DRAFT_01574	EC:6.3.5.7	Glutaminyl-tRNA synthase (glutamine-hydrolyzing).			
2558670906	DRAFT_01574	TIGR00134	glutamyl-tRNA(Gln) amidotransferase, subunit E			0.00E+00
2558670906	DRAFT_01574	KO:K03330	glutamyl-tRNA(Gln) amidotransferase subunit E [EC:6.3.5.7]			0.00E+00
2558670906	DRAFT_01574	ITERM:01533	glutamyl-tRNA(Gln) amidotransferase subunit E (EC 6.3.5.7)			
2558670906	DRAFT_01574	Locus_type		CDS		
2558670906	DRAFT_01574	Product_name		glutamyl-tRNA(Gln) amidotransferase subunit E (EC 6.3.5.7)		
2558670906	DRAFT_01574	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44		
2558670906	DRAFT_01574	Coordinates		7466..9385(+)		
2558670906	DRAFT_01574	DNA_length		1920bp		
2558670906	DRAFT_01574	Protein_length		639aa		
2558670906	DRAFT_01574	GC			0.59	
2558670907	DRAFT_01575	Locus_type		CDS		
2558670907	DRAFT_01575	Product_name		hypothetical protein		
2558670907	DRAFT_01575	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44		
2558670907	DRAFT_01575	Coordinates		9454..10005(-)		
2558670907	DRAFT_01575	DNA_length		552bp		
2558670907	DRAFT_01575	Protein_length		183aa		
2558670907	DRAFT_01575	GC			0.59	
2558670907	DRAFT_01575	Transmembrane		Yes		
2558670908	DRAFT_01576	COG_category	[R] General function prediction only			
2558670908	DRAFT_01576	COG1721	Uncharacterized conserved protein (some members contain a von Will			5.00E-27
2558670908	DRAFT_01576	pfam01882	DUF58			5.40E-13
2558670908	DRAFT_01576	Locus_type		CDS		
2558670908	DRAFT_01576	Product_name		Uncharacterized conserved protein (some members contain a von Wi		
2558670908	DRAFT_01576	Scaffold		DRAFT_contig_70_523_len_11378_read_count_163908.44		
2558670908	DRAFT_01576	Coordinates		9954..11375(-)		
2558670908	DRAFT_01576	DNA_length		1422bp		
2558670908	DRAFT_01576	Protein_length		473aa		
2558670908	DRAFT_01576	GC			0.59	
2558670908	DRAFT_01576	Transmembrane		Yes		

2558670909	DRAFT_01577	Locus_type		CDS		
2558670909	DRAFT_01577	Product_name		hypothetical protein		
2558670909	DRAFT_01577	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45		
2558670909	DRAFT_01577	Coordinates		3..539(+)		
2558670909	DRAFT_01577	DNA_length		537bp		
2558670909	DRAFT_01577	Protein_length		178aa		
2558670909	DRAFT_01577	GC			0.52	
2558670910	DRAFT_01578	Locus_type		CDS		
2558670910	DRAFT_01578	Product_name		hypothetical protein		
2558670910	DRAFT_01578	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45		
2558670910	DRAFT_01578	Coordinates		962..1258(+)		
2558670910	DRAFT_01578	DNA_length		297bp		
2558670910	DRAFT_01578	Protein_length		98aa		
2558670910	DRAFT_01578	GC			0.59	
2558670911	DRAFT_01579	Locus_type		CDS		
2558670911	DRAFT_01579	Product_name		hypothetical protein		
2558670911	DRAFT_01579	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45		
2558670911	DRAFT_01579	Coordinates		1255..1416(+)		
2558670911	DRAFT_01579	DNA_length		162bp		
2558670911	DRAFT_01579	Protein_length		53aa		
2558670911	DRAFT_01579	GC			0.51	
2558670912	DRAFT_01580	Locus_type		CDS		
2558670912	DRAFT_01580	Product_name		hypothetical protein		
2558670912	DRAFT_01580	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45		
2558670912	DRAFT_01580	Coordinates		1413..1535(+)		
2558670912	DRAFT_01580	DNA_length		123bp		
2558670912	DRAFT_01580	Protein_length		40aa		
2558670912	DRAFT_01580	GC			0.5	
2558670913	DRAFT_01581	pfam04307	DUF457			5.80E-14

2558670913	DRAFT_01581	Locus_type		CDS		
2558670913	DRAFT_01581	Product_name		Predicted membrane-bound metal-dependent hydrolase (DUF457)		
2558670913	DRAFT_01581	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45		
2558670913	DRAFT_01581	Coordinates		1815..2720(+)		
2558670913	DRAFT_01581	DNA_length		906bp		
2558670913	DRAFT_01581	Protein_length		301aa		
2558670913	DRAFT_01581	GC			0.51	
2558670913	DRAFT_01581	Transmembrane		Yes		
2558670914	DRAFT_01582	Locus_type		CDS		
2558670914	DRAFT_01582	Product_name		hypothetical protein		
2558670914	DRAFT_01582	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45		
2558670914	DRAFT_01582	Coordinates		2835..3308(-)		
2558670914	DRAFT_01582	DNA_length		474bp		
2558670914	DRAFT_01582	Protein_length		157aa		
2558670914	DRAFT_01582	GC			0.46	
2558670914	DRAFT_01582	Transmembrane		Yes		
2558670915	DRAFT_01583	Locus_type		CDS		
2558670915	DRAFT_01583	Product_name		hypothetical protein		
2558670915	DRAFT_01583	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45		
2558670915	DRAFT_01583	Coordinates		3317..3532(+)		
2558670915	DRAFT_01583	DNA_length		216bp		
2558670915	DRAFT_01583	Protein_length		71aa		
2558670915	DRAFT_01583	GC			0.53	
2558670916	DRAFT_01584	pfam11177	DUF2964			1.40E-04
2558670916	DRAFT_01584	Locus_type		CDS		
2558670916	DRAFT_01584	Product_name		Protein of unknown function (DUF2964)		
2558670916	DRAFT_01584	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45		
2558670916	DRAFT_01584	Coordinates		3635..4570(+)		
2558670916	DRAFT_01584	DNA_length		936bp		
2558670916	DRAFT_01584	Protein_length		311aa		
2558670916	DRAFT_01584	GC			0.61	

2558670916	DRAFT_01584	Transmembrane		Yes	

2558670917	DRAFT_01585	Locus_type		CDS	
2558670917	DRAFT_01585	Product_name		hypothetical protein	
2558670917	DRAFT_01585	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45	
2558670917	DRAFT_01585	Coordinates		4866..5174(-)	
2558670917	DRAFT_01585	DNA_length		309bp	
2558670917	DRAFT_01585	Protein_length		102aa	
2558670917	DRAFT_01585	GC		0.56	

2558670918	DRAFT_01586	COG_category	[C] Energy production and conversion		
2558670918	DRAFT_01586	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)		2.00E-88
2558670918	DRAFT_01586	pfam00248	Aldo_ket_red		2.50E-79
2558670918	DRAFT_01586	EC:1.1.1.91	Aryl-alcohol dehydrogenase (NADP(+)).		
2558670918	DRAFT_01586	KO:K05882	aryl-alcohol dehydrogenase (NADP+) [EC:1.1.1.91]		0.00E+00
2558670918	DRAFT_01586	Locus_type		CDS	
2558670918	DRAFT_01586	Product_name		Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	
2558670918	DRAFT_01586	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45	
2558670918	DRAFT_01586	Coordinates		5332..6315(+)	
2558670918	DRAFT_01586	DNA_length		984bp	
2558670918	DRAFT_01586	Protein_length		327aa	
2558670918	DRAFT_01586	GC		0.59	

2558670919	DRAFT_01587	COG_category	[G] Carbohydrate transport and metabolism		
2558670919	DRAFT_01587	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670919	DRAFT_01587	COG0451	Nucleoside-diphosphate-sugar epimerases		1.00E-39
2558670919	DRAFT_01587	pfam01370	Epimerase		3.50E-37
2558670919	DRAFT_01587	Locus_type		CDS	
2558670919	DRAFT_01587	Product_name		Nucleoside-diphosphate-sugar epimerases	
2558670919	DRAFT_01587	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45	
2558670919	DRAFT_01587	Coordinates		6502..7590(-)	
2558670919	DRAFT_01587	DNA_length		1089bp	
2558670919	DRAFT_01587	Protein_length		362aa	
2558670919	DRAFT_01587	GC		0.57	

2558670920	DRAFT_01588	pfam13231	PMT_2		2.60E-10
2558670920	DRAFT_01588	Locus_type		CDS	
2558670920	DRAFT_01588	Product_name		4-amino-4-deoxy-L-arabinose transferase and related glycosyltransfer	
2558670920	DRAFT_01588	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45	
2558670920	DRAFT_01588	Coordinates		7803..9206(-)	
2558670920	DRAFT_01588	DNA_length		1404bp	
2558670920	DRAFT_01588	Protein_length		467aa	
2558670920	DRAFT_01588	GC		0.56	
2558670920	DRAFT_01588	Transmembrane		Yes	
2558670921	DRAFT_01589	KEGG_module	M00248: Putative antibiotic transport system		
2558670921	DRAFT_01589	COG_category	[V] Defense mechanisms		
2558670921	DRAFT_01589	COG0842	ABC-type multidrug transport system, permease component		2.00E-05
2558670921	DRAFT_01589	pfam01061	ABC2_membrane		6.60E-27
2558670921	DRAFT_01589	TIGR00025	ABC transporter efflux protein, DrrB family		1.90E-21
2558670921	DRAFT_01589	KO:K09686	antibiotic transport system permease protein		4.20E-45
2558670921	DRAFT_01589	Locus_type		CDS	
2558670921	DRAFT_01589	Product_name		ABC-type multidrug transport system, permease component	
2558670921	DRAFT_01589	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45	
2558670921	DRAFT_01589	Coordinates		9456..10286(-)	
2558670921	DRAFT_01589	DNA_length		831bp	
2558670921	DRAFT_01589	Protein_length		276aa	
2558670921	DRAFT_01589	GC		0.62	
2558670921	DRAFT_01589	Transmembrane		Yes	
2558670922	DRAFT_01590	KEGG_module	M00248: Putative antibiotic transport system		
2558670922	DRAFT_01590	COG_category	[V] Defense mechanisms		
2558670922	DRAFT_01590	COG1131	ABC-type multidrug transport system, ATPase component		1.00E-76
2558670922	DRAFT_01590	pfam13732	DUF4162		1.60E-07
2558670922	DRAFT_01590	pfam00005	ABC_tran		2.90E-29
2558670922	DRAFT_01590	TIGR01188	daunorubicin resistance ABC transporter ATP-binding subunit		1.30E-109
2558670922	DRAFT_01590	KO:K09687	antibiotic transport system ATP-binding protein		0.00E+00
2558670922	DRAFT_01590	Locus_type		CDS	

2558670922	DRAFT_01590	Product_name		daunorubicin resistance ABC transporter ATP-binding subunit	
2558670922	DRAFT_01590	Scaffold		DRAFT_contig_70_531_len_11320_read_count_197274.45	
2558670922	DRAFT_01590	Coordinates		10289..11317(-)	
2558670922	DRAFT_01590	DNA_length		1029bp	
2558670922	DRAFT_01590	Protein_length		342aa	
2558670922	DRAFT_01590	GC		0.62	
2558670923	DRAFT_01591	Locus_type		CDS	
2558670923	DRAFT_01591	Product_name		hypothetical protein	
2558670923	DRAFT_01591	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46	
2558670923	DRAFT_01591	Coordinates		160..627(+)	
2558670923	DRAFT_01591	DNA_length		468bp	
2558670923	DRAFT_01591	Protein_length		155aa	
2558670923	DRAFT_01591	GC		0.54	
2558670924	DRAFT_01592	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism		
2558670924	DRAFT_01592	COG1228	Imidazolonepropionase and related amidohydrolases		2.00E-44
2558670924	DRAFT_01592	pfam01979	Amidohydro_1		6.90E-27
2558670924	DRAFT_01592	Locus_type		CDS	
2558670924	DRAFT_01592	Product_name		Imidazolonepropionase and related amidohydrolases	
2558670924	DRAFT_01592	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46	
2558670924	DRAFT_01592	Coordinates		1006..2217(-)	
2558670924	DRAFT_01592	DNA_length		1212bp	
2558670924	DRAFT_01592	Protein_length		403aa	
2558670924	DRAFT_01592	GC		0.61	
2558670925	DRAFT_01593	Locus_type		CDS	
2558670925	DRAFT_01593	Product_name		hypothetical protein	
2558670925	DRAFT_01593	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46	
2558670925	DRAFT_01593	Coordinates		2378..5122(+)	
2558670925	DRAFT_01593	DNA_length		2745bp	
2558670925	DRAFT_01593	Protein_length		914aa	
2558670925	DRAFT_01593	GC		0.6	
2558670925	DRAFT_01593	Transmembrane		Yes	

2558670926	DRAFT_01594	Locus_type		CDS	
2558670926	DRAFT_01594	Product_name		hypothetical protein	
2558670926	DRAFT_01594	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46	
2558670926	DRAFT_01594	Coordinates		5134..5421(-)	
2558670926	DRAFT_01594	DNA_length		288bp	
2558670926	DRAFT_01594	Protein_length		95aa	
2558670926	DRAFT_01594	GC		0.57	
2558670926	DRAFT_01594	Transmembrane		Yes	
2558670927	DRAFT_01595	COG_category	[R] General function prediction only		
2558670927	DRAFT_01595	COG_category	[E] Amino acid transport and metabolism		
2558670927	DRAFT_01595	COG1387	Histidinol phosphatase and related hydrolases of the PHP family		6.00E-14
2558670927	DRAFT_01595	pfam02811	PHP		7.90E-05
2558670927	DRAFT_01595	TIGR01856	histidinol phosphate phosphatase, HisJ family		6.40E-19
2558670927	DRAFT_01595	Locus_type		CDS	
2558670927	DRAFT_01595	Product_name		Histidinol phosphatase and related hydrolases of the PHP family	
2558670927	DRAFT_01595	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46	
2558670927	DRAFT_01595	Coordinates		5510..6280(-)	
2558670927	DRAFT_01595	DNA_length		771bp	
2558670927	DRAFT_01595	Protein_length		256aa	
2558670927	DRAFT_01595	GC		0.52	
2558670928	DRAFT_01596	Locus_type		CDS	
2558670928	DRAFT_01596	Product_name		hypothetical protein	
2558670928	DRAFT_01596	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46	
2558670928	DRAFT_01596	Coordinates		6302..6460(-)	
2558670928	DRAFT_01596	DNA_length		159bp	
2558670928	DRAFT_01596	Protein_length		52aa	
2558670928	DRAFT_01596	GC		0.54	
2558670929	DRAFT_01597	Locus_type		CDS	
2558670929	DRAFT_01597	Product_name		hypothetical protein	
2558670929	DRAFT_01597	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46	

2558670929	DRAFT_01597	Coordinates		6525..6668(-)		
2558670929	DRAFT_01597	DNA_length		144bp		
2558670929	DRAFT_01597	Protein_length		47aa		
2558670929	DRAFT_01597	GC			0.43	
2558670930	DRAFT_01598	pfam13847	Methyltransf_31			5.90E-08
2558670930	DRAFT_01598	Locus_type		CDS		
2558670930	DRAFT_01598	Product_name		Methyltransferase domain		
2558670930	DRAFT_01598	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46		
2558670930	DRAFT_01598	Coordinates		6976..7296(-)		
2558670930	DRAFT_01598	DNA_length		321bp		
2558670930	DRAFT_01598	Protein_length		106aa		
2558670930	DRAFT_01598	GC			0.53	
2558670931	DRAFT_01599	Locus_type		CDS		
2558670931	DRAFT_01599	Product_name		hypothetical protein		
2558670931	DRAFT_01599	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46		
2558670931	DRAFT_01599	Coordinates		7323..8084(+)		
2558670931	DRAFT_01599	DNA_length		762bp		
2558670931	DRAFT_01599	Protein_length		253aa		
2558670931	DRAFT_01599	GC			0.5	
2558670931	DRAFT_01599	Transmembrane		Yes		
2558670932	DRAFT_01600	Locus_type		CDS		
2558670932	DRAFT_01600	Product_name		hypothetical protein		
2558670932	DRAFT_01600	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46		
2558670932	DRAFT_01600	Coordinates		8110..8547(-)		
2558670932	DRAFT_01600	DNA_length		438bp		
2558670932	DRAFT_01600	Protein_length		145aa		
2558670932	DRAFT_01600	GC			0.53	
2558670932	DRAFT_01600	Transmembrane		Yes		
2558670933	DRAFT_01601	Locus_type		CDS		
2558670933	DRAFT_01601	Product_name		hypothetical protein		

2558670933	DRAFT_01601	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46		
2558670933	DRAFT_01601	Coordinates		8924..9526(+)		
2558670933	DRAFT_01601	DNA_length		603bp		
2558670933	DRAFT_01601	Protein_length		200aa		
2558670933	DRAFT_01601	GC			0.49	
2558670933	DRAFT_01601	Transmembrane		Yes		
2558670934	DRAFT_01602	Locus_type		CDS		
2558670934	DRAFT_01602	Product_name		hypothetical protein		
2558670934	DRAFT_01602	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46		
2558670934	DRAFT_01602	Coordinates		10131..10349(-)		
2558670934	DRAFT_01602	DNA_length		219bp		
2558670934	DRAFT_01602	Protein_length		72aa		
2558670934	DRAFT_01602	GC			0.52	
2558670934	DRAFT_01602	Transmembrane		Yes		
2558670935	DRAFT_01603	KEGG_module	M00135: GABA biosynthesis, eukaryotes, putrescine => GABA			
2558670935	DRAFT_01603	Metacyc	PWY-0: putrescine degradation III			
2558670935	DRAFT_01603	Metacyc	PWY-6117: spermine and spermidine degradation I			
2558670935	DRAFT_01603	pfam00583	Acetyltransf_1			2.20E-13
2558670935	DRAFT_01603	EC:2.3.1.57	Diamine N-acetyltransferase.			
2558670935	DRAFT_01603	KO:K00657	diamine N-acetyltransferase [EC:2.3.1.57]			5.40E-29
2558670935	DRAFT_01603	Locus_type		CDS		
2558670935	DRAFT_01603	Product_name		Acetyltransferases		
2558670935	DRAFT_01603	Scaffold		DRAFT_contig_70_538_len_11243_read_count_219486.46		
2558670935	DRAFT_01603	Coordinates		10477..10977(-)		
2558670935	DRAFT_01603	DNA_length		501bp		
2558670935	DRAFT_01603	Protein_length		166aa		
2558670935	DRAFT_01603	GC			0.51	
2558670936	DRAFT_01604	Locus_type		CDS		
2558670936	DRAFT_01604	Product_name		hypothetical protein		
2558670936	DRAFT_01604	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670936	DRAFT_01604	Coordinates		2..331(-)		

2558670936	DRAFT_01604	DNA_length		330bp		
2558670936	DRAFT_01604	Protein_length		110aa		
2558670936	DRAFT_01604	GC			0.57	
2558670936	DRAFT_01604	Transmembrane		Yes		
2558670937	DRAFT_01605	IMG_pathway	433: Archaeal nucleoid proteins			
2558670937	DRAFT_01605	COG_category	[K] Transcription			
2558670937	DRAFT_01605	COG1581	Archaeal DNA-binding protein			6.00E-21
2558670937	DRAFT_01605	pfam01918	Alba			1.50E-18
2558670937	DRAFT_01605	TIGR00285	DNA-binding protein Alba			3.20E-39
2558670937	DRAFT_01605	KO:K03622	archaea-specific DNA-binding protein			2.70E-21
2558670937	DRAFT_01605	ITERM:00143	nucleoid protein Alba			
2558670937	DRAFT_01605	Locus_type		CDS		
2558670937	DRAFT_01605	Product_name		nucleoid protein Alba		
2558670937	DRAFT_01605	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670937	DRAFT_01605	Coordinates		692..988(-)		
2558670937	DRAFT_01605	DNA_length		297bp		
2558670937	DRAFT_01605	Protein_length		98aa		
2558670937	DRAFT_01605	GC			0.52	
2558670938	DRAFT_01606	Locus_type		CDS		
2558670938	DRAFT_01606	Product_name		hypothetical protein		
2558670938	DRAFT_01606	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670938	DRAFT_01606	Coordinates		1261..1440(-)		
2558670938	DRAFT_01606	DNA_length		180bp		
2558670938	DRAFT_01606	Protein_length		59aa		
2558670938	DRAFT_01606	GC			0.52	
2558670939	DRAFT_01607	COG_category	[L] Replication, recombination and repair			
2558670939	DRAFT_01607	COG3316	Transposase and inactivated derivatives			3.00E-09
2558670939	DRAFT_01607	pfam13610	DDE_Tnp_IS240			5.50E-16
2558670939	DRAFT_01607	Locus_type		CDS		
2558670939	DRAFT_01607	Product_name		Transposase and inactivated derivatives		
2558670939	DRAFT_01607	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		

2558670939	DRAFT_01607	Coordinates		1622..2782(+)		
2558670939	DRAFT_01607	DNA_length		1161bp		
2558670939	DRAFT_01607	Protein_length		386aa		
2558670939	DRAFT_01607	GC			0.55	
2558670940	DRAFT_01608	Locus_type		CDS		
2558670940	DRAFT_01608	Product_name		hypothetical protein		
2558670940	DRAFT_01608	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670940	DRAFT_01608	Coordinates		2808..3026(+)		
2558670940	DRAFT_01608	DNA_length		219bp		
2558670940	DRAFT_01608	Protein_length		72aa		
2558670940	DRAFT_01608	GC			0.57	
2558670941	DRAFT_01609	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			
2558670941	DRAFT_01609	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2558670941	DRAFT_01609	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)			
2558670941	DRAFT_01609	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2558670941	DRAFT_01609	Metacyc	PWY-5538: pyruvate fermentation to acetate VI			
2558670941	DRAFT_01609	Metacyc	PWY-5392: reductive TCA cycle II			
2558670941	DRAFT_01609	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)			
2558670941	DRAFT_01609	Metacyc	P23-PWY: reductive TCA cycle I			
2558670941	DRAFT_01609	Metacyc	PWY-6728: methylaspartate cycle			
2558670941	DRAFT_01609	Metacyc	PWY-5537: pyruvate fermentation to acetate V			
2558670941	DRAFT_01609	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2558670941	DRAFT_01609	Metacyc	PWY-5690: TCA cycle II (eukaryotic)			
2558670941	DRAFT_01609	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2558670941	DRAFT_01609	Metacyc	TCA: TCA cycle I (prokaryotic)			
2558670941	DRAFT_01609	COG_category	[C] Energy production and conversion			
2558670941	DRAFT_01609	COG0045	Succinyl-CoA synthetase, beta subunit			8.00E-88
2558670941	DRAFT_01609	pfam08442	ATP-grasp_2			1.90E-41
2558670941	DRAFT_01609	pfam00549	Ligase_CoA			3.60E-06
2558670941	DRAFT_01609	EC:6.2.1.5	Succinate--CoA ligase (ADP-forming).			
2558670941	DRAFT_01609	TIGR01016	succinyl-CoA synthetase, beta subunit			4.60E-99
2558670941	DRAFT_01609	KO:K01903	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]			0.00E+00

2558670941	DRAFT_01609	Locus_type		CDS	
2558670941	DRAFT_01609	Product_name		Succinyl-CoA synthetase, beta subunit	
2558670941	DRAFT_01609	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47	
2558670941	DRAFT_01609	Coordinates		3214..4311(+)	
2558670941	DRAFT_01609	DNA_length		1098bp	
2558670941	DRAFT_01609	Protein_length		365aa	
2558670941	DRAFT_01609	GC		0.6	

2558670942	DRAFT_01610	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)		
2558670942	DRAFT_01610	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2558670942	DRAFT_01610	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2558670942	DRAFT_01610	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2558670942	DRAFT_01610	Metacyc	TCA: TCA cycle I (prokaryotic)		
2558670942	DRAFT_01610	Metacyc	PWY-5690: TCA cycle II (eukaryotic)		
2558670942	DRAFT_01610	Metacyc	PWY-5392: reductive TCA cycle II		
2558670942	DRAFT_01610	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558670942	DRAFT_01610	Metacyc	PWY-6728: methylaspartate cycle		
2558670942	DRAFT_01610	Metacyc	PWY-5537: pyruvate fermentation to acetate V		
2558670942	DRAFT_01610	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)		
2558670942	DRAFT_01610	Metacyc	P23-PWY: reductive TCA cycle I		
2558670942	DRAFT_01610	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558670942	DRAFT_01610	Metacyc	PWY-5538: pyruvate fermentation to acetate VI		
2558670942	DRAFT_01610	COG_category	[C] Energy production and conversion		
2558670942	DRAFT_01610	COG0074	Succinyl-CoA synthetase, alpha subunit		4.00E-88
2558670942	DRAFT_01610	pfam02629	CoA_binding		2.30E-20
2558670942	DRAFT_01610	pfam13607	Succ_CoA_lig		8.80E-11
2558670942	DRAFT_01610	EC:6.2.1.5	Succinate--CoA ligase (ADP-forming).		
2558670942	DRAFT_01610	TIGR01019	succinyl-CoA synthetase, alpha subunit		2.80E-108
2558670942	DRAFT_01610	KO:K01902	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]		0.00E+00
2558670942	DRAFT_01610	Locus_type		CDS	
2558670942	DRAFT_01610	Product_name		succinyl-CoA synthetase (ADP-forming) alpha subunit (EC 6.2.1.5)	
2558670942	DRAFT_01610	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47	
2558670942	DRAFT_01610	Coordinates		4311..5180(+)	
2558670942	DRAFT_01610	DNA_length		870bp	

2558670942	DRAFT_01610	Protein_length		289aa		
2558670942	DRAFT_01610	GC			0.62	
2558670943	DRAFT_01611	KEGG_module	M00177: Ribosome, eukaryotes			
2558670943	DRAFT_01611	KEGG_module	M00179: Ribosome, archaea			
2558670943	DRAFT_01611	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558670943	DRAFT_01611	COG1552	Ribosomal protein L40E			3.00E-04
2558670943	DRAFT_01611	KO:K02927	large subunit ribosomal protein L40e			5.60E-16
2558670943	DRAFT_01611	Locus_type		CDS		
2558670943	DRAFT_01611	Product_name		Ribosomal protein L40E		
2558670943	DRAFT_01611	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670943	DRAFT_01611	Coordinates		5251..5418(+)		
2558670943	DRAFT_01611	DNA_length		168bp		
2558670943	DRAFT_01611	Protein_length		55aa		
2558670943	DRAFT_01611	GC			0.56	
2558670944	DRAFT_01612	Locus_type		tRNA		
2558670944	DRAFT_01612	Product_name		tRNA_Undet_???		
2558670944	DRAFT_01612	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670944	DRAFT_01612	Coordinates		5453..5576(+)		
2558670944	DRAFT_01612	DNA_length		124bp		
2558670944	DRAFT_01612	GC			0.65	
2558670945	DRAFT_01613	Locus_type		CDS		
2558670945	DRAFT_01613	Product_name		hypothetical protein		
2558670945	DRAFT_01613	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670945	DRAFT_01613	Coordinates		5645..6115(+)		
2558670945	DRAFT_01613	DNA_length		471bp		
2558670945	DRAFT_01613	Protein_length		156aa		
2558670945	DRAFT_01613	GC			0.55	
2558670946	DRAFT_01614	Locus_type		CDS		
2558670946	DRAFT_01614	Product_name		hypothetical protein		
2558670946	DRAFT_01614	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		

2558670946	DRAFT_01614	Coordinates		6112..6303(+)		
2558670946	DRAFT_01614	DNA_length		192bp		
2558670946	DRAFT_01614	Protein_length		63aa		
2558670946	DRAFT_01614	GC			0.54	
2558670947	DRAFT_01615	pfam04055	Radical_SAM			3.00E-10
2558670947	DRAFT_01615	Locus_type		CDS		
2558670947	DRAFT_01615	Product_name		DNA repair photolyase		
2558670947	DRAFT_01615	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670947	DRAFT_01615	Coordinates		6315..7058(+)		
2558670947	DRAFT_01615	DNA_length		744bp		
2558670947	DRAFT_01615	Protein_length		247aa		
2558670947	DRAFT_01615	GC			0.52	
2558670948	DRAFT_01616	pfam13520	AA_permease_2			2.20E-18
2558670948	DRAFT_01616	Locus_type		CDS		
2558670948	DRAFT_01616	Product_name		Amino acid transporters		
2558670948	DRAFT_01616	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670948	DRAFT_01616	Coordinates		7048..7560(-)		
2558670948	DRAFT_01616	DNA_length		513bp		
2558670948	DRAFT_01616	Protein_length		170aa		
2558670948	DRAFT_01616	GC			0.57	
2558670948	DRAFT_01616	Transmembrane		Yes		
2558670949	DRAFT_01617	Locus_type		CDS		
2558670949	DRAFT_01617	Product_name		hypothetical protein		
2558670949	DRAFT_01617	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670949	DRAFT_01617	Coordinates		7542..7742(-)		
2558670949	DRAFT_01617	DNA_length		201bp		
2558670949	DRAFT_01617	Protein_length		66aa		
2558670949	DRAFT_01617	GC			0.63	
2558670949	DRAFT_01617	Transmembrane		Yes		
2558670950	DRAFT_01618	COG_category	[S] Function unknown			

2558670950	DRAFT_01618	COG4089	Predicted membrane protein			1.00E-37
2558670950	DRAFT_01618	pfam07758	DUF1614			1.00E-48
2558670950	DRAFT_01618	Locus_type		CDS		
2558670950	DRAFT_01618	Product_name		Predicted membrane protein		
2558670950	DRAFT_01618	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670950	DRAFT_01618	Coordinates		7876..8577(-)		
2558670950	DRAFT_01618	DNA_length		702bp		
2558670950	DRAFT_01618	Protein_length		233aa		
2558670950	DRAFT_01618	GC			0.61	
2558670950	DRAFT_01618	Transmembrane		Yes		

2558670951	DRAFT_01619	pfam03477	ATP-cone			2.40E-07
2558670951	DRAFT_01619	Locus_type		CDS		
2558670951	DRAFT_01619	Product_name		ATP cone domain		
2558670951	DRAFT_01619	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670951	DRAFT_01619	Coordinates		8629..8898(-)		
2558670951	DRAFT_01619	DNA_length		270bp		
2558670951	DRAFT_01619	Protein_length		89aa		
2558670951	DRAFT_01619	GC			0.53	

2558670952	DRAFT_01620	COG_category	[K] Transcription			
2558670952	DRAFT_01620	COG2101	TATA-box binding protein (TBP), component of TFIID and TFIIIB			3.00E-56
2558670952	DRAFT_01620	pfam00352	TBP			7.80E-29
2558670952	DRAFT_01620	pfam00352	TBP			7.50E-30
2558670952	DRAFT_01620	KO:K03120	transcription initiation factor TFIID TATA-box-binding protein			0.00E+00
2558670952	DRAFT_01620	ITERM:01960	TATA binding protein of transcription factor TFIID			
2558670952	DRAFT_01620	Locus_type		CDS		
2558670952	DRAFT_01620	Product_name		TATA binding protein of transcription factor TFIID		
2558670952	DRAFT_01620	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47		
2558670952	DRAFT_01620	Coordinates		9698..10282(+)		
2558670952	DRAFT_01620	DNA_length		585bp		
2558670952	DRAFT_01620	Protein_length		194aa		
2558670952	DRAFT_01620	GC			0.52	

2558670953	DRAFT_01621	Locus_type		CDS	
2558670953	DRAFT_01621	Product_name		hypothetical protein	
2558670953	DRAFT_01621	Scaffold		DRAFT_contig_70_589_len_10771_read_count_176040.47	
2558670953	DRAFT_01621	Coordinates		10370..10645(-)	
2558670953	DRAFT_01621	DNA_length		276bp	
2558670953	DRAFT_01621	Protein_length		91aa	
2558670953	DRAFT_01621	GC		0.46	

2558670954	DRAFT_01622	pfam12849	PBP_like_2		3.60E-35
2558670954	DRAFT_01622	TIGR00975	phosphate ABC transporter, phosphate-binding protein		2.40E-56
2558670954	DRAFT_01622	Locus_type		CDS	
2558670954	DRAFT_01622	Product_name		ABC-type phosphate transport system, periplasmic component	
2558670954	DRAFT_01622	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48	
2558670954	DRAFT_01622	Coordinates		3..755(-)	
2558670954	DRAFT_01622	DNA_length		753bp	
2558670954	DRAFT_01622	Protein_length		251aa	
2558670954	DRAFT_01622	GC		0.55	
2558670954	DRAFT_01622	Transmembrane		Yes	

2558670955	DRAFT_01623	COG_category	[P] Inorganic ion transport and metabolism		
2558670955	DRAFT_01623	COG0704	Phosphate uptake regulator		2.00E-24
2558670955	DRAFT_01623	pfam01895	PhoU		1.30E-16
2558670955	DRAFT_01623	pfam04014	Antitoxin-MazE		1.30E-08
2558670955	DRAFT_01623	pfam01895	PhoU		5.50E-05
2558670955	DRAFT_01623	Locus_type		CDS	
2558670955	DRAFT_01623	Product_name		Phosphate uptake regulator	
2558670955	DRAFT_01623	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48	
2558670955	DRAFT_01623	Coordinates		894..1904(+)	
2558670955	DRAFT_01623	DNA_length		1011bp	
2558670955	DRAFT_01623	Protein_length		336aa	
2558670955	DRAFT_01623	GC		0.55	

2558670956	DRAFT_01624	Locus_type		CDS	
2558670956	DRAFT_01624	Product_name		hypothetical protein	

2558670956	DRAFT_01624	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48		
2558670956	DRAFT_01624	Coordinates		1940..2248(-)		
2558670956	DRAFT_01624	DNA_length		309bp		
2558670956	DRAFT_01624	Protein_length		102aa		
2558670956	DRAFT_01624	GC			0.55	
2558670957	DRAFT_01625	KEGG_module	M00248: Putative antibiotic transport system			
2558670957	DRAFT_01625	COG_category	[V] Defense mechanisms			
2558670957	DRAFT_01625	COG0842	ABC-type multidrug transport system, permease component			1.00E-08
2558670957	DRAFT_01625	pfam01061	ABC2_membrane			5.40E-37
2558670957	DRAFT_01625	TIGR00025	ABC transporter efflux protein, DrrB family			4.90E-20
2558670957	DRAFT_01625	TIGR01247	daunorubicin resistance ABC transporter membrane protein			6.50E-44
2558670957	DRAFT_01625	KO:K09686	antibiotic transport system permease protein			0.00E+00
2558670957	DRAFT_01625	Locus_type		CDS		
2558670957	DRAFT_01625	Product_name		ABC-type multidrug transport system, permease component		
2558670957	DRAFT_01625	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48		
2558670957	DRAFT_01625	Coordinates		2357..3163(-)		
2558670957	DRAFT_01625	DNA_length		807bp		
2558670957	DRAFT_01625	Protein_length		268aa		
2558670957	DRAFT_01625	GC			0.57	
2558670957	DRAFT_01625	Transmembrane		Yes		
2558670958	DRAFT_01626	KEGG_module	M00248: Putative antibiotic transport system			
2558670958	DRAFT_01626	COG_category	[V] Defense mechanisms			
2558670958	DRAFT_01626	COG1131	ABC-type multidrug transport system, ATPase component			7.00E-73
2558670958	DRAFT_01626	pfam00005	ABC_tran			3.00E-27
2558670958	DRAFT_01626	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2558670958	DRAFT_01626	Locus_type		CDS		
2558670958	DRAFT_01626	Product_name		ABC-type multidrug transport system, ATPase component		
2558670958	DRAFT_01626	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48		
2558670958	DRAFT_01626	Coordinates		3165..3959(-)		
2558670958	DRAFT_01626	DNA_length		795bp		
2558670958	DRAFT_01626	Protein_length		264aa		
2558670958	DRAFT_01626	GC			0.57	

2558670959	DRAFT_01627	Locus_type		CDS		
2558670959	DRAFT_01627	Product_name		hypothetical protein		
2558670959	DRAFT_01627	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48		
2558670959	DRAFT_01627	Coordinates		4596..5411(-)		
2558670959	DRAFT_01627	DNA_length		816bp		
2558670959	DRAFT_01627	Protein_length		271aa		
2558670959	DRAFT_01627	GC			0.51	
2558670960	DRAFT_01628	COG_category	[R] General function prediction only			
2558670960	DRAFT_01628	COG2910	Putative NADH-flavin reductase			3.00E-16
2558670960	DRAFT_01628	pfam13460	NAD_binding_10			1.30E-37
2558670960	DRAFT_01628	Locus_type		CDS		
2558670960	DRAFT_01628	Product_name		Putative NADH-flavin reductase		
2558670960	DRAFT_01628	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48		
2558670960	DRAFT_01628	Coordinates		5593..6228(-)		
2558670960	DRAFT_01628	DNA_length		636bp		
2558670960	DRAFT_01628	Protein_length		211aa		
2558670960	DRAFT_01628	GC			0.52	
2558670961	DRAFT_01629	KEGG_module	M00248: Putative antibiotic transport system			
2558670961	DRAFT_01629	COG_category	[V] Defense mechanisms			
2558670961	DRAFT_01629	COG0842	ABC-type multidrug transport system, permease component			3.00E-17
2558670961	DRAFT_01629	pfam12698	ABC2_membrane_3			1.50E-50
2558670961	DRAFT_01629	KO:K09686	antibiotic transport system permease protein			0.00E+00
2558670961	DRAFT_01629	Locus_type		CDS		
2558670961	DRAFT_01629	Product_name		ABC-type multidrug transport system, permease component		
2558670961	DRAFT_01629	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48		
2558670961	DRAFT_01629	Coordinates		6289..7482(-)		
2558670961	DRAFT_01629	DNA_length		1194bp		
2558670961	DRAFT_01629	Protein_length		397aa		
2558670961	DRAFT_01629	GC			0.57	
2558670961	DRAFT_01629	Transmembrane		Yes		

2558670962	DRAFT_01630	KEGG_module	M00248: Putative antibiotic transport system		
2558670962	DRAFT_01630	COG_category	[V] Defense mechanisms		
2558670962	DRAFT_01630	COG1131	ABC-type multidrug transport system, ATPase component		9.00E-76
2558670962	DRAFT_01630	pfam00005	ABC_tran		6.50E-31
2558670962	DRAFT_01630	TIGR01188	daunorubicin resistance ABC transporter ATP-binding subunit		1.10E-103
2558670962	DRAFT_01630	KO:K09687	antibiotic transport system ATP-binding protein		0.00E+00
2558670962	DRAFT_01630	Locus_type		CDS	
2558670962	DRAFT_01630	Product_name		daunorubicin resistance ABC transporter ATP-binding subunit	
2558670962	DRAFT_01630	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48	
2558670962	DRAFT_01630	Coordinates		7489..8493(-)	
2558670962	DRAFT_01630	DNA_length		1005bp	
2558670962	DRAFT_01630	Protein_length		334aa	
2558670962	DRAFT_01630	GC		0.56	
2558670963	DRAFT_01631	pfam03551	PadR		1.80E-18
2558670963	DRAFT_01631	Locus_type		CDS	
2558670963	DRAFT_01631	Product_name		Predicted transcriptional regulators	
2558670963	DRAFT_01631	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48	
2558670963	DRAFT_01631	Coordinates		8541..9185(-)	
2558670963	DRAFT_01631	DNA_length		645bp	
2558670963	DRAFT_01631	Protein_length		214aa	
2558670963	DRAFT_01631	GC		0.58	
2558670964	DRAFT_01632	Locus_type		CDS	
2558670964	DRAFT_01632	Product_name		hypothetical protein	
2558670964	DRAFT_01632	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48	
2558670964	DRAFT_01632	Coordinates		9420..9620(-)	
2558670964	DRAFT_01632	DNA_length		201bp	
2558670964	DRAFT_01632	Protein_length		66aa	
2558670964	DRAFT_01632	GC		0.5	
2558670965	DRAFT_01633	Locus_type		CDS	
2558670965	DRAFT_01633	Product_name		hypothetical protein	
2558670965	DRAFT_01633	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48	

2558670965	DRAFT_01633	Coordinates		9617..9880(-)		
2558670965	DRAFT_01633	DNA_length		264bp		
2558670965	DRAFT_01633	Protein_length		87aa		
2558670965	DRAFT_01633	GC			0.49	
2558670966	DRAFT_01634	Locus_type		CDS		
2558670966	DRAFT_01634	Product_name		hypothetical protein		
2558670966	DRAFT_01634	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48		
2558670966	DRAFT_01634	Coordinates		9893..10018(-)		
2558670966	DRAFT_01634	DNA_length		126bp		
2558670966	DRAFT_01634	Protein_length		41aa		
2558670966	DRAFT_01634	GC			0.43	
2558670967	DRAFT_01635	pfam07883	Cupin_2			4.70E-05
2558670967	DRAFT_01635	Locus_type		CDS		
2558670967	DRAFT_01635	Product_name		Cupin domain		
2558670967	DRAFT_01635	Scaffold		DRAFT_contig_70_600_len_10654_read_count_197271.48		
2558670967	DRAFT_01635	Coordinates		10066..10218(-)		
2558670967	DRAFT_01635	DNA_length		153bp		
2558670967	DRAFT_01635	Protein_length		50aa		
2558670967	DRAFT_01635	GC			0.54	
2558670968	DRAFT_01636	Locus_type		CDS		
2558670968	DRAFT_01636	Product_name		hypothetical protein		
2558670968	DRAFT_01636	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49		
2558670968	DRAFT_01636	Coordinates		1..174(-)		
2558670968	DRAFT_01636	DNA_length		174bp		
2558670968	DRAFT_01636	Protein_length		58aa		
2558670968	DRAFT_01636	GC			0.6	
2558670969	DRAFT_01637	COG_category	[G] Carbohydrate transport and metabolism			
2558670969	DRAFT_01637	COG2814	Arabinose efflux permease			8.00E-12
2558670969	DRAFT_01637	pfam07690	MFS_1			3.30E-20
2558670969	DRAFT_01637	pfam07690	MFS_1			4.50E-27

2558670969	DRAFT_01637	Locus_type		CDS		
2558670969	DRAFT_01637	Product_name		Arabinose efflux permease		
2558670969	DRAFT_01637	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49		
2558670969	DRAFT_01637	Coordinates		217..1395(-)		
2558670969	DRAFT_01637	DNA_length		1179bp		
2558670969	DRAFT_01637	Protein_length		392aa		
2558670969	DRAFT_01637	GC			0.63	
2558670969	DRAFT_01637	Transmembrane		Yes		

2558670970	DRAFT_01638	COG_category	[S] Function unknown			
2558670970	DRAFT_01638	COG4275	Uncharacterized conserved protein			6.00E-17
2558670970	DRAFT_01638	pfam09828	Chrome_Resist			1.80E-29
2558670970	DRAFT_01638	Locus_type		CDS		
2558670970	DRAFT_01638	Product_name		Uncharacterized conserved protein		
2558670970	DRAFT_01638	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49		
2558670970	DRAFT_01638	Coordinates		1392..1841(-)		
2558670970	DRAFT_01638	DNA_length		450bp		
2558670970	DRAFT_01638	Protein_length		149aa		
2558670970	DRAFT_01638	GC			0.63	

2558670971	DRAFT_01639	COG_category	[S] Function unknown			
2558670971	DRAFT_01639	COG4275	Uncharacterized conserved protein			2.00E-41
2558670971	DRAFT_01639	pfam09828	Chrome_Resist			4.40E-49
2558670971	DRAFT_01639	Locus_type		CDS		
2558670971	DRAFT_01639	Product_name		Uncharacterized conserved protein		
2558670971	DRAFT_01639	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49		
2558670971	DRAFT_01639	Coordinates		1845..2276(-)		
2558670971	DRAFT_01639	DNA_length		432bp		
2558670971	DRAFT_01639	Protein_length		143aa		
2558670971	DRAFT_01639	GC			0.6	

2558670972	DRAFT_01640	COG_category	[R] General function prediction only			
2558670972	DRAFT_01640	COG2405	Predicted nucleic acid-binding protein, contains PIN domain			1.00E-03
2558670972	DRAFT_01640	Locus_type		CDS		

2558670972	DRAFT_01640	Product_name		Predicted nucleic acid-binding protein, contains PIN domain	
2558670972	DRAFT_01640	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49	
2558670972	DRAFT_01640	Coordinates		2499..2981(-)	
2558670972	DRAFT_01640	DNA_length		483bp	
2558670972	DRAFT_01640	Protein_length		160aa	
2558670972	DRAFT_01640	GC		0.5	
2558670973	DRAFT_01641	Locus_type		CDS	
2558670973	DRAFT_01641	Product_name		hypothetical protein	
2558670973	DRAFT_01641	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49	
2558670973	DRAFT_01641	Coordinates		2978..3550(-)	
2558670973	DRAFT_01641	DNA_length		573bp	
2558670973	DRAFT_01641	Protein_length		190aa	
2558670973	DRAFT_01641	GC		0.51	
2558670974	DRAFT_01642	Locus_type		CDS	
2558670974	DRAFT_01642	Product_name		hypothetical protein	
2558670974	DRAFT_01642	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49	
2558670974	DRAFT_01642	Coordinates		3584..4663(+)	
2558670974	DRAFT_01642	DNA_length		1080bp	
2558670974	DRAFT_01642	Protein_length		359aa	
2558670974	DRAFT_01642	GC		0.5	
2558670975	DRAFT_01643	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558670975	DRAFT_01643	COG0638	20S proteasome, alpha and beta subunits		3.00E-07
2558670975	DRAFT_01643	pfam00227	Proteasome		1.40E-09
2558670975	DRAFT_01643	Locus_type		CDS	
2558670975	DRAFT_01643	Product_name		20S proteasome, alpha and beta subunits	
2558670975	DRAFT_01643	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49	
2558670975	DRAFT_01643	Coordinates		4788..5702(+)	
2558670975	DRAFT_01643	DNA_length		915bp	
2558670975	DRAFT_01643	Protein_length		304aa	
2558670975	DRAFT_01643	GC		0.51	

2558670976	DRAFT_01644	pfam01545	Cation_efflux		1.60E-05
2558670976	DRAFT_01644	Locus_type		CDS	
2558670976	DRAFT_01644	Product_name		Predicted Co/Zn/Cd cation transporters	
2558670976	DRAFT_01644	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49	
2558670976	DRAFT_01644	Coordinates		6190..6780(-)	
2558670976	DRAFT_01644	DNA_length		591bp	
2558670976	DRAFT_01644	Protein_length		196aa	
2558670976	DRAFT_01644	GC		0.53	
2558670976	DRAFT_01644	Transmembrane		Yes	
2558670977	DRAFT_01645	COG_category	[P] Inorganic ion transport and metabolism		
2558670977	DRAFT_01645	COG1914	Mn2+ and Fe2+ transporters of the NRAMP family		8.00E-66
2558670977	DRAFT_01645	pfam01566	Nramp		1.50E-105
2558670977	DRAFT_01645	TIGR01197	NRAMP (natural resistance-associated macrophage protein) metal ion		2.50E-86
2558670977	DRAFT_01645	KO:K03322	manganese transport protein		0.00E+00
2558670977	DRAFT_01645	Locus_type		CDS	
2558670977	DRAFT_01645	Product_name		NRAMP (natural resistance-associated macrophage protein) metal ior	
2558670977	DRAFT_01645	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49	
2558670977	DRAFT_01645	Coordinates		7160..8452(-)	
2558670977	DRAFT_01645	DNA_length		1293bp	
2558670977	DRAFT_01645	Protein_length		430aa	
2558670977	DRAFT_01645	GC		0.55	
2558670977	DRAFT_01645	Transmembrane		Yes	
2558670978	DRAFT_01646	COG_category	[K] Transcription		
2558670978	DRAFT_01646	COG1321	Mn-dependent transcriptional regulator		2.00E-24
2558670978	DRAFT_01646	pfam01325	Fe_dep_repress		2.40E-19
2558670978	DRAFT_01646	pfam02742	Fe_dep_repr_C		7.00E-14
2558670978	DRAFT_01646	ITERM:02272	iron (metal) dependent repressor, DtxR family		
2558670978	DRAFT_01646	Locus_type		CDS	
2558670978	DRAFT_01646	Product_name		iron (metal) dependent repressor, DtxR family	
2558670978	DRAFT_01646	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49	
2558670978	DRAFT_01646	Coordinates		8569..9042(+)	
2558670978	DRAFT_01646	DNA_length		474bp	

2558670978	DRAFT_01646	Protein_length		157aa		
2558670978	DRAFT_01646	GC			0.53	
2558670979	DRAFT_01647	pfam13240	zinc_ribbon_2			8.90E-08
2558670979	DRAFT_01647	Locus_type		CDS		
2558670979	DRAFT_01647	Product_name		zinc-ribbon domain		
2558670979	DRAFT_01647	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49		
2558670979	DRAFT_01647	Coordinates		9338..9745(-)		
2558670979	DRAFT_01647	DNA_length		408bp		
2558670979	DRAFT_01647	Protein_length		135aa		
2558670979	DRAFT_01647	GC			0.55	
2558670979	DRAFT_01647	Transmembrane		Yes		
2558670980	DRAFT_01648	pfam13414	TPR_11			3.10E-09
2558670980	DRAFT_01648	Locus_type		CDS		
2558670980	DRAFT_01648	Product_name		TPR repeat		
2558670980	DRAFT_01648	Scaffold		DRAFT_contig_70_607_len_10577_read_count_184089.49		
2558670980	DRAFT_01648	Coordinates		9883..10575(-)		
2558670980	DRAFT_01648	DNA_length		693bp		
2558670980	DRAFT_01648	Protein_length		230aa		
2558670980	DRAFT_01648	GC			0.56	
2558670981	DRAFT_01649	Locus_type		tRNA		
2558670981	DRAFT_01649	Product_name		tRNA_Undet_???		
2558670981	DRAFT_01649	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50		
2558670981	DRAFT_01649	Coordinates		42..143(+)		
2558670981	DRAFT_01649	DNA_length		102bp		
2558670981	DRAFT_01649	GC			0.61	
2558670982	DRAFT_01650	TIGR01376	Chlamydial polymorphic outer membrane protein repeat			4.00E-06
2558670982	DRAFT_01650	Locus_type		CDS		
2558670982	DRAFT_01650	Product_name		hypothetical protein		
2558670982	DRAFT_01650	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50		
2558670982	DRAFT_01650	Coordinates		441..602(+)		

2558670982	DRAFT_01650	DNA_length		162bp		
2558670982	DRAFT_01650	Protein_length		53aa		
2558670982	DRAFT_01650	GC			0.6	
2558670983	DRAFT_01651	Locus_type		CDS		
2558670983	DRAFT_01651	Product_name		hypothetical protein		
2558670983	DRAFT_01651	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50		
2558670983	DRAFT_01651	Coordinates		728..3334(-)		
2558670983	DRAFT_01651	DNA_length		2607bp		
2558670983	DRAFT_01651	Protein_length		868aa		
2558670983	DRAFT_01651	GC			0.48	
2558670983	DRAFT_01651	Transmembrane		Yes		
2558670984	DRAFT_01652	pfam13231	PMT_2			4.30E-10
2558670984	DRAFT_01652	Locus_type		CDS		
2558670984	DRAFT_01652	Product_name		4-amino-4-deoxy-L-arabinose transferase and related glycosyltransfer		
2558670984	DRAFT_01652	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50		
2558670984	DRAFT_01652	Coordinates		3337..5178(-)		
2558670984	DRAFT_01652	DNA_length		1842bp		
2558670984	DRAFT_01652	Protein_length		613aa		
2558670984	DRAFT_01652	GC			0.48	
2558670984	DRAFT_01652	Transmembrane		Yes		
2558670985	DRAFT_01653	COG_category	[S] Function unknown			
2558670985	DRAFT_01653	COG2246	Predicted membrane protein			1.00E-15
2558670985	DRAFT_01653	pfam00535	Glycos_transf_2			8.50E-24
2558670985	DRAFT_01653	pfam04138	GtrA			4.60E-20
2558670985	DRAFT_01653	Locus_type		CDS		
2558670985	DRAFT_01653	Product_name		Predicted membrane protein		
2558670985	DRAFT_01653	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50		
2558670985	DRAFT_01653	Coordinates		5262..6518(-)		
2558670985	DRAFT_01653	DNA_length		1257bp		
2558670985	DRAFT_01653	Protein_length		418aa		
2558670985	DRAFT_01653	GC			0.51	

2558670985	DRAFT_01653	Transmembrane		Yes		
2558670986	DRAFT_01654	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2558670986	DRAFT_01654	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2558670986	DRAFT_01654	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2558670986	DRAFT_01654	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			
2558670986	DRAFT_01654	Metacyc	PWY-6397: mycolyl-arabinogalactan-peptidoglycan complex biosynthesis			
2558670986	DRAFT_01654	Metacyc	PWY-3821: galactose degradation III			
2558670986	DRAFT_01654	Metacyc	PWY-6527: stachyose degradation			
2558670986	DRAFT_01654	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558670986	DRAFT_01654	COG_category	[G] Carbohydrate transport and metabolism			
2558670986	DRAFT_01654	COG0451	Nucleoside-diphosphate-sugar epimerases			7.00E-46
2558670986	DRAFT_01654	pfam01370	Epimerase			1.70E-44
2558670986	DRAFT_01654	EC:5.1.3.2	UDP-glucose 4-epimerase.			
2558670986	DRAFT_01654	KO:K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]			0.00E+00
2558670986	DRAFT_01654	Locus_type		CDS		
2558670986	DRAFT_01654	Product_name		Nucleoside-diphosphate-sugar epimerases		
2558670986	DRAFT_01654	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50		
2558670986	DRAFT_01654	Coordinates		6543..7568(-)		
2558670986	DRAFT_01654	DNA_length		1026bp		
2558670986	DRAFT_01654	Protein_length		341aa		
2558670986	DRAFT_01654	GC			0.52	
2558670987	DRAFT_01655	Locus_type		CDS		
2558670987	DRAFT_01655	Product_name		hypothetical protein		
2558670987	DRAFT_01655	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50		
2558670987	DRAFT_01655	Coordinates		7625..7843(-)		
2558670987	DRAFT_01655	DNA_length		219bp		
2558670987	DRAFT_01655	Protein_length		72aa		
2558670987	DRAFT_01655	GC			0.45	
2558670987	DRAFT_01655	Transmembrane		Yes		
2558670988	DRAFT_01656	pfam08241	Methyltransf_11			2.10E-05
2558670988	DRAFT_01656	Locus_type		CDS		

2558670988	DRAFT_01656	Product_name		Predicted RNA methylase	
2558670988	DRAFT_01656	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50	
2558670988	DRAFT_01656	Coordinates		8089..8667(-)	
2558670988	DRAFT_01656	DNA_length		579bp	
2558670988	DRAFT_01656	Protein_length		192aa	
2558670988	DRAFT_01656	GC			0.55
2558670989	DRAFT_01657	Locus_type		CDS	
2558670989	DRAFT_01657	Product_name		hypothetical protein	
2558670989	DRAFT_01657	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50	
2558670989	DRAFT_01657	Coordinates		8973..9239(-)	
2558670989	DRAFT_01657	DNA_length		267bp	
2558670989	DRAFT_01657	Protein_length		88aa	
2558670989	DRAFT_01657	GC			0.47
2558670990	DRAFT_01658	pfam04851	ResIII		1.20E-21
2558670990	DRAFT_01658	Locus_type		CDS	
2558670990	DRAFT_01658	Product_name		DNA or RNA helicases of superfamily II	
2558670990	DRAFT_01658	Scaffold		DRAFT_contig_70_610_len_10561_read_count_224801.50	
2558670990	DRAFT_01658	Coordinates		9617..10558(+)	
2558670990	DRAFT_01658	DNA_length		942bp	
2558670990	DRAFT_01658	Protein_length		314aa	
2558670990	DRAFT_01658	GC			0.56
2558670991	DRAFT_01659	Locus_type		CDS	
2558670991	DRAFT_01659	Product_name		hypothetical protein	
2558670991	DRAFT_01659	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558670991	DRAFT_01659	Coordinates		2..373(-)	
2558670991	DRAFT_01659	DNA_length		372bp	
2558670991	DRAFT_01659	Protein_length		124aa	
2558670991	DRAFT_01659	GC			0.56
2558670991	DRAFT_01659	Transmembrane		Yes	
2558670992	DRAFT_01660	Locus_type		CDS	

2558670992	DRAFT_01660	Product_name		hypothetical protein	
2558670992	DRAFT_01660	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558670992	DRAFT_01660	Coordinates		508..1158(+)	
2558670992	DRAFT_01660	DNA_length		651bp	
2558670992	DRAFT_01660	Protein_length		216aa	
2558670992	DRAFT_01660	GC		0.52	
2558670992	DRAFT_01660	Transmembrane		Yes	

2558670993	DRAFT_01661	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2558670993	DRAFT_01661	COG_category	[G] Carbohydrate transport and metabolism		
2558670993	DRAFT_01661	COG0451	Nucleoside-diphosphate-sugar epimerases		9.00E-09
2558670993	DRAFT_01661	pfam13460	NAD_binding_10		4.00E-05
2558670993	DRAFT_01661	pfam01370	Epimerase		5.20E-05
2558670993	DRAFT_01661	Locus_type		CDS	
2558670993	DRAFT_01661	Product_name		NADH(P)-binding/NAD dependent epimerase/dehydratase family	
2558670993	DRAFT_01661	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558670993	DRAFT_01661	Coordinates		1345..2325(-)	
2558670993	DRAFT_01661	DNA_length		981bp	
2558670993	DRAFT_01661	Protein_length		326aa	
2558670993	DRAFT_01661	GC		0.6	

2558670994	DRAFT_01662	Locus_type		CDS	
2558670994	DRAFT_01662	Product_name		hypothetical protein	
2558670994	DRAFT_01662	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558670994	DRAFT_01662	Coordinates		2642..3289(-)	
2558670994	DRAFT_01662	DNA_length		648bp	
2558670994	DRAFT_01662	Protein_length		215aa	
2558670994	DRAFT_01662	GC		0.57	
2558670994	DRAFT_01662	Transmembrane		Yes	

2558670995	DRAFT_01663	pfam14417	MEDS		8.20E-09
2558670995	DRAFT_01663	Locus_type		CDS	
2558670995	DRAFT_01663	Product_name		MEDS: MEthanogen/methylotroph, DcmR Sensory domain	
2558670995	DRAFT_01663	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	

2558670995	DRAFT_01663	Coordinates		3404..4009(-)	
2558670995	DRAFT_01663	DNA_length		606bp	
2558670995	DRAFT_01663	Protein_length		201aa	
2558670995	DRAFT_01663	GC			0.55
2558670996	DRAFT_01664	Locus_type		CDS	
2558670996	DRAFT_01664	Product_name		hypothetical protein	
2558670996	DRAFT_01664	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558670996	DRAFT_01664	Coordinates		4193..4543(+)	
2558670996	DRAFT_01664	DNA_length		351bp	
2558670996	DRAFT_01664	Protein_length		116aa	
2558670996	DRAFT_01664	GC			0.54
2558670997	DRAFT_01665	Locus_type		CDS	
2558670997	DRAFT_01665	Product_name		hypothetical protein	
2558670997	DRAFT_01665	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558670997	DRAFT_01665	Coordinates		4540..4737(+)	
2558670997	DRAFT_01665	DNA_length		198bp	
2558670997	DRAFT_01665	Protein_length		65aa	
2558670997	DRAFT_01665	GC			0.53
2558670998	DRAFT_01666	Locus_type		CDS	
2558670998	DRAFT_01666	Product_name		hypothetical protein	
2558670998	DRAFT_01666	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558670998	DRAFT_01666	Coordinates		4894..5829(+)	
2558670998	DRAFT_01666	DNA_length		936bp	
2558670998	DRAFT_01666	Protein_length		311aa	
2558670998	DRAFT_01666	GC			0.57
2558670999	DRAFT_01667	pfam01978	TrmB		1.30E-05
2558670999	DRAFT_01667	Locus_type		CDS	
2558670999	DRAFT_01667	Product_name		Sugar-specific transcriptional regulator TrmB	
2558670999	DRAFT_01667	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558670999	DRAFT_01667	Coordinates		5970..6353(+)	

2558670999	DRAFT_01667	DNA_length		384bp	
2558670999	DRAFT_01667	Protein_length		127aa	
2558670999	DRAFT_01667	GC			0.58

2558671000	DRAFT_01668	Locus_type		CDS	
2558671000	DRAFT_01668	Product_name		hypothetical protein	
2558671000	DRAFT_01668	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558671000	DRAFT_01668	Coordinates		6454..6792(+)	
2558671000	DRAFT_01668	DNA_length		339bp	
2558671000	DRAFT_01668	Protein_length		112aa	
2558671000	DRAFT_01668	GC			0.58
2558671000	DRAFT_01668	Transmembrane		Yes	

2558671001	DRAFT_01669	Locus_type		CDS	
2558671001	DRAFT_01669	Product_name		hypothetical protein	
2558671001	DRAFT_01669	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558671001	DRAFT_01669	Coordinates		7053..7217(+)	
2558671001	DRAFT_01669	DNA_length		165bp	
2558671001	DRAFT_01669	Protein_length		54aa	
2558671001	DRAFT_01669	GC			0.56

2558671002	DRAFT_01670	pfam14321	DUF4382		8.80E-18
2558671002	DRAFT_01670	Locus_type		CDS	
2558671002	DRAFT_01670	Product_name		Domain of unknown function (DUF4382)	
2558671002	DRAFT_01670	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558671002	DRAFT_01670	Coordinates		7578..8705(-)	
2558671002	DRAFT_01670	DNA_length		1128bp	
2558671002	DRAFT_01670	Protein_length		375aa	
2558671002	DRAFT_01670	GC			0.57

2558671003	DRAFT_01671	Locus_type		CDS	
2558671003	DRAFT_01671	Product_name		hypothetical protein	
2558671003	DRAFT_01671	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51	
2558671003	DRAFT_01671	Coordinates		8921..9376(-)	

2558671003	DRAFT_01671	DNA_length		456bp		
2558671003	DRAFT_01671	Protein_length		151aa		
2558671003	DRAFT_01671	GC			0.54	
2558671004	DRAFT_01672	Locus_type		CDS		
2558671004	DRAFT_01672	Product_name		hypothetical protein		
2558671004	DRAFT_01672	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51		
2558671004	DRAFT_01672	Coordinates		9504..9809(-)		
2558671004	DRAFT_01672	DNA_length		306bp		
2558671004	DRAFT_01672	Protein_length		101aa		
2558671004	DRAFT_01672	GC			0.56	
2558671005	DRAFT_01673	pfam07790	DUF1628			5.60E-08
2558671005	DRAFT_01673	TIGR02537	archaeal flagellin N-terminal-like domain			5.20E-11
2558671005	DRAFT_01673	Locus_type		CDS		
2558671005	DRAFT_01673	Product_name		archaeal flagellin N-terminal-like domain		
2558671005	DRAFT_01673	Scaffold		DRAFT_contig_70_633_len_10267_read_count_171144.51		
2558671005	DRAFT_01673	Coordinates		9946..10266(+)		
2558671005	DRAFT_01673	DNA_length		321bp		
2558671005	DRAFT_01673	Protein_length		107aa		
2558671005	DRAFT_01673	GC			0.53	
2558671005	DRAFT_01673	Transmembrane		Yes		
2558671006	DRAFT_01674	pfam02683	DsbD			6.30E-08
2558671006	DRAFT_01674	pfam02683	DsbD			2.60E-24
2558671006	DRAFT_01674	KO:K06196	cytochrome c-type biogenesis protein			8.90E-36
2558671006	DRAFT_01674	Locus_type		CDS		
2558671006	DRAFT_01674	Product_name		Cytochrome c biogenesis protein		
2558671006	DRAFT_01674	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52		
2558671006	DRAFT_01674	Coordinates		94..771(-)		
2558671006	DRAFT_01674	DNA_length		678bp		
2558671006	DRAFT_01674	Protein_length		225aa		
2558671006	DRAFT_01674	GC			0.52	
2558671006	DRAFT_01674	Transmembrane		Yes		

2558671007	DRAFT_01675	Locus_type		CDS		
2558671007	DRAFT_01675	Product_name		hypothetical protein		
2558671007	DRAFT_01675	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52		
2558671007	DRAFT_01675	Coordinates		1148..1939(+)		
2558671007	DRAFT_01675	DNA_length		792bp		
2558671007	DRAFT_01675	Protein_length		263aa		
2558671007	DRAFT_01675	GC			0.58	
2558671007	DRAFT_01675	Transmembrane		Yes		
2558671008	DRAFT_01676	Metacyc	PWY-6654: phosphopantothenate biosynthesis III			
2558671008	DRAFT_01676	COG_category	[R] General function prediction only			
2558671008	DRAFT_01676	COG1829	Predicted archaeal kinase (sugar kinase superfamily)			6.00E-24
2558671008	DRAFT_01676	pfam00288	GHMP_kinases_N			1.10E-04
2558671008	DRAFT_01676	EC:2.7.1.169	Pantoate kinase.			
2558671008	DRAFT_01676	KO:K06982	pantoate kinase [EC:2.7.1.169]			5.20E-24
2558671008	DRAFT_01676	Locus_type		CDS		
2558671008	DRAFT_01676	Product_name		Predicted archaeal kinase (sugar kinase superfamily)		
2558671008	DRAFT_01676	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52		
2558671008	DRAFT_01676	Coordinates		2049..2879(+)		
2558671008	DRAFT_01676	DNA_length		831bp		
2558671008	DRAFT_01676	Protein_length		276aa		
2558671008	DRAFT_01676	GC			0.61	
2558671008	DRAFT_01676	Transmembrane		Yes		
2558671009	DRAFT_01677	COG_category	[E] Amino acid transport and metabolism			
2558671009	DRAFT_01677	COG0006	Xaa-Pro aminopeptidase			3.00E-57
2558671009	DRAFT_01677	pfam00557	Peptidase_M24			1.80E-50
2558671009	DRAFT_01677	EC:3.4.13.9	Xaa-Pro dipeptidase.			
2558671009	DRAFT_01677	KO:K01271	Xaa-Pro dipeptidase [EC:3.4.13.9]			0.00E+00
2558671009	DRAFT_01677	Locus_type		CDS		
2558671009	DRAFT_01677	Product_name		Xaa-Pro aminopeptidase		
2558671009	DRAFT_01677	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52		
2558671009	DRAFT_01677	Coordinates		2876..3922(-)		

2558671009	DRAFT_01677	DNA_length		1047bp	
2558671009	DRAFT_01677	Protein_length		348aa	
2558671009	DRAFT_01677	GC		0.61	
2558671010	DRAFT_01678	COG_category	[D] Cell cycle control, cell division, chromosome partitioning		
2558671010	DRAFT_01678	COG1196	Chromosome segregation ATPases		7.00E-125
2558671010	DRAFT_01678	pfam02463	SMC_N		8.10E-57
2558671010	DRAFT_01678	pfam06470	SMC_hinge		3.50E-15
2558671010	DRAFT_01678	KO:K03529	chromosome segregation protein		0.00E+00
2558671010	DRAFT_01678	Locus_type		CDS	
2558671010	DRAFT_01678	Product_name		Chromosome segregation ATPases	
2558671010	DRAFT_01678	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52	
2558671010	DRAFT_01678	Coordinates		3964..7554(+)	
2558671010	DRAFT_01678	DNA_length		3591bp	
2558671010	DRAFT_01678	Protein_length		1196aa	
2558671010	DRAFT_01678	GC		0.61	
2558671011	DRAFT_01679	COG_category	[S] Function unknown		
2558671011	DRAFT_01679	COG1354	Uncharacterized conserved protein		1.00E-04
2558671011	DRAFT_01679	KO:K05896	segregation and condensation protein A		4.20E-30
2558671011	DRAFT_01679	ITERM:00133	condensin subunit ScpA		
2558671011	DRAFT_01679	Locus_type		CDS	
2558671011	DRAFT_01679	Product_name		condensin subunit ScpA	
2558671011	DRAFT_01679	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52	
2558671011	DRAFT_01679	Coordinates		7547..8212(+)	
2558671011	DRAFT_01679	DNA_length		666bp	
2558671011	DRAFT_01679	Protein_length		221aa	
2558671011	DRAFT_01679	GC		0.59	
2558671012	DRAFT_01680	COG_category	[K] Transcription		
2558671012	DRAFT_01680	COG1386	Predicted transcriptional regulator containing the HTH domain		1.00E-20
2558671012	DRAFT_01680	pfam04079	DUF387		2.60E-30
2558671012	DRAFT_01680	TIGR00281	segregation and condensation protein B		1.90E-28
2558671012	DRAFT_01680	KO:K06024	segregation and condensation protein B		1.50E-33

2558671012	DRAFT_01680	Locus_type		CDS	
2558671012	DRAFT_01680	Product_name		Predicted transcriptional regulator containing the HTH domain	
2558671012	DRAFT_01680	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52	
2558671012	DRAFT_01680	Coordinates		8214..8744(+)	
2558671012	DRAFT_01680	DNA_length		531bp	
2558671012	DRAFT_01680	Protein_length		176aa	
2558671012	DRAFT_01680	GC		0.61	

2558671013	DRAFT_01681	KEGG_module	M00179: Ribosome, archaea		
2558671013	DRAFT_01681	KEGG_module	M00177: Ribosome, eukaryotes		
2558671013	DRAFT_01681	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558671013	DRAFT_01681	COG2007	Ribosomal protein S8E		5.00E-23
2558671013	DRAFT_01681	pfam01201	Ribosomal_S8e		2.90E-23
2558671013	DRAFT_01681	TIGR00307	ribosomal protein S8.e		9.30E-31
2558671013	DRAFT_01681	KO:K02995	small subunit ribosomal protein S8e		8.30E-31
2558671013	DRAFT_01681	Locus_type		CDS	
2558671013	DRAFT_01681	Product_name		ribosomal protein S8.e	
2558671013	DRAFT_01681	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52	
2558671013	DRAFT_01681	Coordinates		8905..9402(+)	
2558671013	DRAFT_01681	DNA_length		498bp	
2558671013	DRAFT_01681	Protein_length		165aa	
2558671013	DRAFT_01681	GC		0.58	

2558671014	DRAFT_01682	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport		
2558671014	DRAFT_01682	COG1400	Signal recognition particle 19 kDa protein		3.00E-10
2558671014	DRAFT_01682	pfam01922	SRP19		5.90E-17
2558671014	DRAFT_01682	KO:K03105	signal recognition particle subunit SRP19		4.40E-12
2558671014	DRAFT_01682	Locus_type		CDS	
2558671014	DRAFT_01682	Product_name		Signal recognition particle 19 kDa protein	
2558671014	DRAFT_01682	Scaffold		DRAFT_contig_70_700_len_9743_read_count_155629.52	
2558671014	DRAFT_01682	Coordinates		9403..9732(+)	
2558671014	DRAFT_01682	DNA_length		330bp	
2558671014	DRAFT_01682	Protein_length		109aa	
2558671014	DRAFT_01682	GC		0.56	

2558671015	DRAFT_01683	Locus_type		CDS	
2558671015	DRAFT_01683	Product_name		hypothetical protein	
2558671015	DRAFT_01683	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53	
2558671015	DRAFT_01683	Coordinates		204..614(+)	
2558671015	DRAFT_01683	DNA_length		411bp	
2558671015	DRAFT_01683	Protein_length		136aa	
2558671015	DRAFT_01683	GC		0.52	

2558671016	DRAFT_01684	Locus_type		CDS	
2558671016	DRAFT_01684	Product_name		hypothetical protein	
2558671016	DRAFT_01684	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53	
2558671016	DRAFT_01684	Coordinates		940..1371(-)	
2558671016	DRAFT_01684	DNA_length		432bp	
2558671016	DRAFT_01684	Protein_length		143aa	
2558671016	DRAFT_01684	GC		0.53	

2558671017	DRAFT_01685	pfam05594	Fil_haemagg		9.10E+01
2558671017	DRAFT_01685	pfam05594	Fil_haemagg		1.50E-01
2558671017	DRAFT_01685	pfam05594	Fil_haemagg		7.50E-02
2558671017	DRAFT_01685	pfam05594	Fil_haemagg		2.60E+00
2558671017	DRAFT_01685	TIGR01731	adhesin HecA family 20-residue repeat (two copies)		2.30E-04
2558671017	DRAFT_01685	Locus_type		CDS	
2558671017	DRAFT_01685	Product_name		Haemagluttinin repeat	
2558671017	DRAFT_01685	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53	
2558671017	DRAFT_01685	Coordinates		1796..3256(+)	
2558671017	DRAFT_01685	DNA_length		1461bp	
2558671017	DRAFT_01685	Protein_length		486aa	
2558671017	DRAFT_01685	GC		0.5	
2558671017	DRAFT_01685	Signal_peptide		Yes	
2558671017	DRAFT_01685	Transmembrane		Yes	

2558671018	DRAFT_01686	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2558671018	DRAFT_01686	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		

2558671018	DRAFT_01686	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2558671018	DRAFT_01686	IMG_pathway	492: Glycine ligation to tRNA(Gly)			
2558671018	DRAFT_01686	pfam03129	HGTP_anticodon			8.40E-19
2558671018	DRAFT_01686	pfam00587	tRNA-synt_2b			1.90E-43
2558671018	DRAFT_01686	EC:6.1.1.14	Glycine--tRNA ligase.			
2558671018	DRAFT_01686	TIGR00389	glycyl-tRNA synthetase, dimeric type			2.00E-106
2558671018	DRAFT_01686	KO:K01880	glycyl-tRNA synthetase [EC:6.1.1.14]			0.00E+00
2558671018	DRAFT_01686	ITERM:01945	glycyl-tRNA synthetase (EC 6.1.1.14)			
2558671018	DRAFT_01686	Locus_type		CDS		
2558671018	DRAFT_01686	Product_name		glycyl-tRNA synthetase (EC 6.1.1.14)		
2558671018	DRAFT_01686	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53		
2558671018	DRAFT_01686	Coordinates		3634..5097(+)		
2558671018	DRAFT_01686	DNA_length		1464bp		
2558671018	DRAFT_01686	Protein_length		487aa		
2558671018	DRAFT_01686	GC			0.57	

2558671019	DRAFT_01687	COG_category	[S] Function unknown			
2558671019	DRAFT_01687	COG1836	Predicted membrane protein			2.00E-30
2558671019	DRAFT_01687	pfam01940	DUF92			1.80E-56
2558671019	DRAFT_01687	TIGR00297	TIGR00297 family protein			3.80E-45
2558671019	DRAFT_01687	Locus_type		CDS		
2558671019	DRAFT_01687	Product_name		Predicted membrane protein		
2558671019	DRAFT_01687	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53		
2558671019	DRAFT_01687	Coordinates		5081..5896(-)		
2558671019	DRAFT_01687	DNA_length		816bp		
2558671019	DRAFT_01687	Protein_length		271aa		
2558671019	DRAFT_01687	GC			0.56	
2558671019	DRAFT_01687	Transmembrane		Yes		

2558671020	DRAFT_01688	Locus_type		CDS		
2558671020	DRAFT_01688	Product_name		hypothetical protein		
2558671020	DRAFT_01688	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53		
2558671020	DRAFT_01688	Coordinates		5979..6971(-)		
2558671020	DRAFT_01688	DNA_length		993bp		

2558671020	DRAFT_01688	Protein_length		330aa	
2558671020	DRAFT_01688	GC		0.59	
2558671021	DRAFT_01689	COG_category	[K] Transcription		
2558671021	DRAFT_01689	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatic		2.00E-74
2558671021	DRAFT_01689	pfam08271	TF_Zn_Ribbon		3.60E-12
2558671021	DRAFT_01689	pfam00382	TFIIB		8.50E-18
2558671021	DRAFT_01689	pfam00382	TFIIB		7.90E-20
2558671021	DRAFT_01689	KO:K03124	transcription initiation factor TFIIB		0.00E+00
2558671021	DRAFT_01689	Locus_type		CDS	
2558671021	DRAFT_01689	Product_name		Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiat	
2558671021	DRAFT_01689	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53	
2558671021	DRAFT_01689	Coordinates		7073..8101(+)	
2558671021	DRAFT_01689	DNA_length		1029bp	
2558671021	DRAFT_01689	Protein_length		342aa	
2558671021	DRAFT_01689	GC		0.56	
2558671021	DRAFT_01689	Transmembrane		Yes	
2558671022	DRAFT_01690	pfam02517	Abi		2.40E-09
2558671022	DRAFT_01690	Locus_type		CDS	
2558671022	DRAFT_01690	Product_name		CAAX protease self-immunity	
2558671022	DRAFT_01690	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53	
2558671022	DRAFT_01690	Coordinates		8265..9296(-)	
2558671022	DRAFT_01690	DNA_length		1032bp	
2558671022	DRAFT_01690	Protein_length		343aa	
2558671022	DRAFT_01690	GC		0.6	
2558671022	DRAFT_01690	Transmembrane		Yes	
2558671023	DRAFT_01691	Locus_type		CDS	
2558671023	DRAFT_01691	Product_name		hypothetical protein	
2558671023	DRAFT_01691	Scaffold		DRAFT_contig_70_711_len_9632_read_count_162759.53	
2558671023	DRAFT_01691	Coordinates		9299..9631(-)	
2558671023	DRAFT_01691	DNA_length		333bp	
2558671023	DRAFT_01691	Protein_length		110aa	

2558671023	DRAFT_01691	GC			0.56	
2558671024	DRAFT_01692	COG_category	[L] Replication, recombination and repair			
2558671024	DRAFT_01692	COG0417	DNA polymerase elongation subunit (family B)			7.00E-105
2558671024	DRAFT_01692	pfam00136	DNA_pol_B			3.30E-77
2558671024	DRAFT_01692	pfam03104	DNA_pol_B_exo1			4.10E-31
2558671024	DRAFT_01692	EC:2.7.7.7	DNA-directed DNA polymerase.			
2558671024	DRAFT_01692	KO:K02319	DNA polymerase I [EC:2.7.7.7]			0.00E+00
2558671024	DRAFT_01692	Locus_type		CDS		
2558671024	DRAFT_01692	Product_name		DNA polymerase elongation subunit (family B)		
2558671024	DRAFT_01692	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54		
2558671024	DRAFT_01692	Coordinates		237..2777(-)		
2558671024	DRAFT_01692	DNA_length		2541bp		
2558671024	DRAFT_01692	Protein_length		846aa		
2558671024	DRAFT_01692	GC			0.57	
2558671025	DRAFT_01693	Locus_type		CDS		
2558671025	DRAFT_01693	Product_name		hypothetical protein		
2558671025	DRAFT_01693	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54		
2558671025	DRAFT_01693	Coordinates		2879..3247(+)		
2558671025	DRAFT_01693	DNA_length		369bp		
2558671025	DRAFT_01693	Protein_length		122aa		
2558671025	DRAFT_01693	GC			0.55	
2558671025	DRAFT_01693	Transmembrane		Yes		
2558671026	DRAFT_01694	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558671026	DRAFT_01694	COG0399	Predicted pyridoxal phosphate-dependent enzyme apparently involved			3.00E-106
2558671026	DRAFT_01694	pfam01041	DegT_DnrJ_EryC1			3.40E-116
2558671026	DRAFT_01694	Locus_type		CDS		
2558671026	DRAFT_01694	Product_name		Predicted pyridoxal phosphate-dependent enzyme apparently involve		
2558671026	DRAFT_01694	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54		
2558671026	DRAFT_01694	Coordinates		3448..4560(+)		
2558671026	DRAFT_01694	DNA_length		1113bp		
2558671026	DRAFT_01694	Protein_length		370aa		

2558671026	DRAFT_01694	GC			0.57	
2558671027	DRAFT_01695	Metacyc	MANNOSYL-CHITO-DOLICHOL-BIOSYNTHESIS: dolichyl-diphosphooligosaccharide biosynthesis			
2558671027	DRAFT_01695	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558671027	DRAFT_01695	COG0463	Glycosyltransferases involved in cell wall biogenesis			6.00E-17
2558671027	DRAFT_01695	pfam00535	Glycos_transf_2			7.60E-26
2558671027	DRAFT_01695	EC:2.4.1.83	Dolichyl-phosphate beta-D-mannosyltransferase.			
2558671027	DRAFT_01695	KO:K00721	dolichol-phosphate mannosyltransferase [EC:2.4.1.83]			1.40E-45
2558671027	DRAFT_01695	Locus_type		CDS		
2558671027	DRAFT_01695	Product_name		Glycosyltransferases involved in cell wall biogenesis		
2558671027	DRAFT_01695	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54		
2558671027	DRAFT_01695	Coordinates		4572..5285(+)		
2558671027	DRAFT_01695	DNA_length		714bp		
2558671027	DRAFT_01695	Protein_length		237aa		
2558671027	DRAFT_01695	GC			0.59	
2558671028	DRAFT_01696	KEGG_module	M00184: RNA polymerase, archaea			
2558671028	DRAFT_01696	COG_category	[K] Transcription			
2558671028	DRAFT_01696	COG1996	DNA-directed RNA polymerase, subunit RPC10 (contains C4-type Zn-fin			1.00E-03
2558671028	DRAFT_01696	EC:2.7.7.6	DNA-directed RNA polymerase.			
2558671028	DRAFT_01696	KO:K03059	DNA-directed RNA polymerase subunit P [EC:2.7.7.6]			4.10E-15
2558671028	DRAFT_01696	Locus_type		CDS		
2558671028	DRAFT_01696	Product_name		DNA-directed RNA polymerase, subunit RPC10 (contains C4-type Zn-fi		
2558671028	DRAFT_01696	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54		
2558671028	DRAFT_01696	Coordinates		5420..5608(+)		
2558671028	DRAFT_01696	DNA_length		189bp		
2558671028	DRAFT_01696	Protein_length		62aa		
2558671028	DRAFT_01696	GC			0.53	
2558671029	DRAFT_01697	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			
2558671029	DRAFT_01697	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone			
2558671029	DRAFT_01697	Metacyc	PWY66-367: ketogenesis			
2558671029	DRAFT_01697	Metacyc	PWY-922: mevalonate pathway I			
2558671029	DRAFT_01697	Metacyc	PWY-6174: mevalonate pathway II (archaea)			

2558671029	DRAFT_01697	IMG_pathway	178: Mevalonate pathway for isopentenyl pyrophopsphate synthesis		
2558671029	DRAFT_01697	IMG_pathway	591: Archaeal mevalonate pathway for isopentenyl pyrophosphate synthesis		
2558671029	DRAFT_01697	COG_category	[I] Lipid transport and metabolism		
2558671029	DRAFT_01697	COG3425	3-hydroxy-3-methylglutaryl CoA synthase		8.00E-90
2558671029	DRAFT_01697	pfam08541	ACP_syn_III_C		2.20E-12
2558671029	DRAFT_01697	EC:2.3.3.10	Hydroxymethylglutaryl-CoA synthase.		
2558671029	DRAFT_01697	TIGR00748	hydroxymethylglutaryl-CoA synthase, putative		0.00E+00
2558671029	DRAFT_01697	KO:K01641	hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]		0.00E+00
2558671029	DRAFT_01697	ITERM:00461	hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)		
2558671029	DRAFT_01697	Locus_type		CDS	
2558671029	DRAFT_01697	Product_name		hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)	
2558671029	DRAFT_01697	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54	
2558671029	DRAFT_01697	Coordinates		5802..6845(+)	
2558671029	DRAFT_01697	DNA_length		1044bp	
2558671029	DRAFT_01697	Protein_length		347aa	
2558671029	DRAFT_01697	GC		0.56	
2558671030	DRAFT_01698	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2558671030	DRAFT_01698	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone		
2558671030	DRAFT_01698	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway		
2558671030	DRAFT_01698	KEGG_module	M00373: Ethylmalonyl pathway		
2558671030	DRAFT_01698	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle		
2558671030	DRAFT_01698	Metacyc	PWY-5741: ethylmalonyl pathway		
2558671030	DRAFT_01698	Metacyc	PWY66-367: ketogenesis		
2558671030	DRAFT_01698	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)		
2558671030	DRAFT_01698	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2558671030	DRAFT_01698	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis		
2558671030	DRAFT_01698	Metacyc	PWY-6174: mevalonate pathway II (archaea)		
2558671030	DRAFT_01698	Metacyc	PWY-922: mevalonate pathway I		
2558671030	DRAFT_01698	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II		
2558671030	DRAFT_01698	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2558671030	DRAFT_01698	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2558671030	DRAFT_01698	Metacyc	PWY-6883: pyruvate fermentation to butanol II		
2558671030	DRAFT_01698	Metacyc	PWY-5177: glutaryl-CoA degradation		

2558671030	DRAFT_01698	Metacyc	PWY-6863: pyruvate fermentation to hexanol			
2558671030	DRAFT_01698	Metacyc	PWY-6583: pyruvate fermentation to butanol I			
2558671030	DRAFT_01698	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate			
2558671030	DRAFT_01698	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis			
2558671030	DRAFT_01698	Metacyc	PWY-6876: isopropanol biosynthesis			
2558671030	DRAFT_01698	Metacyc	PWY-7003: glycerol degradation to butanol			
2558671030	DRAFT_01698	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate			
2558671030	DRAFT_01698	Metacyc	PWY66-368: ketolysis			
2558671030	DRAFT_01698	COG_category	[I] Lipid transport and metabolism			
2558671030	DRAFT_01698	COG0183	Acetyl-CoA acetyltransferase			5.00E-54
2558671030	DRAFT_01698	pfam02803	Thiolase_C			7.50E-09
2558671030	DRAFT_01698	pfam00108	Thiolase_N			4.20E-07
2558671030	DRAFT_01698	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.			
2558671030	DRAFT_01698	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]			0.00E+00
2558671030	DRAFT_01698	Locus_type		CDS		
2558671030	DRAFT_01698	Product_name		Acetyl-CoA acetyltransferase		
2558671030	DRAFT_01698	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54		
2558671030	DRAFT_01698	Coordinates		6855..8018(+)		
2558671030	DRAFT_01698	DNA_length		1164bp		
2558671030	DRAFT_01698	Protein_length		387aa		
2558671030	DRAFT_01698	GC			0.59	
2558671031	DRAFT_01699	COG_category	[R] General function prediction only			
2558671031	DRAFT_01699	COG1545	Predicted nucleic-acid-binding protein containing a Zn-ribbon			8.00E-27
2558671031	DRAFT_01699	pfam01796	DUF35			7.70E-15
2558671031	DRAFT_01699	pfam12172	DUF35_N			1.20E-08
2558671031	DRAFT_01699	Locus_type		CDS		
2558671031	DRAFT_01699	Product_name		Predicted nucleic-acid-binding protein containing a Zn-ribbon		
2558671031	DRAFT_01699	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54		
2558671031	DRAFT_01699	Coordinates		8019..8408(+)		
2558671031	DRAFT_01699	DNA_length		390bp		
2558671031	DRAFT_01699	Protein_length		129aa		
2558671031	DRAFT_01699	GC			0.54	

2558671032	DRAFT_01700	pfam13632	Glyco_trans_2_3		5.20E-19
2558671032	DRAFT_01700	Locus_type		CDS	
2558671032	DRAFT_01700	Product_name		Glycosyltransferases, probably involved in cell wall biogenesis	
2558671032	DRAFT_01700	Scaffold		DRAFT_contig_70_728_len_9512_read_count_148120.54	
2558671032	DRAFT_01700	Coordinates		8679..9509(+)	
2558671032	DRAFT_01700	DNA_length		831bp	
2558671032	DRAFT_01700	Protein_length		277aa	
2558671032	DRAFT_01700	GC		0.54	
2558671033	DRAFT_01701	Locus_type		CDS	
2558671033	DRAFT_01701	Product_name		hypothetical protein	
2558671033	DRAFT_01701	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671033	DRAFT_01701	Coordinates		1..168(+)	
2558671033	DRAFT_01701	DNA_length		168bp	
2558671033	DRAFT_01701	Protein_length		55aa	
2558671033	DRAFT_01701	GC		0.56	
2558671033	DRAFT_01701	Transmembrane		Yes	
2558671034	DRAFT_01702	pfam08423	Rad51		7.80E-07
2558671034	DRAFT_01702	Locus_type		CDS	
2558671034	DRAFT_01702	Product_name		Rad51	
2558671034	DRAFT_01702	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671034	DRAFT_01702	Coordinates		199..1143(+)	
2558671034	DRAFT_01702	DNA_length		945bp	
2558671034	DRAFT_01702	Protein_length		314aa	
2558671034	DRAFT_01702	GC		0.61	
2558671035	DRAFT_01703	Locus_type		CDS	
2558671035	DRAFT_01703	Product_name		hypothetical protein	
2558671035	DRAFT_01703	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671035	DRAFT_01703	Coordinates		1143..1412(+)	
2558671035	DRAFT_01703	DNA_length		270bp	
2558671035	DRAFT_01703	Protein_length		89aa	
2558671035	DRAFT_01703	GC		0.6	

2558671036	DRAFT_01704	Locus_type		CDS	
2558671036	DRAFT_01704	Product_name		hypothetical protein	
2558671036	DRAFT_01704	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671036	DRAFT_01704	Coordinates		1409..1675(+)	
2558671036	DRAFT_01704	DNA_length		267bp	
2558671036	DRAFT_01704	Protein_length		88aa	
2558671036	DRAFT_01704	GC		0.59	
2558671037	DRAFT_01705	COG_category	[L] Replication, recombination and repair		
2558671037	DRAFT_01705	COG0417	DNA polymerase elongation subunit (family B)		1.00E-87
2558671037	DRAFT_01705	pfam03104	DNA_pol_B_exo1		5.40E-05
2558671037	DRAFT_01705	pfam00136	DNA_pol_B		1.00E-36
2558671037	DRAFT_01705	EC:2.7.7.7	DNA-directed DNA polymerase.		
2558671037	DRAFT_01705	KO:K02319	DNA polymerase I [EC:2.7.7.7]		0.00E+00
2558671037	DRAFT_01705	Locus_type		CDS	
2558671037	DRAFT_01705	Product_name		DNA polymerase elongation subunit (family B)	
2558671037	DRAFT_01705	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671037	DRAFT_01705	Coordinates		1656..3911(+)	
2558671037	DRAFT_01705	DNA_length		2256bp	
2558671037	DRAFT_01705	Protein_length		751aa	
2558671037	DRAFT_01705	GC		0.57	
2558671038	DRAFT_01706	pfam01243	Pyridox_oxidase		6.40E-22
2558671038	DRAFT_01706	TIGR03618	PPOX class probable F420-dependent enzyme		9.00E-24
2558671038	DRAFT_01706	Locus_type		CDS	
2558671038	DRAFT_01706	Product_name		Predicted flavin-nucleotide-binding protein	
2558671038	DRAFT_01706	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671038	DRAFT_01706	Coordinates		3924..4313(-)	
2558671038	DRAFT_01706	DNA_length		390bp	
2558671038	DRAFT_01706	Protein_length		129aa	
2558671038	DRAFT_01706	GC		0.53	
2558671039	DRAFT_01707	Locus_type		tRNA	

2558671039	DRAFT_01707	Product_name		tRNA_Thr_GGT	
2558671039	DRAFT_01707	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671039	DRAFT_01707	Coordinates		4355..4428(-)	
2558671039	DRAFT_01707	DNA_length		74bp	
2558671039	DRAFT_01707	GC		0.62	
2558671040	DRAFT_01708	Locus_type		CDS	
2558671040	DRAFT_01708	Product_name		hypothetical protein	
2558671040	DRAFT_01708	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671040	DRAFT_01708	Coordinates		4980..5105(+)	
2558671040	DRAFT_01708	DNA_length		126bp	
2558671040	DRAFT_01708	Protein_length		41aa	
2558671040	DRAFT_01708	GC		0.48	
2558671040	DRAFT_01708	Transmembrane		Yes	
2558671041	DRAFT_01709	KEGG_module	M00288: RPA complex		
2558671041	DRAFT_01709	COG_category	[L] Replication, recombination and repair		
2558671041	DRAFT_01709	COG1599	Single-stranded DNA-binding replication protein A (RPA), large (70 kD)		4.00E-09
2558671041	DRAFT_01709	KO:K07466	replication factor A1		0.00E+00
2558671041	DRAFT_01709	Locus_type		CDS	
2558671041	DRAFT_01709	Product_name		Single-stranded DNA-binding replication protein A (RPA), large (70 kD	
2558671041	DRAFT_01709	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55	
2558671041	DRAFT_01709	Coordinates		5102..6505(-)	
2558671041	DRAFT_01709	DNA_length		1404bp	
2558671041	DRAFT_01709	Protein_length		467aa	
2558671041	DRAFT_01709	GC		0.56	
2558671042	DRAFT_01710	KEGG_module	M00027: GABA (gamma-Aminobutyrate) shunt		
2558671042	DRAFT_01710	Metacyc	BETA-ALA-DEGRADATION-I-PWY: β-alanine degradation I		
2558671042	DRAFT_01710	Metacyc	PWY-6537: 4-aminobutyrate degradation II		
2558671042	DRAFT_01710	Metacyc	PWY-6536: 4-aminobutyrate degradation III		
2558671042	DRAFT_01710	Metacyc	GLUDEG-I-PWY: glutamate degradation III (via 4-aminobutyrate)		
2558671042	DRAFT_01710	Metacyc	PWY-5022: 4-aminobutyrate degradation V		
2558671042	DRAFT_01710	Metacyc	P181-PWY: nicotine degradation I		

2558671042	DRAFT_01710	Metacyc	PWY-6535: 4-aminobutyrate degradation I			
2558671042	DRAFT_01710	Metacyc	PWY-4321: glutamate degradation IV			
2558671042	DRAFT_01710	COG_category	[E] Amino acid transport and metabolism			
2558671042	DRAFT_01710	COG0160	4-aminobutyrate aminotransferase and related aminotransferases			0.00E+00
2558671042	DRAFT_01710	pfam00202	Aminotran_3			2.10E-97
2558671042	DRAFT_01710	EC:2.6.1.19	4-aminobutyrate--2-oxoglutarate transaminase.			
2558671042	DRAFT_01710	TIGR00700	4-aminobutyrate aminotransferase, prokaryotic type			2.60E-112
2558671042	DRAFT_01710	KO:K00823	4-aminobutyrate aminotransferase [EC:2.6.1.19]			0.00E+00
2558671042	DRAFT_01710	Locus_type		CDS		
2558671042	DRAFT_01710	Product_name		4-aminobutyrate aminotransferase and related aminotransferases		
2558671042	DRAFT_01710	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55		
2558671042	DRAFT_01710	Coordinates		6509..7861(-)		
2558671042	DRAFT_01710	DNA_length		1353bp		
2558671042	DRAFT_01710	Protein_length		450aa		
2558671042	DRAFT_01710	GC			0.55	
2558671043	DRAFT_01711	IMG_pathway	433: Archaeal nucleoid proteins			
2558671043	DRAFT_01711	COG_category	[K] Transcription			
2558671043	DRAFT_01711	COG1581	Archaeal DNA-binding protein			1.00E-16
2558671043	DRAFT_01711	pfam01918	Alba			5.30E-11
2558671043	DRAFT_01711	TIGR00285	DNA-binding protein Alba			5.00E-28
2558671043	DRAFT_01711	KO:K03622	archaea-specific DNA-binding protein			6.60E-17
2558671043	DRAFT_01711	ITERM:00143	nucleoid protein Alba			
2558671043	DRAFT_01711	Locus_type		CDS		
2558671043	DRAFT_01711	Product_name		nucleoid protein Alba		
2558671043	DRAFT_01711	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55		
2558671043	DRAFT_01711	Coordinates		7903..8187(-)		
2558671043	DRAFT_01711	DNA_length		285bp		
2558671043	DRAFT_01711	Protein_length		94aa		
2558671043	DRAFT_01711	GC			0.52	
2558671044	DRAFT_01712	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558671044	DRAFT_01712	COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family			2.00E-31
2558671044	DRAFT_01712	pfam00160	Pro_isomerase			4.10E-37

2558671044	DRAFT_01712	EC:5.2.1.8	Peptidylprolyl isomerase.			
2558671044	DRAFT_01712	KO:K01802	peptidylprolyl isomerase [EC:5.2.1.8]			3.60E-23
2558671044	DRAFT_01712	Locus_type		CDS		
2558671044	DRAFT_01712	Product_name		Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family		
2558671044	DRAFT_01712	Scaffold		DRAFT_contig_70_800_len_9042_read_count_162732.55		
2558671044	DRAFT_01712	Coordinates		8284..8979(+)		
2558671044	DRAFT_01712	DNA_length		696bp		
2558671044	DRAFT_01712	Protein_length		231aa		
2558671044	DRAFT_01712	GC			0.51	
2558671044	DRAFT_01712	Transmembrane		Yes		
2558671045	DRAFT_01713	IMG_pathway	433: Archaeal nucleoid proteins			
2558671045	DRAFT_01713	COG_category	[K] Transcription			
2558671045	DRAFT_01713	COG1581	Archaeal DNA-binding protein			2.00E-15
2558671045	DRAFT_01713	pfam01918	Alba			7.60E-16
2558671045	DRAFT_01713	TIGR00285	DNA-binding protein Alba			4.50E-28
2558671045	DRAFT_01713	KO:K03622	archaea-specific DNA-binding protein			1.60E-15
2558671045	DRAFT_01713	ITERM:00143	nucleoid protein Alba			
2558671045	DRAFT_01713	Locus_type		CDS		
2558671045	DRAFT_01713	Product_name		nucleoid protein Alba		
2558671045	DRAFT_01713	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56		
2558671045	DRAFT_01713	Coordinates		172..450(+)		
2558671045	DRAFT_01713	DNA_length		279bp		
2558671045	DRAFT_01713	Protein_length		92aa		
2558671045	DRAFT_01713	GC			0.54	
2558671046	DRAFT_01714	COG_category	[L] Replication, recombination and repair			
2558671046	DRAFT_01714	COG2827	Predicted endonuclease containing a URI domain			1.00E-24
2558671046	DRAFT_01714	pfam01541	GIY-YIG			3.70E-10
2558671046	DRAFT_01714	KO:K07461	putative endonuclease			1.70E-21
2558671046	DRAFT_01714	Locus_type		CDS		
2558671046	DRAFT_01714	Product_name		Predicted endonuclease containing a URI domain		
2558671046	DRAFT_01714	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56		
2558671046	DRAFT_01714	Coordinates		491..766(-)		

2558671046	DRAFT_01714	DNA_length		276bp	
2558671046	DRAFT_01714	Protein_length		91aa	
2558671046	DRAFT_01714	GC		0.56	
2558671047	DRAFT_01715	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds		
2558671047	DRAFT_01715	Metacyc	P122-PWY: heterolactic fermentation		
2558671047	DRAFT_01715	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)		
2558671047	DRAFT_01715	Metacyc	GLYCOLYSIS: glycolysis I		
2558671047	DRAFT_01715	Metacyc	PWY-5484: glycolysis II (from fructose-6P)		
2558671047	DRAFT_01715	Metacyc	PWY-7003: glycerol degradation to butanol		
2558671047	DRAFT_01715	Metacyc	P341-PWY: glycolysis V (Pyrococcus)		
2558671047	DRAFT_01715	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis		
2558671047	DRAFT_01715	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)		
2558671047	DRAFT_01715	Metacyc	PWY-6901: xylose degradation IV		
2558671047	DRAFT_01715	Metacyc	GLUCONEO-PWY: gluconeogenesis I		
2558671047	DRAFT_01715	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2558671047	DRAFT_01715	Metacyc	PWY-5723: Rubisco shunt		
2558671047	DRAFT_01715	Metacyc	PWY-7124: ethylene biosynthesis V		
2558671047	DRAFT_01715	Metacyc	PWY-1042: glycolysis IV (plant cytosol)		
2558671047	DRAFT_01715	Metacyc	P124-PWY: Bifidobacterium shunt		
2558671047	DRAFT_01715	Metacyc	PWY-2221: Entner-Doudoroff pathway III (semi-phosphorylative)		
2558671047	DRAFT_01715	COG_category	[G] Carbohydrate transport and metabolism		
2558671047	DRAFT_01715	COG3635	Predicted phosphoglycerate mutase, AP superfamily		2.00E-88
2558671047	DRAFT_01715	pfam01676	Metalloenzyme		4.00E-22
2558671047	DRAFT_01715	pfam10143	PhosphMutase		1.30E-45
2558671047	DRAFT_01715	EC:5.4.2.1	Phosphoglycerate mutase.		
2558671047	DRAFT_01715	TIGR00306	2,3-bisphosphoglycerate-independent phosphoglycerate mutase, archa		5.00E-96
2558671047	DRAFT_01715	KO:K15635	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.		0.00E+00
2558671047	DRAFT_01715	Locus_type		CDS	
2558671047	DRAFT_01715	Product_name		2,3-bisphosphoglycerate-independent phosphoglycerate mutase, arch	
2558671047	DRAFT_01715	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56	
2558671047	DRAFT_01715	Coordinates		933..2180(-)	
2558671047	DRAFT_01715	DNA_length		1248bp	
2558671047	DRAFT_01715	Protein_length		415aa	

2558671047	DRAFT_01715	GC			0.6	
2558671048	DRAFT_01716	KEGG_module	M00554: Nucleotide sugar biosynthesis, galactose => UDP-galactose			
2558671048	DRAFT_01716	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2558671048	DRAFT_01716	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2558671048	DRAFT_01716	KEGG_module	M00549: Nucleotide sugar biosynthesis, glucose => UDP-glucose			
2558671048	DRAFT_01716	Metacyc	PWY-6527: stachyose degradation			
2558671048	DRAFT_01716	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2558671048	DRAFT_01716	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			
2558671048	DRAFT_01716	COG_category	[C] Energy production and conversion			
2558671048	DRAFT_01716	COG1085	Galactose-1-phosphate uridylyltransferase			4.00E-41
2558671048	DRAFT_01716	pfam01087	GalP_UDP_transf			5.80E-05
2558671048	DRAFT_01716	EC:2.7.7.12	UDP-glucose--hexose-1-phosphate uridylyltransferase.			
2558671048	DRAFT_01716	KO:K00965	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]			0.00E+00
2558671048	DRAFT_01716	Locus_type		CDS		
2558671048	DRAFT_01716	Product_name		Galactose-1-phosphate uridylyltransferase		
2558671048	DRAFT_01716	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56		
2558671048	DRAFT_01716	Coordinates		2277..3311(+)		
2558671048	DRAFT_01716	DNA_length		1035bp		
2558671048	DRAFT_01716	Protein_length		344aa		
2558671048	DRAFT_01716	GC			0.58	
2558671049	DRAFT_01717	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)			
2558671049	DRAFT_01717	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2558671049	DRAFT_01717	KEGG_module	M00114: Ascorbate biosynthesis, plants, glucose-6P => ascorbate			
2558671049	DRAFT_01717	Metacyc	PWY-5659: GDP-mannose biosynthesis			
2558671049	DRAFT_01717	Metacyc	PWY-5054: sorbitol biosynthesis I			
2558671049	DRAFT_01717	Metacyc	GLYCOLYSIS: glycolysis I			
2558671049	DRAFT_01717	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2558671049	DRAFT_01717	Metacyc	PWY-6531: mannitol cycle			
2558671049	DRAFT_01717	Metacyc	PWY-3861: mannitol degradation II			
2558671049	DRAFT_01717	Metacyc	PWY-5384: sucrose degradation IV			
2558671049	DRAFT_01717	Metacyc	P341-PWY: glycolysis V (Pyrococcus)			
2558671049	DRAFT_01717	Metacyc	P124-PWY: Bifidobacterium shunt			

2558671049	DRAFT_01717	Metacyc	ANAEROFRUCAT-PWY: homolactic fermentation		
2558671049	DRAFT_01717	Metacyc	RUMP-PWY: formaldehyde oxidation I		
2558671049	DRAFT_01717	Metacyc	SUCSYN-PWY: sucrose biosynthesis		
2558671049	DRAFT_01717	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2558671049	DRAFT_01717	Metacyc	PWY-3881: mannitol biosynthesis		
2558671049	DRAFT_01717	Metacyc	PWY-3801: sucrose degradation VI (anaerobic)		
2558671049	DRAFT_01717	Metacyc	MANNCAT-PWY: D-mannose degradation		
2558671049	DRAFT_01717	Metacyc	GLUCONEO-PWY: gluconeogenesis I		
2558671049	DRAFT_01717	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)		
2558671049	DRAFT_01717	Metacyc	P122-PWY: heterolactic fermentation		
2558671049	DRAFT_01717	Metacyc	PWY-6981: chitin biosynthesis		
2558671049	DRAFT_01717	Metacyc	PWY-622: starch biosynthesis		
2558671049	DRAFT_01717	Metacyc	PWY-5514: UDP-<i>N</i>-acetyl-D-galactosamine biosynthesis II		
2558671049	DRAFT_01717	Metacyc	PWY-621: sucrose degradation III		
2558671049	DRAFT_01717	IMG_pathway	404: D-Mannose conversion to fructose-6-phosphate		
2558671049	DRAFT_01717	IMG_pathway	406: GDP-mannose formation from fructose 6-phosphate		
2558671049	DRAFT_01717	pfam10432	bact-PGI_C		5.30E-37
2558671049	DRAFT_01717	EC:5.3.1.9	Glucose-6-phosphate isomerase.		
2558671049	DRAFT_01717	EC:5.3.1.8	Mannose-6-phosphate isomerase.		
2558671049	DRAFT_01717	TIGR02128	bifunctional phosphoglucose/phosphomannose isomerase		2.60E-59
2558671049	DRAFT_01717	KO:K15916	glucose/mannose-6-phosphate isomerase [EC:5.3.1.9 5.3.1.8]		1.90E-36
2558671049	DRAFT_01717	ITERM:06272	bifunctional phosphoglucose/phosphomannose isomerase (EC 5.3.1.8; EC 5.3.1.9)		
2558671049	DRAFT_01717	Locus_type		CDS	
2558671049	DRAFT_01717	Product_name		bifunctional phosphoglucose/phosphomannose isomerase (EC 5.3.1.8	
2558671049	DRAFT_01717	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56	
2558671049	DRAFT_01717	Coordinates		3315..4340(-)	
2558671049	DRAFT_01717	DNA_length		1026bp	
2558671049	DRAFT_01717	Protein_length		341aa	
2558671049	DRAFT_01717	GC		0.59	

2558671050	DRAFT_01718	pfam13562	NTP_transf_4		1.50E-07
2558671050	DRAFT_01718	TIGR03991	UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate		8.10E-80
2558671050	DRAFT_01718	Locus_type		CDS	
2558671050	DRAFT_01718	Product_name		UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate	

2558671050	DRAFT_01718	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56	
2558671050	DRAFT_01718	Coordinates		4490..5731(-)	
2558671050	DRAFT_01718	DNA_length		1242bp	
2558671050	DRAFT_01718	Protein_length		413aa	
2558671050	DRAFT_01718	GC		0.61	
2558671051	DRAFT_01719	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes		
2558671051	DRAFT_01719	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes		
2558671051	DRAFT_01719	KEGG_module	M00114: Ascorbate biosynthesis, plants, glucose-6P => ascorbate		
2558671051	DRAFT_01719	Metacyc	PWY-5659: GDP-mannose biosynthesis		
2558671051	DRAFT_01719	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)		
2558671051	DRAFT_01719	Metacyc	PWY-6082: alginate biosynthesis II		
2558671051	DRAFT_01719	Metacyc	PWY-6073: alginate biosynthesis I		
2558671051	DRAFT_01719	pfam00483	NTP_transferase		9.80E-21
2558671051	DRAFT_01719	EC:2.7.7.13	Mannose-1-phosphate guanylyltransferase.		
2558671051	DRAFT_01719	KO:K00966	mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]		0.00E+00
2558671051	DRAFT_01719	Locus_type		CDS	
2558671051	DRAFT_01719	Product_name		Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopol	
2558671051	DRAFT_01719	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56	
2558671051	DRAFT_01719	Coordinates		5736..6365(-)	
2558671051	DRAFT_01719	DNA_length		630bp	
2558671051	DRAFT_01719	Protein_length		209aa	
2558671051	DRAFT_01719	GC		0.54	
2558671052	DRAFT_01720	Locus_type		CDS	
2558671052	DRAFT_01720	Product_name		hypothetical protein	
2558671052	DRAFT_01720	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56	
2558671052	DRAFT_01720	Coordinates		6439..7170(-)	
2558671052	DRAFT_01720	DNA_length		732bp	
2558671052	DRAFT_01720	Protein_length		243aa	
2558671052	DRAFT_01720	GC		0.59	
2558671053	DRAFT_01721	Locus_type		CDS	
2558671053	DRAFT_01721	Product_name		hypothetical protein	

2558671053	DRAFT_01721	Scaffold		DRAFT_contig_70_809_len_8972_read_count_133314.56	
2558671053	DRAFT_01721	Coordinates		7306..7311(-)	
2558671053	DRAFT_01721	DNA_length		6bp	
2558671053	DRAFT_01721	Protein_length		1aa	
2558671053	DRAFT_01721	GC			0.33

2558671054	DRAFT_01722	Locus_type		CDS	
2558671054	DRAFT_01722	Product_name		hypothetical protein	
2558671054	DRAFT_01722	Scaffold		DRAFT_contig_70_925_len_8329_read_count_151445.57	
2558671054	DRAFT_01722	Coordinates		2..145(-)	
2558671054	DRAFT_01722	DNA_length		144bp	
2558671054	DRAFT_01722	Protein_length		48aa	
2558671054	DRAFT_01722	GC			0.54
2558671054	DRAFT_01722	Transmembrane		Yes	

2558671055	DRAFT_01723	Locus_type		CDS	
2558671055	DRAFT_01723	Product_name		hypothetical protein	
2558671055	DRAFT_01723	Scaffold		DRAFT_contig_70_925_len_8329_read_count_151445.57	
2558671055	DRAFT_01723	Coordinates		576..1340(+)	
2558671055	DRAFT_01723	DNA_length		765bp	
2558671055	DRAFT_01723	Protein_length		254aa	
2558671055	DRAFT_01723	GC			0.52
2558671055	DRAFT_01723	Transmembrane		Yes	

2558671056	DRAFT_01724	TIGR02537	archaeal flagellin N-terminal-like domain		2.30E-08
2558671056	DRAFT_01724	Locus_type		CDS	
2558671056	DRAFT_01724	Product_name		archaeal flagellin N-terminal-like domain	
2558671056	DRAFT_01724	Scaffold		DRAFT_contig_70_925_len_8329_read_count_151445.57	
2558671056	DRAFT_01724	Coordinates		1615..3375(+)	
2558671056	DRAFT_01724	DNA_length		1761bp	
2558671056	DRAFT_01724	Protein_length		586aa	
2558671056	DRAFT_01724	GC			0.55
2558671056	DRAFT_01724	Transmembrane		Yes	

2558671057	DRAFT_01725	Locus_type		CDS	
2558671057	DRAFT_01725	Product_name		hypothetical protein	
2558671057	DRAFT_01725	Scaffold		DRAFT_contig_70_925_len_8329_read_count_151445.57	
2558671057	DRAFT_01725	Coordinates		3470..4066(+)	
2558671057	DRAFT_01725	DNA_length		597bp	
2558671057	DRAFT_01725	Protein_length		198aa	
2558671057	DRAFT_01725	GC			0.54
2558671057	DRAFT_01725	Transmembrane		Yes	
2558671058	DRAFT_01726	Locus_type		CDS	
2558671058	DRAFT_01726	Product_name		hypothetical protein	
2558671058	DRAFT_01726	Scaffold		DRAFT_contig_70_925_len_8329_read_count_151445.57	
2558671058	DRAFT_01726	Coordinates		4076..5845(+)	
2558671058	DRAFT_01726	DNA_length		1770bp	
2558671058	DRAFT_01726	Protein_length		589aa	
2558671058	DRAFT_01726	GC			0.54
2558671058	DRAFT_01726	Transmembrane		Yes	
2558671059	DRAFT_01727	TIGR02537	archaeal flagellin N-terminal-like domain		7.60E-08
2558671059	DRAFT_01727	Locus_type		CDS	
2558671059	DRAFT_01727	Product_name		archaeal flagellin N-terminal-like domain	
2558671059	DRAFT_01727	Scaffold		DRAFT_contig_70_925_len_8329_read_count_151445.57	
2558671059	DRAFT_01727	Coordinates		5857..8328(+)	
2558671059	DRAFT_01727	DNA_length		2472bp	
2558671059	DRAFT_01727	Protein_length		824aa	
2558671059	DRAFT_01727	GC			0.56
2558671059	DRAFT_01727	Transmembrane		Yes	
2558671060	DRAFT_01728	pfam12695	Abhydrolase_5		9.60E-12
2558671060	DRAFT_01728	Locus_type		CDS	
2558671060	DRAFT_01728	Product_name		Dienelactone hydrolase and related enzymes	
2558671060	DRAFT_01728	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58	
2558671060	DRAFT_01728	Coordinates		1..450(+)	
2558671060	DRAFT_01728	DNA_length		450bp	

2558671060	DRAFT_01728	Protein_length		149aa		
2558671060	DRAFT_01728	GC			0.62	
2558671061	DRAFT_01729	Locus_type		CDS		
2558671061	DRAFT_01729	Product_name		hypothetical protein		
2558671061	DRAFT_01729	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58		
2558671061	DRAFT_01729	Coordinates		526..1005(-)		
2558671061	DRAFT_01729	DNA_length		480bp		
2558671061	DRAFT_01729	Protein_length		159aa		
2558671061	DRAFT_01729	GC			0.57	
2558671062	DRAFT_01730	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558671062	DRAFT_01730	COG0695	Glutaredoxin and related proteins			1.00E-02
2558671062	DRAFT_01730	Locus_type		CDS		
2558671062	DRAFT_01730	Product_name		hypothetical protein		
2558671062	DRAFT_01730	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58		
2558671062	DRAFT_01730	Coordinates		992..1339(-)		
2558671062	DRAFT_01730	DNA_length		348bp		
2558671062	DRAFT_01730	Protein_length		115aa		
2558671062	DRAFT_01730	GC			0.55	
2558671063	DRAFT_01731	COG_category	[R] General function prediction only			
2558671063	DRAFT_01731	COG0456	Acetyltransferases			2.00E-15
2558671063	DRAFT_01731	pfam00583	Acetyltransf_1			8.90E-15
2558671063	DRAFT_01731	EC:2.3.1.128	Ribosomal-protein-alanine N-acetyltransferase.			
2558671063	DRAFT_01731	KO:K03789	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]			1.50E-13
2558671063	DRAFT_01731	Locus_type		CDS		
2558671063	DRAFT_01731	Product_name		Acetyltransferases		
2558671063	DRAFT_01731	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58		
2558671063	DRAFT_01731	Coordinates		1549..2025(-)		
2558671063	DRAFT_01731	DNA_length		477bp		
2558671063	DRAFT_01731	Protein_length		158aa		
2558671063	DRAFT_01731	GC			0.53	

2558671064	DRAFT_01732	Locus_type		CDS		
2558671064	DRAFT_01732	Product_name		hypothetical protein		
2558671064	DRAFT_01732	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58		
2558671064	DRAFT_01732	Coordinates		2156..2506(+)		
2558671064	DRAFT_01732	DNA_length		351bp		
2558671064	DRAFT_01732	Protein_length		116aa		
2558671064	DRAFT_01732	GC			0.62	
2558671065	DRAFT_01733	COG_category	[F] Nucleotide transport and metabolism			
2558671065	DRAFT_01733	COG2169	Adenosine deaminase			2.00E-41
2558671065	DRAFT_01733	pfam01035	DNA_binding_1			5.10E-31
2558671065	DRAFT_01733	pfam02805	Ada_Zn_binding			4.40E-28
2558671065	DRAFT_01733	pfam12833	HTH_18			3.10E-10
2558671065	DRAFT_01733	EC:2.1.1.63	Methylated-DNA--[protein]-cysteine S-methyltransferase.			
2558671065	DRAFT_01733	TIGR00589	O-6-methylguanine DNA methyltransferase			1.30E-37
2558671065	DRAFT_01733	KO:K10778	AraC family transcriptional regulator, regulatory protein of adaptative			0.00E+00
2558671065	DRAFT_01733	Locus_type		CDS		
2558671065	DRAFT_01733	Product_name		Adenosine deaminase		
2558671065	DRAFT_01733	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58		
2558671065	DRAFT_01733	Coordinates		2558..3736(+)		
2558671065	DRAFT_01733	DNA_length		1179bp		
2558671065	DRAFT_01733	Protein_length		392aa		
2558671065	DRAFT_01733	GC			0.59	
2558671065	DRAFT_01733	Fused_gene		Yes		
2558671066	DRAFT_01734	Locus_type		CDS		
2558671066	DRAFT_01734	Product_name		hypothetical protein		
2558671066	DRAFT_01734	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58		
2558671066	DRAFT_01734	Coordinates		4018..4539(-)		
2558671066	DRAFT_01734	DNA_length		522bp		
2558671066	DRAFT_01734	Protein_length		173aa		
2558671066	DRAFT_01734	GC			0.57	
2558671067	DRAFT_01735	pfam01844	HNH			3.00E-09

2558671067	DRAFT_01735	Locus_type		CDS	
2558671067	DRAFT_01735	Product_name		Restriction endonuclease	
2558671067	DRAFT_01735	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58	
2558671067	DRAFT_01735	Coordinates		4925..5464(+)	
2558671067	DRAFT_01735	DNA_length		540bp	
2558671067	DRAFT_01735	Protein_length		179aa	
2558671067	DRAFT_01735	GC		0.56	

2558671068	DRAFT_01736	IMG_pathway	224: Nucleotide incision repair		
2558671068	DRAFT_01736	IMG_pathway	616: Abasic site processing by AP endonuclease activity		
2558671068	DRAFT_01736	COG_category	[L] Replication, recombination and repair		
2558671068	DRAFT_01736	COG1515	Deoxyinosine 3'endonuclease (endonuclease V)		1.00E-25
2558671068	DRAFT_01736	pfam04493	Endonuclease_5		1.60E-30
2558671068	DRAFT_01736	EC:3.1.21.7	Deoxyribonuclease V.		
2558671068	DRAFT_01736	KO:K05982	deoxyribonuclease V [EC:3.1.21.7]		1.10E-24
2558671068	DRAFT_01736	ITERM:00592	Endonuclease V (EC 3.1.21.-)		
2558671068	DRAFT_01736	Locus_type		CDS	
2558671068	DRAFT_01736	Product_name		Endonuclease V (EC 3.1.21.-)	
2558671068	DRAFT_01736	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58	
2558671068	DRAFT_01736	Coordinates		5724..6368(+)	
2558671068	DRAFT_01736	DNA_length		645bp	
2558671068	DRAFT_01736	Protein_length		214aa	
2558671068	DRAFT_01736	GC		0.56	

2558671069	DRAFT_01737	pfam05048	NosD		6.40E-10
2558671069	DRAFT_01737	pfam05048	NosD		4.60E-13
2558671069	DRAFT_01737	TIGR03804	parallel beta-helix repeat (two copies)		2.40E-09
2558671069	DRAFT_01737	Locus_type		CDS	
2558671069	DRAFT_01737	Product_name		parallel beta-helix repeat (two copies)	
2558671069	DRAFT_01737	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58	
2558671069	DRAFT_01737	Coordinates		6465..7793(+)	
2558671069	DRAFT_01737	DNA_length		1329bp	
2558671069	DRAFT_01737	Protein_length		442aa	
2558671069	DRAFT_01737	GC		0.56	

2558671069	DRAFT_01737	Transmembrane		Yes		
2558671070	DRAFT_01738	Locus_type		CDS		
2558671070	DRAFT_01738	Product_name		hypothetical protein		
2558671070	DRAFT_01738	Scaffold		DRAFT_contig_70_970_len_8171_read_count_141304.58		
2558671070	DRAFT_01738	Coordinates		7983..8168(+)		
2558671070	DRAFT_01738	DNA_length		186bp		
2558671070	DRAFT_01738	Protein_length		62aa		
2558671070	DRAFT_01738	GC			0.61	
2558671071	DRAFT_01739	Locus_type		CDS		
2558671071	DRAFT_01739	Product_name		hypothetical protein		
2558671071	DRAFT_01739	Scaffold		DRAFT_contig_70_1011_len_7975_read_count_148262.59		
2558671071	DRAFT_01739	Coordinates		1..231(+)		
2558671071	DRAFT_01739	DNA_length		231bp		
2558671071	DRAFT_01739	Protein_length		76aa		
2558671071	DRAFT_01739	GC			0.55	
2558671072	DRAFT_01740	KEGG_module	M00358: Coenzyme M biosynthesis			
2558671072	DRAFT_01740	COG_category	[C] Energy production and conversion			
2558671072	DRAFT_01740	COG2055	Malate/L-lactate dehydrogenases			2.00E-95
2558671072	DRAFT_01740	pfam02615	Ldh_2			7.00E-104
2558671072	DRAFT_01740	EC:1.1.1.272	(R)-2-hydroxyacid dehydrogenase.			
2558671072	DRAFT_01740	KO:K05884	(R)-2-hydroxyacid dehydrogenase [EC:1.1.1.272]			0.00E+00
2558671072	DRAFT_01740	Locus_type		CDS		
2558671072	DRAFT_01740	Product_name		Malate/L-lactate dehydrogenases		
2558671072	DRAFT_01740	Scaffold		DRAFT_contig_70_1011_len_7975_read_count_148262.59		
2558671072	DRAFT_01740	Coordinates		299..1339(+)		
2558671072	DRAFT_01740	DNA_length		1041bp		
2558671072	DRAFT_01740	Protein_length		346aa		
2558671072	DRAFT_01740	GC			0.54	
2558671073	DRAFT_01741	Locus_type		CDS		
2558671073	DRAFT_01741	Product_name		hypothetical protein		

2558671073	DRAFT_01741	Scaffold		DRAFT_contig_70_1011_len_7975_read_count_148262.59	
2558671073	DRAFT_01741	Coordinates		1405..2790(-)	
2558671073	DRAFT_01741	DNA_length		1386bp	
2558671073	DRAFT_01741	Protein_length		461aa	
2558671073	DRAFT_01741	GC		0.52	

2558671074	DRAFT_01742	KEGG_module	M00119: Pantothenate biosynthesis, valine/L-aspartate => pantothenate		
2558671074	DRAFT_01742	KEGG_module	M00019: Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine		
2558671074	DRAFT_01742	KEGG_module	M00570: Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine		
2558671074	DRAFT_01742	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA		
2558671074	DRAFT_01742	Metacyc	ILEUSYN-PWY: isoleucine biosynthesis I (from threonine)		
2558671074	DRAFT_01742	Metacyc	PWY-5108: isoleucine biosynthesis V		
2558671074	DRAFT_01742	Metacyc	PWY-5104: isoleucine biosynthesis IV		
2558671074	DRAFT_01742	Metacyc	LEUSYN-PWY: leucine biosynthesis		
2558671074	DRAFT_01742	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2558671074	DRAFT_01742	Metacyc	PWY-5076: leucine degradation III		
2558671074	DRAFT_01742	Metacyc	VALDEG-PWY: valine degradation I		
2558671074	DRAFT_01742	Metacyc	PWY-5057: valine degradation II		
2558671074	DRAFT_01742	Metacyc	ALANINE-VALINESYN-PWY: alanine biosynthesis I		
2558671074	DRAFT_01742	Metacyc	PWY-5103: isoleucine biosynthesis III		
2558671074	DRAFT_01742	Metacyc	PWY-5101: isoleucine biosynthesis II		
2558671074	DRAFT_01742	Metacyc	VALSYN-PWY: valine biosynthesis		
2558671074	DRAFT_01742	Metacyc	PWY-5078: isoleucine degradation II		
2558671074	DRAFT_01742	Metacyc	LEU-DEG2-PWY: leucine degradation I		
2558671074	DRAFT_01742	COG_category	[H] Coenzyme transport and metabolism		
2558671074	DRAFT_01742	COG_category	[E] Amino acid transport and metabolism		
2558671074	DRAFT_01742	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorism		2.00E-65
2558671074	DRAFT_01742	pfam01063	Aminotran_4		5.90E-44
2558671074	DRAFT_01742	EC:2.6.1.42	Branched-chain-amino-acid transaminase.		
2558671074	DRAFT_01742	TIGR01122	branched-chain amino acid aminotransferase, group I		5.10E-120
2558671074	DRAFT_01742	KO:K00826	branched-chain amino acid aminotransferase [EC:2.6.1.42]		0.00E+00
2558671074	DRAFT_01742	Locus_type		CDS	
2558671074	DRAFT_01742	Product_name		branched-chain amino acid aminotransferase, group I	
2558671074	DRAFT_01742	Scaffold		DRAFT_contig_70_1011_len_7975_read_count_148262.59	

2558671074	DRAFT_01742	Coordinates		2825..3769(-)	
2558671074	DRAFT_01742	DNA_length		945bp	
2558671074	DRAFT_01742	Protein_length		314aa	
2558671074	DRAFT_01742	GC		0.55	
2558671075	DRAFT_01743	COG_category	[C] Energy production and conversion		
2558671075	DRAFT_01743	COG1042	Acyl-CoA synthetase (NDP forming)		0.00E+00
2558671075	DRAFT_01743	pfam13380	CoA_binding_2		6.70E-21
2558671075	DRAFT_01743	pfam13607	Succ_CoA_lig		1.20E-54
2558671075	DRAFT_01743	pfam13302	Acetyltransf_3		1.90E-08
2558671075	DRAFT_01743	pfam13549	ATP-grasp_5		4.40E-69
2558671075	DRAFT_01743	TIGR02717	acetyl coenzyme A synthetase (ADP forming), alpha domain		0.00E+00
2558671075	DRAFT_01743	KO:K09181	hypothetical protein		0.00E+00
2558671075	DRAFT_01743	Locus_type		CDS	
2558671075	DRAFT_01743	Product_name		Acyl-CoA synthetase (NDP forming)	
2558671075	DRAFT_01743	Scaffold		DRAFT_contig_70_1011_len_7975_read_count_148262.59	
2558671075	DRAFT_01743	Coordinates		3905..6706(-)	
2558671075	DRAFT_01743	DNA_length		2802bp	
2558671075	DRAFT_01743	Protein_length		933aa	
2558671075	DRAFT_01743	GC		0.6	
2558671075	DRAFT_01743	Fused_gene		Yes	
2558671076	DRAFT_01744	Locus_type		CDS	
2558671076	DRAFT_01744	Product_name		hypothetical protein	
2558671076	DRAFT_01744	Scaffold		DRAFT_contig_70_1011_len_7975_read_count_148262.59	
2558671076	DRAFT_01744	Coordinates		6892..7974(-)	
2558671076	DRAFT_01744	DNA_length		1083bp	
2558671076	DRAFT_01744	Protein_length		360aa	
2558671076	DRAFT_01744	GC		0.56	
2558671077	DRAFT_01745	COG_category	[T] Signal transduction mechanisms		
2558671077	DRAFT_01745	COG0467	RecA-superfamily ATPases implicated in signal transduction		1.00E-09
2558671077	DRAFT_01745	pfam07088	GvpD		9.90E-29
2558671077	DRAFT_01745	Locus_type		CDS	

2558671077	DRAFT_01745	Product_name		GvpD gas vesicle protein		
2558671077	DRAFT_01745	Scaffold		DRAFT_contig_70_1019_len_7928_read_count_151901.60		
2558671077	DRAFT_01745	Coordinates		3..962(-)		
2558671077	DRAFT_01745	DNA_length		960bp		
2558671077	DRAFT_01745	Protein_length		320aa		
2558671077	DRAFT_01745	GC			0.5	
2558671078	DRAFT_01746	Locus_type		CDS		
2558671078	DRAFT_01746	Product_name		hypothetical protein		
2558671078	DRAFT_01746	Scaffold		DRAFT_contig_70_1019_len_7928_read_count_151901.60		
2558671078	DRAFT_01746	Coordinates		959..1279(-)		
2558671078	DRAFT_01746	DNA_length		321bp		
2558671078	DRAFT_01746	Protein_length		106aa		
2558671078	DRAFT_01746	GC			0.51	
2558671079	DRAFT_01747	Locus_type		CDS		
2558671079	DRAFT_01747	Product_name		hypothetical protein		
2558671079	DRAFT_01747	Scaffold		DRAFT_contig_70_1019_len_7928_read_count_151901.60		
2558671079	DRAFT_01747	Coordinates		1682..1972(-)		
2558671079	DRAFT_01747	DNA_length		291bp		
2558671079	DRAFT_01747	Protein_length		96aa		
2558671079	DRAFT_01747	GC			0.5	
2558671079	DRAFT_01747	Transmembrane		Yes		
2558671080	DRAFT_01748	Locus_type		CDS		
2558671080	DRAFT_01748	Product_name		hypothetical protein		
2558671080	DRAFT_01748	Scaffold		DRAFT_contig_70_1019_len_7928_read_count_151901.60		
2558671080	DRAFT_01748	Coordinates		2208..2378(-)		
2558671080	DRAFT_01748	DNA_length		171bp		
2558671080	DRAFT_01748	Protein_length		56aa		
2558671080	DRAFT_01748	GC			0.49	
2558671081	DRAFT_01749	pfam04138	GtrA			5.40E-07
2558671081	DRAFT_01749	pfam03706	UPF0104			2.00E-13

2558671081	DRAFT_01749	Locus_type		CDS	
2558671081	DRAFT_01749	Product_name		GtrA-like protein/Uncharacterised protein family (UPF0104)	
2558671081	DRAFT_01749	Scaffold		DRAFT_contig_70_1019_len_7928_read_count_151901.60	
2558671081	DRAFT_01749	Coordinates		2801..4333(+)	
2558671081	DRAFT_01749	DNA_length		1533bp	
2558671081	DRAFT_01749	Protein_length		510aa	
2558671081	DRAFT_01749	GC		0.56	
2558671081	DRAFT_01749	Transmembrane		Yes	
2558671082	DRAFT_01750	Locus_type		CDS	
2558671082	DRAFT_01750	Product_name		hypothetical protein	
2558671082	DRAFT_01750	Scaffold		DRAFT_contig_70_1019_len_7928_read_count_151901.60	
2558671082	DRAFT_01750	Coordinates		4657..4818(+)	
2558671082	DRAFT_01750	DNA_length		162bp	
2558671082	DRAFT_01750	Protein_length		53aa	
2558671082	DRAFT_01750	GC		0.57	
2558671083	DRAFT_01751	pfam00583	Acetyltransf_1		4.50E-11
2558671083	DRAFT_01751	Locus_type		CDS	
2558671083	DRAFT_01751	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins	
2558671083	DRAFT_01751	Scaffold		DRAFT_contig_70_1019_len_7928_read_count_151901.60	
2558671083	DRAFT_01751	Coordinates		5321..5863(+)	
2558671083	DRAFT_01751	DNA_length		543bp	
2558671083	DRAFT_01751	Protein_length		180aa	
2558671083	DRAFT_01751	GC		0.51	
2558671084	DRAFT_01752	Locus_type		CDS	
2558671084	DRAFT_01752	Product_name		hypothetical protein	
2558671084	DRAFT_01752	Scaffold		DRAFT_contig_70_1019_len_7928_read_count_151901.60	
2558671084	DRAFT_01752	Coordinates		6137..6313(+)	
2558671084	DRAFT_01752	DNA_length		177bp	
2558671084	DRAFT_01752	Protein_length		58aa	
2558671084	DRAFT_01752	GC		0.5	

2558671085	DRAFT_01753	Locus_type	CDS	
2558671085	DRAFT_01753	Product_name	hypothetical protein	
2558671085	DRAFT_01753	Scaffold	DRAFT_contig_70_1019_len_7928_read_count_151901.60	
2558671085	DRAFT_01753	Coordinates	6540..6995(-)	
2558671085	DRAFT_01753	DNA_length	456bp	
2558671085	DRAFT_01753	Protein_length	151aa	
2558671085	DRAFT_01753	GC		0.47
2558671086	DRAFT_01754	Locus_type	CDS	
2558671086	DRAFT_01754	Product_name	hypothetical protein	
2558671086	DRAFT_01754	Scaffold	DRAFT_contig_70_1019_len_7928_read_count_151901.60	
2558671086	DRAFT_01754	Coordinates	7053..7214(-)	
2558671086	DRAFT_01754	DNA_length	162bp	
2558671086	DRAFT_01754	Protein_length	53aa	
2558671086	DRAFT_01754	GC		0.51
2558671086	DRAFT_01754	Transmembrane	Yes	
2558671087	DRAFT_01755	Locus_type	CDS	
2558671087	DRAFT_01755	Product_name	hypothetical protein	
2558671087	DRAFT_01755	Scaffold	DRAFT_contig_70_1019_len_7928_read_count_151901.60	
2558671087	DRAFT_01755	Coordinates	7331..7762(+)	
2558671087	DRAFT_01755	DNA_length	432bp	
2558671087	DRAFT_01755	Protein_length	143aa	
2558671087	DRAFT_01755	GC		0.55
2558671087	DRAFT_01755	Transmembrane	Yes	
2558671088	DRAFT_01756	Locus_type	CDS	
2558671088	DRAFT_01756	Product_name	hypothetical protein	
2558671088	DRAFT_01756	Scaffold	DRAFT_contig_70_1067_len_7725_read_count_134975.61	
2558671088	DRAFT_01756	Coordinates	1..303(+)	
2558671088	DRAFT_01756	DNA_length	303bp	
2558671088	DRAFT_01756	Protein_length	100aa	
2558671088	DRAFT_01756	GC		0.54
2558671088	DRAFT_01756	Transmembrane	Yes	

2558671089	DRAFT_01757	KEGG_module	M00222: Phosphate transport system			
2558671089	DRAFT_01757	COG_category	[P] Inorganic ion transport and metabolism			
2558671089	DRAFT_01757	COG0573	ABC-type phosphate transport system, permease component			4.00E-63
2558671089	DRAFT_01757	pfam00528	BPD_transp_1			1.00E-15
2558671089	DRAFT_01757	TIGR02138	phosphate ABC transporter, permease protein PstC			2.50E-95
2558671089	DRAFT_01757	KO:K02037	phosphate transport system permease protein			0.00E+00
2558671089	DRAFT_01757	ITERM:05784	phosphate ABC transporter membrane protein 1, PhoT family (TC 3.A.1.7.1)			
2558671089	DRAFT_01757	Locus_type		CDS		
2558671089	DRAFT_01757	Product_name		phosphate ABC transporter membrane protein 1, PhoT family (TC 3.A		
2558671089	DRAFT_01757	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671089	DRAFT_01757	Coordinates		350..1294(+)		
2558671089	DRAFT_01757	DNA_length		945bp		
2558671089	DRAFT_01757	Protein_length		314aa		
2558671089	DRAFT_01757	GC			0.56	
2558671089	DRAFT_01757	Transmembrane		Yes		
2558671090	DRAFT_01758	KEGG_module	M00222: Phosphate transport system			
2558671090	DRAFT_01758	COG_category	[P] Inorganic ion transport and metabolism			
2558671090	DRAFT_01758	COG0581	ABC-type phosphate transport system, permease component			3.00E-48
2558671090	DRAFT_01758	pfam00528	BPD_transp_1			9.20E-16
2558671090	DRAFT_01758	TIGR00974	phosphate ABC transporter, permease protein PstA			1.20E-73
2558671090	DRAFT_01758	KO:K02038	phosphate transport system permease protein			0.00E+00
2558671090	DRAFT_01758	ITERM:06114	phosphate ABC transporter membrane protein 2, PhoT family (TC 3.A.1.7.1)			
2558671090	DRAFT_01758	Locus_type		CDS		
2558671090	DRAFT_01758	Product_name		phosphate ABC transporter membrane protein 2, PhoT family (TC 3.A		
2558671090	DRAFT_01758	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671090	DRAFT_01758	Coordinates		1312..2127(+)		
2558671090	DRAFT_01758	DNA_length		816bp		
2558671090	DRAFT_01758	Protein_length		271aa		
2558671090	DRAFT_01758	GC			0.58	
2558671090	DRAFT_01758	Transmembrane		Yes		
2558671091	DRAFT_01759	KEGG_module	M00222: Phosphate transport system			

2558671091	DRAFT_01759	COG_category	[P] Inorganic ion transport and metabolism			
2558671091	DRAFT_01759	COG1117	ABC-type phosphate transport system, ATPase component			3.00E-118
2558671091	DRAFT_01759	pfam00005	ABC_tran			3.50E-31
2558671091	DRAFT_01759	EC:3.6.3.27	Phosphate-transporting ATPase.			
2558671091	DRAFT_01759	TIGR00972	phosphate ABC transporter, ATP-binding protein			1.70E-121
2558671091	DRAFT_01759	KO:K02036	phosphate transport system ATP-binding protein [EC:3.6.3.27]			0.00E+00
2558671091	DRAFT_01759	ITERM:05785	phosphate ABC transporter ATP-binding protein, PhoT family (TC 3.A.1.7.1)			
2558671091	DRAFT_01759	Locus_type		CDS		
2558671091	DRAFT_01759	Product_name		phosphate ABC transporter ATP-binding protein, PhoT family (TC 3.A.		
2558671091	DRAFT_01759	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671091	DRAFT_01759	Coordinates		2120..2947(+)		
2558671091	DRAFT_01759	DNA_length		828bp		
2558671091	DRAFT_01759	Protein_length		275aa		
2558671091	DRAFT_01759	GC			0.57	
2558671092	DRAFT_01760	COG_category	[P] Inorganic ion transport and metabolism			
2558671092	DRAFT_01760	COG0704	Phosphate uptake regulator			2.00E-23
2558671092	DRAFT_01760	pfam01895	PhoU			2.00E-06
2558671092	DRAFT_01760	pfam01895	PhoU			1.10E-15
2558671092	DRAFT_01760	KO:K02039	phosphate transport system protein			0.00E+00
2558671092	DRAFT_01760	Locus_type		CDS		
2558671092	DRAFT_01760	Product_name		Phosphate uptake regulator		
2558671092	DRAFT_01760	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671092	DRAFT_01760	Coordinates		2970..3584(+)		
2558671092	DRAFT_01760	DNA_length		615bp		
2558671092	DRAFT_01760	Protein_length		204aa		
2558671092	DRAFT_01760	GC			0.6	
2558671093	DRAFT_01761	pfam01513	NAD_kinase			1.00E-10
2558671093	DRAFT_01761	Locus_type		CDS		
2558671093	DRAFT_01761	Product_name		Predicted sugar kinase		
2558671093	DRAFT_01761	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671093	DRAFT_01761	Coordinates		3585..4409(-)		
2558671093	DRAFT_01761	DNA_length		825bp		

2558671093	DRAFT_01761	Protein_length		274aa		
2558671093	DRAFT_01761	GC			0.59	
2558671094	DRAFT_01762	COG_category	[S] Function unknown			
2558671094	DRAFT_01762	COG1801	Uncharacterized conserved protein			2.00E-54
2558671094	DRAFT_01762	pfam01904	DUF72			1.10E-62
2558671094	DRAFT_01762	Locus_type		CDS		
2558671094	DRAFT_01762	Product_name		Uncharacterized conserved protein		
2558671094	DRAFT_01762	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671094	DRAFT_01762	Coordinates		4387..5244(-)		
2558671094	DRAFT_01762	DNA_length		858bp		
2558671094	DRAFT_01762	Protein_length		285aa		
2558671094	DRAFT_01762	GC			0.57	
2558671095	DRAFT_01763	COG_category	[S] Function unknown			
2558671095	DRAFT_01763	COG1469	Uncharacterized conserved protein			2.00E-17
2558671095	DRAFT_01763	pfam02649	GCHY-1			3.70E-20
2558671095	DRAFT_01763	Locus_type		CDS		
2558671095	DRAFT_01763	Product_name		Uncharacterized conserved protein		
2558671095	DRAFT_01763	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671095	DRAFT_01763	Coordinates		5298..6047(-)		
2558671095	DRAFT_01763	DNA_length		750bp		
2558671095	DRAFT_01763	Protein_length		249aa		
2558671095	DRAFT_01763	GC			0.59	
2558671096	DRAFT_01764	COG_category	[R] General function prediction only			
2558671096	DRAFT_01764	COG0603	Predicted PP-loop superfamily ATPase			4.00E-32
2558671096	DRAFT_01764	pfam06508	QueC			2.60E-34
2558671096	DRAFT_01764	TIGR00364	queuosine biosynthesis protein QueC			2.50E-31
2558671096	DRAFT_01764	KO:K06920	queuosine biosynthesis protein QueC			9.50E-34
2558671096	DRAFT_01764	Locus_type		CDS		
2558671096	DRAFT_01764	Product_name		Predicted PP-loop superfamily ATPase		
2558671096	DRAFT_01764	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671096	DRAFT_01764	Coordinates		6074..6667(-)		

2558671096	DRAFT_01764	DNA_length		594bp		
2558671096	DRAFT_01764	Protein_length		197aa		
2558671096	DRAFT_01764	GC			0.56	
2558671097	DRAFT_01765	COG_category	[H] Coenzyme transport and metabolism			
2558671097	DRAFT_01765	COG0720	6-pyruvoyl-tetrahydropterin synthase			2.00E-11
2558671097	DRAFT_01765	pfam01242	PTPS			2.40E-19
2558671097	DRAFT_01765	Locus_type		CDS		
2558671097	DRAFT_01765	Product_name		6-pyruvoyl-tetrahydropterin synthase		
2558671097	DRAFT_01765	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671097	DRAFT_01765	Coordinates		6712..7557(-)		
2558671097	DRAFT_01765	DNA_length		846bp		
2558671097	DRAFT_01765	Protein_length		281aa		
2558671097	DRAFT_01765	GC			0.56	
2558671098	DRAFT_01766	Locus_type		tRNA		
2558671098	DRAFT_01766	Product_name		tRNA_Gly_CCC		
2558671098	DRAFT_01766	Scaffold		DRAFT_contig_70_1067_len_7725_read_count_134975.61		
2558671098	DRAFT_01766	Coordinates		7632..7724(+)		
2558671098	DRAFT_01766	DNA_length		79bp		
2558671098	DRAFT_01766	GC			0.68	
2558671099	DRAFT_01767	Locus_type		CDS		
2558671099	DRAFT_01767	Product_name		hypothetical protein		
2558671099	DRAFT_01767	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62		
2558671099	DRAFT_01767	Coordinates		3..677(+)		
2558671099	DRAFT_01767	DNA_length		675bp		
2558671099	DRAFT_01767	Protein_length		224aa		
2558671099	DRAFT_01767	GC			0.55	
2558671100	DRAFT_01768	pfam13248	zf-ribbon_3			1.20E-07
2558671100	DRAFT_01768	Locus_type		CDS		
2558671100	DRAFT_01768	Product_name		zinc-ribbon domain		
2558671100	DRAFT_01768	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62		

2558671100	DRAFT_01768	Coordinates		1002..1700(+)	
2558671100	DRAFT_01768	DNA_length		699bp	
2558671100	DRAFT_01768	Protein_length		232aa	
2558671100	DRAFT_01768	GC		0.53	
2558671101	DRAFT_01769	Locus_type		CDS	
2558671101	DRAFT_01769	Product_name		hypothetical protein	
2558671101	DRAFT_01769	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62	
2558671101	DRAFT_01769	Coordinates		1869..2708(+)	
2558671101	DRAFT_01769	DNA_length		840bp	
2558671101	DRAFT_01769	Protein_length		279aa	
2558671101	DRAFT_01769	GC		0.53	
2558671102	DRAFT_01770	Locus_type		CDS	
2558671102	DRAFT_01770	Product_name		hypothetical protein	
2558671102	DRAFT_01770	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62	
2558671102	DRAFT_01770	Coordinates		2828..2974(+)	
2558671102	DRAFT_01770	DNA_length		147bp	
2558671102	DRAFT_01770	Protein_length		48aa	
2558671102	DRAFT_01770	GC		0.58	
2558671102	DRAFT_01770	Transmembrane		Yes	
2558671103	DRAFT_01771	Locus_type		CDS	
2558671103	DRAFT_01771	Product_name		hypothetical protein	
2558671103	DRAFT_01771	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62	
2558671103	DRAFT_01771	Coordinates		3203..3457(+)	
2558671103	DRAFT_01771	DNA_length		255bp	
2558671103	DRAFT_01771	Protein_length		84aa	
2558671103	DRAFT_01771	GC		0.5	
2558671104	DRAFT_01772	COG_category	[R] General function prediction only		
2558671104	DRAFT_01772	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa		4.00E-27
2558671104	DRAFT_01772	pfam12697	Abhydrolase_6		6.10E-37
2558671104	DRAFT_01772	Locus_type		CDS	

2558671104	DRAFT_01772	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super	
2558671104	DRAFT_01772	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62	
2558671104	DRAFT_01772	Coordinates		3590..4384(+)	
2558671104	DRAFT_01772	DNA_length		795bp	
2558671104	DRAFT_01772	Protein_length		264aa	
2558671104	DRAFT_01772	GC		0.5	
2558671105	DRAFT_01773	Locus_type		CDS	
2558671105	DRAFT_01773	Product_name		hypothetical protein	
2558671105	DRAFT_01773	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62	
2558671105	DRAFT_01773	Coordinates		4734..4895(-)	
2558671105	DRAFT_01773	DNA_length		162bp	
2558671105	DRAFT_01773	Protein_length		53aa	
2558671105	DRAFT_01773	GC		0.49	
2558671105	DRAFT_01773	Transmembrane		Yes	
2558671106	DRAFT_01774	Locus_type		CDS	
2558671106	DRAFT_01774	Product_name		hypothetical protein	
2558671106	DRAFT_01774	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62	
2558671106	DRAFT_01774	Coordinates		5069..5215(+)	
2558671106	DRAFT_01774	DNA_length		147bp	
2558671106	DRAFT_01774	Protein_length		48aa	
2558671106	DRAFT_01774	GC		0.51	
2558671107	DRAFT_01775	pfam13240	zinc_ribbon_2		1.30E-07
2558671107	DRAFT_01775	Locus_type		CDS	
2558671107	DRAFT_01775	Product_name		zinc-ribbon domain	
2558671107	DRAFT_01775	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62	
2558671107	DRAFT_01775	Coordinates		6251..7138(-)	
2558671107	DRAFT_01775	DNA_length		888bp	
2558671107	DRAFT_01775	Protein_length		295aa	
2558671107	DRAFT_01775	GC		0.59	
2558671107	DRAFT_01775	Transmembrane		Yes	

2558671108	DRAFT_01776	Locus_type		CDS		
2558671108	DRAFT_01776	Product_name		hypothetical protein		
2558671108	DRAFT_01776	Scaffold		DRAFT_contig_70_1087_len_7658_read_count_135041.62		
2558671108	DRAFT_01776	Coordinates		7368..7655(+)		
2558671108	DRAFT_01776	DNA_length		288bp		
2558671108	DRAFT_01776	Protein_length		96aa		
2558671108	DRAFT_01776	GC			0.51	
2558671108	DRAFT_01776	Transmembrane		Yes		

2558671109	DRAFT_01777	COG_category	[R] General function prediction only			
2558671109	DRAFT_01777	COG0456	Acetyltransferases			6.00E-04
2558671109	DRAFT_01777	pfam13673	Acetyltransf_10			1.90E-08
2558671109	DRAFT_01777	Locus_type		CDS		
2558671109	DRAFT_01777	Product_name		Acetyltransferases		
2558671109	DRAFT_01777	Scaffold		DRAFT_contig_70_1231_len_7151_read_count_125048.63		
2558671109	DRAFT_01777	Coordinates		1..972(+)		
2558671109	DRAFT_01777	DNA_length		972bp		
2558671109	DRAFT_01777	Protein_length		323aa		
2558671109	DRAFT_01777	GC			0.51	

2558671110	DRAFT_01778	COG_category	[S] Function unknown			
2558671110	DRAFT_01778	COG5616	Predicted integral membrane protein			2.00E-34
2558671110	DRAFT_01778	pfam13414	TPR_11			3.70E-10
2558671110	DRAFT_01778	pfam00211	Guanylate_cyc			1.00E-22
2558671110	DRAFT_01778	pfam13414	TPR_11			3.30E-09
2558671110	DRAFT_01778	pfam13414	TPR_11			1.60E-06
2558671110	DRAFT_01778	EC:4.6.1.1	Adenylate cyclase.			
2558671110	DRAFT_01778	KO:K01768	adenylate cyclase [EC:4.6.1.1]			0.00E+00
2558671110	DRAFT_01778	Locus_type		CDS		
2558671110	DRAFT_01778	Product_name		Predicted integral membrane protein		
2558671110	DRAFT_01778	Scaffold		DRAFT_contig_70_1231_len_7151_read_count_125048.63		
2558671110	DRAFT_01778	Coordinates		1282..3240(+)		
2558671110	DRAFT_01778	DNA_length		1959bp		
2558671110	DRAFT_01778	Protein_length		652aa		

2558671110	DRAFT_01778	GC			0.57	
2558671111	DRAFT_01779	COG_category	[R] General function prediction only			
2558671111	DRAFT_01779	COG2910	Putative NADH-flavin reductase			5.00E-18
2558671111	DRAFT_01779	pfam13460	NAD_binding_10			2.00E-33
2558671111	DRAFT_01779	Locus_type		CDS		
2558671111	DRAFT_01779	Product_name		Putative NADH-flavin reductase		
2558671111	DRAFT_01779	Scaffold		DRAFT_contig_70_1231_len_7151_read_count_125048.63		
2558671111	DRAFT_01779	Coordinates		3362..4060(+)		
2558671111	DRAFT_01779	DNA_length		699bp		
2558671111	DRAFT_01779	Protein_length		232aa		
2558671111	DRAFT_01779	GC			0.63	
2558671112	DRAFT_01780	Metacyc	PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I			
2558671112	DRAFT_01780	Metacyc	PWY-6797: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (archaea)			
2558671112	DRAFT_01780	Metacyc	PWY-7206: pyrimidine deoxyribonucleotides dephosphorylation			
2558671112	DRAFT_01780	Metacyc	PWY-6575: juvenile hormone III biosynthesis I			
2558671112	DRAFT_01780	Metacyc	PWY-6502: oxidized GTP and dGTP detoxification			
2558671112	DRAFT_01780	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis			
2558671112	DRAFT_01780	COG_category	[F] Nucleotide transport and metabolism			
2558671112	DRAFT_01780	COG1051	ADP-ribose pyrophosphatase			6.00E-20
2558671112	DRAFT_01780	pfam00293	NUDIX			7.40E-20
2558671112	DRAFT_01780	EC:3.6.1.-	Hydrolases. Acting on acid anhydrides. In phosphorous-containing anhydrides.			
2558671112	DRAFT_01780	KO:K03574	7,8-dihydro-8-oxoguanine triphosphatase [EC:3.6.1.-]			9.00E-16
2558671112	DRAFT_01780	Locus_type		CDS		
2558671112	DRAFT_01780	Product_name		ADP-ribose pyrophosphatase		
2558671112	DRAFT_01780	Scaffold		DRAFT_contig_70_1231_len_7151_read_count_125048.63		
2558671112	DRAFT_01780	Coordinates		4118..4573(-)		
2558671112	DRAFT_01780	DNA_length		456bp		
2558671112	DRAFT_01780	Protein_length		151aa		
2558671112	DRAFT_01780	GC			0.55	
2558671113	DRAFT_01781	pfam08445	FR47			1.10E-13
2558671113	DRAFT_01781	Locus_type		CDS		

2558671113	DRAFT_01781	Product_name		Sortase and related acyltransferases		
2558671113	DRAFT_01781	Scaffold		DRAFT_contig_70_1231_len_7151_read_count_125048.63		
2558671113	DRAFT_01781	Coordinates		4843..5202(+)		
2558671113	DRAFT_01781	DNA_length		360bp		
2558671113	DRAFT_01781	Protein_length		119aa		
2558671113	DRAFT_01781	GC			0.58	
2558671114	DRAFT_01782	pfam13847	Methyltransf_31			3.20E-24
2558671114	DRAFT_01782	Locus_type		CDS		
2558671114	DRAFT_01782	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2558671114	DRAFT_01782	Scaffold		DRAFT_contig_70_1231_len_7151_read_count_125048.63		
2558671114	DRAFT_01782	Coordinates		5255..6058(-)		
2558671114	DRAFT_01782	DNA_length		804bp		
2558671114	DRAFT_01782	Protein_length		267aa		
2558671114	DRAFT_01782	GC			0.48	
2558671115	DRAFT_01783	pfam06197	DUF998			2.90E-08
2558671115	DRAFT_01783	Locus_type		CDS		
2558671115	DRAFT_01783	Product_name		Protein of unknown function (DUF998)		
2558671115	DRAFT_01783	Scaffold		DRAFT_contig_70_1231_len_7151_read_count_125048.63		
2558671115	DRAFT_01783	Coordinates		6143..6532(+)		
2558671115	DRAFT_01783	DNA_length		390bp		
2558671115	DRAFT_01783	Protein_length		129aa		
2558671115	DRAFT_01783	GC			0.57	
2558671115	DRAFT_01783	Transmembrane		Yes		
2558671116	DRAFT_01784	pfam10604	Polyketide_cyc2			6.60E-05
2558671116	DRAFT_01784	Locus_type		CDS		
2558671116	DRAFT_01784	Product_name		Polyketide cyclase / dehydrase and lipid transport		
2558671116	DRAFT_01784	Scaffold		DRAFT_contig_70_1231_len_7151_read_count_125048.63		
2558671116	DRAFT_01784	Coordinates		6777..7148(-)		
2558671116	DRAFT_01784	DNA_length		372bp		
2558671116	DRAFT_01784	Protein_length		123aa		
2558671116	DRAFT_01784	GC			0.53	

2558671117	DRAFT_01785	COG_category	[S] Function unknown			
2558671117	DRAFT_01785	COG1814	Uncharacterized membrane protein			5.00E-12
2558671117	DRAFT_01785	pfam01988	VIT1			7.60E-44
2558671117	DRAFT_01785	Locus_type		CDS		
2558671117	DRAFT_01785	Product_name		Uncharacterized membrane protein		
2558671117	DRAFT_01785	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671117	DRAFT_01785	Coordinates		3..647(-)		
2558671117	DRAFT_01785	DNA_length		645bp		
2558671117	DRAFT_01785	Protein_length		215aa		
2558671117	DRAFT_01785	GC			0.55	
2558671117	DRAFT_01785	Transmembrane		Yes		

2558671118	DRAFT_01786	pfam08241	Methyltransf_11			7.80E-21
2558671118	DRAFT_01786	Locus_type		CDS		
2558671118	DRAFT_01786	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2558671118	DRAFT_01786	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671118	DRAFT_01786	Coordinates		788..1567(-)		
2558671118	DRAFT_01786	DNA_length		780bp		
2558671118	DRAFT_01786	Protein_length		259aa		
2558671118	DRAFT_01786	GC			0.56	
2558671118	DRAFT_01786	Transmembrane		Yes		

2558671119	DRAFT_01787	Locus_type		CDS		
2558671119	DRAFT_01787	Product_name		hypothetical protein		
2558671119	DRAFT_01787	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671119	DRAFT_01787	Coordinates		1775..1984(-)		
2558671119	DRAFT_01787	DNA_length		210bp		
2558671119	DRAFT_01787	Protein_length		69aa		
2558671119	DRAFT_01787	GC			0.47	

2558671120	DRAFT_01788	IMG_pathway	146: Chorismate synthesis			
2558671120	DRAFT_01788	IMG_pathway	519: Archaeal chorismate synthesis			
2558671120	DRAFT_01788	COG_category	[E] Amino acid transport and metabolism			

2558671120	DRAFT_01788	COG0703	Shikimate kinase			2.00E-03
2558671120	DRAFT_01788	pfam13238	AAA_18			3.10E-14
2558671120	DRAFT_01788	ITERM:00339	shikimate kinase (EC 2.7.1.71)			
2558671120	DRAFT_01788	Locus_type		CDS		
2558671120	DRAFT_01788	Product_name		shikimate kinase (EC 2.7.1.71)		
2558671120	DRAFT_01788	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671120	DRAFT_01788	Coordinates		2022..2615(-)		
2558671120	DRAFT_01788	DNA_length		594bp		
2558671120	DRAFT_01788	Protein_length		197aa		
2558671120	DRAFT_01788	GC			0.57	
2558671121	DRAFT_01789	Locus_type		CDS		
2558671121	DRAFT_01789	Product_name		hypothetical protein		
2558671121	DRAFT_01789	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671121	DRAFT_01789	Coordinates		2734..2919(-)		
2558671121	DRAFT_01789	DNA_length		186bp		
2558671121	DRAFT_01789	Protein_length		61aa		
2558671121	DRAFT_01789	GC			0.52	
2558671122	DRAFT_01790	Locus_type		CDS		
2558671122	DRAFT_01790	Product_name		hypothetical protein		
2558671122	DRAFT_01790	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671122	DRAFT_01790	Coordinates		3181..3546(+)		
2558671122	DRAFT_01790	DNA_length		366bp		
2558671122	DRAFT_01790	Protein_length		121aa		
2558671122	DRAFT_01790	GC			0.55	
2558671122	DRAFT_01790	Transmembrane		Yes		
2558671123	DRAFT_01791	KEGG_module	M00577: Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin			
2558671123	DRAFT_01791	KEGG_module	M00573: Biotin biosynthesis, BioI pathway, long-chain-acyl-ACP => pimeloyl-ACP => biotin			
2558671123	DRAFT_01791	KEGG_module	M00123: Biotin biosynthesis, pimeloyl-ACP/CoA => biotin			
2558671123	DRAFT_01791	Metacyc	PWY0-1507: biotin biosynthesis from 7-keto-8-aminopelargonate			
2558671123	DRAFT_01791	COG_category	[H] Coenzyme transport and metabolism			
2558671123	DRAFT_01791	COG0502	Biotin synthase and related enzymes			6.00E-26

2558671123	DRAFT_01791	pfam04055	Radical_SAM			2.30E-09
2558671123	DRAFT_01791	EC:2.8.1.6	Biotin synthase.			
2558671123	DRAFT_01791	KO:K01012	biotin synthase [EC:2.8.1.6]			3.00E-42
2558671123	DRAFT_01791	Locus_type		CDS		
2558671123	DRAFT_01791	Product_name		Biotin synthase and related enzymes		
2558671123	DRAFT_01791	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671123	DRAFT_01791	Coordinates		3699..4730(-)		
2558671123	DRAFT_01791	DNA_length		1032bp		
2558671123	DRAFT_01791	Protein_length		343aa		
2558671123	DRAFT_01791	GC			0.56	
2558671124	DRAFT_01792	COG_category	[R] General function prediction only			
2558671124	DRAFT_01792	COG0384	Predicted epimerase, PhzC/PhzF homolog			3.00E-67
2558671124	DRAFT_01792	pfam02567	PhzC-PhzF			1.20E-61
2558671124	DRAFT_01792	TIGR00654	phenazine biosynthesis protein PhzF family			6.40E-66
2558671124	DRAFT_01792	Locus_type		CDS		
2558671124	DRAFT_01792	Product_name		phenazine biosynthesis protein PhzF family		
2558671124	DRAFT_01792	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671124	DRAFT_01792	Coordinates		4861..5982(+)		
2558671124	DRAFT_01792	DNA_length		1122bp		
2558671124	DRAFT_01792	Protein_length		373aa		
2558671124	DRAFT_01792	GC			0.59	
2558671125	DRAFT_01793	Locus_type		CDS		
2558671125	DRAFT_01793	Product_name		hypothetical protein		
2558671125	DRAFT_01793	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		
2558671125	DRAFT_01793	Coordinates		6171..6671(+)		
2558671125	DRAFT_01793	DNA_length		501bp		
2558671125	DRAFT_01793	Protein_length		166aa		
2558671125	DRAFT_01793	GC			0.52	
2558671126	DRAFT_01794	Locus_type		CDS		
2558671126	DRAFT_01794	Product_name		hypothetical protein		
2558671126	DRAFT_01794	Scaffold		DRAFT_contig_70_1291_len_6963_read_count_112826.64		

2558671126	DRAFT_01794	Coordinates		6719..6961(-)	
2558671126	DRAFT_01794	DNA_length		243bp	
2558671126	DRAFT_01794	Protein_length		80aa	
2558671126	DRAFT_01794	GC		0.57	
2558671127	DRAFT_01795	pfam10604	Polyketide_cyc2		4.20E-08
2558671127	DRAFT_01795	Locus_type		CDS	
2558671127	DRAFT_01795	Product_name		Polyketide cyclase / dehydrase and lipid transport	
2558671127	DRAFT_01795	Scaffold		DRAFT_contig_70_1364_len_6738_read_count_111437.65	
2558671127	DRAFT_01795	Coordinates		1..135(-)	
2558671127	DRAFT_01795	DNA_length		135bp	
2558671127	DRAFT_01795	Protein_length		45aa	
2558671127	DRAFT_01795	GC		0.5	
2558671128	DRAFT_01796	Metacyc	PWY-5386: methylglyoxal degradation I		
2558671128	DRAFT_01796	COG_category	[E] Amino acid transport and metabolism		
2558671128	DRAFT_01796	COG0346	Lactoylglutathione lyase and related lyases		2.00E-05
2558671128	DRAFT_01796	pfam13669	Glyoxalase_4		1.60E-12
2558671128	DRAFT_01796	EC:4.4.1.5	Lactoylglutathione lyase.		
2558671128	DRAFT_01796	KO:K01759	lactoylglutathione lyase [EC:4.4.1.5]		5.30E-11
2558671128	DRAFT_01796	Locus_type		CDS	
2558671128	DRAFT_01796	Product_name		Lactoylglutathione lyase and related lyases	
2558671128	DRAFT_01796	Scaffold		DRAFT_contig_70_1364_len_6738_read_count_111437.65	
2558671128	DRAFT_01796	Coordinates		410..817(+)	
2558671128	DRAFT_01796	DNA_length		408bp	
2558671128	DRAFT_01796	Protein_length		135aa	
2558671128	DRAFT_01796	GC		0.55	
2558671129	DRAFT_01797	Locus_type		CDS	
2558671129	DRAFT_01797	Product_name		hypothetical protein	
2558671129	DRAFT_01797	Scaffold		DRAFT_contig_70_1364_len_6738_read_count_111437.65	
2558671129	DRAFT_01797	Coordinates		961..1350(+)	
2558671129	DRAFT_01797	DNA_length		390bp	
2558671129	DRAFT_01797	Protein_length		129aa	

2558671129	DRAFT_01797	GC			0.49	
2558671130	DRAFT_01798	Locus_type		CDS		
2558671130	DRAFT_01798	Product_name		hypothetical protein		
2558671130	DRAFT_01798	Scaffold		DRAFT_contig_70_1364_len_6738_read_count_111437.65		
2558671130	DRAFT_01798	Coordinates		1682..3511(-)		
2558671130	DRAFT_01798	DNA_length		1830bp		
2558671130	DRAFT_01798	Protein_length		609aa		
2558671130	DRAFT_01798	GC			0.59	
2558671130	DRAFT_01798	Transmembrane		Yes		
2558671131	DRAFT_01799	Locus_type		CDS		
2558671131	DRAFT_01799	Product_name		hypothetical protein		
2558671131	DRAFT_01799	Scaffold		DRAFT_contig_70_1364_len_6738_read_count_111437.65		
2558671131	DRAFT_01799	Coordinates		3518..3994(-)		
2558671131	DRAFT_01799	DNA_length		477bp		
2558671131	DRAFT_01799	Protein_length		158aa		
2558671131	DRAFT_01799	GC			0.59	
2558671131	DRAFT_01799	Transmembrane		Yes		
2558671132	DRAFT_01800	Locus_type		CDS		
2558671132	DRAFT_01800	Product_name		hypothetical protein		
2558671132	DRAFT_01800	Scaffold		DRAFT_contig_70_1364_len_6738_read_count_111437.65		
2558671132	DRAFT_01800	Coordinates		4086..5231(+)		
2558671132	DRAFT_01800	DNA_length		1146bp		
2558671132	DRAFT_01800	Protein_length		381aa		
2558671132	DRAFT_01800	GC			0.59	
2558671133	DRAFT_01801	pfam11999	DUF3494			1.30E-70
2558671133	DRAFT_01801	Locus_type		CDS		
2558671133	DRAFT_01801	Product_name		Protein of unknown function (DUF3494)		
2558671133	DRAFT_01801	Scaffold		DRAFT_contig_70_1364_len_6738_read_count_111437.65		
2558671133	DRAFT_01801	Coordinates		5963..6736(-)		
2558671133	DRAFT_01801	DNA_length		774bp		

2558671133	DRAFT_01801	Protein_length		257aa		
2558671133	DRAFT_01801	GC			0.55	
2558671134	DRAFT_01802	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2558671134	DRAFT_01802	COG_category	[L] Replication, recombination and repair			
2558671134	DRAFT_01802	COG1474	Cdc6-related protein, AAA superfamily ATPase			2.00E-44
2558671134	DRAFT_01802	pfam09079	Cdc6_C			2.20E-17
2558671134	DRAFT_01802	pfam13401	AAA_22			2.30E-11
2558671134	DRAFT_01802	TIGR02928	orc1/cdc6 family replication initiation protein			2.40E-74
2558671134	DRAFT_01802	KO:K10725	archaeal cell division control protein 6			0.00E+00
2558671134	DRAFT_01802	Locus_type		CDS		
2558671134	DRAFT_01802	Product_name		orc1/cdc6 family replication initiation protein		
2558671134	DRAFT_01802	Scaffold		DRAFT_contig_70_1487_len_6446_read_count_115261.66		
2558671134	DRAFT_01802	Coordinates		3..1064(+)		
2558671134	DRAFT_01802	DNA_length		1062bp		
2558671134	DRAFT_01802	Protein_length		353aa		
2558671134	DRAFT_01802	GC			0.59	
2558671135	DRAFT_01803	Locus_type		CDS		
2558671135	DRAFT_01803	Product_name		hypothetical protein		
2558671135	DRAFT_01803	Scaffold		DRAFT_contig_70_1487_len_6446_read_count_115261.66		
2558671135	DRAFT_01803	Coordinates		1108..1347(+)		
2558671135	DRAFT_01803	DNA_length		240bp		
2558671135	DRAFT_01803	Protein_length		79aa		
2558671135	DRAFT_01803	GC			0.58	
2558671136	DRAFT_01804	pfam00004	AAA			1.70E-12
2558671136	DRAFT_01804	KO:K04800	replication factor C large subunit			0.00E+00
2558671136	DRAFT_01804	Locus_type		CDS		
2558671136	DRAFT_01804	Product_name		ATPase related to the helicase subunit of the Holliday junction resolva		
2558671136	DRAFT_01804	Scaffold		DRAFT_contig_70_1487_len_6446_read_count_115261.66		
2558671136	DRAFT_01804	Coordinates		1340..2515(-)		
2558671136	DRAFT_01804	DNA_length		1176bp		
2558671136	DRAFT_01804	Protein_length		391aa		

2558671136	DRAFT_01804	GC			0.59	
2558671137	DRAFT_01805	KEGG_module	M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone			
2558671137	DRAFT_01805	Metacyc	PWY-702: methionine biosynthesis II			
2558671137	DRAFT_01805	Metacyc	PWY-4681: kievitone biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-6793: demethylmenaquinol-8 biosynthesis III			
2558671137	DRAFT_01805	Metacyc	PWY-6834: spermidine biosynthesis III			
2558671137	DRAFT_01805	Metacyc	PWY-2681: <i>trans</i>-zeatin biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5893: tridecaprenyl diphosphate biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-6403: carrageenan biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5802: alizarin biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5132: humulone biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5027: phylloquinol biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5770: phenazine-1-carboxylate biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5135: xanthohumol biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-4502: wighteone and luteone biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-7169: hyperxanthone E biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5068: chlorophyll cycle			
2558671137	DRAFT_01805	Metacyc	PWY-6681: neurosporaxanthin biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5808: hyperforin and adhyperforin biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5817: dodecaprenyl diphosphate biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-6262: demethylmenaquinol-8 biosynthesis II			
2558671137	DRAFT_01805	Metacyc	PWY-6936: seleno-amino acid biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5064: chlorophyll <i>a</i> biosynthesis II			
2558671137	DRAFT_01805	Metacyc	PWY-5816: all <i>trans</i> undecaprenyl diphosphate biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5365: linear furanocoumarin biosynthesis			
2558671137	DRAFT_01805	Metacyc	PWY-5133: cohumulone biosynthesis			
2558671137	DRAFT_01805	COG_category	[H] Coenzyme transport and metabolism			
2558671137	DRAFT_01805	COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferas			7.00E-27
2558671137	DRAFT_01805	pfam01040	UbiA			5.30E-34
2558671137	DRAFT_01805	EC:2.5.1.-	Transferases. Transferring alkyl or aryl groups, other than methyl groups. Transferring alkyl or			
2558671137	DRAFT_01805	KO:K03179	4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]			1.40E-43
2558671137	DRAFT_01805	Locus_type		CDS		
2558671137	DRAFT_01805	Product_name		4-hydroxybenzoate polyprenyltransferase and related prenyltransfera		

2558671137	DRAFT_01805	Scaffold		DRAFT_contig_70_1487_len_6446_read_count_115261.66	
2558671137	DRAFT_01805	Coordinates		2516..3313(-)	
2558671137	DRAFT_01805	DNA_length		798bp	
2558671137	DRAFT_01805	Protein_length		265aa	
2558671137	DRAFT_01805	GC		0.6	
2558671137	DRAFT_01805	Transmembrane		Yes	

2558671138	DRAFT_01806	Metacyc	PWY-6689: tRNA splicing		
2558671138	DRAFT_01806	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558671138	DRAFT_01806	COG1676	tRNA splicing endonuclease		1.00E-16
2558671138	DRAFT_01806	pfam02778	tRNA_int_endo_N		1.10E-09
2558671138	DRAFT_01806	pfam01974	tRNA_int_endo		4.50E-19
2558671138	DRAFT_01806	EC:3.1.27.9	tRNA-intron endonuclease.		
2558671138	DRAFT_01806	TIGR00324	tRNA-intron endonuclease		4.80E-25
2558671138	DRAFT_01806	KO:K01170	tRNA-intron endonuclease, archaea type [EC:3.1.27.9]		7.40E-41
2558671138	DRAFT_01806	Locus_type		CDS	
2558671138	DRAFT_01806	Product_name		tRNA-intron endonuclease	
2558671138	DRAFT_01806	Scaffold		DRAFT_contig_70_1487_len_6446_read_count_115261.66	
2558671138	DRAFT_01806	Coordinates		3366..3914(-)	
2558671138	DRAFT_01806	DNA_length		549bp	
2558671138	DRAFT_01806	Protein_length		182aa	
2558671138	DRAFT_01806	GC		0.58	

2558671139	DRAFT_01807	KEGG_module	M00034: Methionine salvage pathway		
2558671139	DRAFT_01807	Metacyc	PWY-7174: <i>S</i>-methyl-5-thio-α-D-ribose 1-phosphate degradation II		
2558671139	DRAFT_01807	Metacyc	PWY-6755: <i>S</i>-methyl-5-thio-α-D-ribose 1-phosphate degradation I		
2558671139	DRAFT_01807	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558671139	DRAFT_01807	COG0182	Predicted translation initiation factor 2B subunit, eIF-2B alpha/beta/de		5.00E-119
2558671139	DRAFT_01807	pfam01008	IF-2B		9.70E-83
2558671139	DRAFT_01807	EC:5.3.1.23	S-methyl-5-thioribose-1-phosphate isomerase.		
2558671139	DRAFT_01807	TIGR00512	S-methyl-5-thioribose-1-phosphate isomerase		2.80E-118
2558671139	DRAFT_01807	TIGR00524	eIF-2B alpha/beta/delta-related uncharacterized proteins		3.80E-117
2558671139	DRAFT_01807	KO:K08963	methylthioribose-1-phosphate isomerase [EC:5.3.1.23]		0.00E+00
2558671139	DRAFT_01807	Locus_type		CDS	

2558671139	DRAFT_01807	Product_name		S-methyl-5-thioribose-1-phosphate isomerase	
2558671139	DRAFT_01807	Scaffold		DRAFT_contig_70_1487_len_6446_read_count_115261.66	
2558671139	DRAFT_01807	Coordinates		4018..5058(+)	
2558671139	DRAFT_01807	DNA_length		1041bp	
2558671139	DRAFT_01807	Protein_length		346aa	
2558671139	DRAFT_01807	GC		0.6	
2558671140	DRAFT_01808	pfam00571	CBS		1.60E-12
2558671140	DRAFT_01808	pfam00571	CBS		1.60E-09
2558671140	DRAFT_01808	Locus_type		CDS	
2558671140	DRAFT_01808	Product_name		Predicted signal-transduction protein containing cAMP-binding and C	
2558671140	DRAFT_01808	Scaffold		DRAFT_contig_70_1487_len_6446_read_count_115261.66	
2558671140	DRAFT_01808	Coordinates		5321..5758(+)	
2558671140	DRAFT_01808	DNA_length		438bp	
2558671140	DRAFT_01808	Protein_length		145aa	
2558671140	DRAFT_01808	GC		0.53	
2558671141	DRAFT_01809	Locus_type		tRNA	
2558671141	DRAFT_01809	Product_name		tRNA_Arg_TCG	
2558671141	DRAFT_01809	Scaffold		DRAFT_contig_70_1487_len_6446_read_count_115261.66	
2558671141	DRAFT_01809	Coordinates		6369..6443(+)	
2558671141	DRAFT_01809	DNA_length		75bp	
2558671141	DRAFT_01809	GC		0.57	
2558671142	DRAFT_01810	COG_category	[P] Inorganic ion transport and metabolism		
2558671142	DRAFT_01810	COG0474	Cation transport ATPase		0.00E+00
2558671142	DRAFT_01810	pfam00702	Hydrolase		1.50E-25
2558671142	DRAFT_01810	pfam00689	Cation_ATPase_C		4.80E-18
2558671142	DRAFT_01810	pfam00122	E1-E2_ATPase		2.70E-57
2558671142	DRAFT_01810	EC:3.6.3.2	Magnesium-importing ATPase.		
2558671142	DRAFT_01810	TIGR01524	magnesium-translocating P-type ATPase		0.00E+00
2558671142	DRAFT_01810	TIGR01494	ATPase, P-type (transporting), HAD superfamily, subfamily IC		9.80E-42
2558671142	DRAFT_01810	KO:K01531	Mg2+-importing ATPase [EC:3.6.3.2]		0.00E+00
2558671142	DRAFT_01810	Locus_type		CDS	

2558671142	DRAFT_01810	Product_name	magnesium-translocating P-type ATPase
2558671142	DRAFT_01810	Scaffold	DRAFT_contig_70_1564_len_6279_read_count_119203.67
2558671142	DRAFT_01810	Coordinates	776..3052(+)
2558671142	DRAFT_01810	DNA_length	2277bp
2558671142	DRAFT_01810	Protein_length	758aa
2558671142	DRAFT_01810	GC	0.58
2558671142	DRAFT_01810	Transmembrane	Yes
2558671143	DRAFT_01811	Locus_type	CDS
2558671143	DRAFT_01811	Product_name	hypothetical protein
2558671143	DRAFT_01811	Scaffold	DRAFT_contig_70_1564_len_6279_read_count_119203.67
2558671143	DRAFT_01811	Coordinates	3397..3939(-)
2558671143	DRAFT_01811	DNA_length	543bp
2558671143	DRAFT_01811	Protein_length	180aa
2558671143	DRAFT_01811	GC	0.55
2558671144	DRAFT_01812	Locus_type	CDS
2558671144	DRAFT_01812	Product_name	hypothetical protein
2558671144	DRAFT_01812	Scaffold	DRAFT_contig_70_1564_len_6279_read_count_119203.67
2558671144	DRAFT_01812	Coordinates	3984..4151(+)
2558671144	DRAFT_01812	DNA_length	168bp
2558671144	DRAFT_01812	Protein_length	55aa
2558671144	DRAFT_01812	GC	0.52
2558671145	DRAFT_01813	Locus_type	CDS
2558671145	DRAFT_01813	Product_name	hypothetical protein
2558671145	DRAFT_01813	Scaffold	DRAFT_contig_70_1564_len_6279_read_count_119203.67
2558671145	DRAFT_01813	Coordinates	5158..5427(-)
2558671145	DRAFT_01813	DNA_length	270bp
2558671145	DRAFT_01813	Protein_length	89aa
2558671145	DRAFT_01813	GC	0.55
2558671146	DRAFT_01814	Locus_type	CDS
2558671146	DRAFT_01814	Product_name	hypothetical protein

2558671146	DRAFT_01814	Scaffold		DRAFT_contig_70_1564_len_6279_read_count_119203.67	
2558671146	DRAFT_01814	Coordinates		6008..6277(-)	
2558671146	DRAFT_01814	DNA_length		270bp	
2558671146	DRAFT_01814	Protein_length		89aa	
2558671146	DRAFT_01814	GC		0.5	
2558671147	DRAFT_01815	KEGG_module	M00254: ABC-2 type transport system		
2558671147	DRAFT_01815	COG_category	[V] Defense mechanisms		
2558671147	DRAFT_01815	COG0842	ABC-type multidrug transport system, permease component		6.00E-06
2558671147	DRAFT_01815	pfam01061	ABC2_membrane		2.60E-14
2558671147	DRAFT_01815	KO:K01992	ABC-2 type transport system permease protein		0.00E+00
2558671147	DRAFT_01815	Locus_type		CDS	
2558671147	DRAFT_01815	Product_name		ABC-type multidrug transport system, permease component	
2558671147	DRAFT_01815	Scaffold		DRAFT_contig_70_1585_len_6250_read_count_103009.68	
2558671147	DRAFT_01815	Coordinates		66..764(-)	
2558671147	DRAFT_01815	DNA_length		699bp	
2558671147	DRAFT_01815	Protein_length		232aa	
2558671147	DRAFT_01815	GC		0.57	
2558671147	DRAFT_01815	Transmembrane		Yes	
2558671148	DRAFT_01816	KEGG_module	M00254: ABC-2 type transport system		
2558671148	DRAFT_01816	COG_category	[V] Defense mechanisms		
2558671148	DRAFT_01816	COG1131	ABC-type multidrug transport system, ATPase component		6.00E-61
2558671148	DRAFT_01816	pfam00005	ABC_tran		3.60E-28
2558671148	DRAFT_01816	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2558671148	DRAFT_01816	Locus_type		CDS	
2558671148	DRAFT_01816	Product_name		ABC-type multidrug transport system, ATPase component	
2558671148	DRAFT_01816	Scaffold		DRAFT_contig_70_1585_len_6250_read_count_103009.68	
2558671148	DRAFT_01816	Coordinates		818..1771(-)	
2558671148	DRAFT_01816	DNA_length		954bp	
2558671148	DRAFT_01816	Protein_length		317aa	
2558671148	DRAFT_01816	GC		0.6	
2558671149	DRAFT_01817	pfam05048	NosD		1.10E-05

2558671149	DRAFT_01817	Locus_type		CDS		
2558671149	DRAFT_01817	Product_name		Periplasmic copper-binding protein (NosD)		
2558671149	DRAFT_01817	Scaffold		DRAFT_contig_70_1585_len_6250_read_count_103009.68		
2558671149	DRAFT_01817	Coordinates		2170..4044(+)		
2558671149	DRAFT_01817	DNA_length		1875bp		
2558671149	DRAFT_01817	Protein_length		624aa		
2558671149	DRAFT_01817	GC			0.54	
2558671149	DRAFT_01817	Transmembrane		Yes		

2558671150	DRAFT_01818	pfam05048	NosD			8.50E-19
2558671150	DRAFT_01818	TIGR03804	parallel beta-helix repeat (two copies)			1.40E-14
2558671150	DRAFT_01818	Locus_type		CDS		
2558671150	DRAFT_01818	Product_name		parallel beta-helix repeat (two copies)		
2558671150	DRAFT_01818	Scaffold		DRAFT_contig_70_1585_len_6250_read_count_103009.68		
2558671150	DRAFT_01818	Coordinates		4314..4919(-)		
2558671150	DRAFT_01818	DNA_length		606bp		
2558671150	DRAFT_01818	Protein_length		201aa		
2558671150	DRAFT_01818	GC			0.54	
2558671150	DRAFT_01818	Transmembrane		Yes		

2558671151	DRAFT_01819	pfam05048	NosD			1.30E-12
2558671151	DRAFT_01819	pfam05048	NosD			2.30E-20
2558671151	DRAFT_01819	TIGR03804	parallel beta-helix repeat (two copies)			1.30E-13
2558671151	DRAFT_01819	Locus_type		CDS		
2558671151	DRAFT_01819	Product_name		parallel beta-helix repeat (two copies)		
2558671151	DRAFT_01819	Scaffold		DRAFT_contig_70_1585_len_6250_read_count_103009.68		
2558671151	DRAFT_01819	Coordinates		5019..6248(-)		
2558671151	DRAFT_01819	DNA_length		1230bp		
2558671151	DRAFT_01819	Protein_length		409aa		
2558671151	DRAFT_01819	GC			0.53	

2558671152	DRAFT_01820	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate
2558671152	DRAFT_01820	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)
2558671152	DRAFT_01820	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)

2558671152	DRAFT_01820	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2558671152	DRAFT_01820	KEGG_module	M00376: 3-Hydroxypropionate bicycle		
2558671152	DRAFT_01820	Metacyc	FERMENTATION-PWY: mixed acid fermentation		
2558671152	DRAFT_01820	Metacyc	TCA: TCA cycle I (prokaryotic)		
2558671152	DRAFT_01820	Metacyc	ANARESP1-PWY: respiration (anaerobic)		
2558671152	DRAFT_01820	Metacyc	PWY-561: superpathway of glyoxylate cycle and fatty acid degradation		
2558671152	DRAFT_01820	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2558671152	DRAFT_01820	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2558671152	DRAFT_01820	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)		
2558671152	DRAFT_01820	Metacyc	P108-PWY: pyruvate fermentation to propionate I		
2558671152	DRAFT_01820	Metacyc	PWY-6728: methylaspartate cycle		
2558671152	DRAFT_01820	Metacyc	P23-PWY: reductive TCA cycle I		
2558671152	DRAFT_01820	Metacyc	PWY-5690: TCA cycle II (eukaryotic)		
2558671152	DRAFT_01820	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)		
2558671152	DRAFT_01820	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2558671152	DRAFT_01820	Metacyc	PWY-5392: reductive TCA cycle II		
2558671152	DRAFT_01820	IMG_pathway	1014: Dicarboxylate/4-hydroxybutyrate cycle		
2558671152	DRAFT_01820	IMG_pathway	308: 2-oxoglutarate synthesis by partial reverse TCA cycle		
2558671152	DRAFT_01820	IMG_pathway	334: Tricarboxylic acid cycle		
2558671152	DRAFT_01820	IMG_pathway	335: Acetyl-CoA synthesis by reverse TCA cycle		
2558671152	DRAFT_01820	IMG_pathway	370: Oxaloacetate conversion to propionate via methylmalonyl-CoA		
2558671152	DRAFT_01820	IMG_pathway	525: Hydroxypropionate cycle		
2558671152	DRAFT_01820	IMG_pathway	960: Glyoxalate from acetyl-CoA via isocitrate lyase cycle		
2558671152	DRAFT_01820	IMG_pathway	962: Glyoxylate from acetyl-CoA via ethylmalonyl-CoA pathway		
2558671152	DRAFT_01820	COG_category	[C] Energy production and conversion		
2558671152	DRAFT_01820	COG0114	Fumarase		0.00E+00
2558671152	DRAFT_01820	pfam00206	Lyase_1		3.30E-81
2558671152	DRAFT_01820	pfam10415	FumaraseC_C		3.00E-07
2558671152	DRAFT_01820	EC:4.2.1.2	Fumarate hydratase.		
2558671152	DRAFT_01820	KO:K01679	fumarate hydratase, class II [EC:4.2.1.2]		0.00E+00
2558671152	DRAFT_01820	ITERM:01347	fumarase, class II (EC 4.2.1.2)		
2558671152	DRAFT_01820	Locus_type		CDS	
2558671152	DRAFT_01820	Product_name		fumarase, class II (EC 4.2.1.2)	
2558671152	DRAFT_01820	Scaffold		DRAFT_contig_70_1826_len_5843_read_count_86513.69	

2558671152	DRAFT_01820	Coordinates		45..1370(+)	
2558671152	DRAFT_01820	DNA_length		1326bp	
2558671152	DRAFT_01820	Protein_length		441aa	
2558671152	DRAFT_01820	GC			0.59
2558671153	DRAFT_01821	Locus_type		CDS	
2558671153	DRAFT_01821	Product_name		hypothetical protein	
2558671153	DRAFT_01821	Scaffold		DRAFT_contig_70_1826_len_5843_read_count_86513.69	
2558671153	DRAFT_01821	Coordinates		1399..1923(-)	
2558671153	DRAFT_01821	DNA_length		525bp	
2558671153	DRAFT_01821	Protein_length		174aa	
2558671153	DRAFT_01821	GC			0.59
2558671154	DRAFT_01822	KEGG_module	M00114: Ascorbate biosynthesis, plants, glucose-6P => ascorbate		
2558671154	DRAFT_01822	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)		
2558671154	DRAFT_01822	Metacyc	PWY-5661: GDP-glucose biosynthesis		
2558671154	DRAFT_01822	Metacyc	PWY-5940: streptomycin biosynthesis		
2558671154	DRAFT_01822	Metacyc	PWY-621: sucrose degradation III		
2558671154	DRAFT_01822	Metacyc	PWY-842: starch degradation I		
2558671154	DRAFT_01822	Metacyc	PWY-3801: sucrose degradation VI (anaerobic)		
2558671154	DRAFT_01822	Metacyc	GLUCOSE1PMETAB-PWY: glucose and glucose-1-phosphate degradation		
2558671154	DRAFT_01822	Metacyc	PWY-5384: sucrose degradation IV		
2558671154	DRAFT_01822	Metacyc	PWY-6731: starch degradation III		
2558671154	DRAFT_01822	Metacyc	PWY-5941: glycogen degradation II		
2558671154	DRAFT_01822	Metacyc	SUCSYN-PWY: sucrose biosynthesis		
2558671154	DRAFT_01822	Metacyc	GLYCOCAT-PWY: glycogen degradation I		
2558671154	DRAFT_01822	Metacyc	PWY-622: starch biosynthesis		
2558671154	DRAFT_01822	Metacyc	PWY-6737: starch degradation V		
2558671154	DRAFT_01822	Metacyc	PWY-5659: GDP-mannose biosynthesis		
2558671154	DRAFT_01822	COG_category	[G] Carbohydrate transport and metabolism		
2558671154	DRAFT_01822	COG1109	Phosphomannomutase		6.00E-67
2558671154	DRAFT_01822	pfam02879	PGM_PMM_II		8.80E-13
2558671154	DRAFT_01822	pfam02880	PGM_PMM_III		1.20E-17
2558671154	DRAFT_01822	pfam00408	PGM_PMM_IV		8.50E-07

2558671154	DRAFT_01822	pfam02878	PGM_PMM_I			8.70E-22
2558671154	DRAFT_01822	EC:5.4.2.2	Phosphoglucomutase.			
2558671154	DRAFT_01822	EC:5.4.2.8	Phosphomannomutase.			
2558671154	DRAFT_01822	KO:K15778	phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]			0.00E+00
2558671154	DRAFT_01822	Locus_type		CDS		
2558671154	DRAFT_01822	Product_name		Phosphomannomutase		
2558671154	DRAFT_01822	Scaffold		DRAFT_contig_70_1826_len_5843_read_count_86513.69		
2558671154	DRAFT_01822	Coordinates		1991..3292(+)		
2558671154	DRAFT_01822	DNA_length		1302bp		
2558671154	DRAFT_01822	Protein_length		433aa		
2558671154	DRAFT_01822	GC			0.6	
2558671155	DRAFT_01823	KEGG_module	M00127: Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P			
2558671155	DRAFT_01823	Metacyc	PWY-6893: thiamin diphosphate biosynthesis II (Bacillus)			
2558671155	DRAFT_01823	Metacyc	PWY-6896: thiamin salvage I			
2558671155	DRAFT_01823	Metacyc	PWY-6894: thiamin diphosphate biosynthesis I (E. coli)			
2558671155	DRAFT_01823	Metacyc	PWY-6897: thiamin salvage II			
2558671155	DRAFT_01823	COG_category	[H] Coenzyme transport and metabolism			
2558671155	DRAFT_01823	COG0611	Thiamine monophosphate kinase			3.00E-55
2558671155	DRAFT_01823	pfam02769	AIRS_C			3.20E-06
2558671155	DRAFT_01823	pfam00586	AIRS			2.30E-13
2558671155	DRAFT_01823	EC:2.7.4.16	Thiamine-phosphate kinase.			
2558671155	DRAFT_01823	TIGR01379	thiamine-monophosphate kinase			4.00E-72
2558671155	DRAFT_01823	KO:K00946	thiamine-monophosphate kinase [EC:2.7.4.16]			0.00E+00
2558671155	DRAFT_01823	Locus_type		CDS		
2558671155	DRAFT_01823	Product_name		thiamine-monophosphate kinase		
2558671155	DRAFT_01823	Scaffold		DRAFT_contig_70_1826_len_5843_read_count_86513.69		
2558671155	DRAFT_01823	Coordinates		3345..4253(+)		
2558671155	DRAFT_01823	DNA_length		909bp		
2558671155	DRAFT_01823	Protein_length		302aa		
2558671155	DRAFT_01823	GC			0.58	
2558671156	DRAFT_01824	KEGG_module	M00114: Ascorbate biosynthesis, plants, glucose-6P => ascorbate			
2558671156	DRAFT_01824	Metacyc	PWY-622: starch biosynthesis			

2558671156	DRAFT_01824	Metacyc	PWY-3801: sucrose degradation VI (anaerobic)		
2558671156	DRAFT_01824	Metacyc	PWY-842: starch degradation I		
2558671156	DRAFT_01824	Metacyc	PWY-5661: GDP-glucose biosynthesis		
2558671156	DRAFT_01824	Metacyc	PWY-5941: glycogen degradation II		
2558671156	DRAFT_01824	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)		
2558671156	DRAFT_01824	Metacyc	SUCSYN-PWY: sucrose biosynthesis		
2558671156	DRAFT_01824	Metacyc	GLUCOSE1PMETAB-PWY: glucose and glucose-1-phosphate degradation		
2558671156	DRAFT_01824	Metacyc	PWY-621: sucrose degradation III		
2558671156	DRAFT_01824	Metacyc	PWY-6731: starch degradation III		
2558671156	DRAFT_01824	Metacyc	PWY-5940: streptomycin biosynthesis		
2558671156	DRAFT_01824	Metacyc	PWY-5384: sucrose degradation IV		
2558671156	DRAFT_01824	Metacyc	PWY-6737: starch degradation V		
2558671156	DRAFT_01824	Metacyc	GLYCOCAT-PWY: glycogen degradation I		
2558671156	DRAFT_01824	Metacyc	PWY-5659: GDP-mannose biosynthesis		
2558671156	DRAFT_01824	COG_category	[G] Carbohydrate transport and metabolism		
2558671156	DRAFT_01824	COG1109	Phosphomannomutase		1.00E-110
2558671156	DRAFT_01824	pfam02878	PGM_PMM_I		3.30E-37
2558671156	DRAFT_01824	pfam02880	PGM_PMM_III		4.00E-20
2558671156	DRAFT_01824	pfam00408	PGM_PMM_IV		3.60E-10
2558671156	DRAFT_01824	pfam02879	PGM_PMM_II		8.40E-24
2558671156	DRAFT_01824	EC:5.4.2.2	Phosphoglucomutase.		
2558671156	DRAFT_01824	EC:5.4.2.8	Phosphomannomutase.		
2558671156	DRAFT_01824	TIGR03990	phosphoglucosamine mutase		0.00E+00
2558671156	DRAFT_01824	KO:K15778	phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]		0.00E+00
2558671156	DRAFT_01824	Locus_type		CDS	
2558671156	DRAFT_01824	Product_name		phosphoglucosamine mutase	
2558671156	DRAFT_01824	Scaffold		DRAFT_contig_70_1826_len_5843_read_count_86513.69	
2558671156	DRAFT_01824	Coordinates		4245..5612(-)	
2558671156	DRAFT_01824	DNA_length		1368bp	
2558671156	DRAFT_01824	Protein_length		455aa	
2558671156	DRAFT_01824	GC		0.6	

2558671157	DRAFT_01825	Locus_type		tRNA	
2558671157	DRAFT_01825	Product_name		tRNA_Ser_CGA	

2558671157	DRAFT_01825	Scaffold		DRAFT_contig_70_1826_len_5843_read_count_86513.69		
2558671157	DRAFT_01825	Coordinates		5728..5840(+)		
2558671157	DRAFT_01825	DNA_length		71bp		
2558671157	DRAFT_01825	GC			0.66	
2558671158	DRAFT_01826	Locus_type		CDS		
2558671158	DRAFT_01826	Product_name		hypothetical protein		
2558671158	DRAFT_01826	Scaffold		DRAFT_contig_70_2034_len_5512_read_count_100863.70		
2558671158	DRAFT_01826	Coordinates		84..842(+)		
2558671158	DRAFT_01826	DNA_length		759bp		
2558671158	DRAFT_01826	Protein_length		252aa		
2558671158	DRAFT_01826	GC			0.54	
2558671159	DRAFT_01827	Locus_type		CDS		
2558671159	DRAFT_01827	Product_name		hypothetical protein		
2558671159	DRAFT_01827	Scaffold		DRAFT_contig_70_2034_len_5512_read_count_100863.70		
2558671159	DRAFT_01827	Coordinates		888..1232(+)		
2558671159	DRAFT_01827	DNA_length		345bp		
2558671159	DRAFT_01827	Protein_length		114aa		
2558671159	DRAFT_01827	GC			0.58	
2558671160	DRAFT_01828	Locus_type		CDS		
2558671160	DRAFT_01828	Product_name		hypothetical protein		
2558671160	DRAFT_01828	Scaffold		DRAFT_contig_70_2034_len_5512_read_count_100863.70		
2558671160	DRAFT_01828	Coordinates		1150..1434(-)		
2558671160	DRAFT_01828	DNA_length		285bp		
2558671160	DRAFT_01828	Protein_length		94aa		
2558671160	DRAFT_01828	GC			0.57	
2558671160	DRAFT_01828	Transmembrane		Yes		
2558671161	DRAFT_01829	pfam00782	DSPc			7.70E-15
2558671161	DRAFT_01829	Locus_type		CDS		
2558671161	DRAFT_01829	Product_name		Predicted protein-tyrosine phosphatase		
2558671161	DRAFT_01829	Scaffold		DRAFT_contig_70_2034_len_5512_read_count_100863.70		

2558671161	DRAFT_01829	Coordinates		1447..1851(-)		
2558671161	DRAFT_01829	DNA_length		405bp		
2558671161	DRAFT_01829	Protein_length		134aa		
2558671161	DRAFT_01829	GC			0.52	
2558671162	DRAFT_01830	pfam13527	Acetyltransf_9			1.80E-16
2558671162	DRAFT_01830	Locus_type		CDS		
2558671162	DRAFT_01830	Product_name		Predicted acetyltransferase involved in intracellular survival and relat		
2558671162	DRAFT_01830	Scaffold		DRAFT_contig_70_2034_len_5512_read_count_100863.70		
2558671162	DRAFT_01830	Coordinates		2011..2949(-)		
2558671162	DRAFT_01830	DNA_length		939bp		
2558671162	DRAFT_01830	Protein_length		312aa		
2558671162	DRAFT_01830	GC			0.51	
2558671163	DRAFT_01831	pfam12847	Methyltransf_18			2.30E-13
2558671163	DRAFT_01831	Locus_type		CDS		
2558671163	DRAFT_01831	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2558671163	DRAFT_01831	Scaffold		DRAFT_contig_70_2034_len_5512_read_count_100863.70		
2558671163	DRAFT_01831	Coordinates		3133..3951(-)		
2558671163	DRAFT_01831	DNA_length		819bp		
2558671163	DRAFT_01831	Protein_length		272aa		
2558671163	DRAFT_01831	GC			0.5	
2558671164	DRAFT_01832	Locus_type		CDS		
2558671164	DRAFT_01832	Product_name		hypothetical protein		
2558671164	DRAFT_01832	Scaffold		DRAFT_contig_70_2034_len_5512_read_count_100863.70		
2558671164	DRAFT_01832	Coordinates		4230..5279(+)		
2558671164	DRAFT_01832	DNA_length		1050bp		
2558671164	DRAFT_01832	Protein_length		349aa		
2558671164	DRAFT_01832	GC			0.53	
2558671165	DRAFT_01833	Locus_type		tRNA		
2558671165	DRAFT_01833	Product_name		tRNA_Leu_CAG		
2558671165	DRAFT_01833	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71		

2558671165	DRAFT_01833	Coordinates		17..101(+)		
2558671165	DRAFT_01833	DNA_length		85bp		
2558671165	DRAFT_01833	GC			0.72	
2558671166	DRAFT_01834	KEGG_module	M00248: Putative antibiotic transport system			
2558671166	DRAFT_01834	COG_category	[V] Defense mechanisms			
2558671166	DRAFT_01834	COG1131	ABC-type multidrug transport system, ATPase component			6.00E-57
2558671166	DRAFT_01834	pfam00005	ABC_tran			1.60E-25
2558671166	DRAFT_01834	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2558671166	DRAFT_01834	Locus_type		CDS		
2558671166	DRAFT_01834	Product_name		ABC-type multidrug transport system, ATPase component		
2558671166	DRAFT_01834	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71		
2558671166	DRAFT_01834	Coordinates		306..1259(+)		
2558671166	DRAFT_01834	DNA_length		954bp		
2558671166	DRAFT_01834	Protein_length		317aa		
2558671166	DRAFT_01834	GC			0.58	
2558671167	DRAFT_01835	KEGG_module	M00248: Putative antibiotic transport system			
2558671167	DRAFT_01835	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2558671167	DRAFT_01835	COG_category	[G] Carbohydrate transport and metabolism			
2558671167	DRAFT_01835	COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease			2.00E-06
2558671167	DRAFT_01835	pfam01061	ABC2_membrane			7.60E-08
2558671167	DRAFT_01835	KO:K09686	antibiotic transport system permease protein			1.10E-10
2558671167	DRAFT_01835	Locus_type		CDS		
2558671167	DRAFT_01835	Product_name		ABC-type polysaccharide/polyol phosphate export systems, permease		
2558671167	DRAFT_01835	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71		
2558671167	DRAFT_01835	Coordinates		1252..2013(+)		
2558671167	DRAFT_01835	DNA_length		762bp		
2558671167	DRAFT_01835	Protein_length		253aa		
2558671167	DRAFT_01835	GC			0.54	
2558671167	DRAFT_01835	Transmembrane		Yes		
2558671168	DRAFT_01836	pfam01061	ABC2_membrane			3.90E-06
2558671168	DRAFT_01836	Locus_type		CDS		

2558671168	DRAFT_01836	Product_name		ABC-type polysaccharide/polyol phosphate export systems, permease	
2558671168	DRAFT_01836	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71	
2558671168	DRAFT_01836	Coordinates		2010..2801(+)	
2558671168	DRAFT_01836	DNA_length		792bp	
2558671168	DRAFT_01836	Protein_length		263aa	
2558671168	DRAFT_01836	GC			0.56
2558671168	DRAFT_01836	Transmembrane		Yes	
2558671169	DRAFT_01837	Locus_type		CDS	
2558671169	DRAFT_01837	Product_name		hypothetical protein	
2558671169	DRAFT_01837	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71	
2558671169	DRAFT_01837	Coordinates		2820..3194(-)	
2558671169	DRAFT_01837	DNA_length		375bp	
2558671169	DRAFT_01837	Protein_length		124aa	
2558671169	DRAFT_01837	GC			0.58
2558671170	DRAFT_01838	Locus_type		CDS	
2558671170	DRAFT_01838	Product_name		hypothetical protein	
2558671170	DRAFT_01838	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71	
2558671170	DRAFT_01838	Coordinates		3326..3592(+)	
2558671170	DRAFT_01838	DNA_length		267bp	
2558671170	DRAFT_01838	Protein_length		88aa	
2558671170	DRAFT_01838	GC			0.54
2558671171	DRAFT_01839	Locus_type		CDS	
2558671171	DRAFT_01839	Product_name		hypothetical protein	
2558671171	DRAFT_01839	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71	
2558671171	DRAFT_01839	Coordinates		3595..4020(-)	
2558671171	DRAFT_01839	DNA_length		426bp	
2558671171	DRAFT_01839	Protein_length		141aa	
2558671171	DRAFT_01839	GC			0.54
2558671172	DRAFT_01840	COG_category	[S] Function unknown		
2558671172	DRAFT_01840	COG1698	Uncharacterized protein conserved in archaea		7.00E-17

2558671172	DRAFT_01840	pfam03685	UPF0147		2.40E-29
2558671172	DRAFT_01840	Locus_type		CDS	
2558671172	DRAFT_01840	Product_name		Uncharacterized protein conserved in archaea	
2558671172	DRAFT_01840	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71	
2558671172	DRAFT_01840	Coordinates		4055..4435(-)	
2558671172	DRAFT_01840	DNA_length		381bp	
2558671172	DRAFT_01840	Protein_length		126aa	
2558671172	DRAFT_01840	GC		0.53	
2558671173	DRAFT_01841	COG_category	[R] General function prediction only		
2558671173	DRAFT_01841	COG1645	Uncharacterized Zn-finger containing protein		1.00E-06
2558671173	DRAFT_01841	pfam06677	Auto_anti-p27		3.70E-09
2558671173	DRAFT_01841	Locus_type		CDS	
2558671173	DRAFT_01841	Product_name		Uncharacterized Zn-finger containing protein	
2558671173	DRAFT_01841	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71	
2558671173	DRAFT_01841	Coordinates		4537..4884(+)	
2558671173	DRAFT_01841	DNA_length		348bp	
2558671173	DRAFT_01841	Protein_length		115aa	
2558671173	DRAFT_01841	GC		0.53	
2558671174	DRAFT_01842	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558671174	DRAFT_01842	COG1225	Peroxiredoxin		2.00E-36
2558671174	DRAFT_01842	pfam00578	AhpC-TSA		3.00E-34
2558671174	DRAFT_01842	Locus_type		CDS	
2558671174	DRAFT_01842	Product_name		Peroxiredoxin	
2558671174	DRAFT_01842	Scaffold		DRAFT_contig_70_2125_len_5392_read_count_101811.71	
2558671174	DRAFT_01842	Coordinates		4911..5390(+)	
2558671174	DRAFT_01842	DNA_length		480bp	
2558671174	DRAFT_01842	Protein_length		159aa	
2558671174	DRAFT_01842	GC		0.55	
2558671175	DRAFT_01843	pfam12846	AAA_10		1.20E-06
2558671175	DRAFT_01843	Locus_type		CDS	
2558671175	DRAFT_01843	Product_name		Predicted ATPase	

2558671175	DRAFT_01843	Scaffold		DRAFT_contig_70_2284_len_5201_read_count_82056.72	
2558671175	DRAFT_01843	Coordinates		3..428(+)	
2558671175	DRAFT_01843	DNA_length		426bp	
2558671175	DRAFT_01843	Protein_length		141aa	
2558671175	DRAFT_01843	GC		0.51	

2558671176	DRAFT_01844	Locus_type		CDS	
2558671176	DRAFT_01844	Product_name		hypothetical protein	
2558671176	DRAFT_01844	Scaffold		DRAFT_contig_70_2284_len_5201_read_count_82056.72	
2558671176	DRAFT_01844	Coordinates		539..724(-)	
2558671176	DRAFT_01844	DNA_length		186bp	
2558671176	DRAFT_01844	Protein_length		61aa	
2558671176	DRAFT_01844	GC		0.56	

2558671177	DRAFT_01845	COG_category	[E] Amino acid transport and metabolism		
2558671177	DRAFT_01845	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases		3.00E-63
2558671177	DRAFT_01845	pfam07676	PD40		1.40E-06
2558671177	DRAFT_01845	pfam00326	Peptidase_S9		1.90E-46
2558671177	DRAFT_01845	Locus_type		CDS	
2558671177	DRAFT_01845	Product_name		Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	
2558671177	DRAFT_01845	Scaffold		DRAFT_contig_70_2284_len_5201_read_count_82056.72	
2558671177	DRAFT_01845	Coordinates		742..2739(+)	
2558671177	DRAFT_01845	DNA_length		1998bp	
2558671177	DRAFT_01845	Protein_length		665aa	
2558671177	DRAFT_01845	GC		0.61	

2558671178	DRAFT_01846	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558671178	DRAFT_01846	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins		2.00E-19
2558671178	DRAFT_01846	pfam13302	Acetyltransf_3		3.10E-24
2558671178	DRAFT_01846	Locus_type		CDS	
2558671178	DRAFT_01846	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins	
2558671178	DRAFT_01846	Scaffold		DRAFT_contig_70_2284_len_5201_read_count_82056.72	
2558671178	DRAFT_01846	Coordinates		2755..3294(-)	
2558671178	DRAFT_01846	DNA_length		540bp	

2558671178	DRAFT_01846	Protein_length		179aa	
2558671178	DRAFT_01846	GC		0.52	
2558671179	DRAFT_01847	COG_category	[E] Amino acid transport and metabolism		
2558671179	DRAFT_01847	COG0346	Lactoylglutathione lyase and related lyases		1.00E-03
2558671179	DRAFT_01847	pfam12681	Glyoxalase_2		3.70E-14
2558671179	DRAFT_01847	Locus_type		CDS	
2558671179	DRAFT_01847	Product_name		Lactoylglutathione lyase and related lyases	
2558671179	DRAFT_01847	Scaffold		DRAFT_contig_70_2284_len_5201_read_count_82056.72	
2558671179	DRAFT_01847	Coordinates		3450..3794(+)	
2558671179	DRAFT_01847	DNA_length		345bp	
2558671179	DRAFT_01847	Protein_length		114aa	
2558671179	DRAFT_01847	GC		0.5	
2558671180	DRAFT_01848	Locus_type		CDS	
2558671180	DRAFT_01848	Product_name		hypothetical protein	
2558671180	DRAFT_01848	Scaffold		DRAFT_contig_70_2284_len_5201_read_count_82056.72	
2558671180	DRAFT_01848	Coordinates		4037..4894(+)	
2558671180	DRAFT_01848	DNA_length		858bp	
2558671180	DRAFT_01848	Protein_length		285aa	
2558671180	DRAFT_01848	GC		0.6	
2558671181	DRAFT_01849	Locus_type		CDS	
2558671181	DRAFT_01849	Product_name		hypothetical protein	
2558671181	DRAFT_01849	Scaffold		DRAFT_contig_70_2284_len_5201_read_count_82056.72	
2558671181	DRAFT_01849	Coordinates		4954..5199(-)	
2558671181	DRAFT_01849	DNA_length		246bp	
2558671181	DRAFT_01849	Protein_length		81aa	
2558671181	DRAFT_01849	GC		0.57	
2558671182	DRAFT_01850	COG_category	[L] Replication, recombination and repair		
2558671182	DRAFT_01850	COG1041	Predicted DNA modification methylase		4.00E-35
2558671182	DRAFT_01850	pfam01170	UPF0020		5.10E-24
2558671182	DRAFT_01850	EC:2.1.1.213	tRNA (guanine(10)-N(2))-dimethyltransferase.		

2558671182	DRAFT_01850	TIGR01177	TIGR01177 family protein		4.40E-57
2558671182	DRAFT_01850	KO:K07446	tRNA (guanine10-N2)-dimethyltransferase [EC:2.1.1.213]		3.00E-29
2558671182	DRAFT_01850	ITERM:05594	N2-methylguanosine tRNA methyltransferase (EC 2.1.1.213)		
2558671182	DRAFT_01850	Locus_type		CDS	
2558671182	DRAFT_01850	Product_name		N2-methylguanosine tRNA methyltransferase (EC 2.1.1.213)	
2558671182	DRAFT_01850	Scaffold		DRAFT_contig_70_2438_len_5030_read_count_74374.73	
2558671182	DRAFT_01850	Coordinates		2..949(-)	
2558671182	DRAFT_01850	DNA_length		948bp	
2558671182	DRAFT_01850	Protein_length		316aa	
2558671182	DRAFT_01850	GC		0.6	
2558671183	DRAFT_01851	KEGG_module	M00005: PRPP biosynthesis, ribose 5P => PRPP		
2558671183	DRAFT_01851	Metacyc	PWY0-662: PRPP biosynthesis I		
2558671183	DRAFT_01851	COG_category	[F] Nucleotide transport and metabolism		
2558671183	DRAFT_01851	COG_category	[E] Amino acid transport and metabolism		
2558671183	DRAFT_01851	COG0462	Phosphoribosylpyrophosphate synthetase		4.00E-74
2558671183	DRAFT_01851	pfam13793	Pribosyltran_N		1.30E-24
2558671183	DRAFT_01851	pfam14572	Pribosyl_synth		5.00E-13
2558671183	DRAFT_01851	EC:2.7.6.1	Ribose-phosphate diphosphokinase.		
2558671183	DRAFT_01851	TIGR01251	ribose-phosphate pyrophosphokinase		1.50E-88
2558671183	DRAFT_01851	KO:K00948	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]		0.00E+00
2558671183	DRAFT_01851	Locus_type		CDS	
2558671183	DRAFT_01851	Product_name		Phosphoribosylpyrophosphate synthetase	
2558671183	DRAFT_01851	Scaffold		DRAFT_contig_70_2438_len_5030_read_count_74374.73	
2558671183	DRAFT_01851	Coordinates		942..1832(-)	
2558671183	DRAFT_01851	DNA_length		891bp	
2558671183	DRAFT_01851	Protein_length		296aa	
2558671183	DRAFT_01851	GC		0.59	
2558671184	DRAFT_01852	Locus_type		CDS	
2558671184	DRAFT_01852	Product_name		hypothetical protein	
2558671184	DRAFT_01852	Scaffold		DRAFT_contig_70_2438_len_5030_read_count_74374.73	
2558671184	DRAFT_01852	Coordinates		1947..2165(+)	
2558671184	DRAFT_01852	DNA_length		219bp	

2558671184	DRAFT_01852	Protein_length		72aa	
2558671184	DRAFT_01852	GC		0.53	
2558671185	DRAFT_01853	COG_category	[F] Nucleotide transport and metabolism		
2558671185	DRAFT_01853	COG1051	ADP-ribose pyrophosphatase		5.00E-18
2558671185	DRAFT_01853	pfam00293	NUDIX		4.00E-22
2558671185	DRAFT_01853	Locus_type		CDS	
2558671185	DRAFT_01853	Product_name		ADP-ribose pyrophosphatase	
2558671185	DRAFT_01853	Scaffold		DRAFT_contig_70_2438_len_5030_read_count_74374.73	
2558671185	DRAFT_01853	Coordinates		2200..2667(-)	
2558671185	DRAFT_01853	DNA_length		468bp	
2558671185	DRAFT_01853	Protein_length		155aa	
2558671185	DRAFT_01853	GC		0.62	
2558671186	DRAFT_01854	COG_category	[G] Carbohydrate transport and metabolism		
2558671186	DRAFT_01854	COG2814	Arabinose efflux permease		9.00E-05
2558671186	DRAFT_01854	pfam05977	MFS_3		3.70E-19
2558671186	DRAFT_01854	Locus_type		CDS	
2558671186	DRAFT_01854	Product_name		Arabinose efflux permease	
2558671186	DRAFT_01854	Scaffold		DRAFT_contig_70_2438_len_5030_read_count_74374.73	
2558671186	DRAFT_01854	Coordinates		2973..4256(-)	
2558671186	DRAFT_01854	DNA_length		1284bp	
2558671186	DRAFT_01854	Protein_length		427aa	
2558671186	DRAFT_01854	GC		0.56	
2558671186	DRAFT_01854	Transmembrane		Yes	
2558671187	DRAFT_01855	TIGR02276	40-residue YVTN family beta-propeller repeat		3.00E-17
2558671187	DRAFT_01855	Locus_type		CDS	
2558671187	DRAFT_01855	Product_name		40-residue YVTN family beta-propeller repeat	
2558671187	DRAFT_01855	Scaffold		DRAFT_contig_70_2438_len_5030_read_count_74374.73	
2558671187	DRAFT_01855	Coordinates		4586..5029(+)	
2558671187	DRAFT_01855	DNA_length		444bp	
2558671187	DRAFT_01855	Protein_length		148aa	
2558671187	DRAFT_01855	GC		0.57	

2558671187	DRAFT_01855	Transmembrane		Yes	

2558671188	DRAFT_01856	Locus_type		CDS	
2558671188	DRAFT_01856	Product_name		hypothetical protein	
2558671188	DRAFT_01856	Scaffold		DRAFT_contig_70_2485_len_4972_read_count_79074.74	
2558671188	DRAFT_01856	Coordinates		3..989(-)	
2558671188	DRAFT_01856	DNA_length		987bp	
2558671188	DRAFT_01856	Protein_length		329aa	
2558671188	DRAFT_01856	GC		0.56	

2558671189	DRAFT_01857	Locus_type		CDS	
2558671189	DRAFT_01857	Product_name		hypothetical protein	
2558671189	DRAFT_01857	Scaffold		DRAFT_contig_70_2485_len_4972_read_count_79074.74	
2558671189	DRAFT_01857	Coordinates		1372..2709(-)	
2558671189	DRAFT_01857	DNA_length		1338bp	
2558671189	DRAFT_01857	Protein_length		445aa	
2558671189	DRAFT_01857	GC		0.6	
2558671189	DRAFT_01857	Transmembrane		Yes	

2558671190	DRAFT_01858	KEGG_module	M00254: ABC-2 type transport system		
2558671190	DRAFT_01858	COG_category	[V] Defense mechanisms		
2558671190	DRAFT_01858	COG1131	ABC-type multidrug transport system, ATPase component		2.00E-52
2558671190	DRAFT_01858	pfam00005	ABC_tran		4.30E-27
2558671190	DRAFT_01858	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2558671190	DRAFT_01858	Locus_type		CDS	
2558671190	DRAFT_01858	Product_name		ABC-type multidrug transport system, ATPase component	
2558671190	DRAFT_01858	Scaffold		DRAFT_contig_70_2485_len_4972_read_count_79074.74	
2558671190	DRAFT_01858	Coordinates		2771..3583(-)	
2558671190	DRAFT_01858	DNA_length		813bp	
2558671190	DRAFT_01858	Protein_length		270aa	
2558671190	DRAFT_01858	GC		0.58	

2558671191	DRAFT_01859	COG_category	[G] Carbohydrate transport and metabolism		
2558671191	DRAFT_01859	COG2211	Na+/melibiose symporter and related transporters		4.00E-08

2558671191	DRAFT_01859	pfam07690	MFS_1		6.20E-24
2558671191	DRAFT_01859	Locus_type		CDS	
2558671191	DRAFT_01859	Product_name		Major Facilitator Superfamily	
2558671191	DRAFT_01859	Scaffold		DRAFT_contig_70_2485_len_4972_read_count_79074.74	
2558671191	DRAFT_01859	Coordinates		3907..4971(+)	
2558671191	DRAFT_01859	DNA_length		1065bp	
2558671191	DRAFT_01859	Protein_length		355aa	
2558671191	DRAFT_01859	GC		0.58	
2558671191	DRAFT_01859	Transmembrane		Yes	
2558671192	DRAFT_01860	COG_category	[R] General function prediction only		
2558671192	DRAFT_01860	COG1234	Metal-dependent hydrolases of the beta-lactamase superfamily III		1.00E-73
2558671192	DRAFT_01860	pfam12706	Lactamase_B_2		2.70E-29
2558671192	DRAFT_01860	EC:3.1.26.11	Ribonuclease Z.		
2558671192	DRAFT_01860	TIGR02651	ribonuclease Z		2.20E-104
2558671192	DRAFT_01860	KO:K00784	ribonuclease Z [EC:3.1.26.11]		0.00E+00
2558671192	DRAFT_01860	Locus_type		CDS	
2558671192	DRAFT_01860	Product_name		ribonuclease Z	
2558671192	DRAFT_01860	Scaffold		DRAFT_contig_70_2628_len_4836_read_count_74891.75	
2558671192	DRAFT_01860	Coordinates		75..995(+)	
2558671192	DRAFT_01860	DNA_length		921bp	
2558671192	DRAFT_01860	Protein_length		306aa	
2558671192	DRAFT_01860	GC		0.6	
2558671192	DRAFT_01860	Fused_gene		Yes	
2558671193	DRAFT_01861	COG_category	[S] Function unknown		
2558671193	DRAFT_01861	COG1931	Uncharacterized protein conserved in archaea		6.00E-21
2558671193	DRAFT_01861	pfam01877	RNA_binding		1.70E-13
2558671193	DRAFT_01861	KO:K09736	hypothetical protein		6.50E-17
2558671193	DRAFT_01861	Locus_type		CDS	
2558671193	DRAFT_01861	Product_name		Uncharacterized protein conserved in archaea	
2558671193	DRAFT_01861	Scaffold		DRAFT_contig_70_2628_len_4836_read_count_74891.75	
2558671193	DRAFT_01861	Coordinates		980..1345(-)	
2558671193	DRAFT_01861	DNA_length		366bp	

2558671193	DRAFT_01861	Protein_length		121aa		
2558671193	DRAFT_01861	GC			0.56	
2558671194	DRAFT_01862	COG_category	[H] Coenzyme transport and metabolism			
2558671194	DRAFT_01862	COG0237	Dephospho-CoA kinase			6.00E-15
2558671194	DRAFT_01862	pfam13207	AAA_17			8.60E-13
2558671194	DRAFT_01862	Locus_type		CDS		
2558671194	DRAFT_01862	Product_name		Dephospho-CoA kinase		
2558671194	DRAFT_01862	Scaffold		DRAFT_contig_70_2628_len_4836_read_count_74891.75		
2558671194	DRAFT_01862	Coordinates		1377..1958(-)		
2558671194	DRAFT_01862	DNA_length		582bp		
2558671194	DRAFT_01862	Protein_length		193aa		
2558671194	DRAFT_01862	GC			0.61	
2558671195	DRAFT_01863	Metacyc	PWY-6689: tRNA splicing			
2558671195	DRAFT_01863	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558671195	DRAFT_01863	COG1514	2'-5' RNA ligase			1.00E-29
2558671195	DRAFT_01863	pfam02834	LigT_PEase			1.60E-05
2558671195	DRAFT_01863	pfam02834	LigT_PEase			6.90E-15
2558671195	DRAFT_01863	EC:6.5.1.-	Ligases. Forming phosphoric ester bonds. Ligases that form phosphoric-ester bonds.			
2558671195	DRAFT_01863	TIGR02258	2'-5' RNA ligase			7.10E-41
2558671195	DRAFT_01863	KO:K01975	2'-5' RNA ligase [EC:6.5.1.-]			3.30E-36
2558671195	DRAFT_01863	Locus_type		CDS		
2558671195	DRAFT_01863	Product_name		2'-5' RNA ligase		
2558671195	DRAFT_01863	Scaffold		DRAFT_contig_70_2628_len_4836_read_count_74891.75		
2558671195	DRAFT_01863	Coordinates		1995..2549(+)		
2558671195	DRAFT_01863	DNA_length		555bp		
2558671195	DRAFT_01863	Protein_length		184aa		
2558671195	DRAFT_01863	GC			0.58	
2558671196	DRAFT_01864	COG_category	[J] Translation, ribosomal structure and biogenesis			
2558671196	DRAFT_01864	COG1746	tRNA nucleotidyltransferase (CCA-adding enzyme)			4.00E-72
2558671196	DRAFT_01864	pfam09249	tRNA_NucTransf2			1.40E-26
2558671196	DRAFT_01864	pfam01909	NTP_transf_2			3.90E-08

2558671196	DRAFT_01864	EC:2.7.7.72	CCA tRNA nucleotidyltransferase.		
2558671196	DRAFT_01864	TIGR03671	CCA-adding enzyme		3.50E-93
2558671196	DRAFT_01864	KO:K07558	tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.72]		0.00E+00
2558671196	DRAFT_01864	Locus_type		CDS	
2558671196	DRAFT_01864	Product_name		CCA-adding enzyme	
2558671196	DRAFT_01864	Scaffold		DRAFT_contig_70_2628_len_4836_read_count_74891.75	
2558671196	DRAFT_01864	Coordinates		2546..3874(+)	
2558671196	DRAFT_01864	DNA_length		1329bp	
2558671196	DRAFT_01864	Protein_length		442aa	
2558671196	DRAFT_01864	GC		0.58	
2558671197	DRAFT_01865	COG_category	[T] Signal transduction mechanisms		
2558671197	DRAFT_01865	COG2112	Predicted Ser/Thr protein kinase		1.00E-29
2558671197	DRAFT_01865	KO:K07176	putative serine/threonine protein kinase		2.80E-45
2558671197	DRAFT_01865	Locus_type		CDS	
2558671197	DRAFT_01865	Product_name		Predicted Ser/Thr protein kinase	
2558671197	DRAFT_01865	Scaffold		DRAFT_contig_70_2628_len_4836_read_count_74891.75	
2558671197	DRAFT_01865	Coordinates		3879..4619(+)	
2558671197	DRAFT_01865	DNA_length		741bp	
2558671197	DRAFT_01865	Protein_length		246aa	
2558671197	DRAFT_01865	GC		0.56	
2558671198	DRAFT_01866	Locus_type		CDS	
2558671198	DRAFT_01866	Product_name		hypothetical protein	
2558671198	DRAFT_01866	Scaffold		DRAFT_contig_70_2628_len_4836_read_count_74891.75	
2558671198	DRAFT_01866	Coordinates		4647..4835(+)	
2558671198	DRAFT_01866	DNA_length		189bp	
2558671198	DRAFT_01866	Protein_length		63aa	
2558671198	DRAFT_01866	GC		0.54	
2558671199	DRAFT_01867	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558671199	DRAFT_01867	COG3277	RNA-binding protein involved in rRNA processing		4.00E-06
2558671199	DRAFT_01867	KO:K07569	RNA-binding protein		2.40E-06
2558671199	DRAFT_01867	Locus_type		CDS	

2558671199	DRAFT_01867	Product_name		RNA-binding protein involved in rRNA processing	
2558671199	DRAFT_01867	Scaffold		DRAFT_contig_70_2774_len_4708_read_count_68402.76	
2558671199	DRAFT_01867	Coordinates		46..267(+)	
2558671199	DRAFT_01867	DNA_length		222bp	
2558671199	DRAFT_01867	Protein_length		73aa	
2558671199	DRAFT_01867	GC		0.63	
2558671200	DRAFT_01868	COG_category	[K] Transcription		
2558671200	DRAFT_01868	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatic		1.00E-57
2558671200	DRAFT_01868	pfam00382	TFIIB		6.30E-09
2558671200	DRAFT_01868	pfam00382	TFIIB		3.60E-17
2558671200	DRAFT_01868	pfam08271	TF_Zn_Ribbon		3.30E-08
2558671200	DRAFT_01868	KO:K03124	transcription initiation factor TFIIB		0.00E+00
2558671200	DRAFT_01868	Locus_type		CDS	
2558671200	DRAFT_01868	Product_name		Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiat	
2558671200	DRAFT_01868	Scaffold		DRAFT_contig_70_2774_len_4708_read_count_68402.76	
2558671200	DRAFT_01868	Coordinates		264..1220(+)	
2558671200	DRAFT_01868	DNA_length		957bp	
2558671200	DRAFT_01868	Protein_length		318aa	
2558671200	DRAFT_01868	GC		0.6	
2558671201	DRAFT_01869	Locus_type		CDS	
2558671201	DRAFT_01869	Product_name		hypothetical protein	
2558671201	DRAFT_01869	Scaffold		DRAFT_contig_70_2774_len_4708_read_count_68402.76	
2558671201	DRAFT_01869	Coordinates		1217..1750(+)	
2558671201	DRAFT_01869	DNA_length		534bp	
2558671201	DRAFT_01869	Protein_length		177aa	
2558671201	DRAFT_01869	GC		0.62	
2558671202	DRAFT_01870	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558671202	DRAFT_01870	COG0293	23S rRNA methylase		2.00E-47
2558671202	DRAFT_01870	pfam01728	FtsJ		1.60E-44
2558671202	DRAFT_01870	EC:2.1.1.166	23S rRNA (uridine(2552)-2'-O)-methyltransferase.		
2558671202	DRAFT_01870	TIGR00438	cell division protein FtsJ		1.60E-56

2558671202	DRAFT_01870	KO:K02427	23S rRNA (uridine2552-2'-O)-methyltransferase [EC:2.1.1.166]		1.10E-43
2558671202	DRAFT_01870	ITERM:06068	23S rRNA Um-2552 2'-O-methyltransferase (EC 2.1.1.166)		
2558671202	DRAFT_01870	Locus_type		CDS	
2558671202	DRAFT_01870	Product_name		23S rRNA Um-2552 2'-O-methyltransferase (EC 2.1.1.166)	
2558671202	DRAFT_01870	Scaffold		DRAFT_contig_70_2774_len_4708_read_count_68402.76	
2558671202	DRAFT_01870	Coordinates		1773..2408(+)	
2558671202	DRAFT_01870	DNA_length		636bp	
2558671202	DRAFT_01870	Protein_length		211aa	
2558671202	DRAFT_01870	GC		0.61	
2558671203	DRAFT_01871	Metacyc	PWY-6829: tRNA methylation (yeast)		
2558671203	DRAFT_01871	COG_category	[J] Translation, ribosomal structure and biogenesis		
2558671203	DRAFT_01871	COG1867	N2,N2-dimethylguanosine tRNA methyltransferase		2.00E-86
2558671203	DRAFT_01871	pfam02005	TRM		5.50E-80
2558671203	DRAFT_01871	EC:2.1.1.216	tRNA (guanine(26)-N(2))-dimethyltransferase.		
2558671203	DRAFT_01871	EC:2.1.1.215	tRNA (guanine(26)-N(2)/guanine(27)-N(2))-dimethyltransferase.		
2558671203	DRAFT_01871	TIGR00308	tRNA(guanine-26,N2-N2) methyltransferase		2.50E-76
2558671203	DRAFT_01871	KO:K00555	tRNA (guanine26-N2/guanine27-N2)-dimethyltransferase [EC:2.1.1.215		0.00E+00
2558671203	DRAFT_01871	Locus_type		CDS	
2558671203	DRAFT_01871	Product_name		N2,N2-dimethylguanosine tRNA methyltransferase	
2558671203	DRAFT_01871	Scaffold		DRAFT_contig_70_2774_len_4708_read_count_68402.76	
2558671203	DRAFT_01871	Coordinates		2425..3570(-)	
2558671203	DRAFT_01871	DNA_length		1146bp	
2558671203	DRAFT_01871	Protein_length		381aa	
2558671203	DRAFT_01871	GC		0.64	
2558671204	DRAFT_01872	Metacyc	PWY-7198: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis IV		
2558671204	DRAFT_01872	Metacyc	PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP		
2558671204	DRAFT_01872	Metacyc	PWY-7185: UTP and CTP dephosphorylation I		
2558671204	DRAFT_01872	Metacyc	PWY-6545: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis III		
2558671204	DRAFT_01872	Metacyc	PWY-7184: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis I		
2558671204	DRAFT_01872	COG_category	[F] Nucleotide transport and metabolism		
2558671204	DRAFT_01872	COG1618	Predicted nucleotide kinase		3.00E-35
2558671204	DRAFT_01872	pfam03266	NTPase_1		5.20E-48

2558671204	DRAFT_01872	EC:3.6.1.15	Nucleoside-triphosphatase.			
2558671204	DRAFT_01872	KO:K06928	nucleoside-triphosphatase THEP1 [EC:3.6.1.15]			6.40E-32
2558671204	DRAFT_01872	Locus_type		CDS		
2558671204	DRAFT_01872	Product_name		Predicted nucleotide kinase		
2558671204	DRAFT_01872	Scaffold		DRAFT_contig_70_2774_len_4708_read_count_68402.76		
2558671204	DRAFT_01872	Coordinates		3672..4223(+)		
2558671204	DRAFT_01872	DNA_length		552bp		
2558671204	DRAFT_01872	Protein_length		183aa		
2558671204	DRAFT_01872	GC			0.62	
2558671205	DRAFT_01873	IMG_pathway	437: Archaeal replication elongation			
2558671205	DRAFT_01873	IMG_pathway	46: Okazaki fragment processing			
2558671205	DRAFT_01873	pfam01351	RNase_HII			1.10E-26
2558671205	DRAFT_01873	TIGR00729	ribonuclease H, mammalian HI/archaeal HII subfamily			3.10E-38
2558671205	DRAFT_01873	ITERM:00110	RNase HII (EC 3.1.26.4)			
2558671205	DRAFT_01873	Locus_type		CDS		
2558671205	DRAFT_01873	Product_name		RNase HII (EC 3.1.26.4)		
2558671205	DRAFT_01873	Scaffold		DRAFT_contig_70_2774_len_4708_read_count_68402.76		
2558671205	DRAFT_01873	Coordinates		4250..4705(+)		
2558671205	DRAFT_01873	DNA_length		456bp		
2558671205	DRAFT_01873	Protein_length		152aa		
2558671205	DRAFT_01873	GC			0.62	
2558671206	DRAFT_01874	Locus_type		CDS		
2558671206	DRAFT_01874	Product_name		hypothetical protein		
2558671206	DRAFT_01874	Scaffold		DRAFT_contig_70_2934_len_4568_read_count_79327.77		
2558671206	DRAFT_01874	Coordinates		7..516(-)		
2558671206	DRAFT_01874	DNA_length		510bp		
2558671206	DRAFT_01874	Protein_length		169aa		
2558671206	DRAFT_01874	GC			0.57	
2558671207	DRAFT_01875	pfam12705	PDDEXK_1			2.10E-08
2558671207	DRAFT_01875	Locus_type		CDS		
2558671207	DRAFT_01875	Product_name		PD-(D/E)XK nuclease superfamily		

2558671207	DRAFT_01875	Scaffold		DRAFT_contig_70_2934_len_4568_read_count_79327.77		
2558671207	DRAFT_01875	Coordinates		789..1589(+)		
2558671207	DRAFT_01875	DNA_length		801bp		
2558671207	DRAFT_01875	Protein_length		266aa		
2558671207	DRAFT_01875	GC			0.6	
2558671208	DRAFT_01876	COG_category	[K] Transcription			
2558671208	DRAFT_01876	COG1309	Transcriptional regulator			3.00E-09
2558671208	DRAFT_01876	pfam13977	TetR_C_6			1.60E-06
2558671208	DRAFT_01876	pfam00440	TetR_N			2.30E-18
2558671208	DRAFT_01876	ITERM:02313	transcriptional regulator, TetR family			
2558671208	DRAFT_01876	Locus_type		CDS		
2558671208	DRAFT_01876	Product_name		transcriptional regulator, TetR family		
2558671208	DRAFT_01876	Scaffold		DRAFT_contig_70_2934_len_4568_read_count_79327.77		
2558671208	DRAFT_01876	Coordinates		1711..2280(-)		
2558671208	DRAFT_01876	DNA_length		570bp		
2558671208	DRAFT_01876	Protein_length		189aa		
2558671208	DRAFT_01876	GC			0.58	
2558671209	DRAFT_01877	Locus_type		CDS		
2558671209	DRAFT_01877	Product_name		hypothetical protein		
2558671209	DRAFT_01877	Scaffold		DRAFT_contig_70_2934_len_4568_read_count_79327.77		
2558671209	DRAFT_01877	Coordinates		2385..2681(+)		
2558671209	DRAFT_01877	DNA_length		297bp		
2558671209	DRAFT_01877	Protein_length		98aa		
2558671209	DRAFT_01877	GC			0.6	
2558671209	DRAFT_01877	Transmembrane		Yes		
2558671210	DRAFT_01878	COG_category	[G] Carbohydrate transport and metabolism			
2558671210	DRAFT_01878	COG2814	Arabinose efflux permease			4.00E-08
2558671210	DRAFT_01878	pfam07690	MFS_1			6.40E-19
2558671210	DRAFT_01878	Locus_type		CDS		
2558671210	DRAFT_01878	Product_name		Arabinose efflux permease		
2558671210	DRAFT_01878	Scaffold		DRAFT_contig_70_2934_len_4568_read_count_79327.77		

2558671210	DRAFT_01878	Coordinates	2688..3938(+)	
2558671210	DRAFT_01878	DNA_length	1251bp	
2558671210	DRAFT_01878	Protein_length	416aa	
2558671210	DRAFT_01878	GC		0.62
2558671210	DRAFT_01878	Transmembrane	Yes	
2558671211	DRAFT_01879	Locus_type	CDS	
2558671211	DRAFT_01879	Product_name	hypothetical protein	
2558671211	DRAFT_01879	Scaffold	DRAFT_contig_70_2934_len_4568_read_count_79327.77	
2558671211	DRAFT_01879	Coordinates	4126..4392(+)	
2558671211	DRAFT_01879	DNA_length	267bp	
2558671211	DRAFT_01879	Protein_length	88aa	
2558671211	DRAFT_01879	GC		0.52
2558671212	DRAFT_01880	Locus_type	CDS	
2558671212	DRAFT_01880	Product_name	hypothetical protein	
2558671212	DRAFT_01880	Scaffold	DRAFT_contig_70_3644_len_4074_read_count_68363.78	
2558671212	DRAFT_01880	Coordinates	1..285(+)	
2558671212	DRAFT_01880	DNA_length	285bp	
2558671212	DRAFT_01880	Protein_length	94aa	
2558671212	DRAFT_01880	GC		0.52
2558671213	DRAFT_01881	Locus_type	CDS	
2558671213	DRAFT_01881	Product_name	hypothetical protein	
2558671213	DRAFT_01881	Scaffold	DRAFT_contig_70_3644_len_4074_read_count_68363.78	
2558671213	DRAFT_01881	Coordinates	369..530(+)	
2558671213	DRAFT_01881	DNA_length	162bp	
2558671213	DRAFT_01881	Protein_length	53aa	
2558671213	DRAFT_01881	GC		0.44
2558671214	DRAFT_01882	Locus_type	CDS	
2558671214	DRAFT_01882	Product_name	hypothetical protein	
2558671214	DRAFT_01882	Scaffold	DRAFT_contig_70_3644_len_4074_read_count_68363.78	
2558671214	DRAFT_01882	Coordinates	499..696(-)	

2558671214	DRAFT_01882	DNA_length		198bp	
2558671214	DRAFT_01882	Protein_length		65aa	
2558671214	DRAFT_01882	GC		0.51	
2558671215	DRAFT_01883	COG_category	[C] Energy production and conversion		
2558671215	DRAFT_01883	COG1042	Acyl-CoA synthetase (NDP forming)		8.00E-129
2558671215	DRAFT_01883	pfam13380	CoA_binding_2		9.40E-23
2558671215	DRAFT_01883	pfam13549	ATP-grasp_5		1.00E-65
2558671215	DRAFT_01883	pfam00583	Acetyltransf_1		5.70E-08
2558671215	DRAFT_01883	pfam13607	Succ_CoA_lig		1.60E-50
2558671215	DRAFT_01883	TIGR02717	acetyl coenzyme A synthetase (ADP forming), alpha domain		0.00E+00
2558671215	DRAFT_01883	Locus_type		CDS	
2558671215	DRAFT_01883	Product_name		Acyl-CoA synthetase (NDP forming)	
2558671215	DRAFT_01883	Scaffold		DRAFT_contig_70_3644_len_4074_read_count_68363.78	
2558671215	DRAFT_01883	Coordinates		865..3420(+)	
2558671215	DRAFT_01883	DNA_length		2556bp	
2558671215	DRAFT_01883	Protein_length		851aa	
2558671215	DRAFT_01883	GC		0.57	
2558671215	DRAFT_01883	Fused_gene		Yes	
2558671216	DRAFT_01884	COG_category	[S] Function unknown		
2558671216	DRAFT_01884	COG0011	Uncharacterized conserved protein		5.00E-12
2558671216	DRAFT_01884	pfam01910	DUF77		1.50E-19
2558671216	DRAFT_01884	TIGR00106	uncharacterized protein, MTH1187 family		1.20E-22
2558671216	DRAFT_01884	Locus_type		CDS	
2558671216	DRAFT_01884	Product_name		Uncharacterized conserved protein	
2558671216	DRAFT_01884	Scaffold		DRAFT_contig_70_3644_len_4074_read_count_68363.78	
2558671216	DRAFT_01884	Coordinates		3647..3994(-)	
2558671216	DRAFT_01884	DNA_length		348bp	
2558671216	DRAFT_01884	Protein_length		115aa	
2558671216	DRAFT_01884	GC		0.49	
2558671217	DRAFT_01885	pfam00881	Nitroreductase		2.50E-07
2558671217	DRAFT_01885	Locus_type		CDS	

2558671217	DRAFT_01885	Product_name		Nitroreductase	
2558671217	DRAFT_01885	Scaffold		DRAFT_contig_70_4003_len_3871_read_count_63941.79	
2558671217	DRAFT_01885	Coordinates		1..231(-)	
2558671217	DRAFT_01885	DNA_length		231bp	
2558671217	DRAFT_01885	Protein_length		77aa	
2558671217	DRAFT_01885	GC		0.54	

2558671218	DRAFT_01886	COG_category	[G] Carbohydrate transport and metabolism		
2558671218	DRAFT_01886	COG2814	Arabinose efflux permease		1.00E-15
2558671218	DRAFT_01886	pfam07690	MFS_1		1.40E-26
2558671218	DRAFT_01886	Locus_type		CDS	
2558671218	DRAFT_01886	Product_name		Arabinose efflux permease	
2558671218	DRAFT_01886	Scaffold		DRAFT_contig_70_4003_len_3871_read_count_63941.79	
2558671218	DRAFT_01886	Coordinates		287..1474(-)	
2558671218	DRAFT_01886	DNA_length		1188bp	
2558671218	DRAFT_01886	Protein_length		395aa	
2558671218	DRAFT_01886	GC		0.59	
2558671218	DRAFT_01886	Transmembrane		Yes	

2558671219	DRAFT_01887	Locus_type		CDS	
2558671219	DRAFT_01887	Product_name		hypothetical protein	
2558671219	DRAFT_01887	Scaffold		DRAFT_contig_70_4003_len_3871_read_count_63941.79	
2558671219	DRAFT_01887	Coordinates		1599..1832(-)	
2558671219	DRAFT_01887	DNA_length		234bp	
2558671219	DRAFT_01887	Protein_length		77aa	
2558671219	DRAFT_01887	GC		0.54	

2558671220	DRAFT_01888	COG_category	[E] Amino acid transport and metabolism		
2558671220	DRAFT_01888	COG0531	Amino acid transporters		2.00E-35
2558671220	DRAFT_01888	pfam13520	AA_permease_2		5.70E-47
2558671220	DRAFT_01888	Locus_type		CDS	
2558671220	DRAFT_01888	Product_name		amino acid/polyamine/organocation transporter, APC superfamily (T	
2558671220	DRAFT_01888	Scaffold		DRAFT_contig_70_4003_len_3871_read_count_63941.79	
2558671220	DRAFT_01888	Coordinates		1922..3319(-)	

2558671220	DRAFT_01888	DNA_length		1398bp	
2558671220	DRAFT_01888	Protein_length		465aa	
2558671220	DRAFT_01888	GC			0.53
2558671220	DRAFT_01888	Transmembrane		Yes	

2558671221	DRAFT_01889	Locus_type		CDS	
2558671221	DRAFT_01889	Product_name		hypothetical protein	
2558671221	DRAFT_01889	Scaffold		DRAFT_contig_70_4003_len_3871_read_count_63941.79	
2558671221	DRAFT_01889	Coordinates		3510..3869(-)	
2558671221	DRAFT_01889	DNA_length		360bp	
2558671221	DRAFT_01889	Protein_length		119aa	
2558671221	DRAFT_01889	GC			0.52

2558671222	DRAFT_01890	Locus_type		CDS	
2558671222	DRAFT_01890	Product_name		hypothetical protein	
2558671222	DRAFT_01890	Scaffold		DRAFT_contig_70_4296_len_3706_read_count_61295.80	
2558671222	DRAFT_01890	Coordinates		3..611(-)	
2558671222	DRAFT_01890	DNA_length		609bp	
2558671222	DRAFT_01890	Protein_length		203aa	
2558671222	DRAFT_01890	GC			0.58
2558671222	DRAFT_01890	Transmembrane		Yes	

2558671223	DRAFT_01891	COG_category	[S] Function unknown		
2558671223	DRAFT_01891	COG1478	Uncharacterized conserved protein		3.00E-53
2558671223	DRAFT_01891	pfam01996	F420_ligase		2.20E-57
2558671223	DRAFT_01891	TIGR01916	F420-0:gamma-glutamyl ligase		2.80E-64
2558671223	DRAFT_01891	Locus_type		CDS	
2558671223	DRAFT_01891	Product_name		Uncharacterized conserved protein	
2558671223	DRAFT_01891	Scaffold		DRAFT_contig_70_4296_len_3706_read_count_61295.80	
2558671223	DRAFT_01891	Coordinates		763..1572(-)	
2558671223	DRAFT_01891	DNA_length		810bp	
2558671223	DRAFT_01891	Protein_length		269aa	
2558671223	DRAFT_01891	GC			0.58

2558671224	DRAFT_01892	COG_category	[R] General function prediction only		
2558671224	DRAFT_01892	COG1719	Predicted hydrocarbon binding protein (contains V4R domain)		2.00E-09
2558671224	DRAFT_01892	pfam02830	V4R		6.20E-12
2558671224	DRAFT_01892	Locus_type		CDS	
2558671224	DRAFT_01892	Product_name		Predicted hydrocarbon binding protein (contains V4R domain)	
2558671224	DRAFT_01892	Scaffold		DRAFT_contig_70_4296_len_3706_read_count_61295.80	
2558671224	DRAFT_01892	Coordinates		2468..3247(-)	
2558671224	DRAFT_01892	DNA_length		780bp	
2558671224	DRAFT_01892	Protein_length		259aa	
2558671224	DRAFT_01892	GC		0.58	

2558671225	DRAFT_01893	KEGG_module	M00244: Putative zinc/manganese transport system		
2558671225	DRAFT_01893	COG_category	[P] Inorganic ion transport and metabolism		
2558671225	DRAFT_01893	COG0803	ABC-type metal ion transport system, periplasmic component/surface		7.00E-30
2558671225	DRAFT_01893	pfam01297	TroA		3.00E-40
2558671225	DRAFT_01893	KO:K02077	zinc/manganese transport system substrate-binding protein		0.00E+00
2558671225	DRAFT_01893	Locus_type		CDS	
2558671225	DRAFT_01893	Product_name		ABC-type metal ion transport system, periplasmic component/surface	
2558671225	DRAFT_01893	Scaffold		DRAFT_contig_70_4344_len_3679_read_count_66053.81	
2558671225	DRAFT_01893	Coordinates		243..1202(+)	
2558671225	DRAFT_01893	DNA_length		960bp	
2558671225	DRAFT_01893	Protein_length		319aa	
2558671225	DRAFT_01893	GC		0.55	
2558671225	DRAFT_01893	Transmembrane		Yes	

2558671226	DRAFT_01894	KEGG_module	M00244: Putative zinc/manganese transport system		
2558671226	DRAFT_01894	COG_category	[P] Inorganic ion transport and metabolism		
2558671226	DRAFT_01894	COG1121	ABC-type Mn/Zn transport systems, ATPase component		2.00E-59
2558671226	DRAFT_01894	pfam00005	ABC_tran		9.30E-27
2558671226	DRAFT_01894	KO:K02074	zinc/manganese transport system ATP-binding protein		0.00E+00
2558671226	DRAFT_01894	Locus_type		CDS	
2558671226	DRAFT_01894	Product_name		ABC-type Mn/Zn transport systems, ATPase component	
2558671226	DRAFT_01894	Scaffold		DRAFT_contig_70_4344_len_3679_read_count_66053.81	
2558671226	DRAFT_01894	Coordinates		1209..1997(+)	

2558671226	DRAFT_01894	DNA_length		789bp		
2558671226	DRAFT_01894	Protein_length		262aa		
2558671226	DRAFT_01894	GC			0.59	
2558671227	DRAFT_01895	KEGG_module	M00244: Putative zinc/manganese transport system			
2558671227	DRAFT_01895	COG_category	[P] Inorganic ion transport and metabolism			
2558671227	DRAFT_01895	COG1108	ABC-type Mn2+/Zn2+ transport systems, permease components			3.00E-34
2558671227	DRAFT_01895	pfam00950	ABC-3			6.70E-49
2558671227	DRAFT_01895	KO:K02075	zinc/manganese transport system permease protein			0.00E+00
2558671227	DRAFT_01895	Locus_type		CDS		
2558671227	DRAFT_01895	Product_name		ABC-type Mn2+/Zn2+ transport systems, permease components		
2558671227	DRAFT_01895	Scaffold		DRAFT_contig_70_4344_len_3679_read_count_66053.81		
2558671227	DRAFT_01895	Coordinates		1994..2893(+)		
2558671227	DRAFT_01895	DNA_length		900bp		
2558671227	DRAFT_01895	Protein_length		299aa		
2558671227	DRAFT_01895	GC			0.56	
2558671227	DRAFT_01895	Transmembrane		Yes		
2558671228	DRAFT_01896	COG_category	[K] Transcription			
2558671228	DRAFT_01896	COG0864	Predicted transcriptional regulators containing the CopG/Arc/MetJ DN			5.00E-16
2558671228	DRAFT_01896	pfam08753	NikR_C			1.90E-08
2558671228	DRAFT_01896	KO:K07722	CopG family transcriptional regulator, nickel-responsive regulator			1.90E-27
2558671228	DRAFT_01896	Locus_type		CDS		
2558671228	DRAFT_01896	Product_name		Predicted transcriptional regulators containing the CopG/Arc/MetJ DN		
2558671228	DRAFT_01896	Scaffold		DRAFT_contig_70_4344_len_3679_read_count_66053.81		
2558671228	DRAFT_01896	Coordinates		3013..3396(+)		
2558671228	DRAFT_01896	DNA_length		384bp		
2558671228	DRAFT_01896	Protein_length		127aa		
2558671228	DRAFT_01896	GC			0.52	
2558671229	DRAFT_01897	pfam05048	NosD			2.20E-06
2558671229	DRAFT_01897	TIGR03804	parallel beta-helix repeat (two copies)			1.30E-07
2558671229	DRAFT_01897	Locus_type		CDS		
2558671229	DRAFT_01897	Product_name		Periplasmic copper-binding protein (NosD)		

2558671229	DRAFT_01897	Scaffold		DRAFT_contig_70_4376_len_3665_read_count_58296.82	
2558671229	DRAFT_01897	Coordinates		1..285(+)	
2558671229	DRAFT_01897	DNA_length		285bp	
2558671229	DRAFT_01897	Protein_length		94aa	
2558671229	DRAFT_01897	GC		0.56	

2558671230	DRAFT_01898	COG_category	[G] Carbohydrate transport and metabolism		
2558671230	DRAFT_01898	COG2814	Arabinose efflux permease		6.00E-08
2558671230	DRAFT_01898	pfam07690	MFS_1		1.90E-26
2558671230	DRAFT_01898	Locus_type		CDS	
2558671230	DRAFT_01898	Product_name		Arabinose efflux permease	
2558671230	DRAFT_01898	Scaffold		DRAFT_contig_70_4376_len_3665_read_count_58296.82	
2558671230	DRAFT_01898	Coordinates		482..1696(-)	
2558671230	DRAFT_01898	DNA_length		1215bp	
2558671230	DRAFT_01898	Protein_length		404aa	
2558671230	DRAFT_01898	GC		0.58	
2558671230	DRAFT_01898	Transmembrane		Yes	

2558671231	DRAFT_01899	Locus_type		CDS	
2558671231	DRAFT_01899	Product_name		hypothetical protein	
2558671231	DRAFT_01899	Scaffold		DRAFT_contig_70_4376_len_3665_read_count_58296.82	
2558671231	DRAFT_01899	Coordinates		1780..2118(-)	
2558671231	DRAFT_01899	DNA_length		339bp	
2558671231	DRAFT_01899	Protein_length		112aa	
2558671231	DRAFT_01899	GC		0.56	
2558671231	DRAFT_01899	Transmembrane		Yes	

2558671232	DRAFT_01900	Locus_type		CDS	
2558671232	DRAFT_01900	Product_name		hypothetical protein	
2558671232	DRAFT_01900	Scaffold		DRAFT_contig_70_4376_len_3665_read_count_58296.82	
2558671232	DRAFT_01900	Coordinates		2222..2767(-)	
2558671232	DRAFT_01900	DNA_length		546bp	
2558671232	DRAFT_01900	Protein_length		181aa	
2558671232	DRAFT_01900	GC		0.6	

2558671232	DRAFT_01900	Transmembrane		Yes		

2558671233	DRAFT_01901	Locus_type		CDS		
2558671233	DRAFT_01901	Product_name		hypothetical protein		
2558671233	DRAFT_01901	Scaffold		DRAFT_contig_70_4376_len_3665_read_count_58296.82		
2558671233	DRAFT_01901	Coordinates		3139..3663(+)		
2558671233	DRAFT_01901	DNA_length		525bp		
2558671233	DRAFT_01901	Protein_length		175aa		
2558671233	DRAFT_01901	GC			0.55	
2558671233	DRAFT_01901	Transmembrane		Yes		

2558671234	DRAFT_01902	pfam12697	Abhydrolase_6			1.00E-11
2558671234	DRAFT_01902	Locus_type		CDS		
2558671234	DRAFT_01902	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase super		
2558671234	DRAFT_01902	Scaffold		DRAFT_contig_70_4496_len_3618_read_count_57001.83		
2558671234	DRAFT_01902	Coordinates		1..360(+)		
2558671234	DRAFT_01902	DNA_length		360bp		
2558671234	DRAFT_01902	Protein_length		119aa		
2558671234	DRAFT_01902	GC			0.58	

2558671235	DRAFT_01903	pfam03029	ATP_bind_1			1.80E-41
2558671235	DRAFT_01903	Locus_type		CDS		
2558671235	DRAFT_01903	Product_name		Conserved hypothetical ATP binding protein		
2558671235	DRAFT_01903	Scaffold		DRAFT_contig_70_4496_len_3618_read_count_57001.83		
2558671235	DRAFT_01903	Coordinates		350..1000(-)		
2558671235	DRAFT_01903	DNA_length		651bp		
2558671235	DRAFT_01903	Protein_length		216aa		
2558671235	DRAFT_01903	GC			0.59	

2558671236	DRAFT_01904	COG_category	[R] General function prediction only			
2558671236	DRAFT_01904	COG1058	Predicted nucleotide-utilizing enzyme related to molybdopterin-biosyn			5.00E-56
2558671236	DRAFT_01904	pfam00994	MoCF_biosynth			1.60E-28
2558671236	DRAFT_01904	TIGR00177	molybdenum cofactor synthesis domain			2.00E-24
2558671236	DRAFT_01904	KO:K03742	competence/damage-inducible protein CinA			0.00E+00

2558671236	DRAFT_01904	Locus_type		CDS	
2558671236	DRAFT_01904	Product_name		Predicted nucleotide-utilizing enzyme related to molybdopterin-biosy	
2558671236	DRAFT_01904	Scaffold		DRAFT_contig_70_4496_len_3618_read_count_57001.83	
2558671236	DRAFT_01904	Coordinates		1115..1942(-)	
2558671236	DRAFT_01904	DNA_length		828bp	
2558671236	DRAFT_01904	Protein_length		275aa	
2558671236	DRAFT_01904	GC		0.56	
2558671237	DRAFT_01905	COG_category	[R] General function prediction only		
2558671237	DRAFT_01905	COG4880	Secreted protein containing C-terminal beta-propeller domain distantl		2.00E-43
2558671237	DRAFT_01905	pfam09826	Beta_propel		4.50E-93
2558671237	DRAFT_01905	Locus_type		CDS	
2558671237	DRAFT_01905	Product_name		Secreted protein containing C-terminal beta-propeller domain distant	
2558671237	DRAFT_01905	Scaffold		DRAFT_contig_70_4496_len_3618_read_count_57001.83	
2558671237	DRAFT_01905	Coordinates		2119..3615(+)	
2558671237	DRAFT_01905	DNA_length		1497bp	
2558671237	DRAFT_01905	Protein_length		499aa	
2558671237	DRAFT_01905	GC		0.59	
2558671237	DRAFT_01905	Transmembrane		Yes	
2558671238	DRAFT_01906	Locus_type		CDS	
2558671238	DRAFT_01906	Product_name		hypothetical protein	
2558671238	DRAFT_01906	Scaffold		DRAFT_contig_70_4712_len_3533_read_count_55690.84	
2558671238	DRAFT_01906	Coordinates		3..812(+)	
2558671238	DRAFT_01906	DNA_length		810bp	
2558671238	DRAFT_01906	Protein_length		269aa	
2558671238	DRAFT_01906	GC		0.56	
2558671239	DRAFT_01907	Locus_type		CDS	
2558671239	DRAFT_01907	Product_name		hypothetical protein	
2558671239	DRAFT_01907	Scaffold		DRAFT_contig_70_4712_len_3533_read_count_55690.84	
2558671239	DRAFT_01907	Coordinates		780..983(-)	
2558671239	DRAFT_01907	DNA_length		204bp	
2558671239	DRAFT_01907	Protein_length		67aa	

2558671239	DRAFT_01907	GC	0.55
2558671240	DRAFT_01908	Locus_type	CDS
2558671240	DRAFT_01908	Product_name	hypothetical protein
2558671240	DRAFT_01908	Scaffold	DRAFT_contig_70_4712_len_3533_read_count_55690.84
2558671240	DRAFT_01908	Coordinates	1458..2024(+)
2558671240	DRAFT_01908	DNA_length	567bp
2558671240	DRAFT_01908	Protein_length	188aa
2558671240	DRAFT_01908	GC	0.57
2558671240	DRAFT_01908	Transmembrane	Yes
2558671241	DRAFT_01909	Locus_type	CDS
2558671241	DRAFT_01909	Product_name	hypothetical protein
2558671241	DRAFT_01909	Scaffold	DRAFT_contig_70_4712_len_3533_read_count_55690.84
2558671241	DRAFT_01909	Coordinates	2259..2561(+)
2558671241	DRAFT_01909	DNA_length	303bp
2558671241	DRAFT_01909	Protein_length	100aa
2558671241	DRAFT_01909	GC	0.57
2558671242	DRAFT_01910	Locus_type	CDS
2558671242	DRAFT_01910	Product_name	hypothetical protein
2558671242	DRAFT_01910	Scaffold	DRAFT_contig_70_4712_len_3533_read_count_55690.84
2558671242	DRAFT_01910	Coordinates	2681..3532(-)
2558671242	DRAFT_01910	DNA_length	852bp
2558671242	DRAFT_01910	Protein_length	283aa
2558671242	DRAFT_01910	GC	0.58
2558671242	DRAFT_01910	Transmembrane	Yes
2558671243	DRAFT_01911	Locus_type	CDS
2558671243	DRAFT_01911	Product_name	hypothetical protein
2558671243	DRAFT_01911	Scaffold	DRAFT_contig_70_4738_len_3521_read_count_76659.85
2558671243	DRAFT_01911	Coordinates	1..219(+)
2558671243	DRAFT_01911	DNA_length	219bp
2558671243	DRAFT_01911	Protein_length	72aa

2558671243	DRAFT_01911	GC		0.58	
2558671244	DRAFT_01912	pfam13659	Methyltransf_26		2.10E-06
2558671244	DRAFT_01912	Locus_type		CDS	
2558671244	DRAFT_01912	Product_name		Methyltransferase domain	
2558671244	DRAFT_01912	Scaffold		DRAFT_contig_70_4738_len_3521_read_count_76659.85	
2558671244	DRAFT_01912	Coordinates		391..2721(-)	
2558671244	DRAFT_01912	DNA_length		2331bp	
2558671244	DRAFT_01912	Protein_length		776aa	
2558671244	DRAFT_01912	GC		0.51	
2558671244	DRAFT_01912	Transmembrane		Yes	
2558671245	DRAFT_01913	Locus_type		CDS	
2558671245	DRAFT_01913	Product_name		hypothetical protein	
2558671245	DRAFT_01913	Scaffold		DRAFT_contig_70_4738_len_3521_read_count_76659.85	
2558671245	DRAFT_01913	Coordinates		3391..3519(-)	
2558671245	DRAFT_01913	DNA_length		129bp	
2558671245	DRAFT_01913	Protein_length		42aa	
2558671245	DRAFT_01913	GC		0.55	
2558671246	DRAFT_01914	Locus_type		CDS	
2558671246	DRAFT_01914	Product_name		hypothetical protein	
2558671246	DRAFT_01914	Scaffold		DRAFT_contig_70_6074_len_3057_read_count_53839.86	
2558671246	DRAFT_01914	Coordinates		2..145(+)	
2558671246	DRAFT_01914	DNA_length		144bp	
2558671246	DRAFT_01914	Protein_length		47aa	
2558671246	DRAFT_01914	GC		0.53	
2558671247	DRAFT_01915	COG_category	[F] Nucleotide transport and metabolism		
2558671247	DRAFT_01915	COG2820	Uridine phosphorylase		8.00E-18
2558671247	DRAFT_01915	pfam01048	PNP_UDP_1		2.50E-34
2558671247	DRAFT_01915	Locus_type		CDS	
2558671247	DRAFT_01915	Product_name		Uridine phosphorylase	
2558671247	DRAFT_01915	Scaffold		DRAFT_contig_70_6074_len_3057_read_count_53839.86	

2558671247	DRAFT_01915	Coordinates		239..1009(-)	
2558671247	DRAFT_01915	DNA_length		771bp	
2558671247	DRAFT_01915	Protein_length		256aa	
2558671247	DRAFT_01915	GC		0.6	
2558671248	DRAFT_01916	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2558671248	DRAFT_01916	COG2039	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase		2.00E-53
2558671248	DRAFT_01916	pfam01470	Peptidase_C15		3.80E-51
2558671248	DRAFT_01916	EC:3.4.19.3	Pyroglutamyl-peptidase I.		
2558671248	DRAFT_01916	TIGR00504	pyroglutamyl-peptidase I		9.30E-55
2558671248	DRAFT_01916	KO:K01304	pyroglutamyl-peptidase [EC:3.4.19.3]		0.00E+00
2558671248	DRAFT_01916	Locus_type		CDS	
2558671248	DRAFT_01916	Product_name		Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidas	
2558671248	DRAFT_01916	Scaffold		DRAFT_contig_70_6074_len_3057_read_count_53839.86	
2558671248	DRAFT_01916	Coordinates		1199..1810(-)	
2558671248	DRAFT_01916	DNA_length		612bp	
2558671248	DRAFT_01916	Protein_length		203aa	
2558671248	DRAFT_01916	GC		0.57	
2558671249	DRAFT_01917	Locus_type		CDS	
2558671249	DRAFT_01917	Product_name		hypothetical protein	
2558671249	DRAFT_01917	Scaffold		DRAFT_contig_70_6074_len_3057_read_count_53839.86	
2558671249	DRAFT_01917	Coordinates		2009..3055(+)	
2558671249	DRAFT_01917	DNA_length		1047bp	
2558671249	DRAFT_01917	Protein_length		349aa	
2558671249	DRAFT_01917	GC		0.55	
2558671250	DRAFT_01918	pfam06197	DUF998		1.50E-08
2558671250	DRAFT_01918	Locus_type		CDS	
2558671250	DRAFT_01918	Product_name		Protein of unknown function (DUF998)	
2558671250	DRAFT_01918	Scaffold		DRAFT_contig_70_6295_len_2997_read_count_50553.87	
2558671250	DRAFT_01918	Coordinates		3..308(+)	
2558671250	DRAFT_01918	DNA_length		306bp	
2558671250	DRAFT_01918	Protein_length		101aa	

2558671250	DRAFT_01918	GC			0.55	
2558671250	DRAFT_01918	Transmembrane		Yes		
2558671251	DRAFT_01919	Metacyc	PWY-6556: pyrimidine ribonucleosides salvage II			
2558671251	DRAFT_01919	Metacyc	PWY0-1295: pyrimidine ribonucleosides degradation			
2558671251	DRAFT_01919	Metacyc	PWY-7181: pyrimidine deoxyribonucleosides degradation			
2558671251	DRAFT_01919	Metacyc	PWY-7199: pyrimidine deoxyribonucleosides salvage			
2558671251	DRAFT_01919	Metacyc	PWY-7193: pyrimidine ribonucleosides salvage I			
2558671251	DRAFT_01919	COG_category	[F] Nucleotide transport and metabolism			
2558671251	DRAFT_01919	COG0295	Cytidine deaminase			1.00E-13
2558671251	DRAFT_01919	EC:3.5.4.5	Cytidine deaminase.			
2558671251	DRAFT_01919	KO:K01489	cytidine deaminase [EC:3.5.4.5]			1.70E-08
2558671251	DRAFT_01919	Locus_type		CDS		
2558671251	DRAFT_01919	Product_name		Cytidine deaminase		
2558671251	DRAFT_01919	Scaffold		DRAFT_contig_70_6295_len_2997_read_count_50553.87		
2558671251	DRAFT_01919	Coordinates		493..915(+)		
2558671251	DRAFT_01919	DNA_length		423bp		
2558671251	DRAFT_01919	Protein_length		140aa		
2558671251	DRAFT_01919	GC			0.51	
2558671252	DRAFT_01920	COG_category	[R] General function prediction only			
2558671252	DRAFT_01920	COG1524	Uncharacterized proteins of the AP superfamily			2.00E-22
2558671252	DRAFT_01920	pfam01663	Phosphodiest			9.30E-21
2558671252	DRAFT_01920	Locus_type		CDS		
2558671252	DRAFT_01920	Product_name		Uncharacterized proteins of the AP superfamily		
2558671252	DRAFT_01920	Scaffold		DRAFT_contig_70_6295_len_2997_read_count_50553.87		
2558671252	DRAFT_01920	Coordinates		1061..2368(+)		
2558671252	DRAFT_01920	DNA_length		1308bp		
2558671252	DRAFT_01920	Protein_length		435aa		
2558671252	DRAFT_01920	GC			0.52	
2558671253	DRAFT_01921	COG_category	[C] Energy production and conversion			
2558671253	DRAFT_01921	COG0778	Nitroreductase			2.00E-08
2558671253	DRAFT_01921	pfam00881	Nitroreductase			5.60E-18

2558671253	DRAFT_01921	TIGR03605	SagB-type dehydrogenase domain			3.40E-33
2558671253	DRAFT_01921	Locus_type		CDS		
2558671253	DRAFT_01921	Product_name		SagB-type dehydrogenase domain		
2558671253	DRAFT_01921	Scaffold		DRAFT_contig_70_6295_len_2997_read_count_50553.87		
2558671253	DRAFT_01921	Coordinates		2542..2994(-)		
2558671253	DRAFT_01921	DNA_length		453bp		
2558671253	DRAFT_01921	Protein_length		150aa		
2558671253	DRAFT_01921	GC			0.56	
2558671254	DRAFT_01922	pfam03415	Peptidase_C11			2.70E-34
2558671254	DRAFT_01922	Locus_type		CDS		
2558671254	DRAFT_01922	Product_name		Clostripain family		
2558671254	DRAFT_01922	Scaffold		DRAFT_contig_70_6366_len_2981_read_count_48437.88		
2558671254	DRAFT_01922	Coordinates		3..2099(+)		
2558671254	DRAFT_01922	DNA_length		2097bp		
2558671254	DRAFT_01922	Protein_length		698aa		
2558671254	DRAFT_01922	GC			0.57	
2558671254	DRAFT_01922	Transmembrane		Yes		
2558671255	DRAFT_01923	Locus_type		CDS		
2558671255	DRAFT_01923	Product_name		hypothetical protein		
2558671255	DRAFT_01923	Scaffold		DRAFT_contig_70_6366_len_2981_read_count_48437.88		
2558671255	DRAFT_01923	Coordinates		2215..2484(+)		
2558671255	DRAFT_01923	DNA_length		270bp		
2558671255	DRAFT_01923	Protein_length		89aa		
2558671255	DRAFT_01923	GC			0.51	
2558671256	DRAFT_01924	Locus_type		CDS		
2558671256	DRAFT_01924	Product_name		hypothetical protein		
2558671256	DRAFT_01924	Scaffold		DRAFT_contig_70_6366_len_2981_read_count_48437.88		
2558671256	DRAFT_01924	Coordinates		2596..2979(+)		
2558671256	DRAFT_01924	DNA_length		384bp		
2558671256	DRAFT_01924	Protein_length		128aa		
2558671256	DRAFT_01924	GC			0.63	

2558671257	DRAFT_01925	pfam05048	NosD			6.00E-14
2558671257	DRAFT_01925	TIGR03804	parallel beta-helix repeat (two copies)			1.30E-18
2558671257	DRAFT_01925	Locus_type		CDS		
2558671257	DRAFT_01925	Product_name		parallel beta-helix repeat (two copies)		
2558671257	DRAFT_01925	Scaffold		DRAFT_contig_70_7259_len_2773_read_count_49723.89		
2558671257	DRAFT_01925	Coordinates		1..507(-)		
2558671257	DRAFT_01925	DNA_length		507bp		
2558671257	DRAFT_01925	Protein_length		169aa		
2558671257	DRAFT_01925	GC			0.55	
2558671257	DRAFT_01925	Transmembrane		Yes		
2558671258	DRAFT_01926	pfam05048	NosD			3.10E-20
2558671258	DRAFT_01926	pfam05048	NosD			4.60E-14
2558671258	DRAFT_01926	TIGR03804	parallel beta-helix repeat (two copies)			4.10E-08
2558671258	DRAFT_01926	Locus_type		CDS		
2558671258	DRAFT_01926	Product_name		Nitrous oxidase accessory protein		
2558671258	DRAFT_01926	Scaffold		DRAFT_contig_70_7259_len_2773_read_count_49723.89		
2558671258	DRAFT_01926	Coordinates		730..1926(+)		
2558671258	DRAFT_01926	DNA_length		1197bp		
2558671258	DRAFT_01926	Protein_length		398aa		
2558671258	DRAFT_01926	GC			0.54	
2558671258	DRAFT_01926	Transmembrane		Yes		
2558671259	DRAFT_01927	pfam13229	Beta_helix			6.20E-26
2558671259	DRAFT_01927	TIGR03804	parallel beta-helix repeat (two copies)			4.80E-12
2558671259	DRAFT_01927	Locus_type		CDS		
2558671259	DRAFT_01927	Product_name		Nitrous oxidase accessory protein		
2558671259	DRAFT_01927	Scaffold		DRAFT_contig_70_7259_len_2773_read_count_49723.89		
2558671259	DRAFT_01927	Coordinates		2095..2772(+)		
2558671259	DRAFT_01927	DNA_length		678bp		
2558671259	DRAFT_01927	Protein_length		226aa		
2558671259	DRAFT_01927	GC			0.54	
2558671259	DRAFT_01927	Signal_peptide		Yes		

2558671260	DRAFT_01928	Locus_type		CDS	
2558671260	DRAFT_01928	Product_name		hypothetical protein	
2558671260	DRAFT_01928	Scaffold		DRAFT_contig_70_8374_len_2565_read_count_45534.90	
2558671260	DRAFT_01928	Coordinates		73..333(-)	
2558671260	DRAFT_01928	DNA_length		261bp	
2558671260	DRAFT_01928	Protein_length		86aa	
2558671260	DRAFT_01928	GC		0.49	
2558671260	DRAFT_01928	Transmembrane		Yes	
2558671261	DRAFT_01929	COG_category	[L] Replication, recombination and repair		
2558671261	DRAFT_01929	COG3316	Transposase and inactivated derivatives		1.00E-12
2558671261	DRAFT_01929	pfam13610	DDE_Tnp_IS240		2.60E-22
2558671261	DRAFT_01929	pfam04434	SWIM		5.60E-05
2558671261	DRAFT_01929	Locus_type		CDS	
2558671261	DRAFT_01929	Product_name		Transposase and inactivated derivatives	
2558671261	DRAFT_01929	Scaffold		DRAFT_contig_70_8374_len_2565_read_count_45534.90	
2558671261	DRAFT_01929	Coordinates		330..1544(-)	
2558671261	DRAFT_01929	DNA_length		1215bp	
2558671261	DRAFT_01929	Protein_length		404aa	
2558671261	DRAFT_01929	GC		0.53	
2558671262	DRAFT_01930	Locus_type		CDS	
2558671262	DRAFT_01930	Product_name		hypothetical protein	
2558671262	DRAFT_01930	Scaffold		DRAFT_contig_70_8374_len_2565_read_count_45534.90	
2558671262	DRAFT_01930	Coordinates		1606..1758(+)	
2558671262	DRAFT_01930	DNA_length		153bp	
2558671262	DRAFT_01930	Protein_length		50aa	
2558671262	DRAFT_01930	GC		0.46	
2558671263	DRAFT_01931	Locus_type		CDS	
2558671263	DRAFT_01931	Product_name		hypothetical protein	
2558671263	DRAFT_01931	Scaffold		DRAFT_contig_70_8374_len_2565_read_count_45534.90	
2558671263	DRAFT_01931	Coordinates		1747..2187(-)	

2558671263	DRAFT_01931	DNA_length	441bp	
2558671263	DRAFT_01931	Protein_length	146aa	
2558671263	DRAFT_01931	GC		0.53