Supplementary information of genes annotated for the Bg1 genome

gene_oid	Locus Tag	Source	Cluster Information	Gene Information	E-value
2572231645	t3m_00001	pfam01458	UPF0051		1.70E-53
2572231645	t3m_00001	Locus_type		CDS	
2572231645	t3m_00001	Product_name		Uncharacterized protein family (UPF0051)	
2572231645	t3m_00001	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231645	t3m_00001	Coordinates		1..651(+)	
2572231645	t3m_00001	DNA_length		651bp	
2572231645	t3m_00001	Protein_length		216aa	
2572231645	t3m_00001	GC		0.66	
2572231646	t3m_00002	COG_category	[S] Function unknown		
2572231646	t3m_00002	COG2259	Predicted membrane protein		4.00E-03
2572231646	t3m_00002	pfam07681	DoxX		5.40E-07
2572231646	t3m_00002	Locus_type		CDS	
2572231646	t3m_00002	Product_name		Predicted membrane protein	
2572231646	t3m_00002	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231646	t3m_00002	Coordinates		874..1422(+)	
2572231646	t3m_00002	DNA_length		549bp	
2572231646	t3m_00002	Protein_length		182aa	
2572231646	t3m_00002	GC		0.64	
2572231646	t3m_00002	Transmembrane		Yes	
2572231647	t3m_00003	Locus_type		CDS	
2572231647	t3m_00003	Product_name		hypothetical protein	
2572231647	t3m_00003	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231647	t3m_00003	Coordinates		1486..1803(-)	
2572231647	t3m_00003	DNA_length		318bp	
2572231647	t3m_00003	Protein_length		105aa	
2572231647	t3m_00003	GC		0.67	
2572231648	t3m_00004	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2572231648	t3m_00004	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease		4.00E-48

2572231648	t3m_00004	pfam01458	UPF0051			4.60E-46
2572231648	t3m_00004	Locus_type		CDS		
2572231648	t3m_00004	Product_name		ABC-type transport system involved in Fe-S cluster assembly, permease		
2572231648	t3m_00004	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231648	t3m_00004	Coordinates		1851..3245(-)		
2572231648	t3m_00004	DNA_length		1395bp		
2572231648	t3m_00004	Protein_length		464aa		
2572231648	t3m_00004	GC			0.68	
2572231649	t3m_00005	COG_category	[C] Energy production and conversion			
2572231649	t3m_00005	COG0822	NifU homolog involved in Fe-S cluster formation			4.00E-26
2572231649	t3m_00005	pfam01592	NifU_N			5.30E-31
2572231649	t3m_00005	TIGR01994	SUF system FeS assembly protein, NifU family			1.30E-31
2572231649	t3m_00005	KO:K04488	nitrogen fixation protein NifU and related proteins			2.30E-27
2572231649	t3m_00005	Locus_type		CDS		
2572231649	t3m_00005	Product_name		SUF system FeS assembly protein, NifU family		
2572231649	t3m_00005	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231649	t3m_00005	Coordinates		3429..3818(+)		
2572231649	t3m_00005	DNA_length		390bp		
2572231649	t3m_00005	Protein_length		129aa		
2572231649	t3m_00005	GC			0.64	
2572231650	t3m_00006	pfam13237	Fer4_10			6.40E-08
2572231650	t3m_00006	Locus_type		CDS		
2572231650	t3m_00006	Product_name		4Fe-4S dicluster domain		
2572231650	t3m_00006	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231650	t3m_00006	Coordinates		3904..4104(+)		
2572231650	t3m_00006	DNA_length		201bp		
2572231650	t3m_00006	Protein_length		66aa		
2572231650	t3m_00006	GC			0.69	
2572231651	t3m_00007	COG_category	[C] Energy production and conversion			
2572231651	t3m_00007	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)			1.00E-26
2572231651	t3m_00007	pfam00248	Aldo_ket_red			1.50E-27

2572231651	t3m_00007	Locus_type		CDS		
2572231651	t3m_00007	Product_name		Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)		
2572231651	t3m_00007	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231651	t3m_00007	Coordinates		4328..5458(+)		
2572231651	t3m_00007	DNA_length		1131bp		
2572231651	t3m_00007	Protein_length		376aa		
2572231651	t3m_00007	GC			0.69	

2572231652	t3m_00008	COG_category	[L] Replication, recombination and repair			
2572231652	t3m_00008	COG0419	ATPase involved in DNA repair			1.00E-40
2572231652	t3m_00008	pfam02463	SMC_N			6.30E-17
2572231652	t3m_00008	Locus_type		CDS		
2572231652	t3m_00008	Product_name		ATPase involved in DNA repair		
2572231652	t3m_00008	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231652	t3m_00008	Coordinates		5493..8060(-)		
2572231652	t3m_00008	DNA_length		2568bp		
2572231652	t3m_00008	Protein_length		855aa		
2572231652	t3m_00008	GC			0.71	

2572231653	t3m_00009	COG_category	[L] Replication, recombination and repair			
2572231653	t3m_00009	COG0420	DNA repair exonuclease			6.00E-25
2572231653	t3m_00009	pfam12850	Metallophos_2			4.10E-11
2572231653	t3m_00009	Locus_type		CDS		
2572231653	t3m_00009	Product_name		DNA repair exonuclease		
2572231653	t3m_00009	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231653	t3m_00009	Coordinates		8070..9353(-)		
2572231653	t3m_00009	DNA_length		1284bp		
2572231653	t3m_00009	Protein_length		427aa		
2572231653	t3m_00009	GC			0.71	

2572231654	t3m_00010	Locus_type		CDS		
2572231654	t3m_00010	Product_name		hypothetical protein		
2572231654	t3m_00010	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231654	t3m_00010	Coordinates		9357..9665(-)		

2572231654	t3m_00010	DNA_length		309bp		
2572231654	t3m_00010	Protein_length		102aa		
2572231654	t3m_00010	GC			0.73	
2572231654	t3m_00010	Transmembrane		Yes		

2572231655	t3m_00011	Locus_type		CDS		
2572231655	t3m_00011	Product_name		hypothetical protein		
2572231655	t3m_00011	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231655	t3m_00011	Coordinates		9874..10233(+)		
2572231655	t3m_00011	DNA_length		360bp		
2572231655	t3m_00011	Protein_length		119aa		
2572231655	t3m_00011	GC			0.68	

2572231656	t3m_00012	COG_category	[C] Energy production and conversion			
2572231656	t3m_00012	COG3808	Inorganic pyrophosphatase			0.00E+00
2572231656	t3m_00012	pfam03030	H_PPase			0.00E+00
2572231656	t3m_00012	EC:3.6.1.1	Inorganic diphosphatase.			
2572231656	t3m_00012	TIGR01104	vacuolar-type H(+)-translocating pyrophosphatase			0.00E+00
2572231656	t3m_00012	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump [EC:3.6.1.1]			0.00E+00
2572231656	t3m_00012	Locus_type		CDS		
2572231656	t3m_00012	Product_name		vacuolar-type H(+)-translocating pyrophosphatase		
2572231656	t3m_00012	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231656	t3m_00012	Coordinates		10472..12598(-)		
2572231656	t3m_00012	DNA_length		2127bp		
2572231656	t3m_00012	Protein_length		708aa		
2572231656	t3m_00012	GC			0.67	
2572231656	t3m_00012	Transmembrane		Yes		

2572231657	t3m_00013	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572231657	t3m_00013	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572231657	t3m_00013	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572231657	t3m_00013	IMG_pathway	504: L-threonine ligation to tRNA(Thr)			
2572231657	t3m_00013	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231657	t3m_00013	COG0441	Threonyl-tRNA synthetase			0.00E+00

2572231657	t3m_00013	pfam07973	tRNA_SAD			3.60E-07
2572231657	t3m_00013	pfam03129	HGTP_anticodon			2.90E-16
2572231657	t3m_00013	pfam00587	tRNA-synt_2b			4.00E-39
2572231657	t3m_00013	EC:6.1.1.3	Threonine--tRNA ligase.			
2572231657	t3m_00013	TIGR00418	threonyl-tRNA synthetase			0.00E+00
2572231657	t3m_00013	KO:K01868	threonyl-tRNA synthetase [EC:6.1.1.3]			0.00E+00
2572231657	t3m_00013	ITERM:00389	threonyl-tRNA synthetase (EC 6.1.1.3)			
2572231657	t3m_00013	Locus_type		CDS		
2572231657	t3m_00013	Product_name		threonyl-tRNA synthetase (EC 6.1.1.3)		
2572231657	t3m_00013	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231657	t3m_00013	Coordinates		12935..14851(-)		
2572231657	t3m_00013	DNA_length		1917bp		
2572231657	t3m_00013	Protein_length		638aa		
2572231657	t3m_00013	GC			0.67	
2572231658	t3m_00014	Locus_type		CDS		
2572231658	t3m_00014	Product_name		hypothetical protein		
2572231658	t3m_00014	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231658	t3m_00014	Coordinates		15109..15342(+)		
2572231658	t3m_00014	DNA_length		234bp		
2572231658	t3m_00014	Protein_length		77aa		
2572231658	t3m_00014	GC			0.67	
2572231659	t3m_00015	Locus_type		CDS		
2572231659	t3m_00015	Product_name		hypothetical protein		
2572231659	t3m_00015	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231659	t3m_00015	Coordinates		15420..15701(-)		
2572231659	t3m_00015	DNA_length		282bp		
2572231659	t3m_00015	Protein_length		93aa		
2572231659	t3m_00015	GC			0.59	
2572231660	t3m_00016	COG_category	[R] General function prediction only			
2572231660	t3m_00016	COG3975	Predicted protease with the C-terminal PDZ domain			1.00E-106
2572231660	t3m_00016	pfam13180	PDZ_2			2.40E-07

2572231660	t3m_00016	pfam05299	Peptidase_M61			8.40E-36
2572231660	t3m_00016	Locus_type		CDS		
2572231660	t3m_00016	Product_name		Predicted protease with the C-terminal PDZ domain		
2572231660	t3m_00016	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231660	t3m_00016	Coordinates		15879..17654(-)		
2572231660	t3m_00016	DNA_length		1776bp		
2572231660	t3m_00016	Protein_length		591aa		
2572231660	t3m_00016	GC			0.64	

2572231661	t3m_00017	Locus_type		CDS		
2572231661	t3m_00017	Product_name		hypothetical protein		
2572231661	t3m_00017	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231661	t3m_00017	Coordinates		17665..17796(-)		
2572231661	t3m_00017	DNA_length		132bp		
2572231661	t3m_00017	Protein_length		43aa		
2572231661	t3m_00017	GC			0.72	

2572231662	t3m_00018	pfam00496	SBP_bac_5			5.50E-09
2572231662	t3m_00018	Locus_type		CDS		
2572231662	t3m_00018	Product_name		Bacterial extracellular solute-binding proteins, family 5 Middle		
2572231662	t3m_00018	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231662	t3m_00018	Coordinates		17814..20957(-)		
2572231662	t3m_00018	DNA_length		3144bp		
2572231662	t3m_00018	Protein_length		1047aa		
2572231662	t3m_00018	GC			0.64	
2572231662	t3m_00018	Transmembrane		Yes		

2572231663	t3m_00019	COG_category	[K] Transcription			
2572231663	t3m_00019	COG1522	Transcriptional regulators			9.00E-24
2572231663	t3m_00019	pfam13412	HTH_24			6.80E-12
2572231663	t3m_00019	pfam01037	AsnC_trans_reg			1.60E-14
2572231663	t3m_00019	ITERM:01884	transcriptional regulator, AsnC family			
2572231663	t3m_00019	Locus_type		CDS		
2572231663	t3m_00019	Product_name		transcriptional regulator, AsnC family		

2572231663	t3m_00019	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231663	t3m_00019	Coordinates		21187..21645(-)		
2572231663	t3m_00019	DNA_length		459bp		
2572231663	t3m_00019	Protein_length		152aa		
2572231663	t3m_00019	GC			0.59	
2572231664	t3m_00020	pfam00977	His_biosynth			1.90E-10
2572231664	t3m_00020	Locus_type		CDS		
2572231664	t3m_00020	Product_name		Histidine biosynthesis protein		
2572231664	t3m_00020	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231664	t3m_00020	Coordinates		22632..23240(-)		
2572231664	t3m_00020	DNA_length		609bp		
2572231664	t3m_00020	Protein_length		202aa		
2572231664	t3m_00020	GC			0.66	
2572231665	t3m_00021	Locus_type		CDS		
2572231665	t3m_00021	Product_name		hypothetical protein		
2572231665	t3m_00021	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231665	t3m_00021	Coordinates		23961..24650(-)		
2572231665	t3m_00021	DNA_length		690bp		
2572231665	t3m_00021	Protein_length		229aa		
2572231665	t3m_00021	GC			0.61	
2572231666	t3m_00022	KEGG_module	M00023: Tryptophan biosynthesis, chorismate => tryptophan			
2572231666	t3m_00022	COG_category	[R] General function prediction only			
2572231666	t3m_00022	COG1350	Predicted alternative tryptophan synthase beta-subunit (paralog of TrpI			0.00E+00
2572231666	t3m_00022	pfam00291	PALP			9.00E-44
2572231666	t3m_00022	EC:4.2.1.20	Tryptophan synthase.			
2572231666	t3m_00022	TIGR01415	pyridoxal-phosphate dependent TrpB-like enzyme			0.00E+00
2572231666	t3m_00022	KO:K06001	tryptophan synthase beta chain [EC:4.2.1.20]			0.00E+00
2572231666	t3m_00022	Locus_type		CDS		
2572231666	t3m_00022	Product_name		pyridoxal-phosphate dependent TrpB-like enzyme		
2572231666	t3m_00022	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231666	t3m_00022	Coordinates		24746..26056(+)		

2572231666	t3m_00022	DNA_length		1311bp		
2572231666	t3m_00022	Protein_length		436aa		
2572231666	t3m_00022	GC			0.64	
2572231667	t3m_00023	pfam07690	MFS_1			2.90E-10
2572231667	t3m_00023	Locus_type		CDS		
2572231667	t3m_00023	Product_name		Major Facilitator Superfamily		
2572231667	t3m_00023	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231667	t3m_00023	Coordinates		26216..27442(+)		
2572231667	t3m_00023	DNA_length		1227bp		
2572231667	t3m_00023	Protein_length		408aa		
2572231667	t3m_00023	GC			0.63	
2572231667	t3m_00023	Transmembrane		Yes		
2572231668	t3m_00024	KEGG_module	M00545: Trans-cinnamate degradation, trans-cinnamate => 2-oxopent-4-enoate + fumarate			
2572231668	t3m_00024	KEGG_module	M00547: Benzene/toluene degradation, benzene => catechol / toluene => 3-methylcatechol			
2572231668	t3m_00024	KEGG_module	M00539: Cumate degradation, p-cumate => 2-oxopent-4-enoate + 2-methylpropanoate			
2572231668	t3m_00024	KEGG_module	M00543: Biphenyl degradation, biphenyl => 2-oxopent-4-enoate + benzoate			
2572231668	t3m_00024	COG_category	[R] General function prediction only			
2572231668	t3m_00024	COG_category	[P] Inorganic ion transport and metabolism			
2572231668	t3m_00024	COG2146	Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxyge			1.00E-11
2572231668	t3m_00024	pfam00355	Rieske			9.40E-15
2572231668	t3m_00024	KO:K05710	dioxygenase ferredoxin subunit			1.60E-07
2572231668	t3m_00024	Locus_type		CDS		
2572231668	t3m_00024	Product_name		Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygen		
2572231668	t3m_00024	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231668	t3m_00024	Coordinates		27542..27943(-)		
2572231668	t3m_00024	DNA_length		402bp		
2572231668	t3m_00024	Protein_length		133aa		
2572231668	t3m_00024	GC			0.62	
2572231669	t3m_00025	COG_category	[G] Carbohydrate transport and metabolism			
2572231669	t3m_00025	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572231669	t3m_00025	COG0702	Predicted nucleoside-diphosphate-sugar epimerases			9.00E-17

2572231669	t3m_00025	pfam05368	NmrA			2.50E-33
2572231669	t3m_00025	Locus_type		CDS		
2572231669	t3m_00025	Product_name		Predicted nucleoside-diphosphate-sugar epimerases		
2572231669	t3m_00025	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231669	t3m_00025	Coordinates		28508..29296(+)		
2572231669	t3m_00025	DNA_length		789bp		
2572231669	t3m_00025	Protein_length		262aa		
2572231669	t3m_00025	GC			0.61	

2572231670	t3m_00026	Locus_type		CDS	
2572231670	t3m_00026	Product_name		hypothetical protein	
2572231670	t3m_00026	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231670	t3m_00026	Coordinates		29497..29811(-)	
2572231670	t3m_00026	DNA_length		315bp	
2572231670	t3m_00026	Protein_length		104aa	
2572231670	t3m_00026	GC			0.6

2572231671	t3m_00027	Locus_type		CDS	
2572231671	t3m_00027	Product_name		hypothetical protein	
2572231671	t3m_00027	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231671	t3m_00027	Coordinates		29964..30110(-)	
2572231671	t3m_00027	DNA_length		147bp	
2572231671	t3m_00027	Protein_length		48aa	
2572231671	t3m_00027	GC			0.5

2572231672	t3m_00028	Locus_type		CDS	
2572231672	t3m_00028	Product_name		hypothetical protein	
2572231672	t3m_00028	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231672	t3m_00028	Coordinates		30309..30434(-)	
2572231672	t3m_00028	DNA_length		126bp	
2572231672	t3m_00028	Protein_length		41aa	
2572231672	t3m_00028	GC			0.58

2572231673	t3m_00029	Locus_type		CDS

2572231673	t3m_00029	Product_name		hypothetical protein		
2572231673	t3m_00029	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231673	t3m_00029	Coordinates		30743..30937(-)		
2572231673	t3m_00029	DNA_length		195bp		
2572231673	t3m_00029	Protein_length		64aa		
2572231673	t3m_00029	GC			0.53	
2572231674	t3m_00030	Locus_type		CDS		
2572231674	t3m_00030	Product_name		hypothetical protein		
2572231674	t3m_00030	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231674	t3m_00030	Coordinates		30952..31317(+)		
2572231674	t3m_00030	DNA_length		366bp		
2572231674	t3m_00030	Protein_length		121aa		
2572231674	t3m_00030	GC			0.58	
2572231674	t3m_00030	Transmembrane		Yes		
2572231675	t3m_00031	Locus_type		CDS		
2572231675	t3m_00031	Product_name		hypothetical protein		
2572231675	t3m_00031	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231675	t3m_00031	Coordinates		31545..31940(-)		
2572231675	t3m_00031	DNA_length		396bp		
2572231675	t3m_00031	Protein_length		131aa		
2572231675	t3m_00031	GC			0.61	
2572231676	t3m_00032	pfam05317	Thermopsin			2.10E-51
2572231676	t3m_00032	EC:3.4.23.42	Thermopsin.			
2572231676	t3m_00032	KO:K01385	thermopsin [EC:3.4.23.42]			0.00E+00
2572231676	t3m_00032	Locus_type		CDS		
2572231676	t3m_00032	Product_name		Thermopsin		
2572231676	t3m_00032	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231676	t3m_00032	Coordinates		32379..34988(+)		
2572231676	t3m_00032	DNA_length		2610bp		
2572231676	t3m_00032	Protein_length		869aa		
2572231676	t3m_00032	GC			0.64	

2572231676	t3m_00032	Signal_peptide		Yes		
2572231676	t3m_00032	Transmembrane		Yes		

2572231677	t3m_00033	Locus_type		CDS		
2572231677	t3m_00033	Product_name		hypothetical protein		
2572231677	t3m_00033	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231677	t3m_00033	Coordinates		35167..35457(-)		
2572231677	t3m_00033	DNA_length		291bp		
2572231677	t3m_00033	Protein_length		96aa		
2572231677	t3m_00033	GC			0.64	

2572231678	t3m_00034	pfam00496	SBP_bac_5			2.10E-12
2572231678	t3m_00034	Locus_type		CDS		
2572231678	t3m_00034	Product_name		Bacterial extracellular solute-binding proteins, family 5 Middle		
2572231678	t3m_00034	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231678	t3m_00034	Coordinates		35532..37883(+)		
2572231678	t3m_00034	DNA_length		2352bp		
2572231678	t3m_00034	Protein_length		783aa		
2572231678	t3m_00034	GC			0.63	
2572231678	t3m_00034	Transmembrane		Yes		

2572231679	t3m_00035	Locus_type		CDS		
2572231679	t3m_00035	Product_name		hypothetical protein		
2572231679	t3m_00035	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231679	t3m_00035	Coordinates		38128..38286(+)		
2572231679	t3m_00035	DNA_length		159bp		
2572231679	t3m_00035	Protein_length		52aa		
2572231679	t3m_00035	GC			0.56	

2572231680	t3m_00036	COG_category	[R] General function prediction only			
2572231680	t3m_00036	COG1988	Predicted membrane-bound metal-dependent hydrolases			1.00E-07
2572231680	t3m_00036	pfam04307	DUF457			1.50E-17
2572231680	t3m_00036	Locus_type		CDS		
2572231680	t3m_00036	Product_name		Predicted membrane-bound metal-dependent hydrolases		

2572231680	t3m_00036	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231680	t3m_00036	Coordinates		38500..39522(+)		
2572231680	t3m_00036	DNA_length		1023bp		
2572231680	t3m_00036	Protein_length		340aa		
2572231680	t3m_00036	GC			0.58	
2572231680	t3m_00036	Transmembrane		Yes		
2572231681	t3m_00037	COG_category	[H] Coenzyme transport and metabolism			
2572231681	t3m_00037	COG0262	Dihydrofolate reductase			1.00E-09
2572231681	t3m_00037	pfam01872	RibD_C			9.70E-17
2572231681	t3m_00037	Locus_type		CDS		
2572231681	t3m_00037	Product_name		Dihydrofolate reductase		
2572231681	t3m_00037	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231681	t3m_00037	Coordinates		39704..40297(+)		
2572231681	t3m_00037	DNA_length		594bp		
2572231681	t3m_00037	Protein_length		197aa		
2572231681	t3m_00037	GC			0.6	
2572231682	t3m_00038	Locus_type		CDS		
2572231682	t3m_00038	Product_name		hypothetical protein		
2572231682	t3m_00038	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231682	t3m_00038	Coordinates		41102..41476(-)		
2572231682	t3m_00038	DNA_length		375bp		
2572231682	t3m_00038	Protein_length		124aa		
2572231682	t3m_00038	GC			0.58	
2572231683	t3m_00039	Locus_type		CDS		
2572231683	t3m_00039	Product_name		hypothetical protein		
2572231683	t3m_00039	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231683	t3m_00039	Coordinates		42085..42501(+)		
2572231683	t3m_00039	DNA_length		417bp		
2572231683	t3m_00039	Protein_length		138aa		
2572231683	t3m_00039	GC			0.63	
2572231683	t3m_00039	Transmembrane		Yes		

2572231684	t3m_00040	pfam02661	Fic			7.30E-26
2572231684	t3m_00040	Locus_type		CDS		
2572231684	t3m_00040	Product_name		Fic/DOC family		
2572231684	t3m_00040	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231684	t3m_00040	Coordinates		42717..43619(-)		
2572231684	t3m_00040	DNA_length		903bp		
2572231684	t3m_00040	Protein_length		300aa		
2572231684	t3m_00040	GC			0.57	
2572231685	t3m_00041	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2572231685	t3m_00041	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231685	t3m_00041	COG2026	Cytotoxic translational repressor of toxin-antitoxin stability system			9.00E-12
2572231685	t3m_00041	pfam05016	Plasmid_stabil			8.40E-11
2572231685	t3m_00041	KO:K06218	RelE protein			2.30E-21
2572231685	t3m_00041	Locus_type		CDS		
2572231685	t3m_00041	Product_name		Cytotoxic translational repressor of toxin-antitoxin stability system		
2572231685	t3m_00041	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231685	t3m_00041	Coordinates		43831..44082(-)		
2572231685	t3m_00041	DNA_length		252bp		
2572231685	t3m_00041	Protein_length		83aa		
2572231685	t3m_00041	GC			0.57	
2572231686	t3m_00042	Locus_type		CDS		
2572231686	t3m_00042	Product_name		hypothetical protein		
2572231686	t3m_00042	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231686	t3m_00042	Coordinates		44082..44303(-)		
2572231686	t3m_00042	DNA_length		222bp		
2572231686	t3m_00042	Protein_length		73aa		
2572231686	t3m_00042	GC			0.57	
2572231687	t3m_00043	pfam08922	DUF1905			3.30E-09
2572231687	t3m_00043	pfam13376	OmdA			1.40E-20
2572231687	t3m_00043	Locus_type		CDS		

2572231687	t3m_00043	Product_name		Bacteriocin-protection, YdeI or OmpD-Associated/Domain of unknown f		
2572231687	t3m_00043	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231687	t3m_00043	Coordinates		44592..44951(+)		
2572231687	t3m_00043	DNA_length		360bp		
2572231687	t3m_00043	Protein_length		119aa		
2572231687	t3m_00043	GC			0.63	
2572231688	t3m_00044	pfam00583	Acetyltransf_1			1.60E-09
2572231688	t3m_00044	Locus_type		CDS		
2572231688	t3m_00044	Product_name		Acetyltransferase (GNAT) family		
2572231688	t3m_00044	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231688	t3m_00044	Coordinates		45142..45993(+)		
2572231688	t3m_00044	DNA_length		852bp		
2572231688	t3m_00044	Protein_length		283aa		
2572231688	t3m_00044	GC			0.59	
2572231689	t3m_00045	Locus_type		CDS		
2572231689	t3m_00045	Product_name		hypothetical protein		
2572231689	t3m_00045	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231689	t3m_00045	Coordinates		46585..47091(-)		
2572231689	t3m_00045	DNA_length		507bp		
2572231689	t3m_00045	Protein_length		168aa		
2572231689	t3m_00045	GC			0.6	
2572231689	t3m_00045	Transmembrane		Yes		
2572231690	t3m_00046	Locus_type		CDS		
2572231690	t3m_00046	Product_name		hypothetical protein		
2572231690	t3m_00046	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231690	t3m_00046	Coordinates		47988..48428(-)		
2572231690	t3m_00046	DNA_length		441bp		
2572231690	t3m_00046	Protein_length		146aa		
2572231690	t3m_00046	GC			0.56	
2572231691	t3m_00047	COG_category	[R] General function prediction only			

2572231691	t3m_00047	COG3324	Predicted enzyme related to lactoylglutathione lyase			2.00E-10
2572231691	t3m_00047	pfam12681	Glyoxalase_2			1.30E-08
2572231691	t3m_00047	Locus_type		CDS		
2572231691	t3m_00047	Product_name		Predicted enzyme related to lactoylglutathione lyase		
2572231691	t3m_00047	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231691	t3m_00047	Coordinates		48606..48992(-)		
2572231691	t3m_00047	DNA_length		387bp		
2572231691	t3m_00047	Protein_length		128aa		
2572231691	t3m_00047	GC			0.61	
2572231692	t3m_00048	KEGG_module	M00258: Putative ABC transport system			
2572231692	t3m_00048	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572231692	t3m_00048	COG4591	ABC-type transport system, involved in lipoprotein release, permease c			2.00E-17
2572231692	t3m_00048	pfam12704	MacB_PCD			5.60E-11
2572231692	t3m_00048	pfam02687	FtsX			4.60E-15
2572231692	t3m_00048	pfam02687	FtsX			9.70E-18
2572231692	t3m_00048	KO:K02004	putative ABC transport system permease protein			0.00E+00
2572231692	t3m_00048	Locus_type		CDS		
2572231692	t3m_00048	Product_name		ABC-type transport system, involved in lipoprotein release, permease cc		
2572231692	t3m_00048	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231692	t3m_00048	Coordinates		49128..52100(-)		
2572231692	t3m_00048	DNA_length		2973bp		
2572231692	t3m_00048	Protein_length		990aa		
2572231692	t3m_00048	GC			0.65	
2572231692	t3m_00048	Transmembrane		Yes		
2572231693	t3m_00049	KEGG_module	M00258: Putative ABC transport system			
2572231693	t3m_00049	COG_category	[V] Defense mechanisms			
2572231693	t3m_00049	COG1136	ABC-type antimicrobial peptide transport system, ATPase component			1.00E-77
2572231693	t3m_00049	pfam00005	ABC_tran			7.70E-33
2572231693	t3m_00049	KO:K02003	putative ABC transport system ATP-binding protein			0.00E+00
2572231693	t3m_00049	Locus_type		CDS		
2572231693	t3m_00049	Product_name		ABC-type antimicrobial peptide transport system, ATPase component		
2572231693	t3m_00049	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		

2572231693	t3m_00049	Coordinates		52106..52783(-)		
2572231693	t3m_00049	DNA_length		678bp		
2572231693	t3m_00049	Protein_length		225aa		
2572231693	t3m_00049	GC			0.63	
2572231694	t3m_00050	Locus_type		CDS		
2572231694	t3m_00050	Product_name		hypothetical protein		
2572231694	t3m_00050	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231694	t3m_00050	Coordinates		52960..53106(+)		
2572231694	t3m_00050	DNA_length		147bp		
2572231694	t3m_00050	Protein_length		48aa		
2572231694	t3m_00050	GC			0.63	
2572231695	t3m_00051	Locus_type		CDS		
2572231695	t3m_00051	Product_name		hypothetical protein		
2572231695	t3m_00051	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231695	t3m_00051	Coordinates		53198..53659(-)		
2572231695	t3m_00051	DNA_length		462bp		
2572231695	t3m_00051	Protein_length		153aa		
2572231695	t3m_00051	GC			0.59	
2572231695	t3m_00051	Transmembrane		Yes		
2572231696	t3m_00052	Locus_type		CDS		
2572231696	t3m_00052	Product_name		hypothetical protein		
2572231696	t3m_00052	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231696	t3m_00052	Coordinates		54065..55198(+)		
2572231696	t3m_00052	DNA_length		1134bp		
2572231696	t3m_00052	Protein_length		377aa		
2572231696	t3m_00052	GC			0.64	
2572231697	t3m_00053	pfam13489	Methyltransf_23			1.70E-20
2572231697	t3m_00053	Locus_type		CDS		
2572231697	t3m_00053	Product_name		Methyltransferase domain		
2572231697	t3m_00053	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		

2572231697	t3m_00053	Coordinates		55201..56016(-)	
2572231697	t3m_00053	DNA_length		816bp	
2572231697	t3m_00053	Protein_length		271aa	
2572231697	t3m_00053	GC		0.66	

2572231698	t3m_00054	COG_category	[T] Signal transduction mechanisms		
2572231698	t3m_00054	COG0589	Universal stress protein UspA and related nucleotide-binding proteins		4.00E-15
2572231698	t3m_00054	pfam00582	Usp		1.20E-24
2572231698	t3m_00054	Locus_type		CDS	
2572231698	t3m_00054	Product_name		Universal stress protein UspA and related nucleotide-binding proteins	
2572231698	t3m_00054	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231698	t3m_00054	Coordinates		56175..56618(+)	
2572231698	t3m_00054	DNA_length		444bp	
2572231698	t3m_00054	Protein_length		147aa	
2572231698	t3m_00054	GC		0.66	

2572231699	t3m_00055	COG_category	[R] General function prediction only		
2572231699	t3m_00055	COG5006	Predicted permease, DMT superfamily		4.00E-04
2572231699	t3m_00055	pfam00892	EamA		1.80E-18
2572231699	t3m_00055	pfam00892	EamA		3.90E-18
2572231699	t3m_00055	Locus_type		CDS	
2572231699	t3m_00055	Product_name		Predicted permease, DMT superfamily	
2572231699	t3m_00055	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231699	t3m_00055	Coordinates		56674..57597(-)	
2572231699	t3m_00055	DNA_length		924bp	
2572231699	t3m_00055	Protein_length		307aa	
2572231699	t3m_00055	GC		0.66	
2572231699	t3m_00055	Transmembrane		Yes	

2572231700	t3m_00056	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP		
2572231700	t3m_00056	Metacyc	PWY-5686: UMP biosynthesis		
2572231700	t3m_00056	IMG_pathway	321: Uridine 5'-monophosphate biosynthesis		
2572231700	t3m_00056	COG_category	[F] Nucleotide transport and metabolism		
2572231700	t3m_00056	COG0540	Aspartate carbamoyltransferase, catalytic chain		1.00E-104

2572231700	t3m_00056	pfam00185	OTCace			7.00E-39
2572231700	t3m_00056	pfam02729	OTCace_N			6.90E-46
2572231700	t3m_00056	EC:2.1.3.2	Aspartate carbamoyltransferase.			
2572231700	t3m_00056	TIGR00670	aspartate carbamoyltransferase			8.40E-119
2572231700	t3m_00056	KO:K00609	aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]			0.00E+00
2572231700	t3m_00056	ITERM:01382	aspartate carbamoyltransferase (EC 2.1.3.2)			
2572231700	t3m_00056	Locus_type		CDS		
2572231700	t3m_00056	Product_name		aspartate carbamoyltransferase (EC 2.1.3.2)		
2572231700	t3m_00056	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231700	t3m_00056	Coordinates		57708..58646(+)		
2572231700	t3m_00056	DNA_length		939bp		
2572231700	t3m_00056	Protein_length		312aa		
2572231700	t3m_00056	GC			0.67	

2572231701	t3m_00057	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP			
2572231701	t3m_00057	COG_category	[F] Nucleotide transport and metabolism			
2572231701	t3m_00057	COG1781	Aspartate carbamoyltransferase, regulatory subunit			5.00E-45
2572231701	t3m_00057	pfam01948	PyrI			5.50E-31
2572231701	t3m_00057	pfam02748	PyrI_C			1.70E-19
2572231701	t3m_00057	TIGR00240	aspartate carbamoyltransferase, regulatory subunit			3.80E-58
2572231701	t3m_00057	KO:K00610	aspartate carbamoyltransferase regulatory subunit			9.00E-40
2572231701	t3m_00057	Locus_type		CDS		
2572231701	t3m_00057	Product_name		aspartate carbamoyltransferase, regulatory subunit		
2572231701	t3m_00057	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231701	t3m_00057	Coordinates		58650..59111(+)		
2572231701	t3m_00057	DNA_length		462bp		
2572231701	t3m_00057	Protein_length		153aa		
2572231701	t3m_00057	GC			0.62	

2572231702	t3m_00058	COG_category	[S] Function unknown			
2572231702	t3m_00058	COG2119	Predicted membrane protein			2.00E-11
2572231702	t3m_00058	pfam01169	UPF0016			1.30E-10
2572231702	t3m_00058	pfam01169	UPF0016			1.60E-08
2572231702	t3m_00058	Locus_type		CDS		

2572231702	t3m_00058	Product_name		Predicted membrane protein		
2572231702	t3m_00058	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231702	t3m_00058	Coordinates		59128..59751(+)		
2572231702	t3m_00058	DNA_length		624bp		
2572231702	t3m_00058	Protein_length		207aa		
2572231702	t3m_00058	GC			0.67	
2572231702	t3m_00058	Transmembrane		Yes		
2572231703	t3m_00059	Locus_type		CDS		
2572231703	t3m_00059	Product_name		hypothetical protein		
2572231703	t3m_00059	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231703	t3m_00059	Coordinates		59704..62016(-)		
2572231703	t3m_00059	DNA_length		2313bp		
2572231703	t3m_00059	Protein_length		770aa		
2572231703	t3m_00059	GC			0.69	
2572231704	t3m_00060	Metacyc	PWY-5905: hypusine biosynthesis			
2572231704	t3m_00060	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572231704	t3m_00060	COG1899	Deoxyhypusine synthase			1.00E-74
2572231704	t3m_00060	pfam01916	DS			2.10E-58
2572231704	t3m_00060	EC:2.5.1.46	Deoxyhypusine synthase.			
2572231704	t3m_00060	TIGR00321	deoxyhypusine synthase			1.20E-75
2572231704	t3m_00060	KO:K00809	deoxyhypusine synthase [EC:2.5.1.46]			0.00E+00
2572231704	t3m_00060	Locus_type		CDS		
2572231704	t3m_00060	Product_name		Deoxyhypusine synthase		
2572231704	t3m_00060	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231704	t3m_00060	Coordinates		62108..63199(+)		
2572231704	t3m_00060	DNA_length		1092bp		
2572231704	t3m_00060	Protein_length		363aa		
2572231704	t3m_00060	GC			0.66	
2572231705	t3m_00061	pfam13191	AAA_16			1.90E-06
2572231705	t3m_00061	Locus_type		CDS		
2572231705	t3m_00061	Product_name		AAA ATPase domain		

2572231705	t3m_00061	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231705	t3m_00061	Coordinates		63758..66187(-)	
2572231705	t3m_00061	DNA_length		2430bp	
2572231705	t3m_00061	Protein_length		809aa	
2572231705	t3m_00061	GC		0.63	
2572231706	t3m_00062	Locus_type		CDS	
2572231706	t3m_00062	Product_name		hypothetical protein	
2572231706	t3m_00062	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231706	t3m_00062	Coordinates		66284..66652(+)	
2572231706	t3m_00062	DNA_length		369bp	
2572231706	t3m_00062	Protein_length		122aa	
2572231706	t3m_00062	GC		0.67	
2572231707	t3m_00063	Locus_type		CDS	
2572231707	t3m_00063	Product_name		hypothetical protein	
2572231707	t3m_00063	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231707	t3m_00063	Coordinates		66652..66858(+)	
2572231707	t3m_00063	DNA_length		207bp	
2572231707	t3m_00063	Protein_length		68aa	
2572231707	t3m_00063	GC		0.68	
2572231708	t3m_00064	Locus_type		CDS	
2572231708	t3m_00064	Product_name		hypothetical protein	
2572231708	t3m_00064	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231708	t3m_00064	Coordinates		67014..67280(+)	
2572231708	t3m_00064	DNA_length		267bp	
2572231708	t3m_00064	Protein_length		88aa	
2572231708	t3m_00064	GC		0.68	
2572231709	t3m_00065	COG_category	[R] General function prediction only		
2572231709	t3m_00065	COG0312	Predicted Zn-dependent proteases and their inactivated homologs		9.00E-47
2572231709	t3m_00065	pfam01523	PmbA_TldD		3.50E-30
2572231709	t3m_00065	KO:K03592	PmbA protein		2.20E-32

2572231709	t3m_00065	Locus_type		CDS	
2572231709	t3m_00065	Product_name		Predicted Zn-dependent proteases and their inactivated homologs	
2572231709	t3m_00065	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231709	t3m_00065	Coordinates		67293..68678(-)	
2572231709	t3m_00065	DNA_length		1386bp	
2572231709	t3m_00065	Protein_length		461aa	
2572231709	t3m_00065	GC		0.67	
2572231710	t3m_00066	COG_category	[R] General function prediction only		
2572231710	t3m_00066	COG0312	Predicted Zn-dependent proteases and their inactivated homologs		1.00E-68
2572231710	t3m_00066	pfam01523	PmbA_TldD		1.80E-45
2572231710	t3m_00066	KO:K03568	TldD protein		0.00E+00
2572231710	t3m_00066	Locus_type		CDS	
2572231710	t3m_00066	Product_name		Predicted Zn-dependent proteases and their inactivated homologs	
2572231710	t3m_00066	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231710	t3m_00066	Coordinates		68702..70135(-)	
2572231710	t3m_00066	DNA_length		1434bp	
2572231710	t3m_00066	Protein_length		477aa	
2572231710	t3m_00066	GC		0.68	
2572231711	t3m_00067	pfam12681	Glyoxalase_2		4.10E-08
2572231711	t3m_00067	Locus_type		CDS	
2572231711	t3m_00067	Product_name		Glyoxalase-like domain	
2572231711	t3m_00067	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231711	t3m_00067	Coordinates		70227..70664(+)	
2572231711	t3m_00067	DNA_length		438bp	
2572231711	t3m_00067	Protein_length		145aa	
2572231711	t3m_00067	GC		0.68	
2572231712	t3m_00068	KEGG_module	M00019: Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine		
2572231712	t3m_00068	KEGG_module	M00570: Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine		
2572231712	t3m_00068	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA		
2572231712	t3m_00068	KEGG_module	M00119: Pantothenate biosynthesis, valine/L-aspartate => pantothenate		
2572231712	t3m_00068	Metacyc	VALSYN-PWY: valine biosynthesis		

2572231712	t3m_00068	Metacyc	PWY-5076: leucine degradation III		
2572231712	t3m_00068	Metacyc	VALDEG-PWY: valine degradation I		
2572231712	t3m_00068	Metacyc	PWY-5101: isoleucine biosynthesis II		
2572231712	t3m_00068	Metacyc	PWY-5108: isoleucine biosynthesis V		
2572231712	t3m_00068	Metacyc	PWY-5104: isoleucine biosynthesis IV		
2572231712	t3m_00068	Metacyc	PWY-5078: isoleucine degradation II		
2572231712	t3m_00068	Metacyc	PWY-5103: isoleucine biosynthesis III		
2572231712	t3m_00068	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2572231712	t3m_00068	Metacyc	LEUSYN-PWY: leucine biosynthesis		
2572231712	t3m_00068	Metacyc	PWY-5057: valine degradation II		
2572231712	t3m_00068	Metacyc	LEU-DEG2-PWY: leucine degradation I		
2572231712	t3m_00068	Metacyc	ILEUSYN-PWY: isoleucine biosynthesis I (from threonine)		
2572231712	t3m_00068	Metacyc	ALANINE-VALINESYN-PWY: alanine biosynthesis I		
2572231712	t3m_00068	COG_category	[E] Amino acid transport and metabolism		
2572231712	t3m_00068	COG_category	[H] Coenzyme transport and metabolism		
2572231712	t3m_00068	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorism		2.00E-64
2572231712	t3m_00068	pfam01063	Aminotran_4		3.90E-46
2572231712	t3m_00068	EC:2.6.1.42	Branched-chain-amino-acid transaminase.		
2572231712	t3m_00068	TIGR01122	branched-chain amino acid aminotransferase, group I		9.20E-114
2572231712	t3m_00068	KO:K00826	branched-chain amino acid aminotransferase [EC:2.6.1.42]		0.00E+00
2572231712	t3m_00068	Locus_type		CDS	
2572231712	t3m_00068	Product_name		branched-chain amino acid aminotransferase, group I	
2572231712	t3m_00068	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231712	t3m_00068	Coordinates		70684..71637(-)	
2572231712	t3m_00068	DNA_length		954bp	
2572231712	t3m_00068	Protein_length		317aa	
2572231712	t3m_00068	GC		0.63	

2572231713	t3m_00069	Locus_type		CDS	
2572231713	t3m_00069	Product_name		hypothetical protein	
2572231713	t3m_00069	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231713	t3m_00069	Coordinates		72228..72941(+)	
2572231713	t3m_00069	DNA_length		714bp	
2572231713	t3m_00069	Protein_length		237aa	

2572231713	t3m_00069	GC			0.63	
2572231713	t3m_00069	Transmembrane		Yes		
2572231714	t3m_00070	pfam01850	PIN			3.60E-09
2572231714	t3m_00070	Locus_type		CDS		
2572231714	t3m_00070	Product_name		PIN domain		
2572231714	t3m_00070	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231714	t3m_00070	Coordinates		73300..73707(-)		
2572231714	t3m_00070	DNA_length		408bp		
2572231714	t3m_00070	Protein_length		135aa		
2572231714	t3m_00070	GC			0.66	
2572231715	t3m_00071	COG_category	[S] Function unknown			
2572231715	t3m_00071	COG3379	Uncharacterized conserved protein			5.00E-97
2572231715	t3m_00071	pfam01663	Phosphodiest			2.70E-41
2572231715	t3m_00071	Locus_type		CDS		
2572231715	t3m_00071	Product_name		Uncharacterized conserved protein		
2572231715	t3m_00071	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231715	t3m_00071	Coordinates		74150..75547(+)		
2572231715	t3m_00071	DNA_length		1398bp		
2572231715	t3m_00071	Protein_length		465aa		
2572231715	t3m_00071	GC			0.66	
2572231716	t3m_00072	KEGG_module	M00358: Coenzyme M biosynthesis			
2572231716	t3m_00072	Metacyc	P261-PWY: coenzyme M biosynthesis I			
2572231716	t3m_00072	IMG_pathway	348: Sulfopyruvate formation from phosphoenolpyruvate			
2572231716	t3m_00072	COG_category	[S] Function unknown			
2572231716	t3m_00072	COG1809	Uncharacterized conserved protein			3.00E-45
2572231716	t3m_00072	pfam02679	ComA			7.90E-59
2572231716	t3m_00072	EC:4.4.1.19	Phosphosulfolactate synthase.			
2572231716	t3m_00072	KO:K08097	phosphosulfolactate synthase [EC:4.4.1.19]			1.60E-41
2572231716	t3m_00072	ITERM:01521	phosphosulfolactate synthase (EC 4.4.1.19)			
2572231716	t3m_00072	Locus_type		CDS		
2572231716	t3m_00072	Product_name		phosphosulfolactate synthase (EC 4.4.1.19)		

2572231716	t3m_00072	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231716	t3m_00072	Coordinates		75636..76637(+)		
2572231716	t3m_00072	DNA_length		1002bp		
2572231716	t3m_00072	Protein_length		333aa		
2572231716	t3m_00072	GC			0.66	

2572231717	t3m_00073	COG_category	[R] General function prediction only			
2572231717	t3m_00073	COG0300	Short-chain dehydrogenases of various substrate specificities			6.00E-27
2572231717	t3m_00073	pfam00106	adh_short			2.40E-17
2572231717	t3m_00073	Locus_type		CDS		
2572231717	t3m_00073	Product_name		Short-chain dehydrogenases of various substrate specificities		
2572231717	t3m_00073	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231717	t3m_00073	Coordinates		76706..77587(+)		
2572231717	t3m_00073	DNA_length		882bp		
2572231717	t3m_00073	Protein_length		293aa		
2572231717	t3m_00073	GC			0.7	

2572231718	t3m_00074	KEGG_module	M00549: Nucleotide sugar biosynthesis, glucose => UDP-glucose			
2572231718	t3m_00074	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2572231718	t3m_00074	Metacyc	TREDEGLOW-PWY: trehalose degradation I (low osmolarity)			
2572231718	t3m_00074	Metacyc	PWY0-1182: trehalose degradation II (trehalase)			
2572231718	t3m_00074	Metacyc	P124-PWY: Bifidobacterium shunt			
2572231718	t3m_00074	Metacyc	GLYCOCAT-PWY: glycogen degradation I			
2572231718	t3m_00074	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2572231718	t3m_00074	Metacyc	P122-PWY: heterolactic fermentation			
2572231718	t3m_00074	Metacyc	GLUCOSE1PMETAB-PWY: glucose and glucose-1-phosphate degradation			
2572231718	t3m_00074	Metacyc	PWY-2723: trehalose degradation V			
2572231718	t3m_00074	Metacyc	PWY-5661: GDP-glucose biosynthesis			
2572231718	t3m_00074	Metacyc	PWY-5514: UDP-<i>N</i>-acetyl-D-galactosamine biosynthesis II			
2572231718	t3m_00074	Metacyc	ANAEROFRUCAT-PWY: homolactic fermentation			
2572231718	t3m_00074	Metacyc	PWY-2722: trehalose degradation IV			
2572231718	t3m_00074	COG_category	[K] Transcription			
2572231718	t3m_00074	COG_category	[G] Carbohydrate transport and metabolism			
2572231718	t3m_00074	COG1940	Transcriptional regulator/sugar kinase			2.00E-42

2572231718	t3m_00074	pfam00480	ROK		9.00E-38
2572231718	t3m_00074	EC:2.7.1.2	Glucokinase.		
2572231718	t3m_00074	KO:K00845	glucokinase [EC:2.7.1.2]		0.00E+00
2572231718	t3m_00074	Locus_type		CDS	
2572231718	t3m_00074	Product_name		Transcriptional regulator/sugar kinase	
2572231718	t3m_00074	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231718	t3m_00074	Coordinates		77584..78540(-)	
2572231718	t3m_00074	DNA_length		957bp	
2572231718	t3m_00074	Protein_length		318aa	
2572231718	t3m_00074	GC		0.7	
2572231719	t3m_00075	COG_category	[G] Carbohydrate transport and metabolism		
2572231719	t3m_00075	COG3387	Glucoamylase and related glycosyl hydrolases		9.00E-88
2572231719	t3m_00075	pfam00723	Glyco_hydro_15		3.40E-09
2572231719	t3m_00075	TIGR01577	oligosaccharide amylase		3.60E-108
2572231719	t3m_00075	ITERM:03202	glucoamylase (EC:3.2.1.3)		
2572231719	t3m_00075	Locus_type		CDS	
2572231719	t3m_00075	Product_name		glucoamylase (EC:3.2.1.3)	
2572231719	t3m_00075	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231719	t3m_00075	Coordinates		78572..80437(-)	
2572231719	t3m_00075	DNA_length		1866bp	
2572231719	t3m_00075	Protein_length		621aa	
2572231719	t3m_00075	GC		0.67	
2572231720	t3m_00076	Metacyc	PWY-842: starch degradation I		
2572231720	t3m_00076	pfam03065	Glyco_hydro_57		5.00E-47
2572231720	t3m_00076	EC:3.2.1.1	Alpha-amylase.		
2572231720	t3m_00076	KO:K07405	alpha-amylase [EC:3.2.1.1]		0.00E+00
2572231720	t3m_00076	Locus_type		CDS	
2572231720	t3m_00076	Product_name		Glycosyl hydrolase family 57	
2572231720	t3m_00076	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231720	t3m_00076	Coordinates		80562..81662(-)	
2572231720	t3m_00076	DNA_length		1101bp	
2572231720	t3m_00076	Protein_length		366aa	

2572231720	t3m_00076	GC			0.67	

2572231721	t3m_00077	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572231721	t3m_00077	COG0438	Glycosyltransferase			4.00E-41
2572231721	t3m_00077	pfam13579	Glyco_trans_4_4			2.60E-23
2572231721	t3m_00077	pfam00534	Glycos_transf_1			2.20E-38
2572231721	t3m_00077	Locus_type		CDS		
2572231721	t3m_00077	Product_name		Glycosyltransferase		
2572231721	t3m_00077	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231721	t3m_00077	Coordinates		81752..82996(-)		
2572231721	t3m_00077	DNA_length		1245bp		
2572231721	t3m_00077	Protein_length		414aa		
2572231721	t3m_00077	GC			0.68	

2572231722	t3m_00078	KEGG_module	M00003: Gluconeogenesis, oxaloacetate => fructose-6P			
2572231722	t3m_00078	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2572231722	t3m_00078	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds			
2572231722	t3m_00078	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			
2572231722	t3m_00078	Metacyc	P341-PWY: glycolysis V (Pyrococcus)			
2572231722	t3m_00078	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2572231722	t3m_00078	Metacyc	PWY66-373: sucrose degradation V (mammalian)			
2572231722	t3m_00078	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2572231722	t3m_00078	Metacyc	PWY-1042: glycolysis IV (plant cytosol)			
2572231722	t3m_00078	Metacyc	GLYCOLYSIS: glycolysis I			
2572231722	t3m_00078	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2572231722	t3m_00078	Metacyc	PWY-7003: glycerol degradation to butanol			
2572231722	t3m_00078	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2572231722	t3m_00078	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)			
2572231722	t3m_00078	IMG_pathway	336: Standard Embden-Meyerhof pathway			
2572231722	t3m_00078	IMG_pathway	337: Embden-Meyerhof pathway without bisphosphoglycerate			
2572231722	t3m_00078	IMG_pathway	527: Calvin cycle			
2572231722	t3m_00078	COG_category	[G] Carbohydrate transport and metabolism			
2572231722	t3m_00078	COG0149	Triosephosphate isomerase			2.00E-31
2572231722	t3m_00078	pfam00121	TIM			3.30E-06

2572231722	t3m_00078	pfam00121	TIM		1.20E-13
2572231722	t3m_00078	EC:5.3.1.1	Triose-phosphate isomerase.		
2572231722	t3m_00078	TIGR00419	triosephosphate isomerase		1.40E-45
2572231722	t3m_00078	KO:K01803	triosephosphate isomerase (TIM) [EC:5.3.1.1]		0.00E+00
2572231722	t3m_00078	ITERM:01475	triosephosphate isomerase (EC 5.3.1.1)		
2572231722	t3m_00078	Locus_type		CDS	
2572231722	t3m_00078	Product_name		triosephosphate isomerase (EC 5.3.1.1)	
2572231722	t3m_00078	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231722	t3m_00078	Coordinates		83292..83897(-)	
2572231722	t3m_00078	DNA_length		606bp	
2572231722	t3m_00078	Protein_length		201aa	
2572231722	t3m_00078	GC		0.73	
2572231723	t3m_00079	Locus_type		CDS	
2572231723	t3m_00079	Product_name		hypothetical protein	
2572231723	t3m_00079	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231723	t3m_00079	Coordinates		83971..84180(-)	
2572231723	t3m_00079	DNA_length		210bp	
2572231723	t3m_00079	Protein_length		69aa	
2572231723	t3m_00079	GC		0.62	
2572231724	t3m_00080	KEGG_module	M00357: Methanogenesis, acetate => methane		
2572231724	t3m_00080	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)		
2572231724	t3m_00080	Metacyc	PWY66-161: oxidative ethanol degradation III		
2572231724	t3m_00080	Metacyc	PWY-6672: <i>cis</i>-genanyl-CoA degradation		
2572231724	t3m_00080	Metacyc	PWY66-21: ethanol degradation II		
2572231724	t3m_00080	Metacyc	PWY66-162: ethanol degradation IV		
2572231724	t3m_00080	Metacyc	PWY0-1313: acetate conversion to acetyl-CoA		
2572231724	t3m_00080	COG_category	[I] Lipid transport and metabolism		
2572231724	t3m_00080	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases		0.00E+00
2572231724	t3m_00080	pfam00501	AMP-binding		1.90E-85
2572231724	t3m_00080	pfam13193	AMP-binding_C		1.80E-14
2572231724	t3m_00080	EC:6.2.1.1	Acetate--CoA ligase.		
2572231724	t3m_00080	TIGR02188	acetate--CoA ligase		0.00E+00

2572231724	t3m_00080	KO:K01895	acetyl-CoA synthetase [EC:6.2.1.1]		0.00E+00
2572231724	t3m_00080	Locus_type		CDS	
2572231724	t3m_00080	Product_name		acetyl-coenzyme A synthetase (EC 6.2.1.1)	
2572231724	t3m_00080	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231724	t3m_00080	Coordinates		84443..86494(+)	
2572231724	t3m_00080	DNA_length		2052bp	
2572231724	t3m_00080	Protein_length		683aa	
2572231724	t3m_00080	GC		0.65	
2572231725	t3m_00081	COG_category	[S] Function unknown		
2572231725	t3m_00081	COG3371	Predicted membrane protein		2.00E-11
2572231725	t3m_00081	pfam06197	DUF998		1.50E-23
2572231725	t3m_00081	Locus_type		CDS	
2572231725	t3m_00081	Product_name		Predicted membrane protein	
2572231725	t3m_00081	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231725	t3m_00081	Coordinates		86587..87330(-)	
2572231725	t3m_00081	DNA_length		744bp	
2572231725	t3m_00081	Protein_length		247aa	
2572231725	t3m_00081	GC		0.66	
2572231725	t3m_00081	Transmembrane		Yes	
2572231726	t3m_00082	Locus_type		CDS	
2572231726	t3m_00082	Product_name		hypothetical protein	
2572231726	t3m_00082	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231726	t3m_00082	Coordinates		87343..87486(-)	
2572231726	t3m_00082	DNA_length		144bp	
2572231726	t3m_00082	Protein_length		47aa	
2572231726	t3m_00082	GC		0.72	
2572231727	t3m_00083	COG_category	[H] Coenzyme transport and metabolism		
2572231727	t3m_00083	COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis		4.00E-04
2572231727	t3m_00083	Locus_type		CDS	
2572231727	t3m_00083	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	
2572231727	t3m_00083	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	

2572231727	t3m_00083	Coordinates		87536..88495(+)		
2572231727	t3m_00083	DNA_length		960bp		
2572231727	t3m_00083	Protein_length		319aa		
2572231727	t3m_00083	GC			0.71	
2572231728	t3m_00084	COG_category	[T] Signal transduction mechanisms			
2572231728	t3m_00084	COG0467	RecA-superfamily ATPases implicated in signal transduction			1.00E-16
2572231728	t3m_00084	pfam06745	KaiC			4.10E-11
2572231728	t3m_00084	Locus_type		CDS		
2572231728	t3m_00084	Product_name		RecA-superfamily ATPases implicated in signal transduction		
2572231728	t3m_00084	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231728	t3m_00084	Coordinates		88527..91226(+)		
2572231728	t3m_00084	DNA_length		2700bp		
2572231728	t3m_00084	Protein_length		899aa		
2572231728	t3m_00084	GC			0.68	
2572231728	t3m_00084	Transmembrane		Yes		
2572231729	t3m_00085	COG_category	[R] General function prediction only			
2572231729	t3m_00085	COG_category	[H] Coenzyme transport and metabolism			
2572231729	t3m_00085	COG_category	[C] Energy production and conversion			
2572231729	t3m_00085	COG1052	Lactate dehydrogenase and related dehydrogenases			1.00E-40
2572231729	t3m_00085	pfam02826	2-Hacid_dh_C			2.40E-36
2572231729	t3m_00085	Locus_type		CDS		
2572231729	t3m_00085	Product_name		Lactate dehydrogenase and related dehydrogenases		
2572231729	t3m_00085	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231729	t3m_00085	Coordinates		91329..92315(-)		
2572231729	t3m_00085	DNA_length		987bp		
2572231729	t3m_00085	Protein_length		328aa		
2572231729	t3m_00085	GC			0.69	
2572231730	t3m_00086	COG_category	[R] General function prediction only			
2572231730	t3m_00086	COG1011	Predicted hydrolase (HAD superfamily)			3.00E-14
2572231730	t3m_00086	pfam13419	HAD_2			1.30E-20
2572231730	t3m_00086	TIGR01549	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m			2.80E-11

2572231730	t3m_00086	KO:K07025	putative hydrolase of the HAD superfamily			1.40E-23
2572231730	t3m_00086	Locus_type		CDS		
2572231730	t3m_00086	Product_name		haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m		
2572231730	t3m_00086	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231730	t3m_00086	Coordinates		92456..93229(+)		
2572231730	t3m_00086	DNA_length		774bp		
2572231730	t3m_00086	Protein_length		257aa		
2572231730	t3m_00086	GC			0.68	
2572231731	t3m_00087	Locus_type		CDS		
2572231731	t3m_00087	Product_name		hypothetical protein		
2572231731	t3m_00087	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231731	t3m_00087	Coordinates		93249..93524(-)		
2572231731	t3m_00087	DNA_length		276bp		
2572231731	t3m_00087	Protein_length		91aa		
2572231731	t3m_00087	GC			0.65	
2572231732	t3m_00088	COG_category	[S] Function unknown			
2572231732	t3m_00088	COG1584	Predicted membrane protein			2.00E-16
2572231732	t3m_00088	pfam01184	Grp1_Fun34_YaaH			1.40E-19
2572231732	t3m_00088	Locus_type		CDS		
2572231732	t3m_00088	Product_name		Predicted membrane protein		
2572231732	t3m_00088	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231732	t3m_00088	Coordinates		93788..94378(+)		
2572231732	t3m_00088	DNA_length		591bp		
2572231732	t3m_00088	Protein_length		196aa		
2572231732	t3m_00088	GC			0.63	
2572231732	t3m_00088	Transmembrane		Yes		
2572231733	t3m_00089	COG_category	[S] Function unknown			
2572231733	t3m_00089	COG2410	Uncharacterized conserved protein			7.00E-18
2572231733	t3m_00089	pfam04250	DUF429			1.00E-25
2572231733	t3m_00089	KO:K09147	hypothetical protein			2.10E-27
2572231733	t3m_00089	Locus_type		CDS		

2572231733	t3m_00089	Product_name		Uncharacterized conserved protein	
2572231733	t3m_00089	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231733	t3m_00089	Coordinates		94467..95189(+)	
2572231733	t3m_00089	DNA_length		723bp	
2572231733	t3m_00089	Protein_length		240aa	
2572231733	t3m_00089	GC		0.67	

2572231734	t3m_00090	COG_category	[S] Function unknown		
2572231734	t3m_00090	COG4280	Predicted membrane protein		7.00E-16
2572231734	t3m_00090	Locus_type		CDS	
2572231734	t3m_00090	Product_name		Predicted membrane protein	
2572231734	t3m_00090	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231734	t3m_00090	Coordinates		95365..96072(-)	
2572231734	t3m_00090	DNA_length		708bp	
2572231734	t3m_00090	Protein_length		235aa	
2572231734	t3m_00090	GC		0.7	
2572231734	t3m_00090	Transmembrane		Yes	

2572231735	t3m_00091	Locus_type		CDS	
2572231735	t3m_00091	Product_name		hypothetical protein	
2572231735	t3m_00091	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231735	t3m_00091	Coordinates		96157..96792(-)	
2572231735	t3m_00091	DNA_length		636bp	
2572231735	t3m_00091	Protein_length		211aa	
2572231735	t3m_00091	GC		0.71	

2572231736	t3m_00092	Metacyc	GLUCONEO-PWY: gluconeogenesis I		
2572231736	t3m_00092	Metacyc	PWY-7118: chitin degradation to ethanol		
2572231736	t3m_00092	COG_category	[C] Energy production and conversion		
2572231736	t3m_00092	COG0281	Malic enzyme		4.00E-106
2572231736	t3m_00092	pfam00390	malic		1.50E-66
2572231736	t3m_00092	pfam03949	Malic_M		8.20E-82
2572231736	t3m_00092	EC:1.1.1.38	Malate dehydrogenase (oxaloacetate-decarboxylating).		
2572231736	t3m_00092	KO:K00027	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]		0.00E+00

2572231736	t3m_00092	Locus_type	CDS
2572231736	t3m_00092	Product_name	NAD-dependent malic enzyme (EC 1.1.1.38)
2572231736	t3m_00092	Scaffold	t3m_contig_70_5_len_122850_read_count_10924403.1
2572231736	t3m_00092	Coordinates	96928..98565(-)
2572231736	t3m_00092	DNA_length	1638bp
2572231736	t3m_00092	Protein_length	545aa
2572231736	t3m_00092	GC	0.67
2572231737	t3m_00093	Locus_type	CDS
2572231737	t3m_00093	Product_name	hypothetical protein
2572231737	t3m_00093	Scaffold	t3m_contig_70_5_len_122850_read_count_10924403.1
2572231737	t3m_00093	Coordinates	98866..99060(+)
2572231737	t3m_00093	DNA_length	195bp
2572231737	t3m_00093	Protein_length	64aa
2572231737	t3m_00093	GC	0.61
2572231737	t3m_00093	Transmembrane	Yes
2572231738	t3m_00094	Locus_type	CDS
2572231738	t3m_00094	Product_name	hypothetical protein
2572231738	t3m_00094	Scaffold	t3m_contig_70_5_len_122850_read_count_10924403.1
2572231738	t3m_00094	Coordinates	99151..99693(-)
2572231738	t3m_00094	DNA_length	543bp
2572231738	t3m_00094	Protein_length	180aa
2572231738	t3m_00094	GC	0.68
2572231739	t3m_00095	Locus_type	CDS
2572231739	t3m_00095	Product_name	hypothetical protein
2572231739	t3m_00095	Scaffold	t3m_contig_70_5_len_122850_read_count_10924403.1
2572231739	t3m_00095	Coordinates	99766..100518(-)
2572231739	t3m_00095	DNA_length	753bp
2572231739	t3m_00095	Protein_length	250aa
2572231739	t3m_00095	GC	0.7
2572231739	t3m_00095	Transmembrane	Yes

2572231740	t3m_00096	Metacyc	PWY-5740: GDP-L-colitose biosynthesis			
2572231740	t3m_00096	Metacyc	PWY-5738: GDP-6-deoxy-D-talose biosynthesis			
2572231740	t3m_00096	Metacyc	PWY-5739: GDP-α-D-perosamine biosynthesis			
2572231740	t3m_00096	Metacyc	GDPRHAMSYN-PWY: GDP-D-rhamnose biosynthesis			
2572231740	t3m_00096	Metacyc	PWY-66: GDP-L-fucose biosynthesis I (from GDP-D-mannose)			
2572231740	t3m_00096	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572231740	t3m_00096	COG_category	[G] Carbohydrate transport and metabolism			
2572231740	t3m_00096	COG0451	Nucleoside-diphosphate-sugar epimerases			3.00E-46
2572231740	t3m_00096	pfam01370	Epimerase			2.10E-48
2572231740	t3m_00096	EC:4.2.1.47	GDP-mannose 4,6-dehydratase.			
2572231740	t3m_00096	KO:K01711	GDPmannose 4,6-dehydratase [EC:4.2.1.47]			0.00E+00
2572231740	t3m_00096	Locus_type		CDS		
2572231740	t3m_00096	Product_name		Nucleoside-diphosphate-sugar epimerases		
2572231740	t3m_00096	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231740	t3m_00096	Coordinates		100603..101556(-)		
2572231740	t3m_00096	DNA_length		954bp		
2572231740	t3m_00096	Protein_length		317aa		
2572231740	t3m_00096	GC			0.68	
2572231741	t3m_00097	Metacyc	MANNOSYL-CHITO-DOLICHOL-BIOSYNTHESIS: dolichyl-diphosphooligosaccharide biosynthesis			
2572231741	t3m_00097	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572231741	t3m_00097	COG0463	Glycosyltransferases involved in cell wall biogenesis			6.00E-22
2572231741	t3m_00097	pfam00535	Glycos_transf_2			1.90E-29
2572231741	t3m_00097	EC:2.4.1.83	Dolichyl-phosphate beta-D-mannosyltransferase.			
2572231741	t3m_00097	KO:K00721	dolichol-phosphate mannosyltransferase [EC:2.4.1.83]			4.20E-42
2572231741	t3m_00097	Locus_type		CDS		
2572231741	t3m_00097	Product_name		Glycosyltransferases involved in cell wall biogenesis		
2572231741	t3m_00097	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231741	t3m_00097	Coordinates		101717..102469(-)		
2572231741	t3m_00097	DNA_length		753bp		
2572231741	t3m_00097	Protein_length		250aa		
2572231741	t3m_00097	GC			0.69	
2572231742	t3m_00098	Metacyc	PWY-6478: GDP-D-<i>glycero</i>-α-D-<i>manno</i>-heptose biosynthesis			

2572231742	t3m_00098	COG_category	[R] General function prediction only			
2572231742	t3m_00098	COG2605	Predicted kinase related to galactokinase and mevalonate kinase			3.00E-86
2572231742	t3m_00098	pfam08544	GHMP_kinases_C			2.30E-12
2572231742	t3m_00098	pfam00288	GHMP_kinases_N			4.00E-12
2572231742	t3m_00098	EC:2.7.1.168	D-glycero-alpha-D-manno-heptose-7-phosphate kinase.			
2572231742	t3m_00098	KO:K07031	D-glycero-alpha-D-manno-heptose-7-phosphate kinase [EC:2.7.1.168]			0.00E+00
2572231742	t3m_00098	Locus_type		CDS		
2572231742	t3m_00098	Product_name		Predicted kinase related to galactokinase and mevalonate kinase		
2572231742	t3m_00098	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231742	t3m_00098	Coordinates		102485..103531(-)		
2572231742	t3m_00098	DNA_length		1047bp		
2572231742	t3m_00098	Protein_length		348aa		
2572231742	t3m_00098	GC			0.64	
2572231743	t3m_00099	Metacyc	PWY-6502: oxidized GTP and dGTP detoxification			
2572231743	t3m_00099	Metacyc	PWY-6575: juvenile hormone III biosynthesis I			
2572231743	t3m_00099	Metacyc	PWY-6797: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (archaea)			
2572231743	t3m_00099	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis			
2572231743	t3m_00099	Metacyc	PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I			
2572231743	t3m_00099	Metacyc	PWY-7206: pyrimidine deoxyribonucleotides dephosphorylation			
2572231743	t3m_00099	COG_category	[F] Nucleotide transport and metabolism			
2572231743	t3m_00099	COG1051	ADP-ribose pyrophosphatase			2.00E-26
2572231743	t3m_00099	pfam00293	NUDIX			3.20E-25
2572231743	t3m_00099	EC:3.6.1.-	Hydrolases. Acting on acid anhydrides. In phosphorous-containing anhydrides.			
2572231743	t3m_00099	KO:K03574	7,8-dihydro-8-oxoguanine triphosphatase [EC:3.6.1.-]			3.60E-28
2572231743	t3m_00099	Locus_type		CDS		
2572231743	t3m_00099	Product_name		ADP-ribose pyrophosphatase		
2572231743	t3m_00099	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231743	t3m_00099	Coordinates		103673..104140(+)		
2572231743	t3m_00099	DNA_length		468bp		
2572231743	t3m_00099	Protein_length		155aa		
2572231743	t3m_00099	GC			0.71	
2572231744	t3m_00100	COG_category	[S] Function unknown			

2572231744	t3m_00100	COG1814	Uncharacterized membrane protein		6.00E-15
2572231744	t3m_00100	pfam01988	VIT1		5.90E-47
2572231744	t3m_00100	TIGR00267	TIGR00267 family protein		9.90E-15
2572231744	t3m_00100	Locus_type		CDS	
2572231744	t3m_00100	Product_name		Uncharacterized membrane protein	
2572231744	t3m_00100	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231744	t3m_00100	Coordinates		104237..104950(+)	
2572231744	t3m_00100	DNA_length		714bp	
2572231744	t3m_00100	Protein_length		237aa	
2572231744	t3m_00100	GC		0.65	
2572231744	t3m_00100	Transmembrane		Yes	
2572231745	t3m_00101	Locus_type		CDS	
2572231745	t3m_00101	Product_name		hypothetical protein	
2572231745	t3m_00101	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231745	t3m_00101	Coordinates		105317..106183(-)	
2572231745	t3m_00101	DNA_length		867bp	
2572231745	t3m_00101	Protein_length		288aa	
2572231745	t3m_00101	GC		0.65	
2572231746	t3m_00102	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572231746	t3m_00102	COG_category	[G] Carbohydrate transport and metabolism		
2572231746	t3m_00102	COG0451	Nucleoside-diphosphate-sugar epimerases		1.00E-15
2572231746	t3m_00102	pfam13460	NAD_binding_10		9.20E-22
2572231746	t3m_00102	EC:1.6.99.3	NADH dehydrogenase.		
2572231746	t3m_00102	KO:K00356	NADH dehydrogenase [EC:1.6.99.3]		4.70E-23
2572231746	t3m_00102	Locus_type		CDS	
2572231746	t3m_00102	Product_name		Nucleoside-diphosphate-sugar epimerases	
2572231746	t3m_00102	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231746	t3m_00102	Coordinates		106274..107194(-)	
2572231746	t3m_00102	DNA_length		921bp	
2572231746	t3m_00102	Protein_length		306aa	
2572231746	t3m_00102	GC		0.69	

2572231747	t3m_00103	Metacyc	PWY-6987: lipoate biosynthesis and incorporation III (Bacillus)			
2572231747	t3m_00103	Metacyc	PWY0-501: lipoate biosynthesis and incorporation I			
2572231747	t3m_00103	COG_category	[H] Coenzyme transport and metabolism			
2572231747	t3m_00103	COG0321	Lipoate-protein ligase B			2.00E-56
2572231747	t3m_00103	pfam03099	BPL_LplA_LipB			1.20E-14
2572231747	t3m_00103	EC:2.3.1.181	Lipoyl(octanoyl) transferase.			
2572231747	t3m_00103	TIGR00214	lipoate-protein ligase B			1.50E-47
2572231747	t3m_00103	KO:K03801	lipoyl(octanoyl) transferase [EC:2.3.1.181]			5.20E-43
2572231747	t3m_00103	Locus_type		CDS		
2572231747	t3m_00103	Product_name		lipoate-protein ligase B		
2572231747	t3m_00103	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231747	t3m_00103	Coordinates		107197..107859(-)		
2572231747	t3m_00103	DNA_length		663bp		
2572231747	t3m_00103	Protein_length		220aa		
2572231747	t3m_00103	GC			0.7	
2572231748	t3m_00104	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA			
2572231748	t3m_00104	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)			
2572231748	t3m_00104	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572231748	t3m_00104	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA			
2572231748	t3m_00104	Metacyc	PYRUVDEHYD-PWY: pyruvate decarboxylation to acetyl CoA			
2572231748	t3m_00104	Metacyc	PWY-5084: 2-oxoglutarate decarboxylation to succinyl-CoA			
2572231748	t3m_00104	Metacyc	PWY-5046: 2-oxoisovalerate decarboxylation to isobutanoyl-CoA			
2572231748	t3m_00104	Metacyc	GLYCLEAV-PWY: glycine cleavage			
2572231748	t3m_00104	COG_category	[C] Energy production and conversion			
2572231748	t3m_00104	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide de			1.00E-125
2572231748	t3m_00104	pfam07992	Pyr_redox_2			1.20E-35
2572231748	t3m_00104	pfam02852	Pyr_redox_dim			2.00E-30
2572231748	t3m_00104	pfam00070	Pyr_redox			3.00E-17
2572231748	t3m_00104	EC:1.8.1.4	Dihydrolipoyl dehydrogenase.			
2572231748	t3m_00104	TIGR01350	dihydrolipoamide dehydrogenase			0.00E+00
2572231748	t3m_00104	KO:K00382	dihydrolipoamide dehydrogenase [EC:1.8.1.4]			0.00E+00
2572231748	t3m_00104	Locus_type		CDS		
2572231748	t3m_00104	Product_name		dihydrolipoamide dehydrogenase		

2572231748	t3m_00104	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231748	t3m_00104	Coordinates		107843..109336(-)		
2572231748	t3m_00104	DNA_length		1494bp		
2572231748	t3m_00104	Protein_length		497aa		
2572231748	t3m_00104	GC			0.68	
2572231749	t3m_00105	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA			
2572231749	t3m_00105	Metacyc	PWY-5046: 2-oxoisovalerate decarboxylation to isobutanoyl-CoA			
2572231749	t3m_00105	COG_category	[C] Energy production and conversion			
2572231749	t3m_00105	COG1071	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1)			7.00E-82
2572231749	t3m_00105	pfam00676	E1_dh			4.80E-70
2572231749	t3m_00105	EC:1.2.4.4	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring).			
2572231749	t3m_00105	KO:K00166	2-oxoisovalerate dehydrogenase E1 component, alpha subunit [EC:1.2.4			0.00E+00
2572231749	t3m_00105	Locus_type		CDS		
2572231749	t3m_00105	Product_name		Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) c		
2572231749	t3m_00105	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231749	t3m_00105	Coordinates		109296..110351(-)		
2572231749	t3m_00105	DNA_length		1056bp		
2572231749	t3m_00105	Protein_length		351aa		
2572231749	t3m_00105	GC			0.67	
2572231750	t3m_00106	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA			
2572231750	t3m_00106	Metacyc	PYRUVDEHYD-PWY: pyruvate decarboxylation to acetyl CoA			
2572231750	t3m_00106	COG_category	[C] Energy production and conversion			
2572231750	t3m_00106	COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide ac			2.00E-106
2572231750	t3m_00106	pfam00364	Biotin_lipoyl			9.30E-22
2572231750	t3m_00106	pfam00198	2-oxoacid_dh			8.10E-81
2572231750	t3m_00106	pfam02817	E3_binding			1.00E-14
2572231750	t3m_00106	EC:2.3.1.12	Dihydrolipoyllysine-residue acetyltransferase.			
2572231750	t3m_00106	KO:K00627	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransf			0.00E+00
2572231750	t3m_00106	Locus_type		CDS		
2572231750	t3m_00106	Product_name		Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acy		
2572231750	t3m_00106	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231750	t3m_00106	Coordinates		110348..111643(-)		

2572231750	t3m_00106	DNA_length		1296bp	
2572231750	t3m_00106	Protein_length		431aa	
2572231750	t3m_00106	GC		0.68	
2572231751	t3m_00107	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA		
2572231751	t3m_00107	Metacyc	PWY-5046: 2-oxoisovalerate decarboxylation to isobutanoyl-CoA		
2572231751	t3m_00107	COG_category	[C] Energy production and conversion		
2572231751	t3m_00107	COG0022	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1)		0.00E+00
2572231751	t3m_00107	pfam02779	Transket_pyr		3.40E-46
2572231751	t3m_00107	pfam02780	Transketolase_C		1.90E-39
2572231751	t3m_00107	EC:1.2.4.4	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring).		
2572231751	t3m_00107	KO:K00167	2-oxoisovalerate dehydrogenase E1 component, beta subunit [EC:1.2.4.		0.00E+00
2572231751	t3m_00107	Locus_type		CDS	
2572231751	t3m_00107	Product_name		Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) c	
2572231751	t3m_00107	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231751	t3m_00107	Coordinates		111653..112630(-)	
2572231751	t3m_00107	DNA_length		978bp	
2572231751	t3m_00107	Protein_length		325aa	
2572231751	t3m_00107	GC		0.66	
2572231752	t3m_00108	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA		
2572231752	t3m_00108	Metacyc	PWY-5046: 2-oxoisovalerate decarboxylation to isobutanoyl-CoA		
2572231752	t3m_00108	COG_category	[C] Energy production and conversion		
2572231752	t3m_00108	COG1071	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1)		9.00E-108
2572231752	t3m_00108	pfam00676	E1_dh		4.40E-94
2572231752	t3m_00108	EC:1.2.4.4	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring).		
2572231752	t3m_00108	TIGR03181	pyruvate dehydrogenase E1 component, alpha subunit		4.50E-126
2572231752	t3m_00108	KO:K00166	2-oxoisovalerate dehydrogenase E1 component, alpha subunit [EC:1.2.		0.00E+00
2572231752	t3m_00108	Locus_type		CDS	
2572231752	t3m_00108	Product_name		Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) c	
2572231752	t3m_00108	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231752	t3m_00108	Coordinates		112627..113706(-)	
2572231752	t3m_00108	DNA_length		1080bp	
2572231752	t3m_00108	Protein_length		359aa	

2572231752	t3m_00108	GC			0.66	
2572231753	t3m_00109	COG_category	[K] Transcription			
2572231753	t3m_00109	COG_category	[L] Replication, recombination and repair			
2572231753	t3m_00109	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231753	t3m_00109	COG0513	Superfamily II DNA and RNA helicases			3.00E-111
2572231753	t3m_00109	pfam00271	Helicase_C			5.00E-27
2572231753	t3m_00109	pfam00270	DEAD			8.00E-45
2572231753	t3m_00109	EC:3.6.4.13	RNA helicase.			
2572231753	t3m_00109	KO:K11927	ATP-dependent RNA helicase RhlE [EC:3.6.4.13]			0.00E+00
2572231753	t3m_00109	Locus_type		CDS		
2572231753	t3m_00109	Product_name		Superfamily II DNA and RNA helicases		
2572231753	t3m_00109	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231753	t3m_00109	Coordinates		113852..115102(-)		
2572231753	t3m_00109	DNA_length		1251bp		
2572231753	t3m_00109	Protein_length		416aa		
2572231753	t3m_00109	GC			0.67	
2572231754	t3m_00110	COG_category	[E] Amino acid transport and metabolism			
2572231754	t3m_00110	COG_category	[T] Signal transduction mechanisms			
2572231754	t3m_00110	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmi			1.00E-22
2572231754	t3m_00110	pfam00497	SBP_bac_3			1.40E-33
2572231754	t3m_00110	ITERM:05951	amino acid ABC transporter substrate-binding protein, PAAT family (TC 3.A.1.3.-)			
2572231754	t3m_00110	Locus_type		CDS		
2572231754	t3m_00110	Product_name		amino acid ABC transporter substrate-binding protein, PAAT family (TC 3		
2572231754	t3m_00110	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231754	t3m_00110	Coordinates		115377..116234(+)		
2572231754	t3m_00110	DNA_length		858bp		
2572231754	t3m_00110	Protein_length		285aa		
2572231754	t3m_00110	GC			0.62	
2572231754	t3m_00110	Transmembrane		Yes		
2572231755	t3m_00111	KEGG_module	M00234: Cystine transport system			
2572231755	t3m_00111	COG_category	[E] Amino acid transport and metabolism			

2572231755	t3m_00111	COG0765	ABC-type amino acid transport system, permease component		3.00E-37
2572231755	t3m_00111	pfam00528	BPD_transp_1		9.90E-17
2572231755	t3m_00111	TIGR01726	amine acid ABC transporter, permease protein, 3-TM region, His/Glu/Gl		6.90E-14
2572231755	t3m_00111	KO:K10009	cystine transport system permease protein		4.40E-32
2572231755	t3m_00111	Locus_type		CDS	
2572231755	t3m_00111	Product_name		ABC-type amino acid transport system, permease component	
2572231755	t3m_00111	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231755	t3m_00111	Coordinates		116347..117273(+)	
2572231755	t3m_00111	DNA_length		927bp	
2572231755	t3m_00111	Protein_length		308aa	
2572231755	t3m_00111	GC		0.65	
2572231755	t3m_00111	Transmembrane		Yes	

2572231756	t3m_00112	KEGG_module	M00236: Putative polar amino acid transport system		
2572231756	t3m_00112	COG_category	[E] Amino acid transport and metabolism		
2572231756	t3m_00112	COG1126	ABC-type polar amino acid transport system, ATPase component		2.00E-102
2572231756	t3m_00112	pfam00005	ABC_tran		5.40E-35
2572231756	t3m_00112	EC:3.6.3.21	Polar-amino-acid-transporting ATPase.		
2572231756	t3m_00112	KO:K02028	polar amino acid transport system ATP-binding protein [EC:3.6.3.21]		0.00E+00
2572231756	t3m_00112	Locus_type		CDS	
2572231756	t3m_00112	Product_name		ABC-type polar amino acid transport system, ATPase component	
2572231756	t3m_00112	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1	
2572231756	t3m_00112	Coordinates		117270..118001(+)	
2572231756	t3m_00112	DNA_length		732bp	
2572231756	t3m_00112	Protein_length		243aa	
2572231756	t3m_00112	GC		0.63	

2572231757	t3m_00113	KEGG_module	M00236: Putative polar amino acid transport system		
2572231757	t3m_00113	COG_category	[E] Amino acid transport and metabolism		
2572231757	t3m_00113	COG0765	ABC-type amino acid transport system, permease component		2.00E-34
2572231757	t3m_00113	pfam00528	BPD_transp_1		2.60E-18
2572231757	t3m_00113	KO:K02029	polar amino acid transport system permease protein		1.40E-24
2572231757	t3m_00113	Locus_type		CDS	
2572231757	t3m_00113	Product_name		ABC-type amino acid transport system, permease component	

2572231757	t3m_00113	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231757	t3m_00113	Coordinates		118122..119132(+)		
2572231757	t3m_00113	DNA_length		1011bp		
2572231757	t3m_00113	Protein_length		336aa		
2572231757	t3m_00113	GC			0.63	
2572231757	t3m_00113	Transmembrane		Yes		
2572231758	t3m_00114	Locus_type		CDS		
2572231758	t3m_00114	Product_name		hypothetical protein		
2572231758	t3m_00114	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231758	t3m_00114	Coordinates		119939..122677(+)		
2572231758	t3m_00114	DNA_length		2739bp		
2572231758	t3m_00114	Protein_length		912aa		
2572231758	t3m_00114	GC			0.63	
2572231759	t3m_00115	Locus_type		tRNA		
2572231759	t3m_00115	Product_name		tRNA_Ile_GAT		
2572231759	t3m_00115	Scaffold		t3m_contig_70_5_len_122850_read_count_10924403.1		
2572231759	t3m_00115	Coordinates		122781..122840(+)		
2572231759	t3m_00115	DNA_length		60bp		
2572231759	t3m_00115	GC			0.57	
2572231760	t3m_00116	pfam13248	zf-ribbon_3			1.10E-05
2572231760	t3m_00116	Locus_type		CDS		
2572231760	t3m_00116	Product_name		zinc-ribbon domain		
2572231760	t3m_00116	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231760	t3m_00116	Coordinates		3..176(+)		
2572231760	t3m_00116	DNA_length		174bp		
2572231760	t3m_00116	Protein_length		57aa		
2572231760	t3m_00116	GC			0.76	
2572231761	t3m_00117	pfam05317	Thermopsin			2.50E-46
2572231761	t3m_00117	EC:3.4.23.42	Thermopsin.			
2572231761	t3m_00117	KO:K01385	thermopsin [EC:3.4.23.42]			0.00E+00

2572231761	t3m_00117	Locus_type		CDS	
2572231761	t3m_00117	Product_name		Thermopsin	
2572231761	t3m_00117	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231761	t3m_00117	Coordinates		655..3168(+)	
2572231761	t3m_00117	DNA_length		2514bp	
2572231761	t3m_00117	Protein_length		837aa	
2572231761	t3m_00117	GC		0.64	
2572231761	t3m_00117	Transmembrane		Yes	
2572231762	t3m_00118	KEGG_module	M00169: CAM (Crassulacean acid metabolism), light		
2572231762	t3m_00118	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2572231762	t3m_00118	KEGG_module	M00172: C4-dicarboxylic acid cycle, NADP+ -malic enzyme type		
2572231762	t3m_00118	KEGG_module	M00171: C4-dicarboxylic acid cycle, NAD+ -malic enzyme type		
2572231762	t3m_00118	Metacyc	PWY-7115: C4 photosynthetic carbon assimilation cycle, NAD-ME type		
2572231762	t3m_00118	Metacyc	PWY-7117: C4 photosynthetic carbon assimilation cycle, PEPCK type		
2572231762	t3m_00118	Metacyc	PWY-6549: glutamine biosynthesis III		
2572231762	t3m_00118	Metacyc	PWY-241: C4 photosynthetic carbon assimilation cycle, NADP-ME type		
2572231762	t3m_00118	IMG_pathway	289: Oxaloacetate synthesis via phosphoenolpyruvate		
2572231762	t3m_00118	COG_category	[G] Carbohydrate transport and metabolism		
2572231762	t3m_00118	COG0574	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase		0.00E+00
2572231762	t3m_00118	pfam00391	PEP-utilizers		1.60E-22
2572231762	t3m_00118	pfam02896	PEP-utilizers_C		1.50E-93
2572231762	t3m_00118	pfam01326	PPDK_N		1.10E-59
2572231762	t3m_00118	EC:2.7.9.1	Pyruvate, phosphate dikinase.		
2572231762	t3m_00118	TIGR01828	pyruvate, phosphate dikinase		0.00E+00
2572231762	t3m_00118	KO:K01006	pyruvate,orthophosphate dikinase [EC:2.7.9.1]		0.00E+00
2572231762	t3m_00118	ITERM:00813	pyruvate phosphate dikinase (EC 2.7.9.1)		
2572231762	t3m_00118	Locus_type		CDS	
2572231762	t3m_00118	Product_name		pyruvate phosphate dikinase (EC 2.7.9.1)	
2572231762	t3m_00118	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231762	t3m_00118	Coordinates		3451..6099(+)	
2572231762	t3m_00118	DNA_length		2649bp	
2572231762	t3m_00118	Protein_length		882aa	
2572231762	t3m_00118	GC		0.67	

2572231763	t3m_00119	KEGG_module	M00248: Putative antibiotic transport system		
2572231763	t3m_00119	COG_category	[V] Defense mechanisms		
2572231763	t3m_00119	COG1131	ABC-type multidrug transport system, ATPase component		4.00E-59
2572231763	t3m_00119	pfam00005	ABC_tran		1.50E-22
2572231763	t3m_00119	KO:K09687	antibiotic transport system ATP-binding protein		0.00E+00
2572231763	t3m_00119	Locus_type		CDS	
2572231763	t3m_00119	Product_name		ABC-type multidrug transport system, ATPase component	
2572231763	t3m_00119	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231763	t3m_00119	Coordinates		6210..7217(+)	
2572231763	t3m_00119	DNA_length		1008bp	
2572231763	t3m_00119	Protein_length		335aa	
2572231763	t3m_00119	GC		0.7	
2572231764	t3m_00120	pfam12730	ABC2_membrane_4		2.70E-12
2572231764	t3m_00120	Locus_type		CDS	
2572231764	t3m_00120	Product_name		ABC-2 family transporter protein	
2572231764	t3m_00120	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231764	t3m_00120	Coordinates		7229..7897(+)	
2572231764	t3m_00120	DNA_length		669bp	
2572231764	t3m_00120	Protein_length		222aa	
2572231764	t3m_00120	GC		0.71	
2572231764	t3m_00120	Transmembrane		Yes	
2572231765	t3m_00121	TIGR02537	archaeal flagellin N-terminal-like domain		3.30E-08
2572231765	t3m_00121	Locus_type		CDS	
2572231765	t3m_00121	Product_name		archaeal flagellin N-terminal-like domain	
2572231765	t3m_00121	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231765	t3m_00121	Coordinates		8013..8654(-)	
2572231765	t3m_00121	DNA_length		642bp	
2572231765	t3m_00121	Protein_length		213aa	
2572231765	t3m_00121	GC		0.65	
2572231765	t3m_00121	Transmembrane		Yes	

2572231766	t3m_00122	COG_category	[S] Function unknown			
2572231766	t3m_00122	COG2246	Predicted membrane protein			4.00E-05
2572231766	t3m_00122	pfam04138	GtrA			8.40E-16
2572231766	t3m_00122	Locus_type		CDS		
2572231766	t3m_00122	Product_name		Predicted membrane protein		
2572231766	t3m_00122	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231766	t3m_00122	Coordinates		8935..9402(-)		
2572231766	t3m_00122	DNA_length		468bp		
2572231766	t3m_00122	Protein_length		155aa		
2572231766	t3m_00122	GC			0.64	
2572231766	t3m_00122	Transmembrane		Yes		

2572231767	t3m_00123	Locus_type		CDS		
2572231767	t3m_00123	Product_name		hypothetical protein		
2572231767	t3m_00123	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231767	t3m_00123	Coordinates		9866..11257(+)		
2572231767	t3m_00123	DNA_length		1392bp		
2572231767	t3m_00123	Protein_length		463aa		
2572231767	t3m_00123	GC			0.67	
2572231767	t3m_00123	Transmembrane		Yes		

2572231768	t3m_00124	Locus_type		CDS		
2572231768	t3m_00124	Product_name		hypothetical protein		
2572231768	t3m_00124	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231768	t3m_00124	Coordinates		11355..11957(+)		
2572231768	t3m_00124	DNA_length		603bp		
2572231768	t3m_00124	Protein_length		200aa		
2572231768	t3m_00124	GC			0.62	

2572231769	t3m_00125	IMG_pathway	667: Ammonium transport via ammonium channel			
2572231769	t3m_00125	COG_category	[P] Inorganic ion transport and metabolism			
2572231769	t3m_00125	COG0004	Ammonia permease			1.00E-112
2572231769	t3m_00125	pfam00909	Ammonium_transp			1.90E-118
2572231769	t3m_00125	TIGR00836	ammonium transporter			0.00E+00

2572231769	t3m_00125	KO:K03320	ammonium transporter, Amt family		0.00E+00
2572231769	t3m_00125	ITERM:05717	ammonium transporter (TC 1.A.11)		
2572231769	t3m_00125	Locus_type		CDS	
2572231769	t3m_00125	Product_name		ammonium transporter (TC 1.A.11)	
2572231769	t3m_00125	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231769	t3m_00125	Coordinates		12221..13453(+)	
2572231769	t3m_00125	DNA_length		1233bp	
2572231769	t3m_00125	Protein_length		410aa	
2572231769	t3m_00125	GC		0.64	
2572231769	t3m_00125	Transmembrane		Yes	
2572231770	t3m_00126	IMG_pathway	667: Ammonium transport via ammonium channel		
2572231770	t3m_00126	COG_category	[P] Inorganic ion transport and metabolism		
2572231770	t3m_00126	COG0004	Ammonia permease		4.00E-98
2572231770	t3m_00126	pfam00909	Ammonium_transp		8.30E-102
2572231770	t3m_00126	TIGR00836	ammonium transporter		4.10E-116
2572231770	t3m_00126	KO:K03320	ammonium transporter, Amt family		0.00E+00
2572231770	t3m_00126	ITERM:05717	ammonium transporter (TC 1.A.11)		
2572231770	t3m_00126	Locus_type		CDS	
2572231770	t3m_00126	Product_name		ammonium transporter (TC 1.A.11)	
2572231770	t3m_00126	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231770	t3m_00126	Coordinates		13737..14951(-)	
2572231770	t3m_00126	DNA_length		1215bp	
2572231770	t3m_00126	Protein_length		404aa	
2572231770	t3m_00126	GC		0.63	
2572231770	t3m_00126	Transmembrane		Yes	
2572231771	t3m_00127	COG_category	[T] Signal transduction mechanisms		
2572231771	t3m_00127	COG0467	RecA-superfamily ATPases implicated in signal transduction		2.00E-08
2572231771	t3m_00127	pfam07088	GvpD		2.70E-26
2572231771	t3m_00127	Locus_type		CDS	
2572231771	t3m_00127	Product_name		RecA-superfamily ATPases implicated in signal transduction	
2572231771	t3m_00127	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231771	t3m_00127	Coordinates		15392..16885(+)	

2572231771	t3m_00127	DNA_length		1494bp	
2572231771	t3m_00127	Protein_length		497aa	
2572231771	t3m_00127	GC		0.65	

2572231772	t3m_00128	Locus_type		CDS	
2572231772	t3m_00128	Product_name		hypothetical protein	
2572231772	t3m_00128	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231772	t3m_00128	Coordinates		17019..17771(-)	
2572231772	t3m_00128	DNA_length		753bp	
2572231772	t3m_00128	Protein_length		250aa	
2572231772	t3m_00128	GC		0.67	
2572231772	t3m_00128	Transmembrane		Yes	

2572231773	t3m_00129	KEGG_module	M00254: ABC-2 type transport system		
2572231773	t3m_00129	COG_category	[V] Defense mechanisms		
2572231773	t3m_00129	COG1131	ABC-type multidrug transport system, ATPase component		4.00E-54
2572231773	t3m_00129	pfam00005	ABC_tran		3.40E-22
2572231773	t3m_00129	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2572231773	t3m_00129	Locus_type		CDS	
2572231773	t3m_00129	Product_name		ABC-type multidrug transport system, ATPase component	
2572231773	t3m_00129	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231773	t3m_00129	Coordinates		17768..18697(-)	
2572231773	t3m_00129	DNA_length		930bp	
2572231773	t3m_00129	Protein_length		309aa	
2572231773	t3m_00129	GC		0.67	

2572231774	t3m_00130	KEGG_module	M00254: ABC-2 type transport system		
2572231774	t3m_00130	COG_category	[R] General function prediction only		
2572231774	t3m_00130	COG1277	ABC-type transport system involved in multi-copper enzyme maturatior		2.00E-10
2572231774	t3m_00130	pfam12730	ABC2_membrane_4		7.00E-17
2572231774	t3m_00130	KO:K01992	ABC-2 type transport system permease protein		2.60E-35
2572231774	t3m_00130	Locus_type		CDS	
2572231774	t3m_00130	Product_name		ABC-type transport system involved in multi-copper enzyme maturation	
2572231774	t3m_00130	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	

2572231774	t3m_00130	Coordinates		18701..19588(-)	
2572231774	t3m_00130	DNA_length		888bp	
2572231774	t3m_00130	Protein_length		295aa	
2572231774	t3m_00130	GC		0.65	
2572231774	t3m_00130	Transmembrane		Yes	

2572231775	t3m_00131	Locus_type		CDS	
2572231775	t3m_00131	Product_name		hypothetical protein	
2572231775	t3m_00131	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231775	t3m_00131	Coordinates		19969..20658(+)	
2572231775	t3m_00131	DNA_length		690bp	
2572231775	t3m_00131	Protein_length		229aa	
2572231775	t3m_00131	GC		0.65	
2572231775	t3m_00131	Transmembrane		Yes	

2572231776	t3m_00132	KEGG_module	M00336: Twin-arginine translocation (Tat) system		
2572231776	t3m_00132	pfam02416	MttA_Hcf106		1.10E-11
2572231776	t3m_00132	TIGR01411	twin arginine-targeting protein translocase, TatA/E family		3.10E-19
2572231776	t3m_00132	KO:K03116	sec-independent protein translocase protein TatA		1.20E-12
2572231776	t3m_00132	Locus_type		CDS	
2572231776	t3m_00132	Product_name		twin arginine-targeting protein translocase, TatA/E family	
2572231776	t3m_00132	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231776	t3m_00132	Coordinates		20781..20987(+)	
2572231776	t3m_00132	DNA_length		207bp	
2572231776	t3m_00132	Protein_length		68aa	
2572231776	t3m_00132	GC		0.63	

2572231777	t3m_00133	KEGG_module	M00336: Twin-arginine translocation (Tat) system		
2572231777	t3m_00133	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport		
2572231777	t3m_00133	COG0805	Sec-independent protein secretion pathway component TatC		2.00E-33
2572231777	t3m_00133	pfam00902	TatC		1.10E-39
2572231777	t3m_00133	TIGR00945	Twin arginine targeting (Tat) protein translocase TatC		6.30E-36
2572231777	t3m_00133	KO:K03118	sec-independent protein translocase protein TatC		0.00E+00
2572231777	t3m_00133	Locus_type		CDS	

2572231777	t3m_00133	Product_name		Sec-independent protein secretion pathway component TatC	
2572231777	t3m_00133	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231777	t3m_00133	Coordinates		21091..21927(+)	
2572231777	t3m_00133	DNA_length		837bp	
2572231777	t3m_00133	Protein_length		278aa	
2572231777	t3m_00133	GC		0.64	
2572231777	t3m_00133	Transmembrane		Yes	
2572231778	t3m_00134	Locus_type		CDS	
2572231778	t3m_00134	Product_name		hypothetical protein	
2572231778	t3m_00134	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231778	t3m_00134	Coordinates		21932..22336(+)	
2572231778	t3m_00134	DNA_length		405bp	
2572231778	t3m_00134	Protein_length		134aa	
2572231778	t3m_00134	GC		0.68	
2572231778	t3m_00134	Transmembrane		Yes	
2572231779	t3m_00135	Locus_type		CDS	
2572231779	t3m_00135	Product_name		hypothetical protein	
2572231779	t3m_00135	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231779	t3m_00135	Coordinates		22333..22515(+)	
2572231779	t3m_00135	DNA_length		183bp	
2572231779	t3m_00135	Protein_length		60aa	
2572231779	t3m_00135	GC		0.66	
2572231779	t3m_00135	Transmembrane		Yes	
2572231780	t3m_00136	COG_category	[C] Energy production and conversion		
2572231780	t3m_00136	COG0723	Rieske Fe-S protein		7.00E-19
2572231780	t3m_00136	pfam00355	Rieske		1.90E-14
2572231780	t3m_00136	TIGR02694	arsenite oxidase, small subunit		6.10E-21
2572231780	t3m_00136	TIGR01409	Tat (twin-arginine translocation) pathway signal sequence		3.30E-08
2572231780	t3m_00136	Locus_type		CDS	
2572231780	t3m_00136	Product_name		Rieske Fe-S protein	
2572231780	t3m_00136	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	

2572231780	t3m_00136	Coordinates		22512..23345(+)		
2572231780	t3m_00136	DNA_length		834bp		
2572231780	t3m_00136	Protein_length		277aa		
2572231780	t3m_00136	GC			0.67	
2572231780	t3m_00136	Transmembrane		Yes		
2572231781	t3m_00137	COG_category	[C] Energy production and conversion			
2572231781	t3m_00137	COG1290	Cytochrome b subunit of the bc complex			5.00E-44
2572231781	t3m_00137	pfam13631	Cytochrom_B_N_2			1.70E-29
2572231781	t3m_00137	pfam00032	Cytochrom_B_C			1.40E-04
2572231781	t3m_00137	Locus_type		CDS		
2572231781	t3m_00137	Product_name		Cytochrome b subunit of the bc complex		
2572231781	t3m_00137	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231781	t3m_00137	Coordinates		23354..24874(+)		
2572231781	t3m_00137	DNA_length		1521bp		
2572231781	t3m_00137	Protein_length		506aa		
2572231781	t3m_00137	GC			0.67	
2572231781	t3m_00137	Transmembrane		Yes		
2572231782	t3m_00138	COG_category	[P] Inorganic ion transport and metabolism			
2572231782	t3m_00138	COG_category	[E] Amino acid transport and metabolism			
2572231782	t3m_00138	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c			2.00E-32
2572231782	t3m_00138	pfam05317	Thermopsin			3.80E-37
2572231782	t3m_00138	pfam00528	BPD_transp_1			7.10E-13
2572231782	t3m_00138	Locus_type		CDS		
2572231782	t3m_00138	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease co		
2572231782	t3m_00138	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231782	t3m_00138	Coordinates		24975..28829(-)		
2572231782	t3m_00138	DNA_length		3855bp		
2572231782	t3m_00138	Protein_length		1284aa		
2572231782	t3m_00138	GC			0.66	
2572231782	t3m_00138	Transmembrane		Yes		
2572231783	t3m_00139	COG_category	[E] Amino acid transport and metabolism			

2572231783	t3m_00139	COG_category	[P] Inorganic ion transport and metabolism			
2572231783	t3m_00139	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c			2.00E-19
2572231783	t3m_00139	pfam00528	BPD_transp_1			5.10E-11
2572231783	t3m_00139	Locus_type		CDS		
2572231783	t3m_00139	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease co		
2572231783	t3m_00139	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231783	t3m_00139	Coordinates		28853..29869(-)		
2572231783	t3m_00139	DNA_length		1017bp		
2572231783	t3m_00139	Protein_length		338aa		
2572231783	t3m_00139	GC			0.65	
2572231783	t3m_00139	Transmembrane		Yes		
2572231784	t3m_00140	Locus_type		CDS		
2572231784	t3m_00140	Product_name		hypothetical protein		
2572231784	t3m_00140	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231784	t3m_00140	Coordinates		30079..30309(+)		
2572231784	t3m_00140	DNA_length		231bp		
2572231784	t3m_00140	Protein_length		76aa		
2572231784	t3m_00140	GC			0.68	
2572231785	t3m_00141	KEGG_module	M00288: RPA complex			
2572231785	t3m_00141	pfam01336	tRNA_anti-codon			2.10E-10
2572231785	t3m_00141	KO:K07466	replication factor A1			9.30E-11
2572231785	t3m_00141	Locus_type		CDS		
2572231785	t3m_00141	Product_name		OB-fold nucleic acid binding domain		
2572231785	t3m_00141	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231785	t3m_00141	Coordinates		30399..30686(-)		
2572231785	t3m_00141	DNA_length		288bp		
2572231785	t3m_00141	Protein_length		95aa		
2572231785	t3m_00141	GC			0.62	
2572231786	t3m_00142	Locus_type		CDS		
2572231786	t3m_00142	Product_name		hypothetical protein		
2572231786	t3m_00142	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		

2572231786	t3m_00142	Coordinates		30753..31178(-)	
2572231786	t3m_00142	DNA_length		426bp	
2572231786	t3m_00142	Protein_length		141aa	
2572231786	t3m_00142	GC		0.67	
2572231787	t3m_00143	Locus_type		CDS	
2572231787	t3m_00143	Product_name		hypothetical protein	
2572231787	t3m_00143	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231787	t3m_00143	Coordinates		31177..31335(+)	
2572231787	t3m_00143	DNA_length		159bp	
2572231787	t3m_00143	Protein_length		52aa	
2572231787	t3m_00143	GC		0.67	
2572231788	t3m_00144	Locus_type		CDS	
2572231788	t3m_00144	Product_name		hypothetical protein	
2572231788	t3m_00144	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231788	t3m_00144	Coordinates		31373..31924(-)	
2572231788	t3m_00144	DNA_length		552bp	
2572231788	t3m_00144	Protein_length		183aa	
2572231788	t3m_00144	GC		0.64	
2572231788	t3m_00144	Transmembrane		Yes	
2572231789	t3m_00145	Locus_type		CDS	
2572231789	t3m_00145	Product_name		hypothetical protein	
2572231789	t3m_00145	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231789	t3m_00145	Coordinates		32088..33335(-)	
2572231789	t3m_00145	DNA_length		1248bp	
2572231789	t3m_00145	Protein_length		415aa	
2572231789	t3m_00145	GC		0.66	
2572231789	t3m_00145	Transmembrane		Yes	
2572231790	t3m_00146	pfam00717	Peptidase_S24		7.60E-06
2572231790	t3m_00146	TIGR02228	signal peptidase I, archaeal type		1.80E-27
2572231790	t3m_00146	Locus_type		CDS	

2572231790	t3m_00146	Product_name		signal peptidase I, archaeal type		
2572231790	t3m_00146	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231790	t3m_00146	Coordinates		33332..34612(-)		
2572231790	t3m_00146	DNA_length		1281bp		
2572231790	t3m_00146	Protein_length		426aa		
2572231790	t3m_00146	GC			0.66	
2572231790	t3m_00146	Transmembrane		Yes		
2572231791	t3m_00147	COG_category	[K] Transcription			
2572231791	t3m_00147	COG3432	Predicted transcriptional regulator			4.00E-06
2572231791	t3m_00147	pfam14947	HTH_45			3.10E-11
2572231791	t3m_00147	Locus_type		CDS		
2572231791	t3m_00147	Product_name		Predicted transcriptional regulator		
2572231791	t3m_00147	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231791	t3m_00147	Coordinates		34693..35271(-)		
2572231791	t3m_00147	DNA_length		579bp		
2572231791	t3m_00147	Protein_length		192aa		
2572231791	t3m_00147	GC			0.67	
2572231792	t3m_00148	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572231792	t3m_00148	COG1247	Sortase and related acyltransferases			2.00E-06
2572231792	t3m_00148	pfam00583	Acetyltransf_1			2.80E-08
2572231792	t3m_00148	Locus_type		CDS		
2572231792	t3m_00148	Product_name		Sortase and related acyltransferases		
2572231792	t3m_00148	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231792	t3m_00148	Coordinates		35518..36267(+)		
2572231792	t3m_00148	DNA_length		750bp		
2572231792	t3m_00148	Protein_length		249aa		
2572231792	t3m_00148	GC			0.69	
2572231793	t3m_00149	Locus_type		CDS		
2572231793	t3m_00149	Product_name		hypothetical protein		
2572231793	t3m_00149	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231793	t3m_00149	Coordinates		36286..37335(-)		

2572231793	t3m_00149	DNA_length	1050bp	
2572231793	t3m_00149	Protein_length	349aa	
2572231793	t3m_00149	GC		0.63
2572231793	t3m_00149	Signal_peptide	Yes	
2572231793	t3m_00149	Transmembrane	Yes	
2572231794	t3m_00150	Locus_type	CDS	
2572231794	t3m_00150	Product_name	hypothetical protein	
2572231794	t3m_00150	Scaffold	t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231794	t3m_00150	Coordinates	37332..38861(-)	
2572231794	t3m_00150	DNA_length	1530bp	
2572231794	t3m_00150	Protein_length	509aa	
2572231794	t3m_00150	GC		0.66
2572231795	t3m_00151	Locus_type	CDS	
2572231795	t3m_00151	Product_name	hypothetical protein	
2572231795	t3m_00151	Scaffold	t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231795	t3m_00151	Coordinates	38863..40101(-)	
2572231795	t3m_00151	DNA_length	1239bp	
2572231795	t3m_00151	Protein_length	412aa	
2572231795	t3m_00151	GC		0.66
2572231796	t3m_00152	Locus_type	CDS	
2572231796	t3m_00152	Product_name	hypothetical protein	
2572231796	t3m_00152	Scaffold	t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231796	t3m_00152	Coordinates	40291..40560(+)	
2572231796	t3m_00152	DNA_length	270bp	
2572231796	t3m_00152	Protein_length	89aa	
2572231796	t3m_00152	GC		0.64
2572231797	t3m_00153	Locus_type	CDS	
2572231797	t3m_00153	Product_name	hypothetical protein	
2572231797	t3m_00153	Scaffold	t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231797	t3m_00153	Coordinates	40672..41676(-)	

2572231797	t3m_00153	DNA_length		1005bp		
2572231797	t3m_00153	Protein_length		334aa		
2572231797	t3m_00153	GC			0.66	
2572231797	t3m_00153	Transmembrane		Yes		
2572231798	t3m_00154	Locus_type		CDS		
2572231798	t3m_00154	Product_name		hypothetical protein		
2572231798	t3m_00154	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231798	t3m_00154	Coordinates		41914..42621(+)		
2572231798	t3m_00154	DNA_length		708bp		
2572231798	t3m_00154	Protein_length		235aa		
2572231798	t3m_00154	GC			0.66	
2572231799	t3m_00155	pfam13632	Glyco_trans_2_3			5.30E-19
2572231799	t3m_00155	Locus_type		CDS		
2572231799	t3m_00155	Product_name		Glycosyl transferase family group 2		
2572231799	t3m_00155	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231799	t3m_00155	Coordinates		42618..43781(-)		
2572231799	t3m_00155	DNA_length		1164bp		
2572231799	t3m_00155	Protein_length		387aa		
2572231799	t3m_00155	GC			0.67	
2572231799	t3m_00155	Transmembrane		Yes		
2572231800	t3m_00156	Locus_type		CDS		
2572231800	t3m_00156	Product_name		hypothetical protein		
2572231800	t3m_00156	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231800	t3m_00156	Coordinates		43778..44719(-)		
2572231800	t3m_00156	DNA_length		942bp		
2572231800	t3m_00156	Protein_length		313aa		
2572231800	t3m_00156	GC			0.7	
2572231800	t3m_00156	Transmembrane		Yes		
2572231801	t3m_00157	Locus_type		CDS		
2572231801	t3m_00157	Product_name		hypothetical protein		

2572231801	t3m_00157	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231801	t3m_00157	Coordinates		44791..45018(-)		
2572231801	t3m_00157	DNA_length		228bp		
2572231801	t3m_00157	Protein_length		75aa		
2572231801	t3m_00157	GC			0.67	
2572231801	t3m_00157	Transmembrane		Yes		
2572231802	t3m_00158	Locus_type		CDS		
2572231802	t3m_00158	Product_name		hypothetical protein		
2572231802	t3m_00158	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231802	t3m_00158	Coordinates		45015..45728(-)		
2572231802	t3m_00158	DNA_length		714bp		
2572231802	t3m_00158	Protein_length		237aa		
2572231802	t3m_00158	GC			0.69	
2572231802	t3m_00158	Signal_peptide		Yes		
2572231802	t3m_00158	Transmembrane		Yes		
2572231803	t3m_00159	pfam05763	DUF835			2.40E-07
2572231803	t3m_00159	pfam08264	Anticodon_1			4.80E-14
2572231803	t3m_00159	pfam00133	tRNA-synt_1			6.20E-25
2572231803	t3m_00159	Locus_type		CDS		
2572231803	t3m_00159	Product_name		tRNA synthetases class I (I, L, M and V)/Protein of unknown function (DU		
2572231803	t3m_00159	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231803	t3m_00159	Coordinates		45809..50614(-)		
2572231803	t3m_00159	DNA_length		4806bp		
2572231803	t3m_00159	Protein_length		1601aa		
2572231803	t3m_00159	GC			0.71	
2572231804	t3m_00160	IMG_pathway	854: Hypusine synthesis			
2572231804	t3m_00160	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231804	t3m_00160	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eI			6.00E-27
2572231804	t3m_00160	pfam01287	eIF-5a			9.80E-12
2572231804	t3m_00160	pfam08207	EFP_N			2.00E-04
2572231804	t3m_00160	TIGR00037	translation elongation factor IF5A			5.90E-51

2572231804	t3m_00160	KO:K03263	translation initiation factor 5A			1.20E-42
2572231804	t3m_00160	ITERM:01965	translation initiation factor 5A precursor (eIF-5A)			
2572231804	t3m_00160	Locus_type		CDS		
2572231804	t3m_00160	Product_name		translation initiation factor 5A precursor (eIF-5A)		
2572231804	t3m_00160	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231804	t3m_00160	Coordinates		50756..51142(+)		
2572231804	t3m_00160	DNA_length		387bp		
2572231804	t3m_00160	Protein_length		128aa		
2572231804	t3m_00160	GC			0.65	
2572231805	t3m_00161	Locus_type		CDS		
2572231805	t3m_00161	Product_name		hypothetical protein		
2572231805	t3m_00161	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231805	t3m_00161	Coordinates		51296..55777(+)		
2572231805	t3m_00161	DNA_length		4482bp		
2572231805	t3m_00161	Protein_length		1493aa		
2572231805	t3m_00161	GC			0.71	
2572231806	t3m_00162	Locus_type		CDS		
2572231806	t3m_00162	Product_name		hypothetical protein		
2572231806	t3m_00162	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231806	t3m_00162	Coordinates		55782..56240(-)		
2572231806	t3m_00162	DNA_length		459bp		
2572231806	t3m_00162	Protein_length		152aa		
2572231806	t3m_00162	GC			0.68	
2572231807	t3m_00163	COG_category	[S] Function unknown			
2572231807	t3m_00163	COG0393	Uncharacterized conserved protein			1.00E-29
2572231807	t3m_00163	pfam01906	YbjQ_1			1.50E-32
2572231807	t3m_00163	Locus_type		CDS		
2572231807	t3m_00163	Product_name		Uncharacterized conserved protein		
2572231807	t3m_00163	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231807	t3m_00163	Coordinates		56324..56728(+)		
2572231807	t3m_00163	DNA_length		405bp		

2572231807	t3m_00163	Protein_length		134aa	
2572231807	t3m_00163	GC		0.68	
2572231808	t3m_00164	Locus_type		tRNA	
2572231808	t3m_00164	Product_name		tRNA_Glu_CTC	
2572231808	t3m_00164	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231808	t3m_00164	Coordinates		56780..56852(+)	
2572231808	t3m_00164	DNA_length		73bp	
2572231808	t3m_00164	GC		0.62	
2572231809	t3m_00165	pfam13248	zf-ribbon_3		2.70E-07
2572231809	t3m_00165	Locus_type		CDS	
2572231809	t3m_00165	Product_name		zinc-ribbon domain	
2572231809	t3m_00165	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231809	t3m_00165	Coordinates		56967..57608(-)	
2572231809	t3m_00165	DNA_length		642bp	
2572231809	t3m_00165	Protein_length		213aa	
2572231809	t3m_00165	GC		0.67	
2572231809	t3m_00165	Transmembrane		Yes	
2572231810	t3m_00166	pfam12695	Abhydrolase_5		5.40E-14
2572231810	t3m_00166	Locus_type		CDS	
2572231810	t3m_00166	Product_name		Alpha/beta hydrolase family	
2572231810	t3m_00166	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231810	t3m_00166	Coordinates		58176..58694(-)	
2572231810	t3m_00166	DNA_length		519bp	
2572231810	t3m_00166	Protein_length		172aa	
2572231810	t3m_00166	GC		0.68	
2572231811	t3m_00167	Locus_type		CDS	
2572231811	t3m_00167	Product_name		hypothetical protein	
2572231811	t3m_00167	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231811	t3m_00167	Coordinates		58917..59726(-)	
2572231811	t3m_00167	DNA_length		810bp	

2572231811	t3m_00167	Protein_length		269aa		
2572231811	t3m_00167	GC			0.67	
2572231811	t3m_00167	Transmembrane		Yes		

2572231812	t3m_00168	pfam08241	Methyltransf_11			2.40E-20
2572231812	t3m_00168	Locus_type		CDS		
2572231812	t3m_00168	Product_name		Methyltransferase domain		
2572231812	t3m_00168	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231812	t3m_00168	Coordinates		60026..60625(+)		
2572231812	t3m_00168	DNA_length		600bp		
2572231812	t3m_00168	Protein_length		199aa		
2572231812	t3m_00168	GC			0.68	

2572231813	t3m_00169	KEGG_module	M00021: Cysteine biosynthesis, serine => cysteine			
2572231813	t3m_00169	Metacyc	PWY-6936: seleno-amino acid biosynthesis			
2572231813	t3m_00169	Metacyc	CYSTSYN-PWY: cysteine biosynthesis I			
2572231813	t3m_00169	COG_category	[E] Amino acid transport and metabolism			
2572231813	t3m_00169	COG0031	Cysteine synthase			5.00E-87
2572231813	t3m_00169	pfam00291	PALP			2.10E-53
2572231813	t3m_00169	EC:2.5.1.47	Cysteine synthase.			
2572231813	t3m_00169	KO:K01738	cysteine synthase A [EC:2.5.1.47]			0.00E+00
2572231813	t3m_00169	Locus_type		CDS		
2572231813	t3m_00169	Product_name		Cysteine synthase		
2572231813	t3m_00169	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231813	t3m_00169	Coordinates		60726..61670(-)		
2572231813	t3m_00169	DNA_length		945bp		
2572231813	t3m_00169	Protein_length		314aa		
2572231813	t3m_00169	GC			0.65	

2572231814	t3m_00170	COG_category	[S] Function unknown			
2572231814	t3m_00170	COG1650	Uncharacterized protein conserved in archaea			2.00E-29
2572231814	t3m_00170	pfam04414	tRNA_deacylase			1.70E-40
2572231814	t3m_00170	KO:K09716	hypothetical protein			1.40E-30
2572231814	t3m_00170	Locus_type		CDS		

2572231814	t3m_00170	Product_name		Uncharacterized protein conserved in archaea	
2572231814	t3m_00170	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231814	t3m_00170	Coordinates		61800..62666(+)	
2572231814	t3m_00170	DNA_length		867bp	
2572231814	t3m_00170	Protein_length		288aa	
2572231814	t3m_00170	GC		0.69	
2572231815	t3m_00171	Locus_type		CDS	
2572231815	t3m_00171	Product_name		hypothetical protein	
2572231815	t3m_00171	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231815	t3m_00171	Coordinates		62632..62889(-)	
2572231815	t3m_00171	DNA_length		258bp	
2572231815	t3m_00171	Protein_length		85aa	
2572231815	t3m_00171	GC		0.63	
2572231816	t3m_00172	Locus_type		CDS	
2572231816	t3m_00172	Product_name		hypothetical protein	
2572231816	t3m_00172	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231816	t3m_00172	Coordinates		63084..63971(-)	
2572231816	t3m_00172	DNA_length		888bp	
2572231816	t3m_00172	Protein_length		295aa	
2572231816	t3m_00172	GC		0.64	
2572231817	t3m_00173	COG_category	[R] General function prediction only		
2572231817	t3m_00173	COG0612	Predicted Zn-dependent peptidases		9.00E-46
2572231817	t3m_00173	pfam00675	Peptidase_M16		9.80E-06
2572231817	t3m_00173	pfam05193	Peptidase_M16_C		6.20E-18
2572231817	t3m_00173	Locus_type		CDS	
2572231817	t3m_00173	Product_name		Predicted Zn-dependent peptidases	
2572231817	t3m_00173	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231817	t3m_00173	Coordinates		64128..65399(-)	
2572231817	t3m_00173	DNA_length		1272bp	
2572231817	t3m_00173	Protein_length		423aa	
2572231817	t3m_00173	GC		0.7	

2572231818	t3m_00174	COG_category	[R] General function prediction only			
2572231818	t3m_00174	COG0612	Predicted Zn-dependent peptidases			2.00E-64
2572231818	t3m_00174	pfam05193	Peptidase_M16_C			1.80E-21
2572231818	t3m_00174	pfam00675	Peptidase_M16			6.50E-27
2572231818	t3m_00174	Locus_type		CDS		
2572231818	t3m_00174	Product_name		Predicted Zn-dependent peptidases		
2572231818	t3m_00174	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231818	t3m_00174	Coordinates		65392..66720(-)		
2572231818	t3m_00174	DNA_length		1329bp		
2572231818	t3m_00174	Protein_length		442aa		
2572231818	t3m_00174	GC			0.7	

2572231819	t3m_00175	KEGG_module	M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone
2572231819	t3m_00175	Metacyc	PWY-5132: humulone biosynthesis
2572231819	t3m_00175	Metacyc	PWY-6834: spermidine biosynthesis III
2572231819	t3m_00175	Metacyc	PWY-5816: all <i>trans</i> undecaprenyl diphosphate biosynthesis
2572231819	t3m_00175	Metacyc	PWY-5817: dodecaprenyl diphosphate biosynthesis
2572231819	t3m_00175	Metacyc	PWY-6262: demethylmenaquinol-8 biosynthesis II
2572231819	t3m_00175	Metacyc	PWY-6403: carrageenan biosynthesis
2572231819	t3m_00175	Metacyc	PWY-2681: <i>trans</i>-zeatin biosynthesis
2572231819	t3m_00175	Metacyc	PWY-5135: xanthohumol biosynthesis
2572231819	t3m_00175	Metacyc	PWY-6681: neurosporaxanthin biosynthesis
2572231819	t3m_00175	Metacyc	PWY-5133: cohumulone biosynthesis
2572231819	t3m_00175	Metacyc	PWY-702: methionine biosynthesis II
2572231819	t3m_00175	Metacyc	PWY-5893: tridecaprenyl diphosphate biosynthesis
2572231819	t3m_00175	Metacyc	PWY-5802: alizarin biosynthesis
2572231819	t3m_00175	Metacyc	PWY-5365: linear furanocoumarin biosynthesis
2572231819	t3m_00175	Metacyc	PWY-7169: hyperxanthone E biosynthesis
2572231819	t3m_00175	Metacyc	PWY-5808: hyperforin and adhyperforin biosynthesis
2572231819	t3m_00175	Metacyc	PWY-5770: phenazine-1-carboxylate biosynthesis
2572231819	t3m_00175	Metacyc	PWY-4681: kievitone biosynthesis
2572231819	t3m_00175	Metacyc	PWY-4502: wighteone and luteone biosynthesis
2572231819	t3m_00175	Metacyc	PWY-6936: seleno-amino acid biosynthesis

2572231819	t3m_00175	Metacyc	PWY-5068: chlorophyll cycle			
2572231819	t3m_00175	Metacyc	PWY-5064: chlorophyll <i>a</i> biosynthesis II			
2572231819	t3m_00175	Metacyc	PWY-5027: phylloquinol biosynthesis			
2572231819	t3m_00175	Metacyc	PWY-6793: demethylmenaquinol-8 biosynthesis III			
2572231819	t3m_00175	IMG_pathway	48: 2,3-Di-O-geranylgeranylglyceryl 3-phosphate biosynthesis			
2572231819	t3m_00175	COG_category	[H] Coenzyme transport and metabolism			
2572231819	t3m_00175	COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferas			1.00E-19
2572231819	t3m_00175	pfam01040	UbiA			5.60E-31
2572231819	t3m_00175	EC:2.5.1.-	Transferases. Transferring alkyl or aryl groups, other than methyl groups. Transferring alkyl or aryl			
2572231819	t3m_00175	KO:K03179	4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]			6.00E-42
2572231819	t3m_00175	ITERM:00052	geranylgeranylglycerol-phosphate geranylgeranyltransferase (EC 2.5.1.42)			
2572231819	t3m_00175	Locus_type		CDS		
2572231819	t3m_00175	Product_name		geranylgeranylglycerol-phosphate geranylgeranyltransferase (EC 2.5.1.4		
2572231819	t3m_00175	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231819	t3m_00175	Coordinates		66847..67674(+)		
2572231819	t3m_00175	DNA_length		828bp		
2572231819	t3m_00175	Protein_length		275aa		
2572231819	t3m_00175	GC			0.68	
2572231819	t3m_00175	Transmembrane		Yes		
2572231820	t3m_00176	Metacyc	PWY-702: methionine biosynthesis II			
2572231820	t3m_00176	Metacyc	PWY-5133: cohumulone biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5808: hyperforin and adhyperforin biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-6834: spermidine biosynthesis III			
2572231820	t3m_00176	Metacyc	PWY-5064: chlorophyll <i>a</i> biosynthesis II			
2572231820	t3m_00176	Metacyc	PWY-6403: carrageenan biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5365: linear furanocoumarin biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-7169: hyperxanthone E biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5132: humulone biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-6262: demethylmenaquinol-8 biosynthesis II			
2572231820	t3m_00176	Metacyc	PWY-6936: seleno-amino acid biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5893: tridecaprenyl diphosphate biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5027: phylloquinol biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-6793: demethylmenaquinol-8 biosynthesis III			

2572231820	t3m_00176	Metacyc	PWY-5068: chlorophyll cycle			
2572231820	t3m_00176	Metacyc	PWY-5816: all <i>trans</i> undecaprenyl diphosphate biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5770: phenazine-1-carboxylate biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-4502: wighteone and luteone biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5817: dodecaprenyl diphosphate biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-2681: <i>trans</i>-zeatin biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5135: xanthohumol biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-4681: kievitone biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-5802: alizarin biosynthesis			
2572231820	t3m_00176	Metacyc	PWY-6681: neurosporaxanthin biosynthesis			
2572231820	t3m_00176	COG_category	[R] General function prediction only			
2572231820	t3m_00176	COG1646	Predicted phosphate-binding enzymes, TIM-barrel fold			2.00E-54
2572231820	t3m_00176	pfam01884	PcrB			6.40E-59
2572231820	t3m_00176	EC:2.5.1.-	Transferases. Transferring alkyl or aryl groups, other than methyl groups. Transferring alkyl or aryl			
2572231820	t3m_00176	TIGR01768	geranylgeranylglyceryl phosphate synthase family protein			1.40E-64
2572231820	t3m_00176	TIGR01769	phosphoglycerol geranylgeranyltransferase			5.00E-66
2572231820	t3m_00176	KO:K07094	putative glycerol-1-phosphate prenyltransferase [EC:2.5.1.-]			0.00E+00
2572231820	t3m_00176	Locus_type		CDS		
2572231820	t3m_00176	Product_name		phosphoglycerol geranylgeranyltransferase		
2572231820	t3m_00176	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231820	t3m_00176	Coordinates		67674..68438(+)		
2572231820	t3m_00176	DNA_length		765bp		
2572231820	t3m_00176	Protein_length		254aa		
2572231820	t3m_00176	GC			0.69	
2572231821	t3m_00177	COG_category	[S] Function unknown			
2572231821	t3m_00177	COG3356	Predicted membrane protein			4.00E-57
2572231821	t3m_00177	pfam09843	DUF2070			9.20E-28
2572231821	t3m_00177	KO:K08979	putative membrane protein			0.00E+00
2572231821	t3m_00177	Locus_type		CDS		
2572231821	t3m_00177	Product_name		Predicted membrane protein		
2572231821	t3m_00177	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231821	t3m_00177	Coordinates		68428..70242(+)		
2572231821	t3m_00177	DNA_length		1815bp		

2572231821	t3m_00177	Protein_length		604aa		
2572231821	t3m_00177	GC			0.68	
2572231821	t3m_00177	Transmembrane		Yes		

2572231822	t3m_00178	pfam01546	Peptidase_M20			6.80E-23
2572231822	t3m_00178	Locus_type		CDS		
2572231822	t3m_00178	Product_name		Peptidase family M20/M25/M40		
2572231822	t3m_00178	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231822	t3m_00178	Coordinates		70250..71881(+)		
2572231822	t3m_00178	DNA_length		1632bp		
2572231822	t3m_00178	Protein_length		543aa		
2572231822	t3m_00178	GC			0.71	

2572231823	t3m_00179	COG_category	[I] Lipid transport and metabolism			
2572231823	t3m_00179	COG0575	CDP-diglyceride synthetase			4.00E-05
2572231823	t3m_00179	pfam01864	DUF46			1.30E-36
2572231823	t3m_00179	Locus_type		CDS		
2572231823	t3m_00179	Product_name		CDP-diglyceride synthetase		
2572231823	t3m_00179	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231823	t3m_00179	Coordinates		71897..72475(+)		
2572231823	t3m_00179	DNA_length		579bp		
2572231823	t3m_00179	Protein_length		192aa		
2572231823	t3m_00179	GC			0.69	
2572231823	t3m_00179	Transmembrane		Yes		

2572231824	t3m_00180	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP			
2572231824	t3m_00180	Metacyc	PWY-5686: UMP biosynthesis			
2572231824	t3m_00180	IMG_pathway	321: Uridine 5'-monophosphate biosynthesis			
2572231824	t3m_00180	COG_category	[F] Nucleotide transport and metabolism			
2572231824	t3m_00180	COG0461	Orotate phosphoribosyltransferase			9.00E-41
2572231824	t3m_00180	pfam00156	Pribosyltran			1.20E-09
2572231824	t3m_00180	EC:2.4.2.10	Orotate phosphoribosyltransferase.			
2572231824	t3m_00180	TIGR00336	orotate phosphoribosyltransferase			6.90E-47
2572231824	t3m_00180	KO:K00762	orotate phosphoribosyltransferase [EC:2.4.2.10]			5.40E-39

2572231824	t3m_00180	ITERM:01392	orotate phosphoribosyltransferase (EC 2.4.2.10)			
2572231824	t3m_00180	Locus_type		CDS		
2572231824	t3m_00180	Product_name		orotate phosphoribosyltransferase (EC 2.4.2.10)		
2572231824	t3m_00180	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231824	t3m_00180	Coordinates		72472..73026(+)		
2572231824	t3m_00180	DNA_length		555bp		
2572231824	t3m_00180	Protein_length		184aa		
2572231824	t3m_00180	GC			0.7	
2572231825	t3m_00181	Metacyc	PWY-6689: tRNA splicing			
2572231825	t3m_00181	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231825	t3m_00181	COG1676	tRNA splicing endonuclease			3.00E-26
2572231825	t3m_00181	pfam01974	tRNA_int_endo			8.70E-09
2572231825	t3m_00181	pfam01974	tRNA_int_endo			2.80E-22
2572231825	t3m_00181	pfam02778	tRNA_int_endo_N			7.90E-10
2572231825	t3m_00181	pfam02778	tRNA_int_endo_N			5.20E-08
2572231825	t3m_00181	EC:3.1.27.9	tRNA-intron endonuclease.			
2572231825	t3m_00181	TIGR00324	tRNA-intron endonuclease			1.10E-18
2572231825	t3m_00181	KO:K01170	tRNA-intron endonuclease, archaea type [EC:3.1.27.9]			0.00E+00
2572231825	t3m_00181	Locus_type		CDS		
2572231825	t3m_00181	Product_name		tRNA splicing endonuclease		
2572231825	t3m_00181	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231825	t3m_00181	Coordinates		73023..74087(+)		
2572231825	t3m_00181	DNA_length		1065bp		
2572231825	t3m_00181	Protein_length		354aa		
2572231825	t3m_00181	GC			0.71	
2572231826	t3m_00182	KEGG_module	M00022: Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate			
2572231826	t3m_00182	Metacyc	PWY-6163: chorismate biosynthesis from 3-dehydroquinate			
2572231826	t3m_00182	IMG_pathway	146: Chorismate synthesis			
2572231826	t3m_00182	IMG_pathway	519: Archaeal chorismate synthesis			
2572231826	t3m_00182	COG_category	[E] Amino acid transport and metabolism			
2572231826	t3m_00182	COG0082	Chorismate synthase			8.00E-111
2572231826	t3m_00182	pfam01264	Chorismate_synt			2.00E-119

2572231826	t3m_00182	EC:4.2.3.5	Chorismate synthase.			
2572231826	t3m_00182	TIGR00033	chorismate synthase			2.50E-119
2572231826	t3m_00182	KO:K01736	chorismate synthase [EC:4.2.3.5]			0.00E+00
2572231826	t3m_00182	ITERM:00348	chorismate synthase (EC 4.2.3.5)			
2572231826	t3m_00182	Locus_type		CDS		
2572231826	t3m_00182	Product_name		chorismate synthase (EC 4.2.3.5)		
2572231826	t3m_00182	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231826	t3m_00182	Coordinates		74107..75189(-)		
2572231826	t3m_00182	DNA_length		1083bp		
2572231826	t3m_00182	Protein_length		360aa		
2572231826	t3m_00182	GC			0.71	

2572231827	t3m_00183	KEGG_module	M00022: Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate			
2572231827	t3m_00183	Metacyc	PWY-6163: chorismate biosynthesis from 3-dehydroquinate			
2572231827	t3m_00183	IMG_pathway	146: Chorismate synthesis			
2572231827	t3m_00183	IMG_pathway	519: Archaeal chorismate synthesis			
2572231827	t3m_00183	COG_category	[E] Amino acid transport and metabolism			
2572231827	t3m_00183	COG0128	5-enolpyruvylshikimate-3-phosphate synthase			3.00E-88
2572231827	t3m_00183	pfam00275	EPSP_synthase			5.80E-82
2572231827	t3m_00183	EC:2.5.1.19	3-phosphoshikimate 1-carboxyvinyltransferase.			
2572231827	t3m_00183	TIGR01356	3-phosphoshikimate 1-carboxyvinyltransferase			1.70E-105
2572231827	t3m_00183	KO:K00800	3-phosphoshikimate 1-carboxyvinyltransferase [EC:2.5.1.19]			0.00E+00
2572231827	t3m_00183	ITERM:00342	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)			
2572231827	t3m_00183	Locus_type		CDS		
2572231827	t3m_00183	Product_name		3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)		
2572231827	t3m_00183	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231827	t3m_00183	Coordinates		75189..76463(-)		
2572231827	t3m_00183	DNA_length		1275bp		
2572231827	t3m_00183	Protein_length		424aa		
2572231827	t3m_00183	GC			0.72	

2572231828	t3m_00184	KEGG_module	M00022: Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate
2572231828	t3m_00184	Metacyc	PWY-6163: chorismate biosynthesis from 3-dehydroquinate
2572231828	t3m_00184	IMG_pathway	146: Chorismate synthesis

2572231828	t3m_00184	IMG_pathway	519: Archaeal chorismate synthesis			
2572231828	t3m_00184	COG_category	[E] Amino acid transport and metabolism			
2572231828	t3m_00184	COG_category	[H] Coenzyme transport and metabolism			
2572231828	t3m_00184	COG1685	Archaeal shikimate kinase			8.00E-41
2572231828	t3m_00184	pfam00288	GHMP_kinases_N			8.90E-08
2572231828	t3m_00184	EC:2.7.1.71	Shikimate kinase.			
2572231828	t3m_00184	TIGR01920	shikimate kinase			1.10E-55
2572231828	t3m_00184	KO:K00891	shikimate kinase [EC:2.7.1.71]			4.40E-27
2572231828	t3m_00184	ITERM:00339	shikimate kinase (EC 2.7.1.71)			
2572231828	t3m_00184	Locus_type		CDS		
2572231828	t3m_00184	Product_name		shikimate kinase (EC 2.7.1.71)		
2572231828	t3m_00184	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231828	t3m_00184	Coordinates		76460..77335(-)		
2572231828	t3m_00184	DNA_length		876bp		
2572231828	t3m_00184	Protein_length		291aa		
2572231828	t3m_00184	GC			0.71	
2572231829	t3m_00185	IMG_pathway	146: Chorismate synthesis			
2572231829	t3m_00185	IMG_pathway	519: Archaeal chorismate synthesis			
2572231829	t3m_00185	COG_category	[E] Amino acid transport and metabolism			
2572231829	t3m_00185	COG0169	Shikimate 5-dehydrogenase			5.00E-43
2572231829	t3m_00185	pfam08501	Shikimate_dh_N			2.90E-16
2572231829	t3m_00185	pfam01487	DHquinase_I			2.30E-16
2572231829	t3m_00185	ITERM:00333	3-dehydroquinate dehydratase (EC 4.2.1.10)			
2572231829	t3m_00185	Locus_type		CDS		
2572231829	t3m_00185	Product_name		3-dehydroquinate dehydratase (EC 4.2.1.10)		
2572231829	t3m_00185	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2		
2572231829	t3m_00185	Coordinates		77332..78762(-)		
2572231829	t3m_00185	DNA_length		1431bp		
2572231829	t3m_00185	Protein_length		476aa		
2572231829	t3m_00185	GC			0.7	
2572231830	t3m_00186	Metacyc	PWY-6422: D-arginine degradation			
2572231830	t3m_00186	IMG_pathway	519: Archaeal chorismate synthesis			

2572231830	t3m_00186	COG_category	[E] Amino acid transport and metabolism		
2572231830	t3m_00186	COG1465	Predicted alternative 3-dehydroquinate synthase		9.00E-51
2572231830	t3m_00186	pfam01959	DHQS		5.40E-75
2572231830	t3m_00186	EC:1.4.1.-	Oxidoreductases. Acting on the CH-NH(2) group of donors. With NAD(+) or NADP(+) as acceptor.		
2572231830	t3m_00186	KO:K11646	dehydroquinate synthase II [EC:1.4.1.-]		1.40E-45
2572231830	t3m_00186	ITERM:03010	3-dehydroquinate synthase II		
2572231830	t3m_00186	Locus_type		CDS	
2572231830	t3m_00186	Product_name		3-dehydroquinate synthase II	
2572231830	t3m_00186	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231830	t3m_00186	Coordinates		78828..79859(-)	
2572231830	t3m_00186	DNA_length		1032bp	
2572231830	t3m_00186	Protein_length		343aa	
2572231830	t3m_00186	GC		0.71	
2572231831	t3m_00187	Metacyc	SUCSYN-PWY: sucrose biosynthesis		
2572231831	t3m_00187	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)		
2572231831	t3m_00187	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)		
2572231831	t3m_00187	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)		
2572231831	t3m_00187	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle		
2572231831	t3m_00187	Metacyc	P341-PWY: glycolysis V (Pyrococcus)		
2572231831	t3m_00187	Metacyc	PWY-5484: glycolysis II (from fructose-6P)		
2572231831	t3m_00187	Metacyc	GLUCONEO-PWY: gluconeogenesis I		
2572231831	t3m_00187	Metacyc	PWY-1042: glycolysis IV (plant cytosol)		
2572231831	t3m_00187	Metacyc	PWY-6160: 3-dehydroquinate biosynthesis II (archaea)		
2572231831	t3m_00187	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2572231831	t3m_00187	Metacyc	GLYCOLYSIS: glycolysis I		
2572231831	t3m_00187	Metacyc	PWY66-373: sucrose degradation V (mammalian)		
2572231831	t3m_00187	COG_category	[G] Carbohydrate transport and metabolism		
2572231831	t3m_00187	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes		2.00E-52
2572231831	t3m_00187	pfam01791	DeoC		3.10E-30
2572231831	t3m_00187	EC:4.1.2.13	Fructose-bisphosphate aldolase.		
2572231831	t3m_00187	EC:2.2.1.10	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase.		
2572231831	t3m_00187	KO:K16306	fructose-bisphosphate aldolase / 2-amino-3,7-dideoxy-D-threo-hept-6-		0.00E+00
2572231831	t3m_00187	Locus_type		CDS	

2572231831	t3m_00187	Product_name		DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	
2572231831	t3m_00187	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231831	t3m_00187	Coordinates		79870..80622(-)	
2572231831	t3m_00187	DNA_length		753bp	
2572231831	t3m_00187	Protein_length		250aa	
2572231831	t3m_00187	GC		0.68	
2572231832	t3m_00188	COG_category	[H] Coenzyme transport and metabolism		
2572231832	t3m_00188	COG5424	Pyrroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C		4.00E-19
2572231832	t3m_00188	pfam03070	TENA_THI-4		5.00E-10
2572231832	t3m_00188	Locus_type		CDS	
2572231832	t3m_00188	Product_name		Pyrroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C	
2572231832	t3m_00188	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231832	t3m_00188	Coordinates		80677..81417(-)	
2572231832	t3m_00188	DNA_length		741bp	
2572231832	t3m_00188	Protein_length		246aa	
2572231832	t3m_00188	GC		0.67	
2572231833	t3m_00189	pfam02515	CoA_transf_3		4.20E-42
2572231833	t3m_00189	Locus_type		CDS	
2572231833	t3m_00189	Product_name		CoA-transferase family III	
2572231833	t3m_00189	Scaffold		t3m_contig_70_18_len_82197_read_count_6592593.2	
2572231833	t3m_00189	Coordinates		81505..82194(+)	
2572231833	t3m_00189	DNA_length		690bp	
2572231833	t3m_00189	Protein_length		230aa	
2572231833	t3m_00189	GC		0.67	
2572231834	t3m_00190	pfam03029	ATP_bind_1		7.20E-29
2572231834	t3m_00190	Locus_type		CDS	
2572231834	t3m_00190	Product_name		Conserved hypothetical ATP binding protein	
2572231834	t3m_00190	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231834	t3m_00190	Coordinates		2..322(-)	
2572231834	t3m_00190	DNA_length		321bp	
2572231834	t3m_00190	Protein_length		107aa	

2572231834	t3m_00190	GC			0.68	
2572231835	t3m_00191	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2572231835	t3m_00191	COG1400	Signal recognition particle 19 kDa protein			5.00E-14
2572231835	t3m_00191	pfam01922	SRP19			9.80E-20
2572231835	t3m_00191	KO:K03105	signal recognition particle subunit SRP19			7.20E-14
2572231835	t3m_00191	Locus_type		CDS		
2572231835	t3m_00191	Product_name		Signal recognition particle 19 kDa protein		
2572231835	t3m_00191	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231835	t3m_00191	Coordinates		326..625(-)		
2572231835	t3m_00191	DNA_length		300bp		
2572231835	t3m_00191	Protein_length		99aa		
2572231835	t3m_00191	GC			0.66	
2572231836	t3m_00192	KEGG_module	M00179: Ribosome, archaea			
2572231836	t3m_00192	KEGG_module	M00177: Ribosome, eukaryotes			
2572231836	t3m_00192	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231836	t3m_00192	COG2007	Ribosomal protein S8E			7.00E-32
2572231836	t3m_00192	pfam01201	Ribosomal_S8e			1.10E-35
2572231836	t3m_00192	TIGR00307	ribosomal protein S8.e			7.60E-47
2572231836	t3m_00192	KO:K02995	small subunit ribosomal protein S8e			2.10E-37
2572231836	t3m_00192	Locus_type		CDS		
2572231836	t3m_00192	Product_name		SSU ribosomal protein S8E		
2572231836	t3m_00192	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231836	t3m_00192	Coordinates		643..1038(-)		
2572231836	t3m_00192	DNA_length		396bp		
2572231836	t3m_00192	Protein_length		131aa		
2572231836	t3m_00192	GC			0.68	
2572231837	t3m_00193	KEGG_module	M00527: Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine			
2572231837	t3m_00193	KEGG_module	M00526: Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine			
2572231837	t3m_00193	KEGG_module	M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine			
2572231837	t3m_00193	KEGG_module	M00525: Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine			
2572231837	t3m_00193	Metacyc	PWY-2942: lysine biosynthesis III			

2572231837	t3m_00193	Metacyc	PWY-2941: lysine biosynthesis II		
2572231837	t3m_00193	Metacyc	PWY-5097: lysine biosynthesis VI		
2572231837	t3m_00193	Metacyc	DAPLYSINESYN-PWY: lysine biosynthesis I		
2572231837	t3m_00193	COG_category	[E] Amino acid transport and metabolism		
2572231837	t3m_00193	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572231837	t3m_00193	COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase		1.00E-57
2572231837	t3m_00193	pfam00701	DHDPS		4.20E-56
2572231837	t3m_00193	EC:4.3.3.7	4-hydroxy-tetrahydrodipicolinate synthase.		
2572231837	t3m_00193	KO:K01714	4-hydroxy-tetrahydrodipicolinate synthase [EC:4.3.3.7]		8.10E-38
2572231837	t3m_00193	Locus_type		CDS	
2572231837	t3m_00193	Product_name		Dihydrodipicolinate synthase/N-acetylneuraminate lyase	
2572231837	t3m_00193	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231837	t3m_00193	Coordinates		1088..2068(-)	
2572231837	t3m_00193	DNA_length		981bp	
2572231837	t3m_00193	Protein_length		326aa	
2572231837	t3m_00193	GC		0.71	
2572231838	t3m_00194	IMG_pathway	437: Archaeal replication elongation		
2572231838	t3m_00194	IMG_pathway	46: Okazaki fragment processing		
2572231838	t3m_00194	COG_category	[L] Replication, recombination and repair		
2572231838	t3m_00194	COG0164	Ribonuclease HII		5.00E-30
2572231838	t3m_00194	pfam01351	RNase_HII		2.70E-35
2572231838	t3m_00194	EC:3.1.26.4	Ribonuclease H.		
2572231838	t3m_00194	TIGR00729	ribonuclease H, mammalian HI/archaeal HII subfamily		6.50E-55
2572231838	t3m_00194	KO:K03470	ribonuclease HII [EC:3.1.26.4]		0.00E+00
2572231838	t3m_00194	ITERM:00110	RNase HII (EC 3.1.26.4)		
2572231838	t3m_00194	Locus_type		CDS	
2572231838	t3m_00194	Product_name		RNase HII (EC 3.1.26.4)	
2572231838	t3m_00194	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231838	t3m_00194	Coordinates		2096..2800(+)	
2572231838	t3m_00194	DNA_length		705bp	
2572231838	t3m_00194	Protein_length		234aa	
2572231838	t3m_00194	GC		0.73	

2572231839	t3m_00195	pfam02036	SCP2			1.40E-13
2572231839	t3m_00195	Locus_type		CDS		
2572231839	t3m_00195	Product_name		SCP-2 sterol transfer family		
2572231839	t3m_00195	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231839	t3m_00195	Coordinates		2797..3132(+)		
2572231839	t3m_00195	DNA_length		336bp		
2572231839	t3m_00195	Protein_length		111aa		
2572231839	t3m_00195	GC			0.65	

2572231840	t3m_00196	KEGG_module	M00133: Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine			
2572231840	t3m_00196	Metacyc	PWY-40: putrescine biosynthesis I			
2572231840	t3m_00196	Metacyc	ARGDEG-III-PWY: arginine degradation IV (arginine decarboxylase/agmatine deiminase pathway)			
2572231840	t3m_00196	Metacyc	PWY0-1299: arginine dependent acid resistance			
2572231840	t3m_00196	Metacyc	PWY0-823: arginine degradation III (arginine decarboxylase/agmatinase pathway)			
2572231840	t3m_00196	Metacyc	PWY-43: putrescine biosynthesis II			
2572231840	t3m_00196	Metacyc	PWY-6305: putrescine biosynthesis IV			
2572231840	t3m_00196	Metacyc	PWY-6834: spermidine biosynthesis III			
2572231840	t3m_00196	IMG_pathway	186: L-arginine degradation by Arg decarboxylase pathway			
2572231840	t3m_00196	IMG_pathway	524: Spermidine synthesis via aminopropylagmatine			
2572231840	t3m_00196	IMG_pathway	823: Putrescine synthesis from L-arginine			
2572231840	t3m_00196	COG_category	[S] Function unknown			
2572231840	t3m_00196	COG1945	Uncharacterized conserved protein			2.00E-17
2572231840	t3m_00196	pfam01862	PvlArgDC			3.70E-27
2572231840	t3m_00196	EC:4.1.1.19	Arginine decarboxylase.			
2572231840	t3m_00196	TIGR00286	arginine decarboxylase, pyruvoyl-dependent			4.80E-25
2572231840	t3m_00196	KO:K02626	arginine decarboxylase [EC:4.1.1.19]			3.40E-12
2572231840	t3m_00196	ITERM:00488	arginine decarboxylase (EC 4.1.1.19)			
2572231840	t3m_00196	Locus_type		CDS		
2572231840	t3m_00196	Product_name		arginine decarboxylase (EC 4.1.1.19)		
2572231840	t3m_00196	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231840	t3m_00196	Coordinates		3157..3597(-)		
2572231840	t3m_00196	DNA_length		441bp		
2572231840	t3m_00196	Protein_length		146aa		
2572231840	t3m_00196	GC			0.66	

2572231841	t3m_00197	KEGG_module	M00345: Formaldehyde assimilation, ribulose monophosphate pathway			
2572231841	t3m_00197	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)			
2572231841	t3m_00197	Metacyc	RUMP-PWY: formaldehyde oxidation I			
2572231841	t3m_00197	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572231841	t3m_00197	COG0794	Predicted sugar phosphate isomerase involved in capsule formation			2.00E-25
2572231841	t3m_00197	pfam01380	SIS			7.70E-15
2572231841	t3m_00197	EC:5.3.1.27	6-phospho-3-hexuloisomerase.			
2572231841	t3m_00197	TIGR03127	6-phospho 3-hexuloisomerase			4.40E-48
2572231841	t3m_00197	KO:K08094	6-phospho-3-hexuloisomerase [EC:5.3.1.27]			5.80E-36
2572231841	t3m_00197	Locus_type		CDS		
2572231841	t3m_00197	Product_name		Predicted sugar phosphate isomerase involved in capsule formation		
2572231841	t3m_00197	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231841	t3m_00197	Coordinates		3709..4281(-)		
2572231841	t3m_00197	DNA_length		573bp		
2572231841	t3m_00197	Protein_length		190aa		
2572231841	t3m_00197	GC			0.67	
2572231842	t3m_00198	COG_category	[L] Replication, recombination and repair			
2572231842	t3m_00198	COG0648	Endonuclease IV			2.00E-24
2572231842	t3m_00198	pfam01261	AP_endonuc_2			8.50E-13
2572231842	t3m_00198	EC:3.1.21.2	Deoxyribonuclease IV (phage-T(4)-induced).			
2572231842	t3m_00198	KO:K01151	deoxyribonuclease IV [EC:3.1.21.2]			0.00E+00
2572231842	t3m_00198	Locus_type		CDS		
2572231842	t3m_00198	Product_name		Endonuclease IV		
2572231842	t3m_00198	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231842	t3m_00198	Coordinates		4259..5461(-)		
2572231842	t3m_00198	DNA_length		1203bp		
2572231842	t3m_00198	Protein_length		400aa		
2572231842	t3m_00198	GC			0.68	
2572231843	t3m_00199	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231843	t3m_00199	COG0293	23S rRNA methylase			4.00E-54
2572231843	t3m_00199	pfam01728	FtsJ			5.70E-49

2572231843	t3m_00199	EC:2.1.1.166	23S rRNA (uridine(2552)-2'-O)-methyltransferase.		
2572231843	t3m_00199	TIGR00438	cell division protein FtsJ		1.60E-67
2572231843	t3m_00199	KO:K02427	23S rRNA (uridine2552-2'-O)-methyltransferase [EC:2.1.1.166]		1.40E-45
2572231843	t3m_00199	Locus_type		CDS	
2572231843	t3m_00199	Product_name		23S rRNA methylase	
2572231843	t3m_00199	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231843	t3m_00199	Coordinates		5507..6160(-)	
2572231843	t3m_00199	DNA_length		654bp	
2572231843	t3m_00199	Protein_length		217aa	
2572231843	t3m_00199	GC		0.71	
2572231844	t3m_00200	Locus_type		tRNA	
2572231844	t3m_00200	Product_name		tRNA_Pro_GGG	
2572231844	t3m_00200	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231844	t3m_00200	Coordinates		6240..6314(-)	
2572231844	t3m_00200	DNA_length		75bp	
2572231844	t3m_00200	GC		0.6	
2572231845	t3m_00201	Locus_type		CDS	
2572231845	t3m_00201	Product_name		hypothetical protein	
2572231845	t3m_00201	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231845	t3m_00201	Coordinates		6441..7157(-)	
2572231845	t3m_00201	DNA_length		717bp	
2572231845	t3m_00201	Protein_length		238aa	
2572231845	t3m_00201	GC		0.71	
2572231846	t3m_00202	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP		
2572231846	t3m_00202	Metacyc	PWY-6596: adenosine nucleotides degradation I		
2572231846	t3m_00202	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II		
2572231846	t3m_00202	Metacyc	PWY-5695: urate biosynthesis/inosine 5'-phosphate degradation		
2572231846	t3m_00202	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis		
2572231846	t3m_00202	COG_category	[R] General function prediction only		
2572231846	t3m_00202	COG0517	FOG: CBS domain		4.00E-13
2572231846	t3m_00202	pfam02195	ParBc		1.80E-08

2572231846	t3m_00202	pfam00571	CBS		3.10E-07
2572231846	t3m_00202	pfam00571	CBS		5.40E-12
2572231846	t3m_00202	EC:1.1.1.205	IMP dehydrogenase.		
2572231846	t3m_00202	KO:K00088	IMP dehydrogenase [EC:1.1.1.205]		0.00E+00
2572231846	t3m_00202	Locus_type		CDS	
2572231846	t3m_00202	Product_name		FOG: CBS domain	
2572231846	t3m_00202	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231846	t3m_00202	Coordinates		7279..8121(-)	
2572231846	t3m_00202	DNA_length		843bp	
2572231846	t3m_00202	Protein_length		280aa	
2572231846	t3m_00202	GC		0.67	
2572231847	t3m_00203	KEGG_module	M00064: ADP-L-glycero-D-manno-heptose biosynthesis		
2572231847	t3m_00203	Metacyc	PWY-6478: GDP-D-<i>glycero</i>-α-D-<i>manno</i>-heptose biosynthesis		
2572231847	t3m_00203	Metacyc	PWY0-1241: ADP-L-<i>glycero</i>-β-D-<i>manno</i>-heptose biosynthesis		
2572231847	t3m_00203	COG_category	[G] Carbohydrate transport and metabolism		
2572231847	t3m_00203	COG0279	Phosphoheptose isomerase		4.00E-29
2572231847	t3m_00203	pfam13580	SIS_2		4.20E-23
2572231847	t3m_00203	EC:5.3.1.28	D-sedoheptulose 7-phosphate isomerase.		
2572231847	t3m_00203	KO:K03271	D-sedoheptulose 7-phosphate isomerase [EC:5.3.1.28]		8.50E-37
2572231847	t3m_00203	Locus_type		CDS	
2572231847	t3m_00203	Product_name		Phosphoheptose isomerase	
2572231847	t3m_00203	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231847	t3m_00203	Coordinates		8121..8723(-)	
2572231847	t3m_00203	DNA_length		603bp	
2572231847	t3m_00203	Protein_length		200aa	
2572231847	t3m_00203	GC		0.68	
2572231848	t3m_00204	Metacyc	PWY-6478: GDP-D-<i>glycero</i>-α-D-<i>manno</i>-heptose biosynthesis		
2572231848	t3m_00204	COG_category	[R] General function prediction only		
2572231848	t3m_00204	COG2605	Predicted kinase related to galactokinase and mevalonate kinase		9.00E-87
2572231848	t3m_00204	pfam08544	GHMP_kinases_C		6.60E-12
2572231848	t3m_00204	pfam00288	GHMP_kinases_N		2.10E-09
2572231848	t3m_00204	EC:2.7.1.168	D-glycero-alpha-D-manno-heptose-7-phosphate kinase.		

2572231848	t3m_00204	KO:K07031	D-glycero-alpha-D-manno-heptose-7-phosphate kinase [EC:2.7.1.168]		0.00E+00
2572231848	t3m_00204	Locus_type		CDS	
2572231848	t3m_00204	Product_name		Predicted kinase related to galactokinase and mevalonate kinase	
2572231848	t3m_00204	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231848	t3m_00204	Coordinates		8720..9697(-)	
2572231848	t3m_00204	DNA_length		978bp	
2572231848	t3m_00204	Protein_length		325aa	
2572231848	t3m_00204	GC		0.68	

2572231849	t3m_00205	KEGG_module	M00290: Holo-TFIIH complex		
2572231849	t3m_00205	COG_category	[L] Replication, recombination and repair		
2572231849	t3m_00205	COG_category	[K] Transcription		
2572231849	t3m_00205	COG1199	Rad3-related DNA helicases		1.00E-70
2572231849	t3m_00205	pfam06733	DEAD_2		1.90E-25
2572231849	t3m_00205	pfam13307	Helicase_C_2		1.60E-32
2572231849	t3m_00205	EC:3.6.4.12	DNA helicase.		
2572231849	t3m_00205	KO:K10844	DNA excision repair protein ERCC-2 [EC:3.6.4.12]		0.00E+00
2572231849	t3m_00205	Locus_type		CDS	
2572231849	t3m_00205	Product_name		Rad3-related DNA helicases	
2572231849	t3m_00205	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231849	t3m_00205	Coordinates		9723..11771(-)	
2572231849	t3m_00205	DNA_length		2049bp	
2572231849	t3m_00205	Protein_length		682aa	
2572231849	t3m_00205	GC		0.7	

2572231850	t3m_00206	COG_category	[C] Energy production and conversion		
2572231850	t3m_00206	COG2440	Ferredoxin-like protein		3.00E-19
2572231850	t3m_00206	KO:K03855	ferredoxin like protein		7.60E-16
2572231850	t3m_00206	Locus_type		CDS	
2572231850	t3m_00206	Product_name		Ferredoxin-like protein	
2572231850	t3m_00206	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231850	t3m_00206	Coordinates		11936..12256(-)	
2572231850	t3m_00206	DNA_length		321bp	
2572231850	t3m_00206	Protein_length		106aa	

2572231850	t3m_00206	GC		0.69
2572231851	t3m_00207	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle	
2572231851	t3m_00207	KEGG_module	M00171: C4-dicarboxylic acid cycle, NAD+ -malic enzyme type	
2572231851	t3m_00207	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)	
2572231851	t3m_00207	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)	
2572231851	t3m_00207	KEGG_module	M00346: Formaldehyde assimilation, serine pathway	
2572231851	t3m_00207	KEGG_module	M00012: Glyoxylate cycle	
2572231851	t3m_00207	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate	
2572231851	t3m_00207	KEGG_module	M00168: CAM (Crassulacean acid metabolism), dark	
2572231851	t3m_00207	Metacyc	TCA: TCA cycle I (prokaryotic)	
2572231851	t3m_00207	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)	
2572231851	t3m_00207	Metacyc	ANARESP1-PWY: respiration (anaerobic)	
2572231851	t3m_00207	Metacyc	PWY-5690: TCA cycle II (eukaryotic)	
2572231851	t3m_00207	Metacyc	P42-PWY: incomplete reductive TCA cycle	
2572231851	t3m_00207	Metacyc	FERMENTATION-PWY: mixed acid fermentation	
2572231851	t3m_00207	Metacyc	GLUCONEO-PWY: gluconeogenesis I	
2572231851	t3m_00207	Metacyc	PWY-6728: methylaspartate cycle	
2572231851	t3m_00207	Metacyc	P108-PWY: pyruvate fermentation to propionate I	
2572231851	t3m_00207	Metacyc	MALATE-ASPARTATE-SHUTTLE-PWY: aspartate degradation II	
2572231851	t3m_00207	Metacyc	PWY-5392: reductive TCA cycle II	
2572231851	t3m_00207	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)	
2572231851	t3m_00207	Metacyc	PWY-561: superpathway of glyoxylate cycle and fatty acid degradation	
2572231851	t3m_00207	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)	
2572231851	t3m_00207	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)	
2572231851	t3m_00207	Metacyc	P23-PWY: reductive TCA cycle I	
2572231851	t3m_00207	Metacyc	GLYOXYLATE-BYPASS: glyoxylate cycle	
2572231851	t3m_00207	Metacyc	PWY-7115: C4 photosynthetic carbon assimilation cycle, NAD-ME type	
2572231851	t3m_00207	IMG_pathway	1014: Dicarboxylate/4-hydroxybutyrate cycle	
2572231851	t3m_00207	IMG_pathway	308: 2-oxoglutarate synthesis by partial reverse TCA cycle	
2572231851	t3m_00207	IMG_pathway	334: Tricarboxylic acid cycle	
2572231851	t3m_00207	IMG_pathway	335: Acetyl-CoA synthesis by reverse TCA cycle	
2572231851	t3m_00207	IMG_pathway	370: Oxaloacetate conversion to propionate via methylmalonyl-CoA	
2572231851	t3m_00207	IMG_pathway	911: Acetyl-CoA assimilation via glyoxylate cycle	

2572231851	t3m_00207	IMG_pathway	913: Acetyl-CoA assimilation via methylaspartate cycle			
2572231851	t3m_00207	IMG_pathway	959: Serine cycle			
2572231851	t3m_00207	IMG_pathway	960: Glyoxalate from acetyl-CoA via isocitrate lyase cycle			
2572231851	t3m_00207	COG_category	[C] Energy production and conversion			
2572231851	t3m_00207	COG0039	Malate/lactate dehydrogenases			3.00E-92
2572231851	t3m_00207	pfam02866	Ldh_1_C			2.50E-28
2572231851	t3m_00207	pfam00056	Ldh_1_N			3.00E-39
2572231851	t3m_00207	EC:1.1.1.37	Malate dehydrogenase.			
2572231851	t3m_00207	TIGR01763	malate dehydrogenase, NAD-dependent			3.60E-118
2572231851	t3m_00207	KO:K00024	malate dehydrogenase [EC:1.1.1.37]			0.00E+00
2572231851	t3m_00207	ITERM:01345	malate dehydrogenase (NAD) (EC 1.1.1.37)			
2572231851	t3m_00207	Locus_type		CDS		
2572231851	t3m_00207	Product_name		malate dehydrogenase (NAD) (EC 1.1.1.37)		
2572231851	t3m_00207	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231851	t3m_00207	Coordinates		12271..13215(-)		
2572231851	t3m_00207	DNA_length		945bp		
2572231851	t3m_00207	Protein_length		314aa		
2572231851	t3m_00207	GC			0.69	
2572231852	t3m_00208	Locus_type		CDS		
2572231852	t3m_00208	Product_name		hypothetical protein		
2572231852	t3m_00208	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231852	t3m_00208	Coordinates		13326..13562(+)		
2572231852	t3m_00208	DNA_length		237bp		
2572231852	t3m_00208	Protein_length		78aa		
2572231852	t3m_00208	GC			0.66	
2572231853	t3m_00209	Locus_type		CDS		
2572231853	t3m_00209	Product_name		hypothetical protein		
2572231853	t3m_00209	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231853	t3m_00209	Coordinates		13534..13758(+)		
2572231853	t3m_00209	DNA_length		225bp		
2572231853	t3m_00209	Protein_length		74aa		
2572231853	t3m_00209	GC			0.68	

2572231854	t3m_00210	KEGG_module	M00119: Pantothenate biosynthesis, valine/L-aspartate => pantothenate			
2572231854	t3m_00210	Metacyc	PWY-6654: phosphopantothenate biosynthesis III			
2572231854	t3m_00210	Metacyc	PANTO-PWY: phosphopantothenate biosynthesis I			
2572231854	t3m_00210	COG_category	[H] Coenzyme transport and metabolism			
2572231854	t3m_00210	COG1893	Ketopantoate reductase			2.00E-53
2572231854	t3m_00210	pfam02558	ApbA			1.30E-26
2572231854	t3m_00210	pfam08546	ApbA_C			1.50E-31
2572231854	t3m_00210	EC:1.1.1.169	2-dehydropantoate 2-reductase.			
2572231854	t3m_00210	TIGR00745	2-dehydropantoate 2-reductase			2.70E-70
2572231854	t3m_00210	KO:K00077	2-dehydropantoate 2-reductase [EC:1.1.1.169]			1.40E-39
2572231854	t3m_00210	Locus_type		CDS		
2572231854	t3m_00210	Product_name		2-dehydropantoate 2-reductase		
2572231854	t3m_00210	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231854	t3m_00210	Coordinates		13787..14722(+)		
2572231854	t3m_00210	DNA_length		936bp		
2572231854	t3m_00210	Protein_length		311aa		
2572231854	t3m_00210	GC			0.72	
2572231855	t3m_00211	KEGG_module	M00003: Gluconeogenesis, oxaloacetate => fructose-6P			
2572231855	t3m_00211	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2572231855	t3m_00211	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)			
2572231855	t3m_00211	KEGG_module	M00166: Reductive pentose phosphate cycle, RuBP + CO2 => glyceraldehyde-3P			
2572231855	t3m_00211	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds			
2572231855	t3m_00211	Metacyc	PWY-6901: xylose degradation IV			
2572231855	t3m_00211	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2572231855	t3m_00211	Metacyc	PWY-7003: glycerol degradation to butanol			
2572231855	t3m_00211	Metacyc	PWY-1042: glycolysis IV (plant cytosol)			
2572231855	t3m_00211	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2572231855	t3m_00211	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2572231855	t3m_00211	Metacyc	P124-PWY: Bifidobacterium shunt			
2572231855	t3m_00211	Metacyc	SUCSYN-PWY: sucrose biosynthesis			
2572231855	t3m_00211	Metacyc	GLYCOLYSIS: glycolysis I			
2572231855	t3m_00211	Metacyc	P122-PWY: heterolactic fermentation			

2572231855	t3m_00211	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis			
2572231855	t3m_00211	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2572231855	t3m_00211	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			
2572231855	t3m_00211	IMG_pathway	336: Standard Embden-Meyerhof pathway			
2572231855	t3m_00211	IMG_pathway	359: Conversion of glyceraldehyde-3-phosphate to pyruvate			
2572231855	t3m_00211	IMG_pathway	527: Calvin cycle			
2572231855	t3m_00211	COG_category	[G] Carbohydrate transport and metabolism			
2572231855	t3m_00211	COG0126	3-phosphoglycerate kinase			1.00E-113
2572231855	t3m_00211	pfam00162	PGK			6.40E-123
2572231855	t3m_00211	EC:2.7.2.3	Phosphoglycerate kinase.			
2572231855	t3m_00211	KO:K00927	phosphoglycerate kinase [EC:2.7.2.3]			0.00E+00
2572231855	t3m_00211	ITERM:01477	phosphoglycerate kinase (EC 2.7.2.3)			
2572231855	t3m_00211	Locus_type		CDS		
2572231855	t3m_00211	Product_name		phosphoglycerate kinase (EC 2.7.2.3)		
2572231855	t3m_00211	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231855	t3m_00211	Coordinates		14747..15928(+)		
2572231855	t3m_00211	DNA_length		1182bp		
2572231855	t3m_00211	Protein_length		393aa		
2572231855	t3m_00211	GC			0.71	

2572231856	t3m_00212	COG_category	[P] Inorganic ion transport and metabolism			
2572231856	t3m_00212	COG1324	Uncharacterized protein involved in tolerance to divalent cations			9.00E-19
2572231856	t3m_00212	pfam03091	CutA1			5.50E-22
2572231856	t3m_00212	KO:K03926	periplasmic divalent cation tolerance protein			1.00E-13
2572231856	t3m_00212	Locus_type		CDS		
2572231856	t3m_00212	Product_name		Uncharacterized protein involved in tolerance to divalent cations		
2572231856	t3m_00212	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231856	t3m_00212	Coordinates		15846..16265(-)		
2572231856	t3m_00212	DNA_length		420bp		
2572231856	t3m_00212	Protein_length		139aa		
2572231856	t3m_00212	GC			0.72	

2572231857	t3m_00213	KEGG_module	M00264: DNA polymerase II complex, archaea			
2572231857	t3m_00213	COG_category	[L] Replication, recombination and repair			

2572231857	t3m_00213	COG1311	Archaeal DNA polymerase II, small subunit/DNA polymerase delta, subu		1.00E-89
2572231857	t3m_00213	pfam04042	DNA_pol_E_B		1.80E-15
2572231857	t3m_00213	EC:2.7.7.7	DNA-directed DNA polymerase.		
2572231857	t3m_00213	KO:K02323	DNA polymerase II small subunit [EC:2.7.7.7]		0.00E+00
2572231857	t3m_00213	Locus_type		CDS	
2572231857	t3m_00213	Product_name		Archaeal DNA polymerase II, small subunit/DNA polymerase delta, subu	
2572231857	t3m_00213	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231857	t3m_00213	Coordinates		16304..17815(-)	
2572231857	t3m_00213	DNA_length		1512bp	
2572231857	t3m_00213	Protein_length		503aa	
2572231857	t3m_00213	GC		0.71	
2572231858	t3m_00214	Locus_type		CDS	
2572231858	t3m_00214	Product_name		hypothetical protein	
2572231858	t3m_00214	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231858	t3m_00214	Coordinates		17947..18597(-)	
2572231858	t3m_00214	DNA_length		651bp	
2572231858	t3m_00214	Protein_length		216aa	
2572231858	t3m_00214	GC		0.65	
2572231859	t3m_00215	COG_category	[L] Replication, recombination and repair		
2572231859	t3m_00215	COG0358	DNA primase (bacterial type)		7.00E-40
2572231859	t3m_00215	pfam13662	Toprim_4		1.40E-09
2572231859	t3m_00215	Locus_type		CDS	
2572231859	t3m_00215	Product_name		DNA primase (bacterial type)	
2572231859	t3m_00215	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231859	t3m_00215	Coordinates		18965..20317(+)	
2572231859	t3m_00215	DNA_length		1353bp	
2572231859	t3m_00215	Protein_length		450aa	
2572231859	t3m_00215	GC		0.68	
2572231860	t3m_00216	pfam13654	AAA_32		4.80E-07
2572231860	t3m_00216	pfam01078	Mg_chelatase		3.10E-08
2572231860	t3m_00216	EC:3.4.21.53	Endopeptidase La.		

2572231860	t3m_00216	TIGR00764	lon-related putative ATP-dependent protease			2.10E-88
2572231860	t3m_00216	KO:K01338	ATP-dependent Lon protease [EC:3.4.21.53]			0.00E+00
2572231860	t3m_00216	Locus_type		CDS		
2572231860	t3m_00216	Product_name		AAA domain/Magnesium chelatase, subunit ChlI		
2572231860	t3m_00216	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231860	t3m_00216	Coordinates		20402..21949(+)		
2572231860	t3m_00216	DNA_length		1548bp		
2572231860	t3m_00216	Protein_length		515aa		
2572231860	t3m_00216	GC			0.7	
2572231861	t3m_00217	Locus_type		tRNA		
2572231861	t3m_00217	Product_name		tRNA_Val_GAC		
2572231861	t3m_00217	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231861	t3m_00217	Coordinates		21998..22070(+)		
2572231861	t3m_00217	DNA_length		73bp		
2572231861	t3m_00217	GC			0.62	
2572231862	t3m_00218	COG_category	[R] General function prediction only			
2572231862	t3m_00218	COG1881	Phospholipid-binding protein			9.00E-39
2572231862	t3m_00218	pfam01161	PBP			3.60E-34
2572231862	t3m_00218	TIGR00481	Raf kinase inhibitor-like protein, YbhB/YbcL family			3.70E-37
2572231862	t3m_00218	Locus_type		CDS		
2572231862	t3m_00218	Product_name		phospholipid-binding protein, PBP family		
2572231862	t3m_00218	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231862	t3m_00218	Coordinates		22261..22725(-)		
2572231862	t3m_00218	DNA_length		465bp		
2572231862	t3m_00218	Protein_length		154aa		
2572231862	t3m_00218	GC			0.66	
2572231863	t3m_00219	COG_category	[K] Transcription			
2572231863	t3m_00219	COG1321	Mn-dependent transcriptional regulator			6.00E-15
2572231863	t3m_00219	pfam02742	Fe_dep_repr_C			3.20E-12
2572231863	t3m_00219	pfam01726	LexA_DNA_bind			2.40E-06
2572231863	t3m_00219	KO:K03709	DtxR family transcriptional regulator, Mn-dependent transcriptional reg			1.50E-12

2572231863	t3m_00219	ITERM:02272	iron (metal) dependent repressor, DtxR family		
2572231863	t3m_00219	Locus_type		CDS	
2572231863	t3m_00219	Product_name		iron (metal) dependent repressor, DtxR family	
2572231863	t3m_00219	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231863	t3m_00219	Coordinates		22960..23391(+)	
2572231863	t3m_00219	DNA_length		432bp	
2572231863	t3m_00219	Protein_length		143aa	
2572231863	t3m_00219	GC		0.68	
2572231864	t3m_00220	KEGG_module	M00244: Putative zinc/manganese transport system		
2572231864	t3m_00220	COG_category	[P] Inorganic ion transport and metabolism		
2572231864	t3m_00220	COG0803	ABC-type metal ion transport system, periplasmic component/surface a		3.00E-28
2572231864	t3m_00220	pfam01297	TroA		1.40E-36
2572231864	t3m_00220	KO:K02077	zinc/manganese transport system substrate-binding protein		0.00E+00
2572231864	t3m_00220	Locus_type		CDS	
2572231864	t3m_00220	Product_name		ABC-type metal ion transport system, periplasmic component/surface a	
2572231864	t3m_00220	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231864	t3m_00220	Coordinates		23428..24498(+)	
2572231864	t3m_00220	DNA_length		1071bp	
2572231864	t3m_00220	Protein_length		356aa	
2572231864	t3m_00220	GC		0.64	
2572231864	t3m_00220	Transmembrane		Yes	
2572231865	t3m_00221	KEGG_module	M00244: Putative zinc/manganese transport system		
2572231865	t3m_00221	COG_category	[P] Inorganic ion transport and metabolism		
2572231865	t3m_00221	COG1121	ABC-type Mn/Zn transport systems, ATPase component		1.00E-56
2572231865	t3m_00221	pfam00005	ABC_tran		7.40E-27
2572231865	t3m_00221	KO:K02074	zinc/manganese transport system ATP-binding protein		0.00E+00
2572231865	t3m_00221	Locus_type		CDS	
2572231865	t3m_00221	Product_name		ABC-type Mn/Zn transport systems, ATPase component	
2572231865	t3m_00221	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231865	t3m_00221	Coordinates		24505..25332(+)	
2572231865	t3m_00221	DNA_length		828bp	
2572231865	t3m_00221	Protein_length		275aa	

2572231865	t3m_00221	GC			0.66	
2572231866	t3m_00222	KEGG_module	M00244: Putative zinc/manganese transport system			
2572231866	t3m_00222	COG_category	[P] Inorganic ion transport and metabolism			
2572231866	t3m_00222	COG1108	ABC-type Mn2+/Zn2+ transport systems, permease components			2.00E-34
2572231866	t3m_00222	pfam00950	ABC-3			8.30E-54
2572231866	t3m_00222	KO:K02075	zinc/manganese transport system permease protein			0.00E+00
2572231866	t3m_00222	Locus_type		CDS		
2572231866	t3m_00222	Product_name		ABC-type Mn2+/Zn2+ transport systems, permease components		
2572231866	t3m_00222	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231866	t3m_00222	Coordinates		25329..26237(+)		
2572231866	t3m_00222	DNA_length		909bp		
2572231866	t3m_00222	Protein_length		302aa		
2572231866	t3m_00222	GC			0.65	
2572231866	t3m_00222	Transmembrane		Yes		
2572231867	t3m_00223	Metacyc	PWY-4722: creatinine degradation II			
2572231867	t3m_00223	Metacyc	PWY-3661: glycine betaine degradation			
2572231867	t3m_00223	Metacyc	CRNFORCAT-PWY: creatinine degradation I			
2572231867	t3m_00223	COG_category	[E] Amino acid transport and metabolism			
2572231867	t3m_00223	COG0665	Glycine/D-amino acid oxidases (deaminating)			2.00E-42
2572231867	t3m_00223	pfam01266	DAO			2.60E-66
2572231867	t3m_00223	EC:1.5.3.1	Sarcosine oxidase.			
2572231867	t3m_00223	KO:K00303	sarcosine oxidase, subunit beta [EC:1.5.3.1]			0.00E+00
2572231867	t3m_00223	Locus_type		CDS		
2572231867	t3m_00223	Product_name		Glycine/D-amino acid oxidases (deaminating)		
2572231867	t3m_00223	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231867	t3m_00223	Coordinates		26262..27434(-)		
2572231867	t3m_00223	DNA_length		1173bp		
2572231867	t3m_00223	Protein_length		390aa		
2572231867	t3m_00223	GC			0.65	
2572231868	t3m_00224	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572231868	t3m_00224	COG0492	Thioredoxin reductase			4.00E-14

2572231868	t3m_00224	pfam04324	Fer2_BFD			9.90E-06
2572231868	t3m_00224	pfam01494	FAD_binding_3			1.90E-06
2572231868	t3m_00224	pfam13510	Fer2_4			3.00E-18
2572231868	t3m_00224	Locus_type		CDS		
2572231868	t3m_00224	Product_name		Thioredoxin reductase		
2572231868	t3m_00224	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231868	t3m_00224	Coordinates		27412..29505(-)		
2572231868	t3m_00224	DNA_length		2094bp		
2572231868	t3m_00224	Protein_length		697aa		
2572231868	t3m_00224	GC			0.66	

2572231869	t3m_00225	Metacyc	HYDROXYPRODEG-PWY: 4-hydroxyproline degradation I			
2572231869	t3m_00225	IMG_pathway	181: L-proline oxidation to L-glutamate			
2572231869	t3m_00225	COG_category	[C] Energy production and conversion			
2572231869	t3m_00225	COG1012	NAD-dependent aldehyde dehydrogenases			1.00E-78
2572231869	t3m_00225	pfam00171	Aldedh			3.70E-89
2572231869	t3m_00225	EC:1.5.1.12	1-pyrroline-5-carboxylate dehydrogenase.			
2572231869	t3m_00225	TIGR01236	delta-1-pyrroline-5-carboxylate dehydrogenase, group 1			0.00E+00
2572231869	t3m_00225	KO:K00294	1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]			0.00E+00
2572231869	t3m_00225	ITERM:00471	delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12)			
2572231869	t3m_00225	Locus_type		CDS		
2572231869	t3m_00225	Product_name		delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12)		
2572231869	t3m_00225	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231869	t3m_00225	Coordinates		29606..31225(+)		
2572231869	t3m_00225	DNA_length		1620bp		
2572231869	t3m_00225	Protein_length		539aa		
2572231869	t3m_00225	GC			0.65	

2572231870	t3m_00226	COG_category	[S] Function unknown			
2572231870	t3m_00226	COG3462	Predicted membrane protein			7.00E-06
2572231870	t3m_00226	pfam09851	SHOCT			2.00E-05
2572231870	t3m_00226	Locus_type		CDS		
2572231870	t3m_00226	Product_name		Predicted membrane protein		
2572231870	t3m_00226	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		

2572231870	t3m_00226	Coordinates		31272..31700(-)		
2572231870	t3m_00226	DNA_length		429bp		
2572231870	t3m_00226	Protein_length		142aa		
2572231870	t3m_00226	GC			0.66	
2572231870	t3m_00226	Transmembrane		Yes		

2572231871	t3m_00227	KEGG_module	M00357: Methanogenesis, acetate => methane			
2572231871	t3m_00227	Metacyc	PWY66-162: ethanol degradation IV			
2572231871	t3m_00227	Metacyc	PWY-6672: <i>cis</i>-genanyl-CoA degradation			
2572231871	t3m_00227	Metacyc	PWY0-1313: acetate conversion to acetyl-CoA			
2572231871	t3m_00227	Metacyc	PWY66-21: ethanol degradation II			
2572231871	t3m_00227	Metacyc	PWY66-161: oxidative ethanol degradation III			
2572231871	t3m_00227	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)			
2572231871	t3m_00227	COG_category	[I] Lipid transport and metabolism			
2572231871	t3m_00227	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases			1.00E-123
2572231871	t3m_00227	pfam13193	AMP-binding_C			6.60E-18
2572231871	t3m_00227	pfam00501	AMP-binding			1.10E-77
2572231871	t3m_00227	EC:6.2.1.1	Acetate--CoA ligase.			
2572231871	t3m_00227	KO:K01895	acetyl-CoA synthetase [EC:6.2.1.1]			0.00E+00
2572231871	t3m_00227	Locus_type		CDS		
2572231871	t3m_00227	Product_name		Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases		
2572231871	t3m_00227	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231871	t3m_00227	Coordinates		31770..33512(-)		
2572231871	t3m_00227	DNA_length		1743bp		
2572231871	t3m_00227	Protein_length		580aa		
2572231871	t3m_00227	GC			0.67	

2572231872	t3m_00228	Locus_type		CDS		
2572231872	t3m_00228	Product_name		hypothetical protein		
2572231872	t3m_00228	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231872	t3m_00228	Coordinates		33587..33985(-)		
2572231872	t3m_00228	DNA_length		399bp		
2572231872	t3m_00228	Protein_length		132aa		
2572231872	t3m_00228	GC			0.63	

2572231872	t3m_00228	Transmembrane		Yes		

2572231873	t3m_00229	KEGG_module	M00527: Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine			
2572231873	t3m_00229	KEGG_module	M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine			
2572231873	t3m_00229	KEGG_module	M00526: Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine			
2572231873	t3m_00229	KEGG_module	M00525: Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine			
2572231873	t3m_00229	Metacyc	PWY-2942: lysine biosynthesis III			
2572231873	t3m_00229	Metacyc	DAPLYSINESYN-PWY: lysine biosynthesis I			
2572231873	t3m_00229	Metacyc	PWY-2941: lysine biosynthesis II			
2572231873	t3m_00229	Metacyc	PWY-5097: lysine biosynthesis VI			
2572231873	t3m_00229	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572231873	t3m_00229	COG_category	[E] Amino acid transport and metabolism			
2572231873	t3m_00229	COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase			1.00E-40
2572231873	t3m_00229	pfam00701	DHDPS			3.70E-31
2572231873	t3m_00229	EC:4.3.3.7	4-hydroxy-tetrahydrodipicolinate synthase.			
2572231873	t3m_00229	KO:K01714	4-hydroxy-tetrahydrodipicolinate synthase [EC:4.3.3.7]			3.50E-40
2572231873	t3m_00229	Locus_type		CDS		
2572231873	t3m_00229	Product_name		Dihydrodipicolinate synthase/N-acetylneuraminate lyase		
2572231873	t3m_00229	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231873	t3m_00229	Coordinates		34127..35104(-)		
2572231873	t3m_00229	DNA_length		978bp		
2572231873	t3m_00229	Protein_length		325aa		
2572231873	t3m_00229	GC			0.64	

2572231874	t3m_00230	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572231874	t3m_00230	COG0425	Predicted redox protein, regulator of disulfide bond formation			1.00E-06
2572231874	t3m_00230	pfam01206	TusA			1.40E-09
2572231874	t3m_00230	Locus_type		CDS		
2572231874	t3m_00230	Product_name		Predicted redox protein, regulator of disulfide bond formation		
2572231874	t3m_00230	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231874	t3m_00230	Coordinates		35147..35431(-)		
2572231874	t3m_00230	DNA_length		285bp		
2572231874	t3m_00230	Protein_length		94aa		
2572231874	t3m_00230	GC			0.67	

2572231875	t3m_00231	COG_category	[S] Function unknown			
2572231875	t3m_00231	COG1891	Uncharacterized protein conserved in archaea			1.00E-47
2572231875	t3m_00231	pfam04476	DUF556			4.50E-57
2572231875	t3m_00231	KO:K09733	hypothetical protein			0.00E+00
2572231875	t3m_00231	Locus_type		CDS		
2572231875	t3m_00231	Product_name		Uncharacterized protein conserved in archaea		
2572231875	t3m_00231	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231875	t3m_00231	Coordinates		35428..36192(-)		
2572231875	t3m_00231	DNA_length		765bp		
2572231875	t3m_00231	Protein_length		254aa		
2572231875	t3m_00231	GC			0.66	
2572231876	t3m_00232	Locus_type		CDS		
2572231876	t3m_00232	Product_name		hypothetical protein		
2572231876	t3m_00232	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231876	t3m_00232	Coordinates		36601..37281(+)		
2572231876	t3m_00232	DNA_length		681bp		
2572231876	t3m_00232	Protein_length		226aa		
2572231876	t3m_00232	GC			0.65	
2572231877	t3m_00233	COG_category	[R] General function prediction only			
2572231877	t3m_00233	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa			1.00E-12
2572231877	t3m_00233	pfam12697	Abhydrolase_6			7.80E-27
2572231877	t3m_00233	Locus_type		CDS		
2572231877	t3m_00233	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfan		
2572231877	t3m_00233	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231877	t3m_00233	Coordinates		37392..38270(-)		
2572231877	t3m_00233	DNA_length		879bp		
2572231877	t3m_00233	Protein_length		292aa		
2572231877	t3m_00233	GC			0.68	
2572231878	t3m_00234	Locus_type		CDS		
2572231878	t3m_00234	Product_name		hypothetical protein		

2572231878	t3m_00234	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231878	t3m_00234	Coordinates		38269..38484(+)		
2572231878	t3m_00234	DNA_length		216bp		
2572231878	t3m_00234	Protein_length		71aa		
2572231878	t3m_00234	GC			0.64	

2572231879	t3m_00235	Locus_type		CDS		
2572231879	t3m_00235	Product_name		hypothetical protein		
2572231879	t3m_00235	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231879	t3m_00235	Coordinates		38481..39155(+)		
2572231879	t3m_00235	DNA_length		675bp		
2572231879	t3m_00235	Protein_length		224aa		
2572231879	t3m_00235	GC			0.64	

2572231880	t3m_00236	KEGG_module	M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate			
2572231880	t3m_00236	Metacyc	PWY-5030: histidine degradation III			
2572231880	t3m_00236	Metacyc	HISHP-PWY: histidine degradation VI			
2572231880	t3m_00236	Metacyc	PWY-5028: histidine degradation II			
2572231880	t3m_00236	Metacyc	HISDEG-PWY: histidine degradation I			
2572231880	t3m_00236	IMG_pathway	189: L-histidine degradation to L-glutamate and formamide			
2572231880	t3m_00236	IMG_pathway	190: L-histidine degradation to L-glutamate and formiminotetrahydrofolate			
2572231880	t3m_00236	COG_category	[E] Amino acid transport and metabolism			
2572231880	t3m_00236	COG2986	Histidine ammonia-lyase			0.00E+00
2572231880	t3m_00236	pfam00221	Lyase_aromatic			0.00E+00
2572231880	t3m_00236	EC:4.3.1.3	Histidine ammonia-lyase.			
2572231880	t3m_00236	TIGR01225	histidine ammonia-lyase			0.00E+00
2572231880	t3m_00236	KO:K01745	histidine ammonia-lyase [EC:4.3.1.3]			0.00E+00
2572231880	t3m_00236	ITERM:00500	histidine ammonia-lyase (EC 4.3.1.3)			
2572231880	t3m_00236	Locus_type		CDS		
2572231880	t3m_00236	Product_name		histidine ammonia-lyase (EC 4.3.1.3)		
2572231880	t3m_00236	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231880	t3m_00236	Coordinates		39191..40714(-)		
2572231880	t3m_00236	DNA_length		1524bp		
2572231880	t3m_00236	Protein_length		507aa		

2572231880	t3m_00236	GC			0.65	
2572231881	t3m_00237	COG_category	[G] Carbohydrate transport and metabolism			
2572231881	t3m_00237	COG2814	Arabinose efflux permease			2.00E-04
2572231881	t3m_00237	pfam07690	MFS_1			1.70E-23
2572231881	t3m_00237	pfam07690	MFS_1			3.00E-12
2572231881	t3m_00237	Locus_type		CDS		
2572231881	t3m_00237	Product_name		Arabinose efflux permease		
2572231881	t3m_00237	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231881	t3m_00237	Coordinates		41980..43737(+)		
2572231881	t3m_00237	DNA_length		1758bp		
2572231881	t3m_00237	Protein_length		585aa		
2572231881	t3m_00237	GC			0.65	
2572231881	t3m_00237	Transmembrane		Yes		
2572231882	t3m_00238	pfam08241	Methyltransf_11			1.20E-16
2572231882	t3m_00238	Locus_type		CDS		
2572231882	t3m_00238	Product_name		Methyltransferase domain		
2572231882	t3m_00238	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231882	t3m_00238	Coordinates		44126..44995(+)		
2572231882	t3m_00238	DNA_length		870bp		
2572231882	t3m_00238	Protein_length		289aa		
2572231882	t3m_00238	GC			0.67	
2572231883	t3m_00239	COG_category	[R] General function prediction only			
2572231883	t3m_00239	COG0491	Zn-dependent hydrolases, including glyoxylases			3.00E-19
2572231883	t3m_00239	pfam00753	Lactamase_B			5.50E-29
2572231883	t3m_00239	Locus_type		CDS		
2572231883	t3m_00239	Product_name		Zn-dependent hydrolases, including glyoxylases		
2572231883	t3m_00239	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231883	t3m_00239	Coordinates		45073..45780(+)		
2572231883	t3m_00239	DNA_length		708bp		
2572231883	t3m_00239	Protein_length		235aa		
2572231883	t3m_00239	GC			0.67	

2572231884	t3m_00240	Locus_type		CDS		
2572231884	t3m_00240	Product_name		hypothetical protein		
2572231884	t3m_00240	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231884	t3m_00240	Coordinates		45844..46320(-)		
2572231884	t3m_00240	DNA_length		477bp		
2572231884	t3m_00240	Protein_length		158aa		
2572231884	t3m_00240	GC			0.68	
2572231885	t3m_00241	KEGG_module	M00288: RPA complex			
2572231885	t3m_00241	pfam01336	tRNA_anti-codon			5.70E-08
2572231885	t3m_00241	KO:K07466	replication factor A1			1.30E-10
2572231885	t3m_00241	Locus_type		CDS		
2572231885	t3m_00241	Product_name		OB-fold nucleic acid binding domain		
2572231885	t3m_00241	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231885	t3m_00241	Coordinates		46400..46708(-)		
2572231885	t3m_00241	DNA_length		309bp		
2572231885	t3m_00241	Protein_length		102aa		
2572231885	t3m_00241	GC			0.66	
2572231886	t3m_00242	Locus_type		CDS		
2572231886	t3m_00242	Product_name		hypothetical protein		
2572231886	t3m_00242	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231886	t3m_00242	Coordinates		46817..47068(-)		
2572231886	t3m_00242	DNA_length		252bp		
2572231886	t3m_00242	Protein_length		83aa		
2572231886	t3m_00242	GC			0.63	
2572231886	t3m_00242	Transmembrane		Yes		
2572231887	t3m_00243	COG_category	[P] Inorganic ion transport and metabolism			
2572231887	t3m_00243	COG1914	Mn2+ and Fe2+ transporters of the NRAMP family			8.00E-30
2572231887	t3m_00243	pfam01566	Nramp			4.00E-38
2572231887	t3m_00243	Locus_type		CDS		
2572231887	t3m_00243	Product_name		Mn2+ and Fe2+ transporters of the NRAMP family		

2572231887	t3m_00243	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231887	t3m_00243	Coordinates		47713..48813(+)	
2572231887	t3m_00243	DNA_length		1101bp	
2572231887	t3m_00243	Protein_length		366aa	
2572231887	t3m_00243	GC		0.66	
2572231887	t3m_00243	Transmembrane		Yes	
2572231888	t3m_00244	Locus_type		CDS	
2572231888	t3m_00244	Product_name		hypothetical protein	
2572231888	t3m_00244	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231888	t3m_00244	Coordinates		48917..49084(+)	
2572231888	t3m_00244	DNA_length		168bp	
2572231888	t3m_00244	Protein_length		55aa	
2572231888	t3m_00244	GC		0.61	
2572231888	t3m_00244	Transmembrane		Yes	
2572231889	t3m_00245	COG_category	[C] Energy production and conversion		
2572231889	t3m_00245	COG1529	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutI		7.00E-54
2572231889	t3m_00245	pfam01315	Ald_Xan_dh_C		1.20E-06
2572231889	t3m_00245	pfam02738	Ald_Xan_dh_C2		2.30E-11
2572231889	t3m_00245	pfam02738	Ald_Xan_dh_C2		2.60E-14
2572231889	t3m_00245	pfam02738	Ald_Xan_dh_C2		7.70E-45
2572231889	t3m_00245	EC:1.3.99.16	Isoquinoline 1-oxidoreductase.		
2572231889	t3m_00245	KO:K00256	isoquinoline 1-oxidoreductase [EC:1.3.99.16]		0.00E+00
2572231889	t3m_00245	Locus_type		CDS	
2572231889	t3m_00245	Product_name		Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL	
2572231889	t3m_00245	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231889	t3m_00245	Coordinates		49152..51254(-)	
2572231889	t3m_00245	DNA_length		2103bp	
2572231889	t3m_00245	Protein_length		700aa	
2572231889	t3m_00245	GC		0.69	
2572231890	t3m_00246	Metacyc	PWY-5372: carbon tetrachloride degradation II		
2572231890	t3m_00246	Metacyc	PWY-6780: hydrogen production VI		

2572231890	t3m_00246	COG_category	[C] Energy production and conversion			
2572231890	t3m_00246	COG2080	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/Cut			7.00E-54
2572231890	t3m_00246	pfam00111	Fer2			3.30E-10
2572231890	t3m_00246	pfam01799	Fer2_2			3.90E-33
2572231890	t3m_00246	EC:1.2.99.2	Carbon-monoxide dehydrogenase (acceptor).			
2572231890	t3m_00246	KO:K03518	carbon-monoxide dehydrogenase small subunit [EC:1.2.99.2]			2.00E-44
2572231890	t3m_00246	Locus_type		CDS		
2572231890	t3m_00246	Product_name		Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS		
2572231890	t3m_00246	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231890	t3m_00246	Coordinates		51251..51730(-)		
2572231890	t3m_00246	DNA_length		480bp		
2572231890	t3m_00246	Protein_length		159aa		
2572231890	t3m_00246	GC			0.68	
2572231891	t3m_00247	Locus_type		CDS		
2572231891	t3m_00247	Product_name		hypothetical protein		
2572231891	t3m_00247	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231891	t3m_00247	Coordinates		51959..53257(+)		
2572231891	t3m_00247	DNA_length		1299bp		
2572231891	t3m_00247	Protein_length		432aa		
2572231891	t3m_00247	GC			0.67	
2572231891	t3m_00247	Transmembrane		Yes		
2572231892	t3m_00248	Locus_type		CDS		
2572231892	t3m_00248	Product_name		hypothetical protein		
2572231892	t3m_00248	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231892	t3m_00248	Coordinates		53254..54708(-)		
2572231892	t3m_00248	DNA_length		1455bp		
2572231892	t3m_00248	Protein_length		484aa		
2572231892	t3m_00248	GC			0.67	
2572231892	t3m_00248	Transmembrane		Yes		
2572231893	t3m_00249	Locus_type		CDS		
2572231893	t3m_00249	Product_name		hypothetical protein		

2572231893	t3m_00249	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231893	t3m_00249	Coordinates		54905..56191(+)		
2572231893	t3m_00249	DNA_length		1287bp		
2572231893	t3m_00249	Protein_length		428aa		
2572231893	t3m_00249	GC			0.67	
2572231893	t3m_00249	Transmembrane		Yes		

2572231894	t3m_00250	pfam09594	DUF2029			7.10E-07
2572231894	t3m_00250	Locus_type		CDS		
2572231894	t3m_00250	Product_name		Protein of unknown function (DUF2029)		
2572231894	t3m_00250	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231894	t3m_00250	Coordinates		56300..57592(+)		
2572231894	t3m_00250	DNA_length		1293bp		
2572231894	t3m_00250	Protein_length		430aa		
2572231894	t3m_00250	GC			0.7	
2572231894	t3m_00250	Transmembrane		Yes		

2572231895	t3m_00251	Metacyc	NADPHOS-DEPHOS-PWY: NAD phosphorylation and dephosphorylation			
2572231895	t3m_00251	COG_category	[C] Energy production and conversion			
2572231895	t3m_00251	COG1282	NAD/NADP transhydrogenase beta subunit			1.00E-116
2572231895	t3m_00251	pfam02233	PNTB			0.00E+00
2572231895	t3m_00251	EC:1.6.1.2	NAD(P)(+) transhydrogenase (AB-specific).			
2572231895	t3m_00251	KO:K00325	NAD(P) transhydrogenase subunit beta [EC:1.6.1.2]			0.00E+00
2572231895	t3m_00251	Locus_type		CDS		
2572231895	t3m_00251	Product_name		NAD/NADP transhydrogenase beta subunit		
2572231895	t3m_00251	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231895	t3m_00251	Coordinates		57579..58994(-)		
2572231895	t3m_00251	DNA_length		1416bp		
2572231895	t3m_00251	Protein_length		471aa		
2572231895	t3m_00251	GC			0.65	
2572231895	t3m_00251	Transmembrane		Yes		

2572231896	t3m_00252	Metacyc	NADPHOS-DEPHOS-PWY: NAD phosphorylation and dephosphorylation			
2572231896	t3m_00252	pfam12769	DUF3814			2.10E-30

2572231896	t3m_00252	EC:1.6.1.2	NAD(P)(+) transhydrogenase (AB-specific).		
2572231896	t3m_00252	KO:K00324	NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]		5.90E-32
2572231896	t3m_00252	Locus_type		CDS	
2572231896	t3m_00252	Product_name		Domain of unknown function (DUF3814)	
2572231896	t3m_00252	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231896	t3m_00252	Coordinates		58991..59293(-)	
2572231896	t3m_00252	DNA_length		303bp	
2572231896	t3m_00252	Protein_length		100aa	
2572231896	t3m_00252	GC		0.64	
2572231896	t3m_00252	Transmembrane		Yes	
2572231897	t3m_00253	Metacyc	NADPHOS-DEPHOS-PWY: NAD phosphorylation and dephosphorylation		
2572231897	t3m_00253	COG_category	[C] Energy production and conversion		
2572231897	t3m_00253	COG3288	NAD/NADP transhydrogenase alpha subunit		3.00E-91
2572231897	t3m_00253	pfam01262	AlaDh_PNT_C		4.50E-49
2572231897	t3m_00253	pfam05222	AlaDh_PNT_N		3.70E-41
2572231897	t3m_00253	EC:1.6.1.2	NAD(P)(+) transhydrogenase (AB-specific).		
2572231897	t3m_00253	TIGR00561	NAD(P) transhydrogenase, alpha subunit		3.80E-101
2572231897	t3m_00253	KO:K00324	NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]		0.00E+00
2572231897	t3m_00253	Locus_type		CDS	
2572231897	t3m_00253	Product_name		NAD/NADP transhydrogenase alpha subunit	
2572231897	t3m_00253	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231897	t3m_00253	Coordinates		59294..60436(-)	
2572231897	t3m_00253	DNA_length		1143bp	
2572231897	t3m_00253	Protein_length		380aa	
2572231897	t3m_00253	GC		0.68	
2572231898	t3m_00254	Metacyc	PWY-5706: alliin degradation		
2572231898	t3m_00254	Metacyc	PWY-181: photorespiration		
2572231898	t3m_00254	Metacyc	PWY-5707: isoalliin degradation		
2572231898	t3m_00254	Metacyc	PWY-7018: paromomycin biosynthesis		
2572231898	t3m_00254	Metacyc	P421-PWY: 4-nitrotoluene degradation I		
2572231898	t3m_00254	Metacyc	PWY-7000: kanamycin biosynthesis		
2572231898	t3m_00254	COG_category	[R] General function prediction only		

2572231898	t3m_00254	COG0579	Predicted dehydrogenase			3.00E-80
2572231898	t3m_00254	pfam01266	DAO			3.70E-51
2572231898	t3m_00254	EC:1.1.3.-	Oxidoreductases. Acting on the CH-OH group of donors. With oxygen as acceptor.			
2572231898	t3m_00254	KO:K15736	L-2-hydroxyglutarate oxidase [EC:1.1.3.-]			0.00E+00
2572231898	t3m_00254	Locus_type		CDS		
2572231898	t3m_00254	Product_name		Predicted dehydrogenase		
2572231898	t3m_00254	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231898	t3m_00254	Coordinates		60540..61742(+)		
2572231898	t3m_00254	DNA_length		1203bp		
2572231898	t3m_00254	Protein_length		400aa		
2572231898	t3m_00254	GC			0.7	

2572231899	t3m_00255	COG_category	[L] Replication, recombination and repair			
2572231899	t3m_00255	COG0863	DNA modification methylase			7.00E-27
2572231899	t3m_00255	pfam01555	N6_N4_Mtase			1.60E-36
2572231899	t3m_00255	EC:2.1.1.72	Site-specific DNA-methyltransferase (adenine-specific).			
2572231899	t3m_00255	KO:K07319	putative adenine-specific DNA-methyltransferase [EC:2.1.1.72]			0.00E+00
2572231899	t3m_00255	Locus_type		CDS		
2572231899	t3m_00255	Product_name		DNA modification methylase		
2572231899	t3m_00255	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231899	t3m_00255	Coordinates		61766..62611(+)		
2572231899	t3m_00255	DNA_length		846bp		
2572231899	t3m_00255	Protein_length		281aa		
2572231899	t3m_00255	GC			0.69	

2572231900	t3m_00256	pfam00535	Glycos_transf_2			1.70E-11
2572231900	t3m_00256	Locus_type		CDS		
2572231900	t3m_00256	Product_name		Glycosyl transferase family 2		
2572231900	t3m_00256	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3		
2572231900	t3m_00256	Coordinates		62608..63645(-)		
2572231900	t3m_00256	DNA_length		1038bp		
2572231900	t3m_00256	Protein_length		345aa		
2572231900	t3m_00256	GC			0.69	

2572231901	t3m_00257	COG_category	[L] Replication, recombination and repair		
2572231901	t3m_00257	COG3359	Predicted exonuclease		8.00E-30
2572231901	t3m_00257	pfam13482	RNase_H_2		3.80E-25
2572231901	t3m_00257	KO:K07502	hypothetical protein		0.00E+00
2572231901	t3m_00257	Locus_type		CDS	
2572231901	t3m_00257	Product_name		Predicted exonuclease	
2572231901	t3m_00257	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231901	t3m_00257	Coordinates		63654..64475(-)	
2572231901	t3m_00257	DNA_length		822bp	
2572231901	t3m_00257	Protein_length		273aa	
2572231901	t3m_00257	GC		0.73	
2572231902	t3m_00258	Locus_type		CDS	
2572231902	t3m_00258	Product_name		hypothetical protein	
2572231902	t3m_00258	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231902	t3m_00258	Coordinates		64519..64899(-)	
2572231902	t3m_00258	DNA_length		381bp	
2572231902	t3m_00258	Protein_length		126aa	
2572231902	t3m_00258	GC		0.71	
2572231903	t3m_00259	Locus_type		rRNA	
2572231903	t3m_00259	Gene_symbol		23S	
2572231903	t3m_00259	Product_name		23S rRNA. Archaeal LSU	
2572231903	t3m_00259	Scaffold		t3m_contig_70_28_len_67510_read_count_6030377.3	
2572231903	t3m_00259	Coordinates		65041..67509(-)	
2572231903	t3m_00259	DNA_length		2469bp	
2572231903	t3m_00259	GC		0.58	
2572231904	t3m_00260	pfam03029	ATP_bind_1		3.10E-25
2572231904	t3m_00260	Locus_type		CDS	
2572231904	t3m_00260	Product_name		Conserved hypothetical ATP binding protein	
2572231904	t3m_00260	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231904	t3m_00260	Coordinates		1..537(+)	
2572231904	t3m_00260	DNA_length		537bp	

2572231904	t3m_00260	Protein_length		178aa		
2572231904	t3m_00260	GC			0.67	
2572231905	t3m_00261	Locus_type		CDS		
2572231905	t3m_00261	Product_name		hypothetical protein		
2572231905	t3m_00261	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231905	t3m_00261	Coordinates		542..844(-)		
2572231905	t3m_00261	DNA_length		303bp		
2572231905	t3m_00261	Protein_length		100aa		
2572231905	t3m_00261	GC			0.69	
2572231906	t3m_00262	pfam01963	TraB			4.60E-18
2572231906	t3m_00262	Locus_type		CDS		
2572231906	t3m_00262	Product_name		TraB family		
2572231906	t3m_00262	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231906	t3m_00262	Coordinates		927..1643(+)		
2572231906	t3m_00262	DNA_length		717bp		
2572231906	t3m_00262	Protein_length		238aa		
2572231906	t3m_00262	GC			0.7	
2572231907	t3m_00263	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2572231907	t3m_00263	COG0489	ATPases involved in chromosome partitioning			5.00E-48
2572231907	t3m_00263	pfam10609	ParA			2.30E-33
2572231907	t3m_00263	Locus_type		CDS		
2572231907	t3m_00263	Product_name		ATPases involved in chromosome partitioning		
2572231907	t3m_00263	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231907	t3m_00263	Coordinates		1615..2391(-)		
2572231907	t3m_00263	DNA_length		777bp		
2572231907	t3m_00263	Protein_length		258aa		
2572231907	t3m_00263	GC			0.67	
2572231908	t3m_00264	COG_category	[C] Energy production and conversion			
2572231908	t3m_00264	COG1042	Acyl-CoA synthetase (NDP forming)			0.00E+00
2572231908	t3m_00264	pfam13549	ATP-grasp_5			1.80E-73

2572231908	t3m_00264	pfam13607	Succ_CoA_lig		2.10E-49
2572231908	t3m_00264	pfam13380	CoA_binding_2		5.10E-23
2572231908	t3m_00264	TIGR02717	acetyl coenzyme A synthetase (ADP forming), alpha domain		0.00E+00
2572231908	t3m_00264	KO:K09181	hypothetical protein		0.00E+00
2572231908	t3m_00264	Locus_type		CDS	
2572231908	t3m_00264	Product_name		Acyl-CoA synthetase (NDP forming)	
2572231908	t3m_00264	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231908	t3m_00264	Coordinates		2557..4692(+)	
2572231908	t3m_00264	DNA_length		2136bp	
2572231908	t3m_00264	Protein_length		711aa	
2572231908	t3m_00264	GC		0.67	
2572231908	t3m_00264	Fused_gene		Yes	
2572231909	t3m_00265	COG_category	[H] Coenzyme transport and metabolism		
2572231909	t3m_00265	COG1977	Molybdopterin converting factor, small subunit		5.00E-08
2572231909	t3m_00265	pfam02597	ThiS		6.10E-11
2572231909	t3m_00265	Locus_type		CDS	
2572231909	t3m_00265	Product_name		Molybdopterin converting factor, small subunit	
2572231909	t3m_00265	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231909	t3m_00265	Coordinates		5053..5310(-)	
2572231909	t3m_00265	DNA_length		258bp	
2572231909	t3m_00265	Protein_length		85aa	
2572231909	t3m_00265	GC		0.64	
2572231910	t3m_00266	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2572231910	t3m_00266	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2572231910	t3m_00266	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2572231910	t3m_00266	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2572231910	t3m_00266	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2572231910	t3m_00266	Metacyc	P23-PWY: reductive TCA cycle I		
2572231910	t3m_00266	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2572231910	t3m_00266	Metacyc	PWY-5392: reductive TCA cycle II		
2572231910	t3m_00266	COG_category	[C] Energy production and conversion		
2572231910	t3m_00266	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o		1.00E-69

2572231910	t3m_00266	pfam01558	POR			3.50E-34
2572231910	t3m_00266	pfam01855	POR_N			6.90E-57
2572231910	t3m_00266	EC:1.2.7.3	2-oxoglutarate synthase.			
2572231910	t3m_00266	TIGR03710	2-oxoacid:acceptor oxidoreductase, alpha subunit			0.00E+00
2572231910	t3m_00266	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]			0.00E+00
2572231910	t3m_00266	Locus_type		CDS		
2572231910	t3m_00266	Product_name		2-oxoacid:acceptor oxidoreductase, alpha subunit		
2572231910	t3m_00266	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231910	t3m_00266	Coordinates		5398..7137(+)		
2572231910	t3m_00266	DNA_length		1740bp		
2572231910	t3m_00266	Protein_length		579aa		
2572231910	t3m_00266	GC			0.67	
2572231911	t3m_00267	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572231911	t3m_00267	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			
2572231911	t3m_00267	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2572231911	t3m_00267	Metacyc	P23-PWY: reductive TCA cycle I			
2572231911	t3m_00267	Metacyc	PWY-5392: reductive TCA cycle II			
2572231911	t3m_00267	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2572231911	t3m_00267	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572231911	t3m_00267	COG_category	[C] Energy production and conversion			
2572231911	t3m_00267	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o			4.00E-80
2572231911	t3m_00267	pfam02775	TPP_enzyme_C			1.80E-29
2572231911	t3m_00267	pfam12367	PFO_beta_C			9.20E-24
2572231911	t3m_00267	EC:1.2.7.3	2-oxoglutarate synthase.			
2572231911	t3m_00267	TIGR02177	2-oxoacid:acceptor oxidoreductase, beta subunit, pyruvate/2-ketoisova			1.10E-111
2572231911	t3m_00267	KO:K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]			0.00E+00
2572231911	t3m_00267	Locus_type		CDS		
2572231911	t3m_00267	Product_name		2-oxoacid:acceptor oxidoreductase, beta subunit, pyruvate/2-ketoisoval		
2572231911	t3m_00267	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231911	t3m_00267	Coordinates		7155..8039(+)		
2572231911	t3m_00267	DNA_length		885bp		
2572231911	t3m_00267	Protein_length		294aa		
2572231911	t3m_00267	GC			0.66	

2572231912	t3m_00268	COG_category	[R] General function prediction only			
2572231912	t3m_00268	COG2244	Membrane protein involved in the export of O-antigen and teichoic aci			2.00E-17
2572231912	t3m_00268	pfam01943	Polysacc_synt			3.00E-20
2572231912	t3m_00268	pfam14667	Polysacc_synt_C			1.70E-11
2572231912	t3m_00268	Locus_type		CDS		
2572231912	t3m_00268	Product_name		Membrane protein involved in the export of O-antigen and teichoic acid		
2572231912	t3m_00268	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231912	t3m_00268	Coordinates		8243..9784(+)		
2572231912	t3m_00268	DNA_length		1542bp		
2572231912	t3m_00268	Protein_length		513aa		
2572231912	t3m_00268	GC			0.67	
2572231912	t3m_00268	Transmembrane		Yes		

2572231913	t3m_00269	Locus_type		CDS		
2572231913	t3m_00269	Product_name		hypothetical protein		
2572231913	t3m_00269	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231913	t3m_00269	Coordinates		9894..10148(+)		
2572231913	t3m_00269	DNA_length		255bp		
2572231913	t3m_00269	Protein_length		84aa		
2572231913	t3m_00269	GC			0.69	

2572231914	t3m_00270	COG_category	[S] Function unknown			
2572231914	t3m_00270	COG0586	Uncharacterized membrane-associated protein			9.00E-21
2572231914	t3m_00270	pfam09335	SNARE_assoc			3.10E-18
2572231914	t3m_00270	Locus_type		CDS		
2572231914	t3m_00270	Product_name		Uncharacterized membrane-associated protein		
2572231914	t3m_00270	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231914	t3m_00270	Coordinates		10188..10892(+)		
2572231914	t3m_00270	DNA_length		705bp		
2572231914	t3m_00270	Protein_length		234aa		
2572231914	t3m_00270	GC			0.67	
2572231914	t3m_00270	Transmembrane		Yes		

2572231915	t3m_00271	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP		
2572231915	t3m_00271	Metacyc	PWY-5686: UMP biosynthesis		
2572231915	t3m_00271	COG_category	[F] Nucleotide transport and metabolism		
2572231915	t3m_00271	COG0044	Dihydroorotase and related cyclic amidohydrolases		3.00E-74
2572231915	t3m_00271	pfam13147	Amidohydro_4		2.40E-13
2572231915	t3m_00271	EC:3.5.2.3	Dihydroorotase.		
2572231915	t3m_00271	TIGR00857	dihydroorotase, multifunctional complex type		9.70E-72
2572231915	t3m_00271	KO:K01465	dihydroorotase [EC:3.5.2.3]		0.00E+00
2572231915	t3m_00271	Locus_type		CDS	
2572231915	t3m_00271	Product_name		Dihydroorotase and related cyclic amidohydrolases	
2572231915	t3m_00271	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231915	t3m_00271	Coordinates		10893..12257(-)	
2572231915	t3m_00271	DNA_length		1365bp	
2572231915	t3m_00271	Protein_length		454aa	
2572231915	t3m_00271	GC		0.72	

2572231916	t3m_00272	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572231916	t3m_00272	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II		
2572231916	t3m_00272	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis		
2572231916	t3m_00272	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I		
2572231916	t3m_00272	IMG_pathway	297: 5-amino-1-(5-phospho-D-ribosyl)imidazole synthesis		
2572231916	t3m_00272	COG_category	[F] Nucleotide transport and metabolism		
2572231916	t3m_00272	COG0150	Phosphoribosylaminoimidazole (AIR) synthetase		8.00E-68
2572231916	t3m_00272	pfam02769	AIRS_C		1.80E-19
2572231916	t3m_00272	pfam00586	AIRS		1.50E-12
2572231916	t3m_00272	EC:6.3.3.1	Phosphoribosylformylglycinamidine cyclo-ligase.		
2572231916	t3m_00272	TIGR00878	phosphoribosylaminoimidazole synthetase		4.00E-74
2572231916	t3m_00272	KO:K01933	phosphoribosylformylglycinamidine cyclo-ligase [EC:6.3.3.1]		0.00E+00
2572231916	t3m_00272	ITERM:01294	phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)		
2572231916	t3m_00272	Locus_type		CDS	
2572231916	t3m_00272	Product_name		phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	
2572231916	t3m_00272	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231916	t3m_00272	Coordinates		12394..13404(+)	
2572231916	t3m_00272	DNA_length		1011bp	

2572231916	t3m_00272	Protein_length		336aa		
2572231916	t3m_00272	GC			0.7	

2572231917	t3m_00273	pfam00892	EamA			3.30E-08
2572231917	t3m_00273	Locus_type		CDS		
2572231917	t3m_00273	Product_name		EamA-like transporter family		
2572231917	t3m_00273	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231917	t3m_00273	Coordinates		13479..14435(+)		
2572231917	t3m_00273	DNA_length		957bp		
2572231917	t3m_00273	Protein_length		318aa		
2572231917	t3m_00273	GC			0.7	
2572231917	t3m_00273	Transmembrane		Yes		

2572231918	t3m_00274	COG_category	[L] Replication, recombination and repair			
2572231918	t3m_00274	COG0417	DNA polymerase elongation subunit (family B)			1.00E-121
2572231918	t3m_00274	pfam00136	DNA_pol_B			6.80E-60
2572231918	t3m_00274	pfam03104	DNA_pol_B_exo1			6.40E-14
2572231918	t3m_00274	EC:2.7.7.7	DNA-directed DNA polymerase.			
2572231918	t3m_00274	KO:K02319	DNA polymerase I [EC:2.7.7.7]			0.00E+00
2572231918	t3m_00274	Locus_type		CDS		
2572231918	t3m_00274	Product_name		DNA polymerase elongation subunit (family B)		
2572231918	t3m_00274	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231918	t3m_00274	Coordinates		14451..16913(-)		
2572231918	t3m_00274	DNA_length		2463bp		
2572231918	t3m_00274	Protein_length		820aa		
2572231918	t3m_00274	GC			0.68	

2572231919	t3m_00275	COG_category	[L] Replication, recombination and repair			
2572231919	t3m_00275	COG1573	Uracil-DNA glycosylase			2.00E-31
2572231919	t3m_00275	pfam03167	UDG			2.40E-34
2572231919	t3m_00275	EC:2.7.7.7	DNA-directed DNA polymerase.			
2572231919	t3m_00275	TIGR00758	uracil-DNA glycosylase, family 4			3.60E-43
2572231919	t3m_00275	KO:K02334	DNA polymerase bacteriophage-type [EC:2.7.7.7]			3.50E-34
2572231919	t3m_00275	Locus_type		CDS		

2572231919	t3m_00275	Product_name		uracil-DNA glycosylase, family 4		
2572231919	t3m_00275	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231919	t3m_00275	Coordinates		16946..17581(-)		
2572231919	t3m_00275	DNA_length		636bp		
2572231919	t3m_00275	Protein_length		211aa		
2572231919	t3m_00275	GC			0.73	
2572231920	t3m_00276	KEGG_module	M00179: Ribosome, archaea			
2572231920	t3m_00276	KEGG_module	M00178: Ribosome, bacteria			
2572231920	t3m_00276	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231920	t3m_00276	COG0048	Ribosomal protein S12			3.00E-36
2572231920	t3m_00276	pfam00164	Ribosom_S12_S23			4.30E-40
2572231920	t3m_00276	TIGR00982	ribosomal protein S23 (S12)			3.70E-75
2572231920	t3m_00276	KO:K02950	small subunit ribosomal protein S12			0.00E+00
2572231920	t3m_00276	Locus_type		CDS		
2572231920	t3m_00276	Product_name		SSU ribosomal protein S12P		
2572231920	t3m_00276	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231920	t3m_00276	Coordinates		17674..18108(+)		
2572231920	t3m_00276	DNA_length		435bp		
2572231920	t3m_00276	Protein_length		144aa		
2572231920	t3m_00276	GC			0.65	
2572231921	t3m_00277	KEGG_module	M00179: Ribosome, archaea			
2572231921	t3m_00277	KEGG_module	M00178: Ribosome, bacteria			
2572231921	t3m_00277	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231921	t3m_00277	COG0049	Ribosomal protein S7			1.00E-34
2572231921	t3m_00277	pfam00177	Ribosomal_S7			8.60E-35
2572231921	t3m_00277	TIGR01028	ribosomal protein S7(archaeal)/S5(eukaryotic)			3.80E-72
2572231921	t3m_00277	KO:K02992	small subunit ribosomal protein S7			0.00E+00
2572231921	t3m_00277	ITERM:01649	SSU ribosomal protein S7P			
2572231921	t3m_00277	Locus_type		CDS		
2572231921	t3m_00277	Product_name		SSU ribosomal protein S7P		
2572231921	t3m_00277	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231921	t3m_00277	Coordinates		18105..18767(+)		

2572231921	t3m_00277	DNA_length		663bp		
2572231921	t3m_00277	Protein_length		220aa		
2572231921	t3m_00277	GC			0.67	
2572231922	t3m_00278	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231922	t3m_00278	COG0480	Translation elongation factors (GTPases)			0.00E+00
2572231922	t3m_00278	pfam14492	EFG_II			7.00E-25
2572231922	t3m_00278	pfam03144	GTP_EFTU_D2			3.00E-13
2572231922	t3m_00278	pfam00009	GTP_EFTU			1.10E-54
2572231922	t3m_00278	pfam00679	EFG_C			7.50E-20
2572231922	t3m_00278	pfam03764	EFG_IV			1.10E-25
2572231922	t3m_00278	TIGR00231	small GTP-binding protein domain			1.80E-23
2572231922	t3m_00278	TIGR00490	translation elongation factor aEF-2			0.00E+00
2572231922	t3m_00278	KO:K03234	elongation factor 2			0.00E+00
2572231922	t3m_00278	Locus_type		CDS		
2572231922	t3m_00278	Product_name		translation elongation factor 2 (EF-2/EF-G)		
2572231922	t3m_00278	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231922	t3m_00278	Coordinates		18787..20988(+)		
2572231922	t3m_00278	DNA_length		2202bp		
2572231922	t3m_00278	Protein_length		733aa		
2572231922	t3m_00278	GC			0.65	
2572231923	t3m_00279	COG_category	[L] Replication, recombination and repair			
2572231923	t3m_00279	COG0350	Methylated DNA-protein cysteine methyltransferase			3.00E-32
2572231923	t3m_00279	pfam01035	DNA_binding_1			2.70E-31
2572231923	t3m_00279	EC:2.1.1.63	Methylated-DNA--[protein]-cysteine S-methyltransferase.			
2572231923	t3m_00279	TIGR00589	O-6-methylguanine DNA methyltransferase			1.80E-36
2572231923	t3m_00279	KO:K00567	methylated-DNA-[protein]-cysteine S-methyltransferase [EC:2.1.1.63]			2.50E-28
2572231923	t3m_00279	Locus_type		CDS		
2572231923	t3m_00279	Product_name		O-6-methylguanine DNA methyltransferase		
2572231923	t3m_00279	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231923	t3m_00279	Coordinates		21015..21614(-)		
2572231923	t3m_00279	DNA_length		600bp		
2572231923	t3m_00279	Protein_length		199aa		

2572231923	t3m_00279	GC			0.69	
2572231924	t3m_00280	COG_category	[L] Replication, recombination and repair			
2572231924	t3m_00280	COG0468	RecA/RadA recombinase			2.00E-36
2572231924	t3m_00280	pfam08423	Rad51			2.00E-22
2572231924	t3m_00280	TIGR02237	DNA repair and recombination protein RadB			2.70E-57
2572231924	t3m_00280	KO:K04484	DNA repair protein RadB			2.70E-40
2572231924	t3m_00280	Locus_type		CDS		
2572231924	t3m_00280	Product_name		DNA repair and recombination protein RadB		
2572231924	t3m_00280	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231924	t3m_00280	Coordinates		21648..22337(-)		
2572231924	t3m_00280	DNA_length		690bp		
2572231924	t3m_00280	Protein_length		229aa		
2572231924	t3m_00280	GC			0.7	
2572231925	t3m_00281	COG_category	[R] General function prediction only			
2572231925	t3m_00281	COG0595	Predicted hydrolase of the metallo-beta-lactamase superfamily			3.00E-38
2572231925	t3m_00281	pfam07521	RMMBL			2.50E-07
2572231925	t3m_00281	pfam12706	Lactamase_B_2			1.20E-16
2572231925	t3m_00281	Locus_type		CDS		
2572231925	t3m_00281	Product_name		Predicted hydrolase of the metallo-beta-lactamase superfamily		
2572231925	t3m_00281	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231925	t3m_00281	Coordinates		22389..23732(-)		
2572231925	t3m_00281	DNA_length		1344bp		
2572231925	t3m_00281	Protein_length		447aa		
2572231925	t3m_00281	GC			0.68	
2572231926	t3m_00282	pfam01909	NTP_transf_2			6.50E-06
2572231926	t3m_00282	Locus_type		CDS		
2572231926	t3m_00282	Product_name		Nucleotidyltransferase domain		
2572231926	t3m_00282	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231926	t3m_00282	Coordinates		23819..24643(+)		
2572231926	t3m_00282	DNA_length		825bp		
2572231926	t3m_00282	Protein_length		274aa		

2572231926	t3m_00282	GC			0.69	
2572231927	t3m_00283	COG_category	[K] Transcription			
2572231927	t3m_00283	COG1996	DNA-directed RNA polymerase, subunit RPC10 (contains C4-type Zn-fin			3.00E-05
2572231927	t3m_00283	Locus_type		CDS		
2572231927	t3m_00283	Product_name		DNA-directed RNA polymerase, subunit P (EC 2.7.7.6)		
2572231927	t3m_00283	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231927	t3m_00283	Coordinates		24662..24796(-)		
2572231927	t3m_00283	DNA_length		135bp		
2572231927	t3m_00283	Protein_length		44aa		
2572231927	t3m_00283	GC			0.61	
2572231928	t3m_00284	KEGG_module	M00177: Ribosome, eukaryotes			
2572231928	t3m_00284	KEGG_module	M00179: Ribosome, archaea			
2572231928	t3m_00284	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231928	t3m_00284	COG1997	Ribosomal protein L37AE/L43A			3.00E-10
2572231928	t3m_00284	pfam01780	Ribosomal_L37ae			4.00E-17
2572231928	t3m_00284	KO:K02921	large subunit ribosomal protein L37Ae			4.60E-12
2572231928	t3m_00284	ITERM:00270	LSU ribosomal protein L37AE			
2572231928	t3m_00284	Locus_type		CDS		
2572231928	t3m_00284	Product_name		LSU ribosomal protein L37AE		
2572231928	t3m_00284	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231928	t3m_00284	Coordinates		24825..25094(-)		
2572231928	t3m_00284	DNA_length		270bp		
2572231928	t3m_00284	Protein_length		89aa		
2572231928	t3m_00284	GC			0.7	
2572231929	t3m_00285	KEGG_module	M00391: Exosome, eukaryotes			
2572231929	t3m_00285	KEGG_module	M00390: Exosome, archaea			
2572231929	t3m_00285	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231929	t3m_00285	COG2123	RNase PH-related exoribonuclease			6.00E-71
2572231929	t3m_00285	pfam03725	RNase_PH_C			1.50E-08
2572231929	t3m_00285	pfam01138	RNase_PH			1.30E-23
2572231929	t3m_00285	KO:K12589	exosome complex component RRP42			0.00E+00

2572231929	t3m_00285	Locus_type		CDS	
2572231929	t3m_00285	Product_name		ribosomal RNA-processing protein RRP42 (EC 3.1.13.-)	
2572231929	t3m_00285	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231929	t3m_00285	Coordinates		25091..25879(-)	
2572231929	t3m_00285	DNA_length		789bp	
2572231929	t3m_00285	Protein_length		262aa	
2572231929	t3m_00285	GC		0.69	
2572231930	t3m_00286	KEGG_module	M00390: Exosome, archaea		
2572231930	t3m_00286	KEGG_module	M00391: Exosome, eukaryotes		
2572231930	t3m_00286	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572231930	t3m_00286	COG0689	RNase PH		2.00E-67
2572231930	t3m_00286	pfam03725	RNase_PH_C		3.30E-11
2572231930	t3m_00286	pfam01138	RNase_PH		1.70E-31
2572231930	t3m_00286	TIGR02065	archaeal exosome-like complex exonuclease 1		1.20E-107
2572231930	t3m_00286	KO:K11600	exosome complex component RRP41		0.00E+00
2572231930	t3m_00286	Locus_type		CDS	
2572231930	t3m_00286	Product_name		archaeal exosome-like complex exonuclease 1	
2572231930	t3m_00286	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231930	t3m_00286	Coordinates		25876..26625(-)	
2572231930	t3m_00286	DNA_length		750bp	
2572231930	t3m_00286	Protein_length		249aa	
2572231930	t3m_00286	GC		0.66	
2572231931	t3m_00287	KEGG_module	M00391: Exosome, eukaryotes		
2572231931	t3m_00287	KEGG_module	M00390: Exosome, archaea		
2572231931	t3m_00287	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572231931	t3m_00287	COG1097	RNA-binding protein Rrp4 and related proteins (contain S1 domain and		2.00E-42
2572231931	t3m_00287	pfam00013	KH_1		6.10E-11
2572231931	t3m_00287	KO:K03679	exosome complex component RRP4		0.00E+00
2572231931	t3m_00287	Locus_type		CDS	
2572231931	t3m_00287	Product_name		RNA-binding protein Rrp4 and related proteins (contain S1 domain and	
2572231931	t3m_00287	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231931	t3m_00287	Coordinates		26656..27372(-)	

2572231931	t3m_00287	DNA_length		717bp		
2572231931	t3m_00287	Protein_length		238aa		
2572231931	t3m_00287	GC			0.71	
2572231932	t3m_00288	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231932	t3m_00288	COG1500	Predicted exosome subunit			5.00E-71
2572231932	t3m_00288	pfam09377	SBDS_C			1.90E-20
2572231932	t3m_00288	pfam01172	SBDS			4.20E-26
2572231932	t3m_00288	TIGR00291	rRNA metabolism protein, SBDS family			2.10E-84
2572231932	t3m_00288	KO:K14574	ribosome maturation protein SDO1			0.00E+00
2572231932	t3m_00288	Locus_type		CDS		
2572231932	t3m_00288	Product_name		rRNA metabolism protein, SBDS family		
2572231932	t3m_00288	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231932	t3m_00288	Coordinates		27562..28257(-)		
2572231932	t3m_00288	DNA_length		696bp		
2572231932	t3m_00288	Protein_length		231aa		
2572231932	t3m_00288	GC			0.65	
2572231933	t3m_00289	KEGG_module	M00343: Archaeal proteasome			
2572231933	t3m_00289	KEGG_module	M00342: Bacterial proteasome			
2572231933	t3m_00289	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572231933	t3m_00289	COG0638	20S proteasome, alpha and beta subunits			2.00E-62
2572231933	t3m_00289	pfam00227	Proteasome			1.20E-52
2572231933	t3m_00289	pfam10584	Proteasome_A_N			1.20E-14
2572231933	t3m_00289	EC:3.4.25.1	Proteasome endopeptidase complex.			
2572231933	t3m_00289	TIGR03633	proteasome endopeptidase complex, archaeal, alpha subunit			2.20E-94
2572231933	t3m_00289	KO:K03432	proteasome alpha subunit [EC:3.4.25.1]			0.00E+00
2572231933	t3m_00289	Locus_type		CDS		
2572231933	t3m_00289	Product_name		proteasome endopeptidase complex, archaeal, alpha subunit		
2572231933	t3m_00289	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231933	t3m_00289	Coordinates		28281..29036(-)		
2572231933	t3m_00289	DNA_length		756bp		
2572231933	t3m_00289	Protein_length		251aa		
2572231933	t3m_00289	GC			0.69	

2572231934	t3m_00290	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2572231934	t3m_00290	COG1331	Highly conserved protein containing a thioredoxin domain		0.00E+00
2572231934	t3m_00290	pfam03190	Thioredox_DsbH		5.40E-61
2572231934	t3m_00290	Locus_type		CDS	
2572231934	t3m_00290	Product_name		Highly conserved protein containing a thioredoxin domain	
2572231934	t3m_00290	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231934	t3m_00290	Coordinates		29191..31311(+)	
2572231934	t3m_00290	DNA_length		2121bp	
2572231934	t3m_00290	Protein_length		706aa	
2572231934	t3m_00290	GC		0.7	
2572231935	t3m_00291	COG_category	[R] General function prediction only		
2572231935	t3m_00291	COG1407	Predicted ICC-like phosphoesterases		2.00E-18
2572231935	t3m_00291	pfam12850	Metallophos_2		1.40E-06
2572231935	t3m_00291	ITERM:01876	putative phosphoesterase		
2572231935	t3m_00291	Locus_type		CDS	
2572231935	t3m_00291	Product_name		putative phosphoesterase	
2572231935	t3m_00291	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231935	t3m_00291	Coordinates		31247..32059(-)	
2572231935	t3m_00291	DNA_length		813bp	
2572231935	t3m_00291	Protein_length		270aa	
2572231935	t3m_00291	GC		0.72	
2572231936	t3m_00292	COG_category	[K] Transcription		
2572231936	t3m_00292	COG1395	Predicted transcriptional regulator		1.00E-54
2572231936	t3m_00292	pfam01381	HTH_3		5.10E-05
2572231936	t3m_00292	KO:K07728	putative transcriptional regulator		0.00E+00
2572231936	t3m_00292	Locus_type		CDS	
2572231936	t3m_00292	Product_name		Predicted transcriptional regulator	
2572231936	t3m_00292	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231936	t3m_00292	Coordinates		32205..33194(+)	
2572231936	t3m_00292	DNA_length		990bp	
2572231936	t3m_00292	Protein_length		329aa	

2572231936	t3m_00292	GC			0.69	
2572231937	t3m_00293	Locus_type		CDS		
2572231937	t3m_00293	Product_name		hypothetical protein		
2572231937	t3m_00293	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231937	t3m_00293	Coordinates		33191..33838(+)		
2572231937	t3m_00293	DNA_length		648bp		
2572231937	t3m_00293	Protein_length		215aa		
2572231937	t3m_00293	GC			0.71	
2572231938	t3m_00294	COG_category	[H] Coenzyme transport and metabolism			
2572231938	t3m_00294	COG0237	Dephospho-CoA kinase			1.00E-16
2572231938	t3m_00294	pfam13238	AAA_18			1.10E-06
2572231938	t3m_00294	Locus_type		CDS		
2572231938	t3m_00294	Product_name		Dephospho-CoA kinase		
2572231938	t3m_00294	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231938	t3m_00294	Coordinates		33854..34396(-)		
2572231938	t3m_00294	DNA_length		543bp		
2572231938	t3m_00294	Protein_length		180aa		
2572231938	t3m_00294	GC			0.69	
2572231939	t3m_00295	Locus_type		CDS		
2572231939	t3m_00295	Product_name		hypothetical protein		
2572231939	t3m_00295	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231939	t3m_00295	Coordinates		34393..35019(-)		
2572231939	t3m_00295	DNA_length		627bp		
2572231939	t3m_00295	Protein_length		208aa		
2572231939	t3m_00295	GC			0.67	
2572231940	t3m_00296	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572231940	t3m_00296	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572231940	t3m_00296	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572231940	t3m_00296	IMG_pathway	492: Glycine ligation to tRNA(Gly)			
2572231940	t3m_00296	COG_category	[J] Translation, ribosomal structure and biogenesis			

2572231940	t3m_00296	COG0423	Glycyl-tRNA synthetase (class II)			8.00E-112
2572231940	t3m_00296	pfam03129	HGTP_anticodon			6.00E-16
2572231940	t3m_00296	pfam00587	tRNA-synt_2b			1.60E-31
2572231940	t3m_00296	EC:6.1.1.14	Glycine--tRNA ligase.			
2572231940	t3m_00296	TIGR00389	glycyl-tRNA synthetase, dimeric type			1.00E-96
2572231940	t3m_00296	KO:K01880	glycyl-tRNA synthetase [EC:6.1.1.14]			0.00E+00
2572231940	t3m_00296	ITERM:01945	glycyl-tRNA synthetase (EC 6.1.1.14)			
2572231940	t3m_00296	Locus_type		CDS		
2572231940	t3m_00296	Product_name		glycyl-tRNA synthetase (EC 6.1.1.14)		
2572231940	t3m_00296	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231940	t3m_00296	Coordinates		35083..36588(-)		
2572231940	t3m_00296	DNA_length		1506bp		
2572231940	t3m_00296	Protein_length		501aa		
2572231940	t3m_00296	GC			0.68	
2572231941	t3m_00297	COG_category	[R] General function prediction only			
2572231941	t3m_00297	COG_category	[F] Nucleotide transport and metabolism			
2572231941	t3m_00297	COG0402	Cytosine deaminase and related metal-dependent hydrolases			3.00E-21
2572231941	t3m_00297	Locus_type		CDS		
2572231941	t3m_00297	Product_name		hypothetical protein		
2572231941	t3m_00297	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231941	t3m_00297	Coordinates		36585..37679(-)		
2572231941	t3m_00297	DNA_length		1095bp		
2572231941	t3m_00297	Protein_length		364aa		
2572231941	t3m_00297	GC			0.71	
2572231942	t3m_00298	Metacyc	RIBOKIN-PWY: ribose degradation			
2572231942	t3m_00298	COG_category	[G] Carbohydrate transport and metabolism			
2572231942	t3m_00298	COG0524	Sugar kinases, ribokinase family			1.00E-31
2572231942	t3m_00298	pfam00294	PfkB			9.80E-36
2572231942	t3m_00298	EC:2.7.1.15	Ribokinase.			
2572231942	t3m_00298	KO:K00852	ribokinase [EC:2.7.1.15]			2.60E-35
2572231942	t3m_00298	Locus_type		CDS		
2572231942	t3m_00298	Product_name		Sugar kinases, ribokinase family		

2572231942	t3m_00298	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231942	t3m_00298	Coordinates		37774..38649(+)	
2572231942	t3m_00298	DNA_length		876bp	
2572231942	t3m_00298	Protein_length		291aa	
2572231942	t3m_00298	GC		0.7	

2572231943	t3m_00299	Metacyc	PWY-6823: molybdenum cofactor biosynthesis		
2572231943	t3m_00299	IMG_pathway	560: Molybdenum cofactor synthesis		
2572231943	t3m_00299	COG_category	[H] Coenzyme transport and metabolism		
2572231943	t3m_00299	COG0303	Molybdopterin biosynthesis enzyme		2.00E-83
2572231943	t3m_00299	pfam00994	MoCF_biosynth		4.20E-23
2572231943	t3m_00299	pfam03454	MoeA_C		1.90E-06
2572231943	t3m_00299	pfam03453	MoeA_N		4.60E-40
2572231943	t3m_00299	EC:2.10.1.1	Molybdopterin molybdotransferase.		
2572231943	t3m_00299	TIGR00177	molybdenum cofactor synthesis domain		2.00E-27
2572231943	t3m_00299	KO:K03750	molybdopterin molybdotransferase [EC:2.10.1.1]		0.00E+00
2572231943	t3m_00299	ITERM:04811	molybdopterin molybdochelatase (EC 2.10.1.1)		
2572231943	t3m_00299	Locus_type		CDS	
2572231943	t3m_00299	Product_name		molybdopterin molybdochelatase (EC 2.10.1.1)	
2572231943	t3m_00299	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231943	t3m_00299	Coordinates		38659..39972(+)	
2572231943	t3m_00299	DNA_length		1314bp	
2572231943	t3m_00299	Protein_length		437aa	
2572231943	t3m_00299	GC		0.72	

2572231944	t3m_00300	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572231944	t3m_00300	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I		
2572231944	t3m_00300	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis		
2572231944	t3m_00300	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II		
2572231944	t3m_00300	COG_category	[F] Nucleotide transport and metabolism		
2572231944	t3m_00300	COG0047	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amido		8.00E-57
2572231944	t3m_00300	pfam13507	GATase_5		1.90E-56
2572231944	t3m_00300	EC:6.3.5.3	Phosphoribosylformylglycinamidine synthase.		
2572231944	t3m_00300	TIGR01737	phosphoribosylformylglycinamidine synthase I		4.50E-66

2572231944	t3m_00300	KO:K01952	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]			0.00E+00
2572231944	t3m_00300	Locus_type		CDS		
2572231944	t3m_00300	Product_name		phosphoribosylformylglycinamidine synthase subunit I (EC 6.3.5.3)		
2572231944	t3m_00300	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231944	t3m_00300	Coordinates		39959..40783(+)		
2572231944	t3m_00300	DNA_length		825bp		
2572231944	t3m_00300	Protein_length		274aa		
2572231944	t3m_00300	GC			0.69	
2572231945	t3m_00301	pfam13659	Methyltransf_26			9.00E-12
2572231945	t3m_00301	TIGR00537	HemK-related putative methylase			1.40E-35
2572231945	t3m_00301	Locus_type		CDS		
2572231945	t3m_00301	Product_name		HemK-related putative methylase		
2572231945	t3m_00301	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231945	t3m_00301	Coordinates		40780..41427(-)		
2572231945	t3m_00301	DNA_length		648bp		
2572231945	t3m_00301	Protein_length		215aa		
2572231945	t3m_00301	GC			0.73	
2572231946	t3m_00302	Metacyc	PWY-7185: UTP and CTP dephosphorylation I			
2572231946	t3m_00302	Metacyc	PWY-7184: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis I			
2572231946	t3m_00302	Metacyc	PWY-6545: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis III			
2572231946	t3m_00302	Metacyc	PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP			
2572231946	t3m_00302	Metacyc	PWY-7198: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis IV			
2572231946	t3m_00302	COG_category	[F] Nucleotide transport and metabolism			
2572231946	t3m_00302	COG1618	Predicted nucleotide kinase			4.00E-38
2572231946	t3m_00302	pfam03266	NTPase_1			2.20E-47
2572231946	t3m_00302	EC:3.6.1.15	Nucleoside-triphosphatase.			
2572231946	t3m_00302	KO:K06928	nucleoside-triphosphatase THEP1 [EC:3.6.1.15]			0.00E+00
2572231946	t3m_00302	Locus_type		CDS		
2572231946	t3m_00302	Product_name		Predicted nucleotide kinase		
2572231946	t3m_00302	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231946	t3m_00302	Coordinates		41460..42017(+)		
2572231946	t3m_00302	DNA_length		558bp		

2572231946	t3m_00302	Protein_length		185aa		
2572231946	t3m_00302	GC			0.64	

2572231947	t3m_00303	Metacyc	PWY-6829: tRNA methylation (yeast)			
2572231947	t3m_00303	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231947	t3m_00303	COG1867	N2,N2-dimethylguanosine tRNA methyltransferase			3.00E-61
2572231947	t3m_00303	pfam02005	TRM			7.80E-19
2572231947	t3m_00303	pfam02005	TRM			5.70E-40
2572231947	t3m_00303	EC:2.1.1.215	tRNA (guanine(26)-N(2)/guanine(27)-N(2))-dimethyltransferase.			
2572231947	t3m_00303	EC:2.1.1.216	tRNA (guanine(26)-N(2))-dimethyltransferase.			
2572231947	t3m_00303	KO:K00555	tRNA (guanine26-N2/guanine27-N2)-dimethyltransferase [EC:2.1.1.215			1.00E-40
2572231947	t3m_00303	Locus_type		CDS		
2572231947	t3m_00303	Product_name		N2,N2-dimethylguanosine tRNA methyltransferase		
2572231947	t3m_00303	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231947	t3m_00303	Coordinates		42113..43096(+)		
2572231947	t3m_00303	DNA_length		984bp		
2572231947	t3m_00303	Protein_length		327aa		
2572231947	t3m_00303	GC			0.72	

2572231948	t3m_00304	COG_category	[R] General function prediction only			
2572231948	t3m_00304	COG1201	Lhr-like helicases			0.00E+00
2572231948	t3m_00304	pfam00270	DEAD			9.80E-25
2572231948	t3m_00304	pfam00271	Helicase_C			1.20E-16
2572231948	t3m_00304	pfam08494	DEAD_assoc			1.70E-23
2572231948	t3m_00304	EC:3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; involved in cellular and subcellul			
2572231948	t3m_00304	KO:K03724	ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.4.-]			0.00E+00
2572231948	t3m_00304	Locus_type		CDS		
2572231948	t3m_00304	Product_name		Lhr-like helicases		
2572231948	t3m_00304	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231948	t3m_00304	Coordinates		43093..45936(-)		
2572231948	t3m_00304	DNA_length		2844bp		
2572231948	t3m_00304	Protein_length		947aa		
2572231948	t3m_00304	GC			0.71	

2572231949	t3m_00305	COG_category	[R] General function prediction only			
2572231949	t3m_00305	COG1661	Predicted DNA-binding protein with PD1-like DNA-binding motif			2.00E-22
2572231949	t3m_00305	pfam03479	DUF296			4.70E-28
2572231949	t3m_00305	Locus_type		CDS		
2572231949	t3m_00305	Product_name		Predicted DNA-binding protein with PD1-like DNA-binding motif		
2572231949	t3m_00305	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231949	t3m_00305	Coordinates		45983..46420(-)		
2572231949	t3m_00305	DNA_length		438bp		
2572231949	t3m_00305	Protein_length		145aa		
2572231949	t3m_00305	GC			0.67	
2572231950	t3m_00306	pfam11528	DUF3224			5.20E-35
2572231950	t3m_00306	Locus_type		CDS		
2572231950	t3m_00306	Product_name		Protein of unknown function (DUF3224)		
2572231950	t3m_00306	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231950	t3m_00306	Coordinates		46553..46954(+)		
2572231950	t3m_00306	DNA_length		402bp		
2572231950	t3m_00306	Protein_length		133aa		
2572231950	t3m_00306	GC			0.64	
2572231951	t3m_00307	COG_category	[R] General function prediction only			
2572231951	t3m_00307	COG1606	ATP-utilizing enzymes of the PP-loop superfamily			6.00E-54
2572231951	t3m_00307	pfam00733	Asn_synthase			2.10E-10
2572231951	t3m_00307	TIGR00268	TIGR00268 family protein			2.20E-60
2572231951	t3m_00307	KO:K06864	uncharacterized protein			0.00E+00
2572231951	t3m_00307	Locus_type		CDS		
2572231951	t3m_00307	Product_name		TIGR00268 family protein		
2572231951	t3m_00307	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231951	t3m_00307	Coordinates		47087..47917(+)		
2572231951	t3m_00307	DNA_length		831bp		
2572231951	t3m_00307	Protein_length		276aa		
2572231951	t3m_00307	GC			0.72	
2572231952	t3m_00308	COG_category	[L] Replication, recombination and repair			

2572231952	t3m_00308	COG0556	Helicase subunit of the DNA excision repair complex			0.00E+00
2572231952	t3m_00308	pfam02151	UVR			1.60E-08
2572231952	t3m_00308	pfam00271	Helicase_C			6.60E-14
2572231952	t3m_00308	pfam12344	UvrB			8.60E-19
2572231952	t3m_00308	pfam04851	ResIII			9.40E-12
2572231952	t3m_00308	TIGR00631	excinuclease ABC, B subunit			0.00E+00
2572231952	t3m_00308	KO:K03702	excinuclease ABC subunit B			0.00E+00
2572231952	t3m_00308	ITERM:00497	Excinuclease ABC subunit B			
2572231952	t3m_00308	Locus_type		CDS		
2572231952	t3m_00308	Product_name		Excinuclease ABC subunit B		
2572231952	t3m_00308	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231952	t3m_00308	Coordinates		47914..49962(+)		
2572231952	t3m_00308	DNA_length		2049bp		
2572231952	t3m_00308	Protein_length		682aa		
2572231952	t3m_00308	GC			0.67	
2572231953	t3m_00309	COG_category	[K] Transcription			
2572231953	t3m_00309	COG1497	Predicted transcriptional regulator			6.00E-27
2572231953	t3m_00309	KO:K07730	putative transcriptional regulator			1.70E-19
2572231953	t3m_00309	Locus_type		CDS		
2572231953	t3m_00309	Product_name		Predicted transcriptional regulator		
2572231953	t3m_00309	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231953	t3m_00309	Coordinates		50022..50858(+)		
2572231953	t3m_00309	DNA_length		837bp		
2572231953	t3m_00309	Protein_length		278aa		
2572231953	t3m_00309	GC			0.73	
2572231954	t3m_00310	KEGG_module	M00240: Iron complex transport system			
2572231954	t3m_00310	COG_category	[H] Coenzyme transport and metabolism			
2572231954	t3m_00310	COG_category	[P] Inorganic ion transport and metabolism			
2572231954	t3m_00310	COG1120	ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase com			2.00E-80
2572231954	t3m_00310	pfam00005	ABC_tran			1.20E-26
2572231954	t3m_00310	EC:3.6.3.34	Iron-chelate-transporting ATPase.			
2572231954	t3m_00310	KO:K02013	iron complex transport system ATP-binding protein [EC:3.6.3.34]			0.00E+00

2572231954	t3m_00310	Locus_type		CDS	
2572231954	t3m_00310	Product_name		ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase com	
2572231954	t3m_00310	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231954	t3m_00310	Coordinates		50852..52153(-)	
2572231954	t3m_00310	DNA_length		1302bp	
2572231954	t3m_00310	Protein_length		433aa	
2572231954	t3m_00310	GC		0.69	
2572231955	t3m_00311	KEGG_module	M00240: Iron complex transport system		
2572231955	t3m_00311	COG_category	[P] Inorganic ion transport and metabolism		
2572231955	t3m_00311	COG0609	ABC-type Fe3+-siderophore transport system, permease component		5.00E-45
2572231955	t3m_00311	pfam01032	FecCD		1.40E-77
2572231955	t3m_00311	KO:K02015	iron complex transport system permease protein		0.00E+00
2572231955	t3m_00311	Locus_type		CDS	
2572231955	t3m_00311	Product_name		ABC-type Fe3+-siderophore transport system, permease component	
2572231955	t3m_00311	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231955	t3m_00311	Coordinates		52150..53193(-)	
2572231955	t3m_00311	DNA_length		1044bp	
2572231955	t3m_00311	Protein_length		347aa	
2572231955	t3m_00311	GC		0.68	
2572231955	t3m_00311	Transmembrane		Yes	
2572231956	t3m_00312	KEGG_module	M00240: Iron complex transport system		
2572231956	t3m_00312	COG_category	[P] Inorganic ion transport and metabolism		
2572231956	t3m_00312	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component		2.00E-29
2572231956	t3m_00312	pfam01497	Peripla_BP_2		8.70E-23
2572231956	t3m_00312	KO:K02016	iron complex transport system substrate-binding protein		8.40E-29
2572231956	t3m_00312	Locus_type		CDS	
2572231956	t3m_00312	Product_name		ABC-type Fe3+-hydroxamate transport system, periplasmic component	
2572231956	t3m_00312	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4	
2572231956	t3m_00312	Coordinates		53264..54298(-)	
2572231956	t3m_00312	DNA_length		1035bp	
2572231956	t3m_00312	Protein_length		344aa	
2572231956	t3m_00312	GC		0.66	

2572231956	t3m_00312	Transmembrane		Yes		

2572231957	t3m_00313	Locus_type		tRNA		
2572231957	t3m_00313	Product_name		tRNA_Trp_CCA		
2572231957	t3m_00313	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231957	t3m_00313	Coordinates		54427..54584(+)		
2572231957	t3m_00313	DNA_length		75bp		
2572231957	t3m_00313	GC			0.59	

2572231958	t3m_00314	Metacyc	PWY-5386: methylglyoxal degradation I			
2572231958	t3m_00314	pfam12681	Glyoxalase_2			2.70E-16
2572231958	t3m_00314	EC:4.4.1.5	Lactoylglutathione lyase.			
2572231958	t3m_00314	KO:K01759	lactoylglutathione lyase [EC:4.4.1.5]			2.90E-09
2572231958	t3m_00314	Locus_type		CDS		
2572231958	t3m_00314	Product_name		Glyoxalase-like domain		
2572231958	t3m_00314	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231958	t3m_00314	Coordinates		54789..55193(+)		
2572231958	t3m_00314	DNA_length		405bp		
2572231958	t3m_00314	Protein_length		134aa		
2572231958	t3m_00314	GC			0.69	

2572231959	t3m_00315	COG_category	[R] General function prediction only			
2572231959	t3m_00315	COG2244	Membrane protein involved in the export of O-antigen and teichoic acic			5.00E-15
2572231959	t3m_00315	pfam14667	Polysacc_synt_C			2.70E-13
2572231959	t3m_00315	pfam01943	Polysacc_synt			7.60E-10
2572231959	t3m_00315	Locus_type		CDS		
2572231959	t3m_00315	Product_name		Membrane protein involved in the export of O-antigen and teichoic acid		
2572231959	t3m_00315	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231959	t3m_00315	Coordinates		55253..56983(+)		
2572231959	t3m_00315	DNA_length		1731bp		
2572231959	t3m_00315	Protein_length		576aa		
2572231959	t3m_00315	GC			0.66	
2572231959	t3m_00315	Transmembrane		Yes		

2572231960	t3m_00316	KEGG_module	M00248: Putative antibiotic transport system			
2572231960	t3m_00316	COG_category	[V] Defense mechanisms			
2572231960	t3m_00316	COG1131	ABC-type multidrug transport system, ATPase component			5.00E-65
2572231960	t3m_00316	pfam00005	ABC_tran			8.90E-30
2572231960	t3m_00316	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2572231960	t3m_00316	Locus_type		CDS		
2572231960	t3m_00316	Product_name		ABC-type multidrug transport system, ATPase component		
2572231960	t3m_00316	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231960	t3m_00316	Coordinates		57313..58239(+)		
2572231960	t3m_00316	DNA_length		927bp		
2572231960	t3m_00316	Protein_length		308aa		
2572231960	t3m_00316	GC			0.67	
2572231961	t3m_00317	Locus_type		CDS		
2572231961	t3m_00317	Product_name		hypothetical protein		
2572231961	t3m_00317	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231961	t3m_00317	Coordinates		58229..58993(+)		
2572231961	t3m_00317	DNA_length		765bp		
2572231961	t3m_00317	Protein_length		254aa		
2572231961	t3m_00317	GC			0.66	
2572231961	t3m_00317	Transmembrane		Yes		
2572231962	t3m_00318	COG_category	[V] Defense mechanisms			
2572231962	t3m_00318	COG0842	ABC-type multidrug transport system, permease component			5.00E-05
2572231962	t3m_00318	pfam01061	ABC2_membrane			1.00E-10
2572231962	t3m_00318	Locus_type		CDS		
2572231962	t3m_00318	Product_name		ABC-type multidrug transport system, permease component		
2572231962	t3m_00318	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231962	t3m_00318	Coordinates		58994..59776(+)		
2572231962	t3m_00318	DNA_length		783bp		
2572231962	t3m_00318	Protein_length		260aa		
2572231962	t3m_00318	GC			0.68	
2572231962	t3m_00318	Transmembrane		Yes		

2572231963	t3m_00319	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231963	t3m_00319	COG0023	Translation initiation factor 1 (eIF-1/SUI1) and related proteins			3.00E-17
2572231963	t3m_00319	pfam01253	SUI1			2.30E-17
2572231963	t3m_00319	TIGR01158	translation initation factor SUI1, putative, prokaryotic			1.70E-23
2572231963	t3m_00319	KO:K03113	translation initiation factor 1			4.00E-15
2572231963	t3m_00319	Locus_type		CDS		
2572231963	t3m_00319	Product_name		Translation initiation factor 1 (eIF-1/SUI1) and related proteins		
2572231963	t3m_00319	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231963	t3m_00319	Coordinates		59939..60256(+)		
2572231963	t3m_00319	DNA_length		318bp		
2572231963	t3m_00319	Protein_length		105aa		
2572231963	t3m_00319	GC			0.7	
2572231964	t3m_00320	Metacyc	PWY-5350: thiosulfate disproportionation III (rhodanese)			
2572231964	t3m_00320	Metacyc	PWY-5329: L-cysteine degradation III			
2572231964	t3m_00320	COG_category	[P] Inorganic ion transport and metabolism			
2572231964	t3m_00320	COG2897	Rhodanese-related sulfurtransferase			5.00E-77
2572231964	t3m_00320	pfam00581	Rhodanese			3.20E-22
2572231964	t3m_00320	pfam00581	Rhodanese			5.90E-15
2572231964	t3m_00320	EC:2.8.1.2	3-mercaptopyruvate sulfurtransferase.			
2572231964	t3m_00320	EC:2.8.1.1	Thiosulfate sulfurtransferase.			
2572231964	t3m_00320	KO:K01011	thiosulfate/3-mercaptopyruvate sulfurtransferase [EC:2.8.1.1 2.8.1.2]			0.00E+00
2572231964	t3m_00320	Locus_type		CDS		
2572231964	t3m_00320	Product_name		Rhodanese-related sulfurtransferase		
2572231964	t3m_00320	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231964	t3m_00320	Coordinates		60378..61232(+)		
2572231964	t3m_00320	DNA_length		855bp		
2572231964	t3m_00320	Protein_length		284aa		
2572231964	t3m_00320	GC			0.67	
2572231965	t3m_00321	COG_category	[E] Amino acid transport and metabolism			
2572231965	t3m_00321	COG0509	Glycine cleavage system H protein (lipoate-binding)			2.00E-17
2572231965	t3m_00321	pfam01597	GCV_H			2.40E-15
2572231965	t3m_00321	pfam01206	TusA			4.40E-08

2572231965	t3m_00321	Locus_type		CDS		
2572231965	t3m_00321	Product_name		Glycine cleavage system H protein (lipoate-binding)		
2572231965	t3m_00321	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231965	t3m_00321	Coordinates		61247..61942(-)		
2572231965	t3m_00321	DNA_length		696bp		
2572231965	t3m_00321	Protein_length		231aa		
2572231965	t3m_00321	GC			0.7	
2572231966	t3m_00322	COG_category	[S] Function unknown			
2572231966	t3m_00322	COG3832	Uncharacterized conserved protein			3.00E-08
2572231966	t3m_00322	pfam08327	AHSA1			8.80E-17
2572231966	t3m_00322	Locus_type		CDS		
2572231966	t3m_00322	Product_name		Uncharacterized conserved protein		
2572231966	t3m_00322	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231966	t3m_00322	Coordinates		62238..62696(-)		
2572231966	t3m_00322	DNA_length		459bp		
2572231966	t3m_00322	Protein_length		152aa		
2572231966	t3m_00322	GC			0.64	
2572231967	t3m_00323	pfam05048	NosD			1.00E-07
2572231967	t3m_00323	pfam08308	PEGA			3.30E-05
2572231967	t3m_00323	pfam05317	Thermopsin			2.20E-57
2572231967	t3m_00323	EC:3.4.23.42	Thermopsin.			
2572231967	t3m_00323	TIGR03804	parallel beta-helix repeat (two copies)			1.30E-07
2572231967	t3m_00323	KO:K01385	thermopsin [EC:3.4.23.42]			0.00E+00
2572231967	t3m_00323	Locus_type		CDS		
2572231967	t3m_00323	Product_name		Periplasmic copper-binding protein (NosD)/PEGA domain/Thermopsin		
2572231967	t3m_00323	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231967	t3m_00323	Coordinates		62875..66162(+)		
2572231967	t3m_00323	DNA_length		3288bp		
2572231967	t3m_00323	Protein_length		1095aa		
2572231967	t3m_00323	GC			0.65	
2572231967	t3m_00323	Transmembrane		Yes		

2572231968	t3m_00324	Locus_type		CDS		
2572231968	t3m_00324	Product_name		hypothetical protein		
2572231968	t3m_00324	Scaffold		t3m_contig_70_29_len_66924_read_count_5585863.4		
2572231968	t3m_00324	Coordinates		66399..66923(+)		
2572231968	t3m_00324	DNA_length		525bp		
2572231968	t3m_00324	Protein_length		175aa		
2572231968	t3m_00324	GC			0.68	
2572231968	t3m_00324	Transmembrane		Yes		

2572231969	t3m_00325	Locus_type		CDS		
2572231969	t3m_00325	Product_name		hypothetical protein		
2572231969	t3m_00325	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231969	t3m_00325	Coordinates		2..223(-)		
2572231969	t3m_00325	DNA_length		222bp		
2572231969	t3m_00325	Protein_length		74aa		
2572231969	t3m_00325	GC			0.63	

2572231970	t3m_00326	COG_category	[G] Carbohydrate transport and metabolism			
2572231970	t3m_00326	COG2211	Na+/melibiose symporter and related transporters			5.00E-08
2572231970	t3m_00326	pfam07690	MFS_1			1.50E-33
2572231970	t3m_00326	Locus_type		CDS		
2572231970	t3m_00326	Product_name		Major Facilitator Superfamily		
2572231970	t3m_00326	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231970	t3m_00326	Coordinates		298..1548(+)		
2572231970	t3m_00326	DNA_length		1251bp		
2572231970	t3m_00326	Protein_length		416aa		
2572231970	t3m_00326	GC			0.69	
2572231970	t3m_00326	Transmembrane		Yes		

2572231971	t3m_00327	KEGG_module	M00254: ABC-2 type transport system			
2572231971	t3m_00327	COG_category	[R] General function prediction only			
2572231971	t3m_00327	COG1277	ABC-type transport system involved in multi-copper enzyme maturatior			5.00E-08
2572231971	t3m_00327	pfam12730	ABC2_membrane_4			6.50E-20
2572231971	t3m_00327	KO:K01992	ABC-2 type transport system permease protein			4.20E-41

2572231971	t3m_00327	Locus_type		CDS	
2572231971	t3m_00327	Product_name		ABC-type transport system involved in multi-copper enzyme maturation	
2572231971	t3m_00327	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572231971	t3m_00327	Coordinates		1571..2464(-)	
2572231971	t3m_00327	DNA_length		894bp	
2572231971	t3m_00327	Protein_length		297aa	
2572231971	t3m_00327	GC		0.65	
2572231971	t3m_00327	Transmembrane		Yes	
2572231972	t3m_00328	KEGG_module	M00254: ABC-2 type transport system		
2572231972	t3m_00328	COG_category	[V] Defense mechanisms		
2572231972	t3m_00328	COG1131	ABC-type multidrug transport system, ATPase component		4.00E-61
2572231972	t3m_00328	pfam00005	ABC_tran		1.80E-26
2572231972	t3m_00328	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2572231972	t3m_00328	Locus_type		CDS	
2572231972	t3m_00328	Product_name		ABC-type multidrug transport system, ATPase component	
2572231972	t3m_00328	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572231972	t3m_00328	Coordinates		2461..3408(-)	
2572231972	t3m_00328	DNA_length		948bp	
2572231972	t3m_00328	Protein_length		315aa	
2572231972	t3m_00328	GC		0.66	
2572231973	t3m_00329	COG_category	[P] Inorganic ion transport and metabolism		
2572231973	t3m_00329	COG2217	Cation transport ATPase		0.00E+00
2572231973	t3m_00329	pfam00702	Hydrolase		2.60E-41
2572231973	t3m_00329	pfam00122	E1-E2_ATPase		7.70E-49
2572231973	t3m_00329	pfam04945	YHS		8.20E-10
2572231973	t3m_00329	EC:3.6.3.4	Copper-exporting ATPase.		
2572231973	t3m_00329	TIGR01511	copper-(or silver)-translocating P-type ATPase		0.00E+00
2572231973	t3m_00329	TIGR01525	heavy metal translocating P-type ATPase		0.00E+00
2572231973	t3m_00329	TIGR01494	ATPase, P-type (transporting), HAD superfamily, subfamily IC		8.30E-43
2572231973	t3m_00329	KO:K01533	Cu2+-exporting ATPase [EC:3.6.3.4]		0.00E+00
2572231973	t3m_00329	Locus_type		CDS	
2572231973	t3m_00329	Product_name		copper-(or silver)-translocating P-type ATPase	

2572231973	t3m_00329	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231973	t3m_00329	Coordinates		3460..5574(-)		
2572231973	t3m_00329	DNA_length		2115bp		
2572231973	t3m_00329	Protein_length		704aa		
2572231973	t3m_00329	GC			0.69	
2572231973	t3m_00329	Transmembrane		Yes		
2572231974	t3m_00330	COG_category	[S] Function unknown			
2572231974	t3m_00330	COG3350	Uncharacterized conserved protein			8.00E-07
2572231974	t3m_00330	pfam04945	YHS			2.10E-08
2572231974	t3m_00330	Locus_type		CDS		
2572231974	t3m_00330	Product_name		Uncharacterized conserved protein		
2572231974	t3m_00330	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231974	t3m_00330	Coordinates		5617..5799(-)		
2572231974	t3m_00330	DNA_length		183bp		
2572231974	t3m_00330	Protein_length		60aa		
2572231974	t3m_00330	GC			0.67	
2572231975	t3m_00331	COG_category	[P] Inorganic ion transport and metabolism			
2572231975	t3m_00331	COG0607	Rhodanese-related sulfurtransferase			2.00E-17
2572231975	t3m_00331	pfam00581	Rhodanese			4.90E-14
2572231975	t3m_00331	Locus_type		CDS		
2572231975	t3m_00331	Product_name		Rhodanese-related sulfurtransferase		
2572231975	t3m_00331	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231975	t3m_00331	Coordinates		5868..6194(+)		
2572231975	t3m_00331	DNA_length		327bp		
2572231975	t3m_00331	Protein_length		108aa		
2572231975	t3m_00331	GC			0.67	
2572231976	t3m_00332	pfam14947	HTH_45			3.80E-09
2572231976	t3m_00332	Locus_type		CDS		
2572231976	t3m_00332	Product_name		Winged helix-turn-helix		
2572231976	t3m_00332	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231976	t3m_00332	Coordinates		6260..6550(-)		

2572231976	t3m_00332	DNA_length		291bp		
2572231976	t3m_00332	Protein_length		96aa		
2572231976	t3m_00332	GC			0.65	
2572231977	t3m_00333	Locus_type		CDS		
2572231977	t3m_00333	Product_name		hypothetical protein		
2572231977	t3m_00333	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231977	t3m_00333	Coordinates		6604..7845(-)		
2572231977	t3m_00333	DNA_length		1242bp		
2572231977	t3m_00333	Protein_length		413aa		
2572231977	t3m_00333	GC			0.69	
2572231978	t3m_00334	COG_category	[L] Replication, recombination and repair			
2572231978	t3m_00334	COG1573	Uracil-DNA glycosylase			2.00E-25
2572231978	t3m_00334	pfam03167	UDG			6.70E-29
2572231978	t3m_00334	TIGR00758	uracil-DNA glycosylase, family 4			3.80E-16
2572231978	t3m_00334	Locus_type		CDS		
2572231978	t3m_00334	Product_name		Uracil-DNA glycosylase		
2572231978	t3m_00334	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231978	t3m_00334	Coordinates		7934..8647(+)		
2572231978	t3m_00334	DNA_length		714bp		
2572231978	t3m_00334	Protein_length		237aa		
2572231978	t3m_00334	GC			0.73	
2572231979	t3m_00335	Metacyc	PWY-6700: queuosine biosynthesis			
2572231979	t3m_00335	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231979	t3m_00335	COG0343	Queuine/archaeosine tRNA-ribosyltransferase			3.00E-76
2572231979	t3m_00335	pfam01702	TGT			2.40E-37
2572231979	t3m_00335	pfam01472	PUA			1.00E-08
2572231979	t3m_00335	EC:2.4.2.29	tRNA-guanine(34) transglycosylase.			
2572231979	t3m_00335	TIGR00432	tRNA-guanine transglycosylase, archaeosine-15-forming			4.70E-113
2572231979	t3m_00335	TIGR00449	tRNA-guanine family transglycosylase			1.00E-72
2572231979	t3m_00335	TIGR00451	uncharacterized domain 2			3.80E-10
2572231979	t3m_00335	KO:K00773	queuine tRNA-ribosyltransferase [EC:2.4.2.29]			0.00E+00

2572231979	t3m_00335	Locus_type		CDS		
2572231979	t3m_00335	Product_name		tRNA-guanine family transglycosylase		
2572231979	t3m_00335	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231979	t3m_00335	Coordinates		8675..10594(+)		
2572231979	t3m_00335	DNA_length		1920bp		
2572231979	t3m_00335	Protein_length		639aa		
2572231979	t3m_00335	GC			0.72	
2572231979	t3m_00335	Fused_gene		Yes		
2572231980	t3m_00336	Locus_type		CDS		
2572231980	t3m_00336	Product_name		hypothetical protein		
2572231980	t3m_00336	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231980	t3m_00336	Coordinates		10692..10922(+)		
2572231980	t3m_00336	DNA_length		231bp		
2572231980	t3m_00336	Protein_length		76aa		
2572231980	t3m_00336	GC			0.65	
2572231981	t3m_00337	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572231981	t3m_00337	COG0533	Metal-dependent proteases with possible chaperone activity			1.00E-95
2572231981	t3m_00337	pfam00814	Peptidase_M22			4.10E-78
2572231981	t3m_00337	TIGR03722	universal archaeal protein Kae1			0.00E+00
2572231981	t3m_00337	TIGR00329	metallohydrolase, glycoprotease/Kae1 family			3.00E-87
2572231981	t3m_00337	KO:K15900	tRNA threonylcarbamoyladenosine biosynthesis protein			0.00E+00
2572231981	t3m_00337	Locus_type		CDS		
2572231981	t3m_00337	Product_name		O-sialoglycoprotein endopeptidase (EC 3.4.24.57)		
2572231981	t3m_00337	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231981	t3m_00337	Coordinates		10980..11966(+)		
2572231981	t3m_00337	DNA_length		987bp		
2572231981	t3m_00337	Protein_length		328aa		
2572231981	t3m_00337	GC			0.71	
2572231982	t3m_00338	COG_category	[C] Energy production and conversion			
2572231982	t3m_00338	COG0644	Dehydrogenases (flavoproteins)			1.00E-58
2572231982	t3m_00338	pfam01494	FAD_binding_3			2.60E-18

2572231982	t3m_00338	TIGR02032	geranylgeranyl reductase family		5.10E-71
2572231982	t3m_00338	Locus_type		CDS	
2572231982	t3m_00338	Product_name		geranylgeranyl reductase family	
2572231982	t3m_00338	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572231982	t3m_00338	Coordinates		12007..13251(+)	
2572231982	t3m_00338	DNA_length		1245bp	
2572231982	t3m_00338	Protein_length		414aa	
2572231982	t3m_00338	GC		0.7	
2572231983	t3m_00339	Locus_type		CDS	
2572231983	t3m_00339	Product_name		hypothetical protein	
2572231983	t3m_00339	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572231983	t3m_00339	Coordinates		13209..13964(-)	
2572231983	t3m_00339	DNA_length		756bp	
2572231983	t3m_00339	Protein_length		251aa	
2572231983	t3m_00339	GC		0.7	
2572231983	t3m_00339	Transmembrane		Yes	
2572231984	t3m_00340	KEGG_module	M00338: Cysteine biosynthesis, homocysteine + serine => cysteine		
2572231984	t3m_00340	KEGG_module	M00035: Methionine degradation		
2572231984	t3m_00340	Metacyc	HOMOCYSDEGR-PWY: cysteine biosynthesis/homocysteine degradation		
2572231984	t3m_00340	Metacyc	PWY-801: homocysteine and cysteine interconversion		
2572231984	t3m_00340	COG_category	[E] Amino acid transport and metabolism		
2572231984	t3m_00340	COG0031	Cysteine synthase		4.00E-101
2572231984	t3m_00340	pfam00571	CBS		1.90E-07
2572231984	t3m_00340	pfam00571	CBS		4.60E-08
2572231984	t3m_00340	pfam00291	PALP		9.90E-68
2572231984	t3m_00340	EC:4.2.1.22	Cystathionine beta-synthase.		
2572231984	t3m_00340	TIGR01137	cystathionine beta-synthase		0.00E+00
2572231984	t3m_00340	KO:K01697	cystathionine beta-synthase [EC:4.2.1.22]		0.00E+00
2572231984	t3m_00340	Locus_type		CDS	
2572231984	t3m_00340	Product_name		Cysteine synthase	
2572231984	t3m_00340	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572231984	t3m_00340	Coordinates		14206..15606(+)	

2572231984	t3m_00340	DNA_length		1401bp		
2572231984	t3m_00340	Protein_length		466aa		
2572231984	t3m_00340	GC			0.68	
2572231985	t3m_00341	KEGG_module	M00338: Cysteine biosynthesis, homocysteine + serine => cysteine			
2572231985	t3m_00341	Metacyc	LCYSDEG-PWY: L-cysteine degradation II			
2572231985	t3m_00341	Metacyc	HOMOCYSDEGR-PWY: cysteine biosynthesis/homocysteine degradation			
2572231985	t3m_00341	Metacyc	PWY-801: homocysteine and cysteine interconversion			
2572231985	t3m_00341	IMG_pathway	197: L-cysteine degradation to pyruvate			
2572231985	t3m_00341	IMG_pathway	517: L-cysteine synthesis from L-cystathionine			
2572231985	t3m_00341	COG_category	[E] Amino acid transport and metabolism			
2572231985	t3m_00341	COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases			5.00E-129
2572231985	t3m_00341	pfam01053	Cys_Met_Meta_PP			0.00E+00
2572231985	t3m_00341	EC:4.4.1.1	Cystathionine gamma-lyase.			
2572231985	t3m_00341	KO:K01758	cystathionine gamma-lyase [EC:4.4.1.1]			0.00E+00
2572231985	t3m_00341	ITERM:00511	cystathionine gamma-lyase (EC 4.4.1.1)			
2572231985	t3m_00341	Locus_type		CDS		
2572231985	t3m_00341	Product_name		cystathionine gamma-lyase (EC 4.4.1.1)		
2572231985	t3m_00341	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231985	t3m_00341	Coordinates		15596..16738(+)		
2572231985	t3m_00341	DNA_length		1143bp		
2572231985	t3m_00341	Protein_length		380aa		
2572231985	t3m_00341	GC			0.7	
2572231986	t3m_00342	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572231986	t3m_00342	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572231986	t3m_00342	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572231986	t3m_00342	IMG_pathway	488: L-cysteine ligation to tRNA(Cys)			
2572231986	t3m_00342	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572231986	t3m_00342	COG0215	Cysteinyl-tRNA synthetase			0.00E+00
2572231986	t3m_00342	pfam01406	tRNA-synt_1e			8.30E-98
2572231986	t3m_00342	pfam09190	DALR_2			6.60E-07
2572231986	t3m_00342	EC:6.1.1.16	Cysteine--tRNA ligase.			
2572231986	t3m_00342	TIGR00435	cysteinyl-tRNA synthetase			7.00E-125

2572231986	t3m_00342	KO:K01883	cysteinyl-tRNA synthetase [EC:6.1.1.16]			0.00E+00
2572231986	t3m_00342	ITERM:00404	cysteinyl-tRNA synthetase (EC 6.1.1.16)			
2572231986	t3m_00342	Locus_type		CDS		
2572231986	t3m_00342	Product_name		cysteinyl-tRNA synthetase (EC 6.1.1.16)		
2572231986	t3m_00342	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231986	t3m_00342	Coordinates		16741..18183(+)		
2572231986	t3m_00342	DNA_length		1443bp		
2572231986	t3m_00342	Protein_length		480aa		
2572231986	t3m_00342	GC			0.7	
2572231987	t3m_00343	COG_category	[R] General function prediction only			
2572231987	t3m_00343	COG1064	Zn-dependent alcohol dehydrogenases			3.00E-61
2572231987	t3m_00343	pfam08240	ADH_N			4.80E-24
2572231987	t3m_00343	pfam00107	ADH_zinc_N			1.60E-31
2572231987	t3m_00343	Locus_type		CDS		
2572231987	t3m_00343	Product_name		Zn-dependent alcohol dehydrogenases		
2572231987	t3m_00343	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231987	t3m_00343	Coordinates		18190..19230(+)		
2572231987	t3m_00343	DNA_length		1041bp		
2572231987	t3m_00343	Protein_length		346aa		
2572231987	t3m_00343	GC			0.71	
2572231988	t3m_00344	pfam12773	DZR			1.20E-07
2572231988	t3m_00344	Locus_type		CDS		
2572231988	t3m_00344	Product_name		Double zinc ribbon		
2572231988	t3m_00344	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231988	t3m_00344	Coordinates		19384..23055(+)		
2572231988	t3m_00344	DNA_length		3672bp		
2572231988	t3m_00344	Protein_length		1223aa		
2572231988	t3m_00344	GC			0.66	
2572231988	t3m_00344	Transmembrane		Yes		
2572231989	t3m_00345	KEGG_module	M00035: Methionine degradation			
2572231989	t3m_00345	Metacyc	PWY-5041: <i>S</i>-adenosyl-L-methionine cycle II			

2572231989	t3m_00345	Metacyc	METHIONINE-DEG1-PWY: methionine degradation I (to homocysteine)		
2572231989	t3m_00345	IMG_pathway	398: S-adenosyl-L-homocysteine hydrolysis		
2572231989	t3m_00345	COG_category	[H] Coenzyme transport and metabolism		
2572231989	t3m_00345	COG0499	S-adenosylhomocysteine hydrolase		0.00E+00
2572231989	t3m_00345	pfam05221	AdoHcyase		1.20E-52
2572231989	t3m_00345	pfam00670	AdoHcyase_NAD		4.00E-50
2572231989	t3m_00345	EC:3.3.1.1	Adenosylhomocysteinase.		
2572231989	t3m_00345	TIGR00936	adenosylhomocysteinase		0.00E+00
2572231989	t3m_00345	KO:K01251	adenosylhomocysteinase [EC:3.3.1.1]		0.00E+00
2572231989	t3m_00345	ITERM:01674	adenosylhomocysteinase (EC 3.3.1.1)		
2572231989	t3m_00345	Locus_type		CDS	
2572231989	t3m_00345	Product_name		adenosylhomocysteinase (EC 3.3.1.1)	
2572231989	t3m_00345	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572231989	t3m_00345	Coordinates		23135..24370(+)	
2572231989	t3m_00345	DNA_length		1236bp	
2572231989	t3m_00345	Protein_length		411aa	
2572231989	t3m_00345	GC		0.7	
2572231990	t3m_00346	KEGG_module	M00532: Photorespiration		
2572231990	t3m_00346	COG_category	[E] Amino acid transport and metabolism		
2572231990	t3m_00346	COG0509	Glycine cleavage system H protein (lipoate-binding)		1.00E-34
2572231990	t3m_00346	pfam01597	GCV_H		5.80E-39
2572231990	t3m_00346	TIGR00527	glycine cleavage system H protein		1.90E-42
2572231990	t3m_00346	KO:K02437	glycine cleavage system H protein		6.00E-31
2572231990	t3m_00346	Locus_type		CDS	
2572231990	t3m_00346	Product_name		glycine cleavage system H protein	
2572231990	t3m_00346	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572231990	t3m_00346	Coordinates		24367..24762(+)	
2572231990	t3m_00346	DNA_length		396bp	
2572231990	t3m_00346	Protein_length		131aa	
2572231990	t3m_00346	GC		0.66	
2572231991	t3m_00347	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2572231991	t3m_00347	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		

2572231991	t3m_00347	Metacyc	GLYCOLYSIS: glycolysis I			
2572231991	t3m_00347	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2572231991	t3m_00347	Metacyc	P23-PWY: reductive TCA cycle I			
2572231991	t3m_00347	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2572231991	t3m_00347	IMG_pathway	1014: Dicarboxylate/4-hydroxybutyrate cycle			
2572231991	t3m_00347	IMG_pathway	289: Oxaloacetate synthesis via phosphoenolpyruvate			
2572231991	t3m_00347	COG_category	[G] Carbohydrate transport and metabolism			
2572231991	t3m_00347	COG0574	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase			0.00E+00
2572231991	t3m_00347	pfam01326	PPDK_N			2.30E-100
2572231991	t3m_00347	pfam02896	PEP-utilizers_C			1.90E-69
2572231991	t3m_00347	pfam00391	PEP-utilizers			1.50E-27
2572231991	t3m_00347	EC:2.7.9.2	Pyruvate, water dikinase.			
2572231991	t3m_00347	TIGR01418	phosphoenolpyruvate synthase			0.00E+00
2572231991	t3m_00347	KO:K01007	pyruvate, water dikinase [EC:2.7.9.2]			0.00E+00
2572231991	t3m_00347	ITERM:00814	phosphoenolpyruvate synthase (EC 2.7.9.2)			
2572231991	t3m_00347	Locus_type		CDS		
2572231991	t3m_00347	Product_name		phosphoenolpyruvate synthase (EC 2.7.9.2)		
2572231991	t3m_00347	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231991	t3m_00347	Coordinates		24860..27184(-)		
2572231991	t3m_00347	DNA_length		2325bp		
2572231991	t3m_00347	Protein_length		774aa		
2572231991	t3m_00347	GC			0.68	

2572231992	t3m_00348	COG_category	[R] General function prediction only			
2572231992	t3m_00348	COG2520	Predicted methyltransferase			4.00E-60
2572231992	t3m_00348	pfam02475	Met_10			1.70E-42
2572231992	t3m_00348	EC:2.1.1.228	tRNA (guanine(37)-N(1))-methyltransferase.			
2572231992	t3m_00348	KO:K15429	tRNA (guanine37-N1)-methyltransferase [EC:2.1.1.228]			0.00E+00
2572231992	t3m_00348	Locus_type		CDS		
2572231992	t3m_00348	Product_name		Predicted methyltransferase		
2572231992	t3m_00348	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231992	t3m_00348	Coordinates		27213..28235(-)		
2572231992	t3m_00348	DNA_length		1023bp		
2572231992	t3m_00348	Protein_length		340aa		

2572231992	t3m_00348	GC			0.69	
2572231993	t3m_00349	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds			
2572231993	t3m_00349	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis			
2572231993	t3m_00349	Metacyc	PWY-7124: ethylene biosynthesis V			
2572231993	t3m_00349	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2572231993	t3m_00349	Metacyc	P341-PWY: glycolysis V (Pyrococcus)			
2572231993	t3m_00349	Metacyc	PWY-6901: xylose degradation IV			
2572231993	t3m_00349	Metacyc	PWY-7003: glycerol degradation to butanol			
2572231993	t3m_00349	Metacyc	PWY-2221: Entner-Doudoroff pathway III (semi-phosphorylative)			
2572231993	t3m_00349	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)			
2572231993	t3m_00349	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2572231993	t3m_00349	Metacyc	PWY-5723: Rubisco shunt			
2572231993	t3m_00349	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2572231993	t3m_00349	Metacyc	GLYCOLYSIS: glycolysis I			
2572231993	t3m_00349	Metacyc	P124-PWY: Bifidobacterium shunt			
2572231993	t3m_00349	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)			
2572231993	t3m_00349	Metacyc	PWY-1042: glycolysis IV (plant cytosol)			
2572231993	t3m_00349	Metacyc	P122-PWY: heterolactic fermentation			
2572231993	t3m_00349	COG_category	[G] Carbohydrate transport and metabolism			
2572231993	t3m_00349	COG3635	Predicted phosphoglycerate mutase, AP superfamily			6.00E-91
2572231993	t3m_00349	pfam10143	PhosphMutase			1.40E-39
2572231993	t3m_00349	pfam01676	Metalloenzyme			1.20E-27
2572231993	t3m_00349	EC:5.4.2.1	Phosphoglycerate mutase.			
2572231993	t3m_00349	TIGR00306	2,3-bisphosphoglycerate-independent phosphoglycerate mutase, archa			6.40E-95
2572231993	t3m_00349	KO:K15635	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.			0.00E+00
2572231993	t3m_00349	Locus_type		CDS		
2572231993	t3m_00349	Product_name		2,3-bisphosphoglycerate-independent phosphoglycerate mutase, archae		
2572231993	t3m_00349	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231993	t3m_00349	Coordinates		28232..29563(-)		
2572231993	t3m_00349	DNA_length		1332bp		
2572231993	t3m_00349	Protein_length		443aa		
2572231993	t3m_00349	GC			0.71	

2572231994	t3m_00350	Locus_type		CDS		
2572231994	t3m_00350	Product_name		hypothetical protein		
2572231994	t3m_00350	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231994	t3m_00350	Coordinates		29601..30722(+)		
2572231994	t3m_00350	DNA_length		1122bp		
2572231994	t3m_00350	Protein_length		373aa		
2572231994	t3m_00350	GC			0.66	
2572231994	t3m_00350	Transmembrane		Yes		
2572231995	t3m_00351	pfam07790	DUF1628			4.20E-07
2572231995	t3m_00351	Locus_type		CDS		
2572231995	t3m_00351	Product_name		Protein of unknown function (DUF1628)		
2572231995	t3m_00351	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231995	t3m_00351	Coordinates		30819..33374(-)		
2572231995	t3m_00351	DNA_length		2556bp		
2572231995	t3m_00351	Protein_length		851aa		
2572231995	t3m_00351	GC			0.66	
2572231995	t3m_00351	Transmembrane		Yes		
2572231996	t3m_00352	Locus_type		CDS		
2572231996	t3m_00352	Product_name		hypothetical protein		
2572231996	t3m_00352	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231996	t3m_00352	Coordinates		33659..34225(-)		
2572231996	t3m_00352	DNA_length		567bp		
2572231996	t3m_00352	Protein_length		188aa		
2572231996	t3m_00352	GC			0.62	
2572231996	t3m_00352	Transmembrane		Yes		
2572231997	t3m_00353	Locus_type		CDS		
2572231997	t3m_00353	Product_name		hypothetical protein		
2572231997	t3m_00353	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231997	t3m_00353	Coordinates		34209..34370(+)		
2572231997	t3m_00353	DNA_length		162bp		
2572231997	t3m_00353	Protein_length		53aa		

2572231997	t3m_00353	GC			0.56	
2572231998	t3m_00354	Locus_type		CDS		
2572231998	t3m_00354	Product_name		hypothetical protein		
2572231998	t3m_00354	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231998	t3m_00354	Coordinates		34753..35250(+)		
2572231998	t3m_00354	DNA_length		498bp		
2572231998	t3m_00354	Protein_length		165aa		
2572231998	t3m_00354	GC			0.69	
2572231999	t3m_00355	pfam00091	Tubulin			4.00E-08
2572231999	t3m_00355	Locus_type		CDS		
2572231999	t3m_00355	Product_name		Tubulin/FtsZ family, GTPase domain		
2572231999	t3m_00355	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572231999	t3m_00355	Coordinates		35291..36211(+)		
2572231999	t3m_00355	DNA_length		921bp		
2572231999	t3m_00355	Protein_length		306aa		
2572231999	t3m_00355	GC			0.7	
2572232000	t3m_00356	Locus_type		CDS		
2572232000	t3m_00356	Product_name		hypothetical protein		
2572232000	t3m_00356	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232000	t3m_00356	Coordinates		36307..36474(+)		
2572232000	t3m_00356	DNA_length		168bp		
2572232000	t3m_00356	Protein_length		55aa		
2572232000	t3m_00356	GC			0.61	
2572232000	t3m_00356	Transmembrane		Yes		
2572232001	t3m_00357	COG_category	[R] General function prediction only			
2572232001	t3m_00357	COG1938	Archaeal enzymes of ATP-grasp superfamily			3.00E-28
2572232001	t3m_00357	pfam09754	PAC2			2.80E-23
2572232001	t3m_00357	KO:K06869	uncharacterized protein			2.30E-22
2572232001	t3m_00357	Locus_type		CDS		
2572232001	t3m_00357	Product_name		Archaeal enzymes of ATP-grasp superfamily		

2572232001	t3m_00357	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572232001	t3m_00357	Coordinates		36503..37303(-)	
2572232001	t3m_00357	DNA_length		801bp	
2572232001	t3m_00357	Protein_length		266aa	
2572232001	t3m_00357	GC		0.7	
2572232002	t3m_00358	Metacyc	P303-PWY: ammonia oxidation II (anaerobic)		
2572232002	t3m_00358	IMG_pathway	437: Archaeal replication elongation		
2572232002	t3m_00358	COG_category	[L] Replication, recombination and repair		
2572232002	t3m_00358	COG0258	5'-3' exonuclease (including N-terminal domain of PolI)		4.00E-31
2572232002	t3m_00358	pfam00867	XPG_I		3.40E-20
2572232002	t3m_00358	pfam00752	XPG_N		3.00E-17
2572232002	t3m_00358	EC:3.-	Hydrolases.		
2572232002	t3m_00358	KO:K04799	flap endonuclease-1 [EC:3.-.-.-]		0.00E+00
2572232002	t3m_00358	ITERM:00111	flap endonuclease 1 (EC 3.1.-.-)		
2572232002	t3m_00358	Locus_type		CDS	
2572232002	t3m_00358	Product_name		flap endonuclease 1 (EC 3.1.-.-)	
2572232002	t3m_00358	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572232002	t3m_00358	Coordinates		37403..38440(+)	
2572232002	t3m_00358	DNA_length		1038bp	
2572232002	t3m_00358	Protein_length		345aa	
2572232002	t3m_00358	GC		0.69	
2572232003	t3m_00359	Metacyc	P164-PWY: purine nucleobases degradation I (anaerobic)		
2572232003	t3m_00359	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2572232003	t3m_00359	Metacyc	PWY-5030: histidine degradation III		
2572232003	t3m_00359	COG_category	[E] Amino acid transport and metabolism		
2572232003	t3m_00359	COG3643	Glutamate formiminotransferase		2.00E-101
2572232003	t3m_00359	pfam02971	FTCD		1.20E-26
2572232003	t3m_00359	pfam07837	FTCD_N		2.00E-67
2572232003	t3m_00359	pfam04961	FTCD_C		5.00E-35
2572232003	t3m_00359	EC:4.3.1.4	Formimidoyltetrahydrofolate cyclodeaminase.		
2572232003	t3m_00359	EC:2.1.2.5	Glutamate formimidoyltransferase.		
2572232003	t3m_00359	TIGR02024	glutamate formiminotransferase		1.60E-117

2572232003	t3m_00359	KO:K13990	glutamate formiminotransferase / formiminotetrahydrofolate cyclodea			0.00E+00
2572232003	t3m_00359	Locus_type		CDS		
2572232003	t3m_00359	Product_name		glutamate formiminotransferase		
2572232003	t3m_00359	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232003	t3m_00359	Coordinates		38437..39912(+)		
2572232003	t3m_00359	DNA_length		1476bp		
2572232003	t3m_00359	Protein_length		491aa		
2572232003	t3m_00359	GC			0.7	
2572232003	t3m_00359	Fused_gene		Yes		

2572232004	t3m_00360	Metacyc	PWY-6168: flavin biosynthesis III (fungi)			
2572232004	t3m_00360	Metacyc	PWY-6167: flavin biosynthesis II (archaea)			
2572232004	t3m_00360	COG_category	[H] Coenzyme transport and metabolism			
2572232004	t3m_00360	COG1985	Pyrimidine reductase, riboflavin biosynthesis			9.00E-47
2572232004	t3m_00360	pfam01872	RibD_C			1.80E-50
2572232004	t3m_00360	EC:1.1.1.302	2,5-diamino-6-(ribosylamino)-4(3H)-pyrimidinone 5'-phosphate reductase.			
2572232004	t3m_00360	TIGR00227	riboflavin-specific deaminase C-terminal domain			3.10E-59
2572232004	t3m_00360	TIGR01508	2,5-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine 1'-reduct			3.60E-57
2572232004	t3m_00360	KO:K14654	2,5-diamino-6-(ribosylamino)-4(3H)-pyrimidinone 5'-phosphate reducta			2.40E-39
2572232004	t3m_00360	Locus_type		CDS		
2572232004	t3m_00360	Product_name		riboflavin-specific deaminase C-terminal domain		
2572232004	t3m_00360	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232004	t3m_00360	Coordinates		39924..40631(+)		
2572232004	t3m_00360	DNA_length		708bp		
2572232004	t3m_00360	Protein_length		235aa		
2572232004	t3m_00360	GC			0.69	

2572232005	t3m_00361	Locus_type		CDS		
2572232005	t3m_00361	Product_name		hypothetical protein		
2572232005	t3m_00361	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232005	t3m_00361	Coordinates		40708..41097(+)		
2572232005	t3m_00361	DNA_length		390bp		
2572232005	t3m_00361	Protein_length		129aa		
2572232005	t3m_00361	GC			0.62	

2572232005	t3m_00361	Transmembrane		Yes	

2572232006	t3m_00362	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism		
2572232006	t3m_00362	COG0179	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydrat		6.00E-54
2572232006	t3m_00362	pfam01557	FAA_hydrolase		1.90E-50
2572232006	t3m_00362	Locus_type		CDS	
2572232006	t3m_00362	Product_name		2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydrata	
2572232006	t3m_00362	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572232006	t3m_00362	Coordinates		41200..42177(+)	
2572232006	t3m_00362	DNA_length		978bp	
2572232006	t3m_00362	Protein_length		325aa	
2572232006	t3m_00362	GC		0.66	

2572232007	t3m_00363	Metacyc	PWY-6679: jadomycin biosynthesis		
2572232007	t3m_00363	Metacyc	PWY-6998: CDP-D-arabitol biosynthesis		
2572232007	t3m_00363	Metacyc	PWY-7127: CDP-D-mannitol biosynthesis		
2572232007	t3m_00363	Metacyc	PWY-6749: CMP-legionaminate biosynthesis I		
2572232007	t3m_00363	Metacyc	PWY-6626: CDP-2-glycerol biosynthesis		
2572232007	t3m_00363	Metacyc	PWY4FS-4: phosphatidylcholine biosynthesis IV		
2572232007	t3m_00363	COG_category	[L] Replication, recombination and repair		
2572232007	t3m_00363	COG1467	Eukaryotic-type DNA primase, catalytic (small) subunit		2.00E-43
2572232007	t3m_00363	pfam01896	DNA_primase_S		1.90E-17
2572232007	t3m_00363	EC:2.7.7.-	Transferases. Transferring phosphorous-containing groups. Nucleotidyltransferases.		
2572232007	t3m_00363	TIGR00335	DNA primase, eukaryotic-type, small subunit, putative		4.80E-42
2572232007	t3m_00363	KO:K02683	DNA primase [EC:2.7.7.-]		0.00E+00
2572232007	t3m_00363	ITERM:00098	DNA primase small subunit (EC 2.7.7.-)		
2572232007	t3m_00363	Locus_type		CDS	
2572232007	t3m_00363	Product_name		DNA primase small subunit (EC 2.7.7.-)	
2572232007	t3m_00363	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5	
2572232007	t3m_00363	Coordinates		42140..43405(-)	
2572232007	t3m_00363	DNA_length		1266bp	
2572232007	t3m_00363	Protein_length		421aa	
2572232007	t3m_00363	GC		0.69	

2572232008	t3m_00364	COG_category	[R] General function prediction only			
2572232008	t3m_00364	COG1094	Predicted RNA-binding protein (contains KH domains)			3.00E-41
2572232008	t3m_00364	pfam00013	KH_1			7.90E-05
2572232008	t3m_00364	pfam00013	KH_1			8.20E-08
2572232008	t3m_00364	TIGR03665	arCOG04150 universal archaeal KH domain protein			6.70E-58
2572232008	t3m_00364	KO:K06961	ribosomal RNA assembly protein			1.60E-41
2572232008	t3m_00364	Locus_type		CDS		
2572232008	t3m_00364	Product_name		arCOG04150 universal archaeal KH domain protein		
2572232008	t3m_00364	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232008	t3m_00364	Coordinates		43410..43982(-)		
2572232008	t3m_00364	DNA_length		573bp		
2572232008	t3m_00364	Protein_length		190aa		
2572232008	t3m_00364	GC			0.71	

2572232009	t3m_00365	COG_category	[T] Signal transduction mechanisms			
2572232009	t3m_00365	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2572232009	t3m_00365	COG1718	Serine/threonine protein kinase involved in cell cycle control			1.00E-59
2572232009	t3m_00365	pfam01163	RIO1			7.20E-49
2572232009	t3m_00365	EC:2.7.11.1	Non-specific serine/threonine protein kinase.			
2572232009	t3m_00365	KO:K07178	RIO kinase 1 [EC:2.7.11.1]			8.80E-43
2572232009	t3m_00365	Locus_type		CDS		
2572232009	t3m_00365	Product_name		Serine/threonine protein kinase involved in cell cycle control		
2572232009	t3m_00365	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232009	t3m_00365	Coordinates		43989..44780(-)		
2572232009	t3m_00365	DNA_length		792bp		
2572232009	t3m_00365	Protein_length		263aa		
2572232009	t3m_00365	GC			0.68	

2572232010	t3m_00366	Locus_type		CDS		
2572232010	t3m_00366	Product_name		hypothetical protein		
2572232010	t3m_00366	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232010	t3m_00366	Coordinates		44922..45488(+)		
2572232010	t3m_00366	DNA_length		567bp		
2572232010	t3m_00366	Protein_length		188aa		

2572232010	t3m_00366	GC			0.69	
2572232011	t3m_00367	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2572232011	t3m_00367	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232011	t3m_00367	COG1585	Membrane protein implicated in regulation of membrane protease acti			7.00E-09
2572232011	t3m_00367	pfam01957	NfeD			5.10E-20
2572232011	t3m_00367	Locus_type		CDS		
2572232011	t3m_00367	Product_name		Membrane protein implicated in regulation of membrane protease activ		
2572232011	t3m_00367	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232011	t3m_00367	Coordinates		45543..46013(+)		
2572232011	t3m_00367	DNA_length		471bp		
2572232011	t3m_00367	Protein_length		156aa		
2572232011	t3m_00367	GC			0.65	
2572232011	t3m_00367	Transmembrane		Yes		
2572232012	t3m_00368	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232012	t3m_00368	COG0330	Membrane protease subunits, stomatin/prohibitin homologs			3.00E-40
2572232012	t3m_00368	pfam01145	Band_7			3.10E-33
2572232012	t3m_00368	Locus_type		CDS		
2572232012	t3m_00368	Product_name		Membrane protease subunits, stomatin/prohibitin homologs		
2572232012	t3m_00368	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232012	t3m_00368	Coordinates		46107..47360(+)		
2572232012	t3m_00368	DNA_length		1254bp		
2572232012	t3m_00368	Protein_length		417aa		
2572232012	t3m_00368	GC			0.66	
2572232012	t3m_00368	Transmembrane		Yes		
2572232013	t3m_00369	Metacyc	PWY0-321: phenylacetate degradation I (aerobic)			
2572232013	t3m_00369	IMG_pathway	1014: Dicarboxylate/4-hydroxybutyrate cycle			
2572232013	t3m_00369	IMG_pathway	222: L-isoleucine degradation to propionyl-CoA and acetyl-CoA			
2572232013	t3m_00369	IMG_pathway	227: L-valine degradation to propionyl-CoA			
2572232013	t3m_00369	IMG_pathway	369: Pyruvate conversion to butyrate			
2572232013	t3m_00369	IMG_pathway	389: Crotonyl-CoA conversion to acetate			
2572232013	t3m_00369	IMG_pathway	596: 3-hydroxypropionate/4-hydroxybutyrate cycle			

2572232013	t3m_00369	IMG_pathway	962: Glyoxylate from acetyl-CoA via ethylmalonyl-CoA pathway			
2572232013	t3m_00369	COG_category	[I] Lipid transport and metabolism			
2572232013	t3m_00369	COG1024	Enoyl-CoA hydratase/carnithine racemase			2.00E-44
2572232013	t3m_00369	pfam00378	ECH			7.40E-53
2572232013	t3m_00369	EC:5.3.3.18	2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase.			
2572232013	t3m_00369	KO:K15866	2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase [EC:5.3.3.18]			0.00E+00
2572232013	t3m_00369	ITERM:00575	short chain enoyl-CoA hydratase (EC 4.2.1.17)			
2572232013	t3m_00369	ITERM:00611	Enoyl-CoA hydratase (EC 4.2.1.17)			
2572232013	t3m_00369	Locus_type		CDS		
2572232013	t3m_00369	Product_name		short chain enoyl-CoA hydratase (EC 4.2.1.17)/Enoyl-CoA hydratase (EC		
2572232013	t3m_00369	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232013	t3m_00369	Coordinates		47487..48275(+)		
2572232013	t3m_00369	DNA_length		789bp		
2572232013	t3m_00369	Protein_length		262aa		
2572232013	t3m_00369	GC			0.73	
2572232014	t3m_00370	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232014	t3m_00370	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins			2.00E-21
2572232014	t3m_00370	pfam13302	Acetyltransf_3			1.60E-21
2572232014	t3m_00370	Locus_type		CDS		
2572232014	t3m_00370	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins		
2572232014	t3m_00370	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232014	t3m_00370	Coordinates		48283..48975(-)		
2572232014	t3m_00370	DNA_length		693bp		
2572232014	t3m_00370	Protein_length		230aa		
2572232014	t3m_00370	GC			0.69	
2572232015	t3m_00371	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232015	t3m_00371	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins			2.00E-18
2572232015	t3m_00371	pfam13302	Acetyltransf_3			4.50E-18
2572232015	t3m_00371	Locus_type		CDS		
2572232015	t3m_00371	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins		
2572232015	t3m_00371	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232015	t3m_00371	Coordinates		48906..49568(-)		

2572232015	t3m_00371	DNA_length		663bp		
2572232015	t3m_00371	Protein_length		220aa		
2572232015	t3m_00371	GC			0.7	
2572232016	t3m_00372	KEGG_module	M00145: NAD(P)H:quinone oxidoreductase, chloroplasts and cyanobacteria			
2572232016	t3m_00372	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572232016	t3m_00372	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2572232016	t3m_00372	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2572232016	t3m_00372	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2572232016	t3m_00372	Metacyc	PWY-6692: Fe(II) oxidation			
2572232016	t3m_00372	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572232016	t3m_00372	COG_category	[C] Energy production and conversion			
2572232016	t3m_00372	COG0838	NADH:ubiquinone oxidoreductase subunit 3 (chain A)			1.00E-11
2572232016	t3m_00372	pfam00507	Oxidored_q4			9.10E-13
2572232016	t3m_00372	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2572232016	t3m_00372	KO:K05574	NAD(P)H-quinone oxidoreductase subunit 3 [EC:1.6.5.3]			9.80E-12
2572232016	t3m_00372	Locus_type		CDS		
2572232016	t3m_00372	Product_name		NADH:ubiquinone oxidoreductase subunit 3 (chain A)		
2572232016	t3m_00372	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232016	t3m_00372	Coordinates		49728..50093(+)		
2572232016	t3m_00372	DNA_length		366bp		
2572232016	t3m_00372	Protein_length		121aa		
2572232016	t3m_00372	GC			0.65	
2572232016	t3m_00372	Transmembrane		Yes		
2572232017	t3m_00373	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2572232017	t3m_00373	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2572232017	t3m_00373	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2572232017	t3m_00373	Metacyc	PWY-6692: Fe(II) oxidation			
2572232017	t3m_00373	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572232017	t3m_00373	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572232017	t3m_00373	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2572232017	t3m_00373	COG_category	[C] Energy production and conversion			
2572232017	t3m_00373	COG0377	NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxido			1.00E-56

2572232017	t3m_00373	pfam01058	Oxidored_q6			8.70E-23
2572232017	t3m_00373	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2572232017	t3m_00373	TIGR01957	NADH-quinone oxidoreductase, B subunit			1.20E-63
2572232017	t3m_00373	KO:K00331	NADH-quinone oxidoreductase subunit B [EC:1.6.5.3]			2.20E-43
2572232017	t3m_00373	Locus_type		CDS		
2572232017	t3m_00373	Product_name		NADH-quinone oxidoreductase, B subunit		
2572232017	t3m_00373	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232017	t3m_00373	Coordinates		50081..50710(+)		
2572232017	t3m_00373	DNA_length		630bp		
2572232017	t3m_00373	Protein_length		209aa		
2572232017	t3m_00373	GC			0.68	
2572232018	t3m_00374	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2572232018	t3m_00374	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2572232018	t3m_00374	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572232018	t3m_00374	Metacyc	PWY-6692: Fe(II) oxidation			
2572232018	t3m_00374	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2572232018	t3m_00374	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2572232018	t3m_00374	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572232018	t3m_00374	pfam00329	Complex1_30kDa			2.50E-27
2572232018	t3m_00374	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2572232018	t3m_00374	KO:K00332	NADH-quinone oxidoreductase subunit C [EC:1.6.5.3]			1.30E-17
2572232018	t3m_00374	Locus_type		CDS		
2572232018	t3m_00374	Product_name		Respiratory-chain NADH dehydrogenase, 30 Kd subunit		
2572232018	t3m_00374	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232018	t3m_00374	Coordinates		50762..51223(+)		
2572232018	t3m_00374	DNA_length		462bp		
2572232018	t3m_00374	Protein_length		153aa		
2572232018	t3m_00374	GC			0.67	
2572232019	t3m_00375	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2572232019	t3m_00375	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2572232019	t3m_00375	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2572232019	t3m_00375	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			

2572232019	t3m_00375	Metacyc	PWY-6692: Fe(II) oxidation			
2572232019	t3m_00375	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2572232019	t3m_00375	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572232019	t3m_00375	COG_category	[C] Energy production and conversion			
2572232019	t3m_00375	COG0649	NADH:ubiquinone oxidoreductase 49 kD subunit 7			5.00E-110
2572232019	t3m_00375	pfam00346	Complex1_49kDa			2.20E-68
2572232019	t3m_00375	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2572232019	t3m_00375	KO:K00333	NADH-quinone oxidoreductase subunit D [EC:1.6.5.3]			0.00E+00
2572232019	t3m_00375	Locus_type		CDS		
2572232019	t3m_00375	Product_name		NADH:ubiquinone oxidoreductase 49 kD subunit 7		
2572232019	t3m_00375	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232019	t3m_00375	Coordinates		51255..52361(+)		
2572232019	t3m_00375	DNA_length		1107bp		
2572232019	t3m_00375	Protein_length		368aa		
2572232019	t3m_00375	GC			0.66	
2572232020	t3m_00376	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2572232020	t3m_00376	Metacyc	PWY-6692: Fe(II) oxidation			
2572232020	t3m_00376	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2572232020	t3m_00376	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2572232020	t3m_00376	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572232020	t3m_00376	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2572232020	t3m_00376	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572232020	t3m_00376	COG_category	[C] Energy production and conversion			
2572232020	t3m_00376	COG1005	NADH:ubiquinone oxidoreductase subunit 1 (chain H)			2.00E-70
2572232020	t3m_00376	pfam00146	NADHdh			5.00E-90
2572232020	t3m_00376	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2572232020	t3m_00376	KO:K00337	NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]			0.00E+00
2572232020	t3m_00376	Locus_type		CDS		
2572232020	t3m_00376	Product_name		NADH:ubiquinone oxidoreductase subunit 1 (chain H)		
2572232020	t3m_00376	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232020	t3m_00376	Coordinates		52374..53498(+)		
2572232020	t3m_00376	DNA_length		1125bp		
2572232020	t3m_00376	Protein_length		374aa		

2572232020	t3m_00376	GC			0.65	
2572232020	t3m_00376	Transmembrane		Yes		
2572232021	t3m_00377	pfam12838	Fer4_7			8.10E-09
2572232021	t3m_00377	pfam00037	Fer4			3.80E-06
2572232021	t3m_00377	Locus_type		CDS		
2572232021	t3m_00377	Product_name		4Fe-4S binding domain/4Fe-4S dicluster domain		
2572232021	t3m_00377	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232021	t3m_00377	Coordinates		53519..54298(+)		
2572232021	t3m_00377	DNA_length		780bp		
2572232021	t3m_00377	Protein_length		259aa		
2572232021	t3m_00377	GC			0.65	
2572232022	t3m_00378	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2572232022	t3m_00378	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2572232022	t3m_00378	Metacyc	PWY-6692: Fe(II) oxidation			
2572232022	t3m_00378	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2572232022	t3m_00378	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572232022	t3m_00378	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572232022	t3m_00378	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2572232022	t3m_00378	COG_category	[C] Energy production and conversion			
2572232022	t3m_00378	COG0839	NADH:ubiquinone oxidoreductase subunit 6 (chain J)			4.00E-07
2572232022	t3m_00378	pfam00499	Oxidored_q3			6.90E-15
2572232022	t3m_00378	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2572232022	t3m_00378	KO:K00339	NADH-quinone oxidoreductase subunit J [EC:1.6.5.3]			8.70E-16
2572232022	t3m_00378	ITERM:05537	NADH dehydrogenase subunit J (EC 1.6.5.3)			
2572232022	t3m_00378	Locus_type		CDS		
2572232022	t3m_00378	Product_name		NADH dehydrogenase subunit J (EC 1.6.5.3)		
2572232022	t3m_00378	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232022	t3m_00378	Coordinates		54295..54783(+)		
2572232022	t3m_00378	DNA_length		489bp		
2572232022	t3m_00378	Protein_length		162aa		
2572232022	t3m_00378	GC			0.67	
2572232022	t3m_00378	Transmembrane		Yes		

2572232023	t3m_00379	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2572232023	t3m_00379	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2572232023	t3m_00379	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572232023	t3m_00379	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572232023	t3m_00379	Metacyc	PWY-6692: Fe(II) oxidation			
2572232023	t3m_00379	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2572232023	t3m_00379	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2572232023	t3m_00379	COG_category	[C] Energy production and conversion			
2572232023	t3m_00379	COG0713	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)			1.00E-09
2572232023	t3m_00379	pfam00420	Oxidored_q2			6.50E-15
2572232023	t3m_00379	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2572232023	t3m_00379	KO:K00340	NADH-quinone oxidoreductase subunit K [EC:1.6.5.3]			3.10E-16
2572232023	t3m_00379	Locus_type		CDS		
2572232023	t3m_00379	Product_name		NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)		
2572232023	t3m_00379	Scaffold		t3m_contig_70_42_len_55050_read_count_4293452.5		
2572232023	t3m_00379	Coordinates		54780..55049(+)		
2572232023	t3m_00379	DNA_length		270bp		
2572232023	t3m_00379	Protein_length		90aa		
2572232023	t3m_00379	GC			0.67	
2572232023	t3m_00379	Transmembrane		Yes		

2572232024	t3m_00380	Locus_type		CDS		
2572232024	t3m_00380	Product_name		hypothetical protein		
2572232024	t3m_00380	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232024	t3m_00380	Coordinates		3..206(-)		
2572232024	t3m_00380	DNA_length		204bp		
2572232024	t3m_00380	Protein_length		68aa		
2572232024	t3m_00380	GC			0.66	

2572232025	t3m_00381	IMG_pathway	217: N-3-alkylpurine repair via base excision			
2572232025	t3m_00381	COG_category	[L] Replication, recombination and repair			
2572232025	t3m_00381	COG2818	3-methyladenine DNA glycosylase			2.00E-65
2572232025	t3m_00381	pfam03352	Adenine_glyco			1.90E-77

2572232025	t3m_00381	EC:3.2.2.20	DNA-3-methyladenine glycosylase I.			
2572232025	t3m_00381	TIGR00624	DNA-3-methyladenine glycosylase I			5.80E-70
2572232025	t3m_00381	KO:K01246	DNA-3-methyladenine glycosylase I [EC:3.2.2.20]			0.00E+00
2572232025	t3m_00381	ITERM:00571	DNA-3-methyladenine glycosylase I (EC 3.2.2.20)			
2572232025	t3m_00381	Locus_type		CDS		
2572232025	t3m_00381	Product_name		DNA-3-methyladenine glycosylase I (EC 3.2.2.20)		
2572232025	t3m_00381	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232025	t3m_00381	Coordinates		256..888(-)		
2572232025	t3m_00381	DNA_length		633bp		
2572232025	t3m_00381	Protein_length		210aa		
2572232025	t3m_00381	GC			0.61	
2572232026	t3m_00382	Locus_type		CDS		
2572232026	t3m_00382	Product_name		hypothetical protein		
2572232026	t3m_00382	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232026	t3m_00382	Coordinates		1431..1979(+)		
2572232026	t3m_00382	DNA_length		549bp		
2572232026	t3m_00382	Protein_length		182aa		
2572232026	t3m_00382	GC			0.59	
2572232027	t3m_00383	COG_category	[E] Amino acid transport and metabolism			
2572232027	t3m_00383	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2572232027	t3m_00383	COG3191	L-aminopeptidase/D-esterase			6.00E-35
2572232027	t3m_00383	pfam03576	Peptidase_S58			8.70E-42
2572232027	t3m_00383	Locus_type		CDS		
2572232027	t3m_00383	Product_name		L-aminopeptidase/D-esterase		
2572232027	t3m_00383	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232027	t3m_00383	Coordinates		2236..3222(+)		
2572232027	t3m_00383	DNA_length		987bp		
2572232027	t3m_00383	Protein_length		328aa		
2572232027	t3m_00383	GC			0.63	
2572232028	t3m_00384	pfam01844	HNH			4.90E-10
2572232028	t3m_00384	Locus_type		CDS		

2572232028	t3m_00384	Product_name	HNH endonuclease
2572232028	t3m_00384	Scaffold	t3m_contig_70_43_len_54376_read_count_5056668.6
2572232028	t3m_00384	Coordinates	4389..4865(+)
2572232028	t3m_00384	DNA_length	477bp
2572232028	t3m_00384	Protein_length	158aa
2572232028	t3m_00384	GC	0.59
2572232029	t3m_00385	Locus_type	CDS
2572232029	t3m_00385	Product_name	hypothetical protein
2572232029	t3m_00385	Scaffold	t3m_contig_70_43_len_54376_read_count_5056668.6
2572232029	t3m_00385	Coordinates	7547..8776(-)
2572232029	t3m_00385	DNA_length	1230bp
2572232029	t3m_00385	Protein_length	409aa
2572232029	t3m_00385	GC	0.66
2572232030	t3m_00386	Locus_type	CDS
2572232030	t3m_00386	Product_name	hypothetical protein
2572232030	t3m_00386	Scaffold	t3m_contig_70_43_len_54376_read_count_5056668.6
2572232030	t3m_00386	Coordinates	10100..10882(+)
2572232030	t3m_00386	DNA_length	783bp
2572232030	t3m_00386	Protein_length	260aa
2572232030	t3m_00386	GC	0.64
2572232031	t3m_00387	Locus_type	CDS
2572232031	t3m_00387	Product_name	hypothetical protein
2572232031	t3m_00387	Scaffold	t3m_contig_70_43_len_54376_read_count_5056668.6
2572232031	t3m_00387	Coordinates	11387..12244(-)
2572232031	t3m_00387	DNA_length	858bp
2572232031	t3m_00387	Protein_length	285aa
2572232031	t3m_00387	GC	0.59
2572232032	t3m_00388	Locus_type	CDS
2572232032	t3m_00388	Product_name	hypothetical protein
2572232032	t3m_00388	Scaffold	t3m_contig_70_43_len_54376_read_count_5056668.6

2572232032	t3m_00388	Coordinates		12286..13554(-)		
2572232032	t3m_00388	DNA_length		1269bp		
2572232032	t3m_00388	Protein_length		422aa		
2572232032	t3m_00388	GC			0.57	
2572232033	t3m_00389	Locus_type		CDS		
2572232033	t3m_00389	Product_name		hypothetical protein		
2572232033	t3m_00389	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232033	t3m_00389	Coordinates		15311..15880(+)		
2572232033	t3m_00389	DNA_length		570bp		
2572232033	t3m_00389	Protein_length		189aa		
2572232033	t3m_00389	GC			0.66	
2572232034	t3m_00390	Locus_type		CDS		
2572232034	t3m_00390	Product_name		hypothetical protein		
2572232034	t3m_00390	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232034	t3m_00390	Coordinates		15877..16452(+)		
2572232034	t3m_00390	DNA_length		576bp		
2572232034	t3m_00390	Protein_length		191aa		
2572232034	t3m_00390	GC			0.63	
2572232035	t3m_00391	Locus_type		CDS		
2572232035	t3m_00391	Product_name		hypothetical protein		
2572232035	t3m_00391	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232035	t3m_00391	Coordinates		16913..17425(-)		
2572232035	t3m_00391	DNA_length		513bp		
2572232035	t3m_00391	Protein_length		170aa		
2572232035	t3m_00391	GC			0.62	
2572232035	t3m_00391	Transmembrane		Yes		
2572232036	t3m_00392	COG_category	[S] Function unknown			
2572232036	t3m_00392	COG2119	Predicted membrane protein			3.00E-10
2572232036	t3m_00392	pfam01169	UPF0016			8.50E-08
2572232036	t3m_00392	pfam01169	UPF0016			3.30E-12

2572232036	t3m_00392	Locus_type		CDS	
2572232036	t3m_00392	Product_name		Predicted membrane protein	
2572232036	t3m_00392	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232036	t3m_00392	Coordinates		17591..18217(-)	
2572232036	t3m_00392	DNA_length		627bp	
2572232036	t3m_00392	Protein_length		208aa	
2572232036	t3m_00392	GC		0.64	
2572232036	t3m_00392	Transmembrane		Yes	
2572232037	t3m_00393	Locus_type		CDS	
2572232037	t3m_00393	Product_name		hypothetical protein	
2572232037	t3m_00393	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232037	t3m_00393	Coordinates		18475..18798(-)	
2572232037	t3m_00393	DNA_length		324bp	
2572232037	t3m_00393	Protein_length		107aa	
2572232037	t3m_00393	GC		0.61	
2572232038	t3m_00394	Locus_type		CDS	
2572232038	t3m_00394	Product_name		hypothetical protein	
2572232038	t3m_00394	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232038	t3m_00394	Coordinates		18788..19045(-)	
2572232038	t3m_00394	DNA_length		258bp	
2572232038	t3m_00394	Protein_length		85aa	
2572232038	t3m_00394	GC		0.64	
2572232039	t3m_00395	pfam01872	RibD_C		5.70E-18
2572232039	t3m_00395	Locus_type		CDS	
2572232039	t3m_00395	Product_name		RibD C-terminal domain	
2572232039	t3m_00395	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232039	t3m_00395	Coordinates		19492..20109(-)	
2572232039	t3m_00395	DNA_length		618bp	
2572232039	t3m_00395	Protein_length		205aa	
2572232039	t3m_00395	GC		0.6	

2572232040	t3m_00396	KEGG_module	M00254: ABC-2 type transport system			
2572232040	t3m_00396	pfam12679	ABC2_membrane_2			1.30E-10
2572232040	t3m_00396	KO:K01992	ABC-2 type transport system permease protein			4.50E-33
2572232040	t3m_00396	Locus_type		CDS		
2572232040	t3m_00396	Product_name		ABC-2 family transporter protein		
2572232040	t3m_00396	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232040	t3m_00396	Coordinates		20351..21088(-)		
2572232040	t3m_00396	DNA_length		738bp		
2572232040	t3m_00396	Protein_length		245aa		
2572232040	t3m_00396	GC			0.61	
2572232040	t3m_00396	Transmembrane		Yes		

2572232041	t3m_00397	KEGG_module	M00248: Putative antibiotic transport system			
2572232041	t3m_00397	COG_category	[V] Defense mechanisms			
2572232041	t3m_00397	COG1131	ABC-type multidrug transport system, ATPase component			5.00E-69
2572232041	t3m_00397	pfam00005	ABC_tran			5.20E-30
2572232041	t3m_00397	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2572232041	t3m_00397	Locus_type		CDS		
2572232041	t3m_00397	Product_name		ABC-type multidrug transport system, ATPase component		
2572232041	t3m_00397	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232041	t3m_00397	Coordinates		21085..22017(-)		
2572232041	t3m_00397	DNA_length		933bp		
2572232041	t3m_00397	Protein_length		310aa		
2572232041	t3m_00397	GC			0.6	

2572232042	t3m_00398	pfam07690	MFS_1			2.40E-37
2572232042	t3m_00398	Locus_type		CDS		
2572232042	t3m_00398	Product_name		Major Facilitator Superfamily		
2572232042	t3m_00398	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232042	t3m_00398	Coordinates		22158..23570(-)		
2572232042	t3m_00398	DNA_length		1413bp		
2572232042	t3m_00398	Protein_length		470aa		
2572232042	t3m_00398	GC			0.59	
2572232042	t3m_00398	Transmembrane		Yes		

2572232043	t3m_00399	pfam14026	DUF4242			1.60E-21
2572232043	t3m_00399	Locus_type		CDS		
2572232043	t3m_00399	Product_name		Protein of unknown function (DUF4242)		
2572232043	t3m_00399	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232043	t3m_00399	Coordinates		24574..24834(-)		
2572232043	t3m_00399	DNA_length		261bp		
2572232043	t3m_00399	Protein_length		86aa		
2572232043	t3m_00399	GC			0.62	
2572232044	t3m_00400	Locus_type		CDS		
2572232044	t3m_00400	Product_name		hypothetical protein		
2572232044	t3m_00400	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232044	t3m_00400	Coordinates		24961..25185(+)		
2572232044	t3m_00400	DNA_length		225bp		
2572232044	t3m_00400	Protein_length		74aa		
2572232044	t3m_00400	GC			0.63	
2572232044	t3m_00400	Transmembrane		Yes		
2572232045	t3m_00401	KEGG_module	M00248: Putative antibiotic transport system			
2572232045	t3m_00401	COG_category	[V] Defense mechanisms			
2572232045	t3m_00401	COG0842	ABC-type multidrug transport system, permease component			7.00E-07
2572232045	t3m_00401	pfam01061	ABC2_membrane			8.90E-21
2572232045	t3m_00401	KO:K09686	antibiotic transport system permease protein			0.00E+00
2572232045	t3m_00401	Locus_type		CDS		
2572232045	t3m_00401	Product_name		ABC-type multidrug transport system, permease component		
2572232045	t3m_00401	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232045	t3m_00401	Coordinates		25422..26222(-)		
2572232045	t3m_00401	DNA_length		801bp		
2572232045	t3m_00401	Protein_length		266aa		
2572232045	t3m_00401	GC			0.63	
2572232045	t3m_00401	Transmembrane		Yes		
2572232046	t3m_00402	KEGG_module	M00248: Putative antibiotic transport system			

2572232046	t3m_00402	COG_category	[V] Defense mechanisms			
2572232046	t3m_00402	COG1131	ABC-type multidrug transport system, ATPase component			5.00E-68
2572232046	t3m_00402	pfam00005	ABC_tran			9.30E-28
2572232046	t3m_00402	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2572232046	t3m_00402	Locus_type		CDS		
2572232046	t3m_00402	Product_name		ABC-type multidrug transport system, ATPase component		
2572232046	t3m_00402	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232046	t3m_00402	Coordinates		26219..27193(-)		
2572232046	t3m_00402	DNA_length		975bp		
2572232046	t3m_00402	Protein_length		324aa		
2572232046	t3m_00402	GC			0.65	
2572232047	t3m_00403	pfam02909	TetR_C			2.80E-16
2572232047	t3m_00403	pfam00440	TetR_N			1.10E-14
2572232047	t3m_00403	ITERM:02313	transcriptional regulator, TetR family			
2572232047	t3m_00403	Locus_type		CDS		
2572232047	t3m_00403	Product_name		transcriptional regulator, TetR family		
2572232047	t3m_00403	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232047	t3m_00403	Coordinates		27321..28010(+)		
2572232047	t3m_00403	DNA_length		690bp		
2572232047	t3m_00403	Protein_length		229aa		
2572232047	t3m_00403	GC			0.64	
2572232048	t3m_00404	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572232048	t3m_00404	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			
2572232048	t3m_00404	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2572232048	t3m_00404	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572232048	t3m_00404	Metacyc	P23-PWY: reductive TCA cycle I			
2572232048	t3m_00404	Metacyc	PWY-5392: reductive TCA cycle II			
2572232048	t3m_00404	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2572232048	t3m_00404	COG_category	[C] Energy production and conversion			
2572232048	t3m_00404	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o			6.00E-17
2572232048	t3m_00404	pfam01558	POR			4.30E-29
2572232048	t3m_00404	EC:1.2.7.3	2-oxoglutarate synthase.			

2572232048	t3m_00404	KO:K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]			1.30E-32
2572232048	t3m_00404	Locus_type		CDS		
2572232048	t3m_00404	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin ox		
2572232048	t3m_00404	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232048	t3m_00404	Coordinates		28114..28743(-)		
2572232048	t3m_00404	DNA_length		630bp		
2572232048	t3m_00404	Protein_length		209aa		
2572232048	t3m_00404	GC			0.63	
2572232049	t3m_00405	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			
2572232049	t3m_00405	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572232049	t3m_00405	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2572232049	t3m_00405	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572232049	t3m_00405	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2572232049	t3m_00405	Metacyc	P23-PWY: reductive TCA cycle I			
2572232049	t3m_00405	Metacyc	PWY-5392: reductive TCA cycle II			
2572232049	t3m_00405	COG_category	[C] Energy production and conversion			
2572232049	t3m_00405	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o			9.00E-38
2572232049	t3m_00405	pfam02775	TPP_enzyme_C			2.10E-22
2572232049	t3m_00405	EC:1.2.7.3	2-oxoglutarate synthase.			
2572232049	t3m_00405	KO:K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]			0.00E+00
2572232049	t3m_00405	Locus_type		CDS		
2572232049	t3m_00405	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin ox		
2572232049	t3m_00405	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232049	t3m_00405	Coordinates		28740..29540(-)		
2572232049	t3m_00405	DNA_length		801bp		
2572232049	t3m_00405	Protein_length		266aa		
2572232049	t3m_00405	GC			0.64	
2572232050	t3m_00406	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572232050	t3m_00406	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			
2572232050	t3m_00406	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2572232050	t3m_00406	Metacyc	P23-PWY: reductive TCA cycle I			
2572232050	t3m_00406	Metacyc	PWY-5392: reductive TCA cycle II			

2572232050	t3m_00406	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2572232050	t3m_00406	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2572232050	t3m_00406	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2572232050	t3m_00406	COG_category	[C] Energy production and conversion		
2572232050	t3m_00406	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o		6.00E-53
2572232050	t3m_00406	pfam01855	POR_N		1.70E-47
2572232050	t3m_00406	EC:1.2.7.3	2-oxoglutarate synthase.		
2572232050	t3m_00406	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]		0.00E+00
2572232050	t3m_00406	Locus_type		CDS	
2572232050	t3m_00406	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin ox	
2572232050	t3m_00406	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232050	t3m_00406	Coordinates		29537..30604(-)	
2572232050	t3m_00406	DNA_length		1068bp	
2572232050	t3m_00406	Protein_length		355aa	
2572232050	t3m_00406	GC		0.65	

2572232051	t3m_00407	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2572232051	t3m_00407	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2572232051	t3m_00407	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2572232051	t3m_00407	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2572232051	t3m_00407	Metacyc	P23-PWY: reductive TCA cycle I		
2572232051	t3m_00407	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2572232051	t3m_00407	Metacyc	PWY-5392: reductive TCA cycle II		
2572232051	t3m_00407	pfam12838	Fer4_7		1.60E-07
2572232051	t3m_00407	EC:1.2.7.3	2-oxoglutarate synthase.		
2572232051	t3m_00407	KO:K00176	2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7.3]		1.50E-14
2572232051	t3m_00407	Locus_type		CDS	
2572232051	t3m_00407	Product_name		4Fe-4S dicluster domain	
2572232051	t3m_00407	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232051	t3m_00407	Coordinates		30601..30855(-)	
2572232051	t3m_00407	DNA_length		255bp	
2572232051	t3m_00407	Protein_length		84aa	
2572232051	t3m_00407	GC		0.62	

2572232052	t3m_00408	Locus_type		CDS		
2572232052	t3m_00408	Product_name		hypothetical protein		
2572232052	t3m_00408	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232052	t3m_00408	Coordinates		31026..31745(-)		
2572232052	t3m_00408	DNA_length		720bp		
2572232052	t3m_00408	Protein_length		239aa		
2572232052	t3m_00408	GC			0.64	
2572232053	t3m_00409	COG_category	[G] Carbohydrate transport and metabolism			
2572232053	t3m_00409	COG2814	Arabinose efflux permease			3.00E-04
2572232053	t3m_00409	pfam07690	MFS_1			2.80E-25
2572232053	t3m_00409	Locus_type		CDS		
2572232053	t3m_00409	Product_name		Arabinose efflux permease		
2572232053	t3m_00409	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232053	t3m_00409	Coordinates		32154..33356(-)		
2572232053	t3m_00409	DNA_length		1203bp		
2572232053	t3m_00409	Protein_length		400aa		
2572232053	t3m_00409	GC			0.65	
2572232053	t3m_00409	Transmembrane		Yes		
2572232054	t3m_00410	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2572232054	t3m_00410	COG1335	Amidases related to nicotinamidase			2.00E-28
2572232054	t3m_00410	pfam00857	Isochorismatase			1.20E-41
2572232054	t3m_00410	Locus_type		CDS		
2572232054	t3m_00410	Product_name		Amidases related to nicotinamidase		
2572232054	t3m_00410	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232054	t3m_00410	Coordinates		33711..34307(+)		
2572232054	t3m_00410	DNA_length		597bp		
2572232054	t3m_00410	Protein_length		198aa		
2572232054	t3m_00410	GC			0.64	
2572232055	t3m_00411	pfam01136	Peptidase_U32			8.10E-19
2572232055	t3m_00411	Locus_type		CDS		
2572232055	t3m_00411	Product_name		Peptidase family U32		

2572232055	t3m_00411	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232055	t3m_00411	Coordinates		34283..35434(-)		
2572232055	t3m_00411	DNA_length		1152bp		
2572232055	t3m_00411	Protein_length		383aa		
2572232055	t3m_00411	GC			0.67	

2572232056	t3m_00412	COG_category	[E] Amino acid transport and metabolism			
2572232056	t3m_00412	COG1605	Chorismate mutase			4.00E-06
2572232056	t3m_00412	pfam01817	CM_2			2.30E-07
2572232056	t3m_00412	Locus_type		CDS		
2572232056	t3m_00412	Product_name		Chorismate mutase		
2572232056	t3m_00412	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232056	t3m_00412	Coordinates		35524..35934(+)		
2572232056	t3m_00412	DNA_length		411bp		
2572232056	t3m_00412	Protein_length		136aa		
2572232056	t3m_00412	GC			0.71	

2572232057	t3m_00413	COG_category	[R] General function prediction only			
2572232057	t3m_00413	COG3413	Predicted DNA binding protein			3.00E-14
2572232057	t3m_00413	pfam04967	HTH_10			1.20E-17
2572232057	t3m_00413	Locus_type		CDS		
2572232057	t3m_00413	Product_name		Predicted DNA binding protein		
2572232057	t3m_00413	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232057	t3m_00413	Coordinates		35985..36656(-)		
2572232057	t3m_00413	DNA_length		672bp		
2572232057	t3m_00413	Protein_length		223aa		
2572232057	t3m_00413	GC			0.71	

2572232058	t3m_00414	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232058	t3m_00414	COG1180	Pyruvate-formate lyase-activating enzyme			5.00E-68
2572232058	t3m_00414	pfam04055	Radical_SAM			3.00E-17
2572232058	t3m_00414	EC:1.97.1.4	[Formate-C-acetyltransferase]-activating enzyme.			
2572232058	t3m_00414	TIGR04337	AmmeMemoRadiSam system radical SAM enzyme			1.50E-99
2572232058	t3m_00414	KO:K04069	pyruvate formate lyase activating enzyme [EC:1.97.1.4]			0.00E+00

2572232058	t3m_00414	Locus_type		CDS	
2572232058	t3m_00414	Product_name		AmmeMemoRadiSam system radical SAM enzyme	
2572232058	t3m_00414	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232058	t3m_00414	Coordinates		36887..37954(-)	
2572232058	t3m_00414	DNA_length		1068bp	
2572232058	t3m_00414	Protein_length		355aa	
2572232058	t3m_00414	GC		0.66	
2572232059	t3m_00415	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232059	t3m_00415	COG1746	tRNA nucleotidyltransferase (CCA-adding enzyme)		2.00E-88
2572232059	t3m_00415	pfam01909	NTP_transf_2		3.80E-08
2572232059	t3m_00415	pfam09249	tRNA_NucTransf2		1.30E-33
2572232059	t3m_00415	EC:2.7.7.72	CCA tRNA nucleotidyltransferase.		
2572232059	t3m_00415	TIGR03671	CCA-adding enzyme		1.60E-117
2572232059	t3m_00415	KO:K07558	tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.72]		0.00E+00
2572232059	t3m_00415	Locus_type		CDS	
2572232059	t3m_00415	Product_name		CCA-adding enzyme	
2572232059	t3m_00415	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232059	t3m_00415	Coordinates		37992..39467(+)	
2572232059	t3m_00415	DNA_length		1476bp	
2572232059	t3m_00415	Protein_length		491aa	
2572232059	t3m_00415	GC		0.71	
2572232060	t3m_00416	Locus_type		CDS	
2572232060	t3m_00416	Product_name		hypothetical protein	
2572232060	t3m_00416	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232060	t3m_00416	Coordinates		39487..39852(-)	
2572232060	t3m_00416	DNA_length		366bp	
2572232060	t3m_00416	Protein_length		121aa	
2572232060	t3m_00416	GC		0.64	
2572232060	t3m_00416	Transmembrane		Yes	
2572232061	t3m_00417	Metacyc	PWY-6987: lipoate biosynthesis and incorporation III (Bacillus)		
2572232061	t3m_00417	Metacyc	PWY0-501: lipoate biosynthesis and incorporation I		

2572232061	t3m_00417	Metacyc	PWY0-1275: lipoate biosynthesis and incorporation II		
2572232061	t3m_00417	COG_category	[H] Coenzyme transport and metabolism		
2572232061	t3m_00417	COG0320	Lipoate synthase		7.00E-104
2572232061	t3m_00417	pfam04055	Radical_SAM		5.30E-12
2572232061	t3m_00417	EC:2.8.1.8	Lipoyl synthase.		
2572232061	t3m_00417	TIGR00510	lipoate synthase		1.40E-108
2572232061	t3m_00417	KO:K03644	lipoic acid synthetase [EC:2.8.1.8]		0.00E+00
2572232061	t3m_00417	Locus_type		CDS	
2572232061	t3m_00417	Product_name		lipoate synthase	
2572232061	t3m_00417	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232061	t3m_00417	Coordinates		39856..40770(-)	
2572232061	t3m_00417	DNA_length		915bp	
2572232061	t3m_00417	Protein_length		304aa	
2572232061	t3m_00417	GC		0.72	
2572232062	t3m_00418	COG_category	[L] Replication, recombination and repair		
2572232062	t3m_00418	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2572232062	t3m_00418	COG1474	Cdc6-related protein, AAA superfamily ATPase		7.00E-43
2572232062	t3m_00418	pfam13401	AAA_22		1.50E-10
2572232062	t3m_00418	pfam09079	Cdc6_C		6.80E-07
2572232062	t3m_00418	TIGR02928	orc1/cdc6 family replication initiation protein		9.30E-60
2572232062	t3m_00418	KO:K10725	archaeal cell division control protein 6		7.10E-41
2572232062	t3m_00418	Locus_type		CDS	
2572232062	t3m_00418	Product_name		orc1/cdc6 family replication initiation protein	
2572232062	t3m_00418	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232062	t3m_00418	Coordinates		40795..41952(-)	
2572232062	t3m_00418	DNA_length		1158bp	
2572232062	t3m_00418	Protein_length		385aa	
2572232062	t3m_00418	GC		0.68	
2572232063	t3m_00419	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP		
2572232063	t3m_00419	COG_category	[F] Nucleotide transport and metabolism		
2572232063	t3m_00419	COG0125	Thymidylate kinase		2.00E-27
2572232063	t3m_00419	pfam02223	Thymidylate_kin		8.50E-29

2572232063	t3m_00419	EC:2.7.4.9	dTMP kinase.			
2572232063	t3m_00419	TIGR00041	thymidylate kinase			5.90E-33
2572232063	t3m_00419	KO:K00943	dTMP kinase [EC:2.7.4.9]			5.30E-18
2572232063	t3m_00419	Locus_type		CDS		
2572232063	t3m_00419	Product_name		thymidylate kinase		
2572232063	t3m_00419	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232063	t3m_00419	Coordinates		41984..42616(-)		
2572232063	t3m_00419	DNA_length		633bp		
2572232063	t3m_00419	Protein_length		210aa		
2572232063	t3m_00419	GC			0.73	

2572232064	t3m_00420	COG_category	[R] General function prediction only			
2572232064	t3m_00420	COG1831	Predicted metal-dependent hydrolase (urease superfamily)			1.00E-61
2572232064	t3m_00420	pfam01026	TatD_DNase			2.10E-21
2572232064	t3m_00420	KO:K07049	TatD-related deoxyribonuclease			2.20E-42
2572232064	t3m_00420	Locus_type		CDS		
2572232064	t3m_00420	Product_name		Predicted metal-dependent hydrolase (urease superfamily)		
2572232064	t3m_00420	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232064	t3m_00420	Coordinates		42613..43488(-)		
2572232064	t3m_00420	DNA_length		876bp		
2572232064	t3m_00420	Protein_length		291aa		
2572232064	t3m_00420	GC			0.71	

2572232065	t3m_00421	COG_category	[K] Transcription			
2572232065	t3m_00421	COG2101	TATA-box binding protein (TBP), component of TFIID and TFIIIB			1.00E-67
2572232065	t3m_00421	pfam00352	TBP			1.10E-31
2572232065	t3m_00421	pfam00352	TBP			8.20E-31
2572232065	t3m_00421	KO:K03120	transcription initiation factor TFIID TATA-box-binding protein			0.00E+00
2572232065	t3m_00421	ITERM:01960	TATA binding protein of transcription factor TFIID			
2572232065	t3m_00421	Locus_type		CDS		
2572232065	t3m_00421	Product_name		TATA binding protein of transcription factor TFIID		
2572232065	t3m_00421	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232065	t3m_00421	Coordinates		43512..44060(-)		
2572232065	t3m_00421	DNA_length		549bp		

2572232065	t3m_00421	Protein_length		182aa		
2572232065	t3m_00421	GC			0.64	
2572232066	t3m_00422	Locus_type		CDS		
2572232066	t3m_00422	Product_name		hypothetical protein		
2572232066	t3m_00422	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232066	t3m_00422	Coordinates		44176..44628(-)		
2572232066	t3m_00422	DNA_length		453bp		
2572232066	t3m_00422	Protein_length		150aa		
2572232066	t3m_00422	GC			0.67	
2572232066	t3m_00422	Transmembrane		Yes		
2572232067	t3m_00423	COG_category	[F] Nucleotide transport and metabolism			
2572232067	t3m_00423	COG1051	ADP-ribose pyrophosphatase			4.00E-06
2572232067	t3m_00423	pfam00293	NUDIX			1.40E-13
2572232067	t3m_00423	Locus_type		CDS		
2572232067	t3m_00423	Product_name		ADP-ribose pyrophosphatase		
2572232067	t3m_00423	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232067	t3m_00423	Coordinates		44688..45332(-)		
2572232067	t3m_00423	DNA_length		645bp		
2572232067	t3m_00423	Protein_length		214aa		
2572232067	t3m_00423	GC			0.7	
2572232068	t3m_00424	Locus_type		CDS		
2572232068	t3m_00424	Product_name		hypothetical protein		
2572232068	t3m_00424	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232068	t3m_00424	Coordinates		45329..45529(-)		
2572232068	t3m_00424	DNA_length		201bp		
2572232068	t3m_00424	Protein_length		66aa		
2572232068	t3m_00424	GC			0.64	
2572232069	t3m_00425	COG_category	[R] General function prediction only			
2572232069	t3m_00425	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa			4.00E-20
2572232069	t3m_00425	pfam12697	Abhydrolase_6			2.30E-36

2572232069	t3m_00425	Locus_type		CDS		
2572232069	t3m_00425	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfan		
2572232069	t3m_00425	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232069	t3m_00425	Coordinates		45557..46378(-)		
2572232069	t3m_00425	DNA_length		822bp		
2572232069	t3m_00425	Protein_length		273aa		
2572232069	t3m_00425	GC			0.66	
2572232070	t3m_00426	pfam02568	ThiI			1.70E-54
2572232070	t3m_00426	TIGR00342	tRNA sulfurtransferase ThiI			3.40E-57
2572232070	t3m_00426	KO:K03151	thiamine biosynthesis protein ThiI			0.00E+00
2572232070	t3m_00426	Locus_type		CDS		
2572232070	t3m_00426	Product_name		Thiamine biosynthesis protein (ThiI)		
2572232070	t3m_00426	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232070	t3m_00426	Coordinates		46472..47098(+)		
2572232070	t3m_00426	DNA_length		627bp		
2572232070	t3m_00426	Protein_length		208aa		
2572232070	t3m_00426	GC			0.64	
2572232071	t3m_00427	pfam13248	zf-ribbon_3			2.30E-07
2572232071	t3m_00427	Locus_type		CDS		
2572232071	t3m_00427	Product_name		zinc-ribbon domain		
2572232071	t3m_00427	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232071	t3m_00427	Coordinates		47177..47749(+)		
2572232071	t3m_00427	DNA_length		573bp		
2572232071	t3m_00427	Protein_length		190aa		
2572232071	t3m_00427	GC			0.64	
2572232071	t3m_00427	Transmembrane		Yes		
2572232072	t3m_00428	Locus_type		CDS		
2572232072	t3m_00428	Product_name		hypothetical protein		
2572232072	t3m_00428	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232072	t3m_00428	Coordinates		47849..48154(+)		
2572232072	t3m_00428	DNA_length		306bp		

2572232072	t3m_00428	Protein_length		101aa		
2572232072	t3m_00428	GC			0.67	
2572232073	t3m_00429	KEGG_module	M00086: beta-Oxidation, acyl-CoA synthesis			
2572232073	t3m_00429	Metacyc	PWY-6001: linoleate biosynthesis II (animals)			
2572232073	t3m_00429	Metacyc	PWY-6944: androstenedione degradation			
2572232073	t3m_00429	Metacyc	PWY-6920: 6-gingerol analog biosynthesis			
2572232073	t3m_00429	Metacyc	PWY-7053: docosahexanoate biosynthesis I			
2572232073	t3m_00429	Metacyc	PWY-5995: linoleate biosynthesis I (plants)			
2572232073	t3m_00429	Metacyc	PWY-5885: wax esters biosynthesis II			
2572232073	t3m_00429	Metacyc	P221-PWY: octane oxidation			
2572232073	t3m_00429	Metacyc	PWY66-388: fatty acid α-oxidation III			
2572232073	t3m_00429	Metacyc	PWY-6945: cholesterol degradation to androstenedione I (cholesterol oxidase)			
2572232073	t3m_00429	Metacyc	PWY-7094: fatty acid salvage			
2572232073	t3m_00429	Metacyc	PWY66-389: phytol degradation			
2572232073	t3m_00429	Metacyc	PWY-6000: γ-linolenate biosynthesis II (animals)			
2572232073	t3m_00429	Metacyc	PWY-5353: arachidonate biosynthesis			
2572232073	t3m_00429	Metacyc	PWY-7049: eicosapentaenoate biosynthesis II (metazoa)			
2572232073	t3m_00429	Metacyc	PWY-5972: stearate biosynthesis I (animals)			
2572232073	t3m_00429	Metacyc	PWY66-391: fatty acid β-oxidation VI (peroxisome)			
2572232073	t3m_00429	Metacyc	FAO-PWY: fatty acid β-oxidation I			
2572232073	t3m_00429	Metacyc	PWY66-387: fatty acid α-oxidation II			
2572232073	t3m_00429	Metacyc	PWY-5136: fatty acid β-oxidation II (peroxisome)			
2572232073	t3m_00429	Metacyc	PWY-6946: cholesterol degradation to androstenedione II (cholesterol dehydrogenase)			
2572232073	t3m_00429	Metacyc	PWY-7033: alkane biosynthesis II			
2572232073	t3m_00429	Metacyc	PWY-7035: (<i>Z</i>)-9-tricosene biosynthesis			
2572232073	t3m_00429	Metacyc	PWY-5143: fatty acid activation			
2572232073	t3m_00429	Metacyc	PWY-6803: phosphatidylcholine acyl editing			
2572232073	t3m_00429	Metacyc	PWY-6951: docosahexanoate biosynthesis II			
2572232073	t3m_00429	Metacyc	PWY-6873: long chain fatty acid ester synthesis for microdiesel production			
2572232073	t3m_00429	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2572232073	t3m_00429	COG_category	[I] Lipid transport and metabolism			
2572232073	t3m_00429	COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II			5.00E-124
2572232073	t3m_00429	pfam13193	AMP-binding_C			1.10E-18

2572232073	t3m_00429	pfam00501	AMP-binding		1.40E-105
2572232073	t3m_00429	EC:6.2.1.3	Long-chain-fatty-acid--CoA ligase.		
2572232073	t3m_00429	KO:K01897	long-chain acyl-CoA synthetase [EC:6.2.1.3]		0.00E+00
2572232073	t3m_00429	Locus_type		CDS	
2572232073	t3m_00429	Product_name		Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	
2572232073	t3m_00429	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232073	t3m_00429	Coordinates		48162..49898(+)	
2572232073	t3m_00429	DNA_length		1737bp	
2572232073	t3m_00429	Protein_length		578aa	
2572232073	t3m_00429	GC		0.68	

2572232074	t3m_00430	COG_category	[R] General function prediction only		
2572232074	t3m_00430	COG2270	Permeases of the major facilitator superfamily		9.00E-10
2572232074	t3m_00430	pfam07690	MFS_1		3.90E-19
2572232074	t3m_00430	pfam07690	MFS_1		4.80E-16
2572232074	t3m_00430	Locus_type		CDS	
2572232074	t3m_00430	Product_name		Permeases of the major facilitator superfamily	
2572232074	t3m_00430	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232074	t3m_00430	Coordinates		49919..51100(+)	
2572232074	t3m_00430	DNA_length		1182bp	
2572232074	t3m_00430	Protein_length		393aa	
2572232074	t3m_00430	GC		0.67	
2572232074	t3m_00430	Transmembrane		Yes	

2572232075	t3m_00431	KEGG_module	M00133: Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine		
2572232075	t3m_00431	Metacyc	PWY-6305: putrescine biosynthesis IV		
2572232075	t3m_00431	Metacyc	PWY0-823: arginine degradation III (arginine decarboxylase/agmatinase pathway)		
2572232075	t3m_00431	Metacyc	PWY-40: putrescine biosynthesis I		
2572232075	t3m_00431	COG_category	[E] Amino acid transport and metabolism		
2572232075	t3m_00431	COG0010	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family		2.00E-54
2572232075	t3m_00431	pfam00491	Arginase		9.30E-77
2572232075	t3m_00431	EC:3.5.3.11	Agmatinase.		
2572232075	t3m_00431	TIGR01230	agmatinase		1.00E-75
2572232075	t3m_00431	KO:K01480	agmatinase [EC:3.5.3.11]		0.00E+00

2572232075	t3m_00431	Locus_type		CDS		
2572232075	t3m_00431	Product_name		agmatinase		
2572232075	t3m_00431	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232075	t3m_00431	Coordinates		51149..52024(+)		
2572232075	t3m_00431	DNA_length		876bp		
2572232075	t3m_00431	Protein_length		291aa		
2572232075	t3m_00431	GC			0.68	
2572232076	t3m_00432	Metacyc	PWY-5129: sphingolipid biosynthesis (plants)			
2572232076	t3m_00432	Metacyc	LIPA-CORESYN-PWY: Lipid A-core biosynthesis			
2572232076	t3m_00432	Metacyc	PWY-5107: phytol salvage pathway			
2572232076	t3m_00432	Metacyc	SPHINGOLIPID-SYN-PWY: sphingolipid biosynthesis (yeast)			
2572232076	t3m_00432	Metacyc	PWY-6577: farnesylcysteine salvage pathway			
2572232076	t3m_00432	Metacyc	PWY-7077: <i>N</i>-acetyl-D-galactosamine degradation			
2572232076	t3m_00432	Metacyc	PWY-6626: CDP-2-glycerol biosynthesis			
2572232076	t3m_00432	Metacyc	PWY-6682: dehydrophos biosynthesis			
2572232076	t3m_00432	COG_category	[T] Signal transduction mechanisms			
2572232076	t3m_00432	COG3642	Mn2+-dependent serine/threonine protein kinase			9.00E-44
2572232076	t3m_00432	EC:2.7.1.-	Transferases. Transferring phosphorous-containing groups. Phosphotransferases with an alcohol g			
2572232076	t3m_00432	TIGR03724	Kae1-associated kinase Bud32			1.30E-53
2572232076	t3m_00432	KO:K07174	Mn2+-dependent serine/threonine protein kinase [EC:2.7.1.-]			5.60E-27
2572232076	t3m_00432	Locus_type		CDS		
2572232076	t3m_00432	Product_name		Kae1-associated kinase Bud32		
2572232076	t3m_00432	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6		
2572232076	t3m_00432	Coordinates		52039..52695(+)		
2572232076	t3m_00432	DNA_length		657bp		
2572232076	t3m_00432	Protein_length		218aa		
2572232076	t3m_00432	GC			0.7	
2572232077	t3m_00433	COG_category	[G] Carbohydrate transport and metabolism			
2572232077	t3m_00433	COG0063	Predicted sugar kinase			9.00E-44
2572232077	t3m_00433	pfam03853	YjeF_N			8.50E-34
2572232077	t3m_00433	pfam01256	Carb_kinase			2.80E-40
2572232077	t3m_00433	TIGR00196	yjeF C-terminal region, hydroxyethylthiazole kinase-related			1.30E-51

2572232077	t3m_00433	TIGR00197	yjeF N-terminal region		8.90E-37
2572232077	t3m_00433	Locus_type		CDS	
2572232077	t3m_00433	Product_name		yjeF C-terminal region, hydroxyethylthiazole kinase-related/yjeF N-term	
2572232077	t3m_00433	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232077	t3m_00433	Coordinates		52711..54207(-)	
2572232077	t3m_00433	DNA_length		1497bp	
2572232077	t3m_00433	Protein_length		498aa	
2572232077	t3m_00433	GC		0.71	
2572232077	t3m_00433	Fused_gene		Yes	

2572232078	t3m_00434	TIGR00523	eukaryotic/archaeal initiation factor 1A		7.60E-13
2572232078	t3m_00434	Locus_type		CDS	
2572232078	t3m_00434	Product_name		hypothetical protein	
2572232078	t3m_00434	Scaffold		t3m_contig_70_43_len_54376_read_count_5056668.6	
2572232078	t3m_00434	Coordinates		54216..54374(-)	
2572232078	t3m_00434	DNA_length		159bp	
2572232078	t3m_00434	Protein_length		52aa	
2572232078	t3m_00434	GC		0.64	

2572232079	t3m_00435	Locus_type		CDS
2572232079	t3m_00435	Product_name		hypothetical protein
2572232079	t3m_00435	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7
2572232079	t3m_00435	Coordinates		1..324(-)
2572232079	t3m_00435	DNA_length		324bp
2572232079	t3m_00435	Protein_length		108aa
2572232079	t3m_00435	GC		0.63

2572232080	t3m_00436	Locus_type		tRNA
2572232080	t3m_00436	Product_name		tRNA_Pseudo_TGT
2572232080	t3m_00436	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7
2572232080	t3m_00436	Coordinates		492..563(+)
2572232080	t3m_00436	DNA_length		72bp
2572232080	t3m_00436	GC		0.56

2572232081	t3m_00437	Locus_type	tRNA
2572232081	t3m_00437	Product_name	tRNA_Thr_CGT
2572232081	t3m_00437	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232081	t3m_00437	Coordinates	568..638(+)
2572232081	t3m_00437	DNA_length	71bp
2572232081	t3m_00437	GC	0.65
2572232082	t3m_00438	Locus_type	tRNA
2572232082	t3m_00438	Product_name	tRNA_Pseudo_GCA
2572232082	t3m_00438	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232082	t3m_00438	Coordinates	640..710(+)
2572232082	t3m_00438	DNA_length	71bp
2572232082	t3m_00438	GC	0.68
2572232083	t3m_00439	Locus_type	tRNA
2572232083	t3m_00439	Product_name	tRNA_Thr_GGT
2572232083	t3m_00439	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232083	t3m_00439	Coordinates	718..788(+)
2572232083	t3m_00439	DNA_length	71bp
2572232083	t3m_00439	GC	0.69
2572232084	t3m_00440	Locus_type	tRNA
2572232084	t3m_00440	Product_name	tRNA_Ala_GGC
2572232084	t3m_00440	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232084	t3m_00440	Coordinates	1151..1221(-)
2572232084	t3m_00440	DNA_length	71bp
2572232084	t3m_00440	GC	0.65
2572232085	t3m_00441	Locus_type	tRNA
2572232085	t3m_00441	Product_name	tRNA_Met_CAT
2572232085	t3m_00441	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232085	t3m_00441	Coordinates	1274..1344(+)
2572232085	t3m_00441	DNA_length	71bp
2572232085	t3m_00441	GC	0.63

2572232086	t3m_00442	Locus_type	tRNA
2572232086	t3m_00442	Product_name	tRNA_Arg_TCT
2572232086	t3m_00442	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232086	t3m_00442	Coordinates	1404..1491(+)
2572232086	t3m_00442	DNA_length	88bp
2572232086	t3m_00442	GC	0.62
2572232087	t3m_00443	Locus_type	tRNA
2572232087	t3m_00443	Product_name	tRNA_Gly_GCC
2572232087	t3m_00443	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232087	t3m_00443	Coordinates	1498..1568(+)
2572232087	t3m_00443	DNA_length	71bp
2572232087	t3m_00443	GC	0.66
2572232088	t3m_00444	Locus_type	tRNA
2572232088	t3m_00444	Product_name	tRNA_Pseudo_GAT
2572232088	t3m_00444	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232088	t3m_00444	Coordinates	1583..1653(-)
2572232088	t3m_00444	DNA_length	71bp
2572232088	t3m_00444	GC	0.58
2572232089	t3m_00445	Locus_type	tRNA
2572232089	t3m_00445	Product_name	tRNA_Ile_TAT
2572232089	t3m_00445	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232089	t3m_00445	Coordinates	1741..1815(-)
2572232089	t3m_00445	DNA_length	75bp
2572232089	t3m_00445	GC	0.65
2572232090	t3m_00446	Locus_type	CDS
2572232090	t3m_00446	Product_name	hypothetical protein
2572232090	t3m_00446	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232090	t3m_00446	Coordinates	1914..2096(-)
2572232090	t3m_00446	DNA_length	183bp

2572232090	t3m_00446	Protein_length	60aa
2572232090	t3m_00446	GC	0.57
2572232091	t3m_00447	Locus_type	CDS
2572232091	t3m_00447	Product_name	hypothetical protein
2572232091	t3m_00447	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232091	t3m_00447	Coordinates	2138..2362(-)
2572232091	t3m_00447	DNA_length	225bp
2572232091	t3m_00447	Protein_length	74aa
2572232091	t3m_00447	GC	0.63
2572232092	t3m_00448	Locus_type	tRNA
2572232092	t3m_00448	Product_name	tRNA_Lys_TTT
2572232092	t3m_00448	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232092	t3m_00448	Coordinates	2475..2547(-)
2572232092	t3m_00448	DNA_length	73bp
2572232092	t3m_00448	GC	0.6
2572232093	t3m_00449	Locus_type	tRNA
2572232093	t3m_00449	Product_name	tRNA_Glu_TTC
2572232093	t3m_00449	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232093	t3m_00449	Coordinates	2557..2629(-)
2572232093	t3m_00449	DNA_length	73bp
2572232093	t3m_00449	GC	0.62
2572232094	t3m_00450	Locus_type	tRNA
2572232094	t3m_00450	Product_name	tRNA_Asp_GTC
2572232094	t3m_00450	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232094	t3m_00450	Coordinates	2818..2888(-)
2572232094	t3m_00450	DNA_length	71bp
2572232094	t3m_00450	GC	0.66
2572232095	t3m_00451	Locus_type	tRNA
2572232095	t3m_00451	Product_name	tRNA_Glu_CTC

2572232095	t3m_00451	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232095	t3m_00451	Coordinates	2895..2968(-)
2572232095	t3m_00451	DNA_length	74bp
2572232095	t3m_00451	GC	0.66
2572232096	t3m_00452	Locus_type	tRNA
2572232096	t3m_00452	Product_name	tRNA_Pseudo_GTA
2572232096	t3m_00452	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232096	t3m_00452	Coordinates	3023..3093(-)
2572232096	t3m_00452	DNA_length	71bp
2572232096	t3m_00452	GC	0.68
2572232097	t3m_00453	Locus_type	tRNA
2572232097	t3m_00453	Product_name	tRNA_Lys_CTT
2572232097	t3m_00453	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232097	t3m_00453	Coordinates	3122..3194(-)
2572232097	t3m_00453	DNA_length	73bp
2572232097	t3m_00453	GC	0.66
2572232098	t3m_00454	Locus_type	tRNA
2572232098	t3m_00454	Product_name	tRNA_Ala_CGC
2572232098	t3m_00454	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232098	t3m_00454	Coordinates	3451..3523(+)
2572232098	t3m_00454	DNA_length	73bp
2572232098	t3m_00454	GC	0.63
2572232099	t3m_00455	Locus_type	tRNA
2572232099	t3m_00455	Product_name	tRNA_Gly_TCC
2572232099	t3m_00455	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232099	t3m_00455	Coordinates	3620..3692(+)
2572232099	t3m_00455	DNA_length	73bp
2572232099	t3m_00455	GC	0.67
2572232100	t3m_00456	Locus_type	tRNA

2572232100	t3m_00456	Product_name	tRNA_Pseudo_CGA
2572232100	t3m_00456	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232100	t3m_00456	Coordinates	3866..3951(+)
2572232100	t3m_00456	DNA_length	86bp
2572232100	t3m_00456	GC	0.58

2572232101	t3m_00457	Locus_type	tRNA
2572232101	t3m_00457	Product_name	tRNA_Trp_CCA
2572232101	t3m_00457	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232101	t3m_00457	Coordinates	3967..4041(+)
2572232101	t3m_00457	DNA_length	75bp
2572232101	t3m_00457	GC	0.65

2572232102	t3m_00458	Locus_type	tRNA
2572232102	t3m_00458	Product_name	tRNA_Pro_TGG
2572232102	t3m_00458	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232102	t3m_00458	Coordinates	4055..4127(+)
2572232102	t3m_00458	DNA_length	73bp
2572232102	t3m_00458	GC	0.66

2572232103	t3m_00459	Locus_type	tRNA
2572232103	t3m_00459	Product_name	tRNA_Leu_TAG
2572232103	t3m_00459	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232103	t3m_00459	Coordinates	4811..4894(+)
2572232103	t3m_00459	DNA_length	84bp
2572232103	t3m_00459	GC	0.65

2572232104	t3m_00460	Locus_type	tRNA
2572232104	t3m_00460	Product_name	tRNA_Arg_GCG
2572232104	t3m_00460	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232104	t3m_00460	Coordinates	4902..4976(+)
2572232104	t3m_00460	DNA_length	75bp
2572232104	t3m_00460	GC	0.64

2572232105	t3m_00461	Locus_type	tRNA
2572232105	t3m_00461	Product_name	tRNA_Arg_TCG
2572232105	t3m_00461	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232105	t3m_00461	Coordinates	4989..5064(+)
2572232105	t3m_00461	DNA_length	76bp
2572232105	t3m_00461	GC	0.67
2572232106	t3m_00462	Locus_type	tRNA
2572232106	t3m_00462	Product_name	tRNA_Pseudo_CAA
2572232106	t3m_00462	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232106	t3m_00462	Coordinates	5068..5150(+)
2572232106	t3m_00462	DNA_length	83bp
2572232106	t3m_00462	GC	0.72
2572232107	t3m_00463	Locus_type	tRNA
2572232107	t3m_00463	Product_name	tRNA_Ser_GCT
2572232107	t3m_00463	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232107	t3m_00463	Coordinates	5161..5245(+)
2572232107	t3m_00463	DNA_length	85bp
2572232107	t3m_00463	GC	0.68
2572232108	t3m_00464	Locus_type	tRNA
2572232108	t3m_00464	Product_name	tRNA_His_GTG
2572232108	t3m_00464	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232108	t3m_00464	Coordinates	5257..5327(-)
2572232108	t3m_00464	DNA_length	71bp
2572232108	t3m_00464	GC	0.69
2572232109	t3m_00465	Locus_type	tRNA
2572232109	t3m_00465	Product_name	tRNA_Gln_TTG
2572232109	t3m_00465	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232109	t3m_00465	Coordinates	5330..5402(-)
2572232109	t3m_00465	DNA_length	73bp
2572232109	t3m_00465	GC	0.59

2572232110	t3m_00466	Locus_type	CDS
2572232110	t3m_00466	Product_name	hypothetical protein
2572232110	t3m_00466	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232110	t3m_00466	Coordinates	5573..5776(-)
2572232110	t3m_00466	DNA_length	204bp
2572232110	t3m_00466	Protein_length	67aa
2572232110	t3m_00466	GC	0.62
2572232111	t3m_00467	Locus_type	CDS
2572232111	t3m_00467	Product_name	hypothetical protein
2572232111	t3m_00467	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232111	t3m_00467	Coordinates	5962..6162(-)
2572232111	t3m_00467	DNA_length	201bp
2572232111	t3m_00467	Protein_length	66aa
2572232111	t3m_00467	GC	0.62
2572232112	t3m_00468	Locus_type	CDS
2572232112	t3m_00468	Product_name	hypothetical protein
2572232112	t3m_00468	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232112	t3m_00468	Coordinates	6170..6589(-)
2572232112	t3m_00468	DNA_length	420bp
2572232112	t3m_00468	Protein_length	139aa
2572232112	t3m_00468	GC	0.66
2572232113	t3m_00469	Locus_type	CDS
2572232113	t3m_00469	Product_name	hypothetical protein
2572232113	t3m_00469	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232113	t3m_00469	Coordinates	6590..6883(-)
2572232113	t3m_00469	DNA_length	294bp
2572232113	t3m_00469	Protein_length	97aa
2572232113	t3m_00469	GC	0.66
2572232114	t3m_00470	Locus_type	CDS

2572232114	t3m_00470	Product_name		hypothetical protein		
2572232114	t3m_00470	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232114	t3m_00470	Coordinates		6884..7501(-)		
2572232114	t3m_00470	DNA_length		618bp		
2572232114	t3m_00470	Protein_length		205aa		
2572232114	t3m_00470	GC			0.65	
2572232115	t3m_00471	pfam00005	ABC_tran			6.00E-10
2572232115	t3m_00471	Locus_type		CDS		
2572232115	t3m_00471	Product_name		ABC transporter		
2572232115	t3m_00471	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232115	t3m_00471	Coordinates		7495..9384(-)		
2572232115	t3m_00471	DNA_length		1890bp		
2572232115	t3m_00471	Protein_length		629aa		
2572232115	t3m_00471	GC			0.65	
2572232116	t3m_00472	Locus_type		CDS		
2572232116	t3m_00472	Product_name		hypothetical protein		
2572232116	t3m_00472	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232116	t3m_00472	Coordinates		9387..10202(-)		
2572232116	t3m_00472	DNA_length		816bp		
2572232116	t3m_00472	Protein_length		271aa		
2572232116	t3m_00472	GC			0.65	
2572232117	t3m_00473	COG_category	[L] Replication, recombination and repair			
2572232117	t3m_00473	COG0417	DNA polymerase elongation subunit (family B)			1.00E-61
2572232117	t3m_00473	pfam00136	DNA_pol_B			6.40E-22
2572232117	t3m_00473	pfam03104	DNA_pol_B_exo1			2.80E-11
2572232117	t3m_00473	EC:2.7.7.7	DNA-directed DNA polymerase.			
2572232117	t3m_00473	KO:K02319	DNA polymerase I [EC:2.7.7.7]			0.00E+00
2572232117	t3m_00473	Locus_type		CDS		
2572232117	t3m_00473	Product_name		DNA polymerase elongation subunit (family B)		
2572232117	t3m_00473	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232117	t3m_00473	Coordinates		10196..12832(-)		

2572232117	t3m_00473	DNA_length		2637bp		
2572232117	t3m_00473	Protein_length		878aa		
2572232117	t3m_00473	GC			0.65	
2572232118	t3m_00474	COG_category	[L] Replication, recombination and repair			
2572232118	t3m_00474	COG0863	DNA modification methylase			4.00E-22
2572232118	t3m_00474	pfam01555	N6_N4_Mtase			4.90E-36
2572232118	t3m_00474	Locus_type		CDS		
2572232118	t3m_00474	Product_name		DNA modification methylase		
2572232118	t3m_00474	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232118	t3m_00474	Coordinates		12826..13743(-)		
2572232118	t3m_00474	DNA_length		918bp		
2572232118	t3m_00474	Protein_length		305aa		
2572232118	t3m_00474	GC			0.65	
2572232119	t3m_00475	COG_category	[S] Function unknown			
2572232119	t3m_00475	COG4333	Uncharacterized protein conserved in bacteria			9.00E-38
2572232119	t3m_00475	pfam07799	DUF1643			9.80E-45
2572232119	t3m_00475	Locus_type		CDS		
2572232119	t3m_00475	Product_name		Uncharacterized protein conserved in bacteria		
2572232119	t3m_00475	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232119	t3m_00475	Coordinates		13740..14264(-)		
2572232119	t3m_00475	DNA_length		525bp		
2572232119	t3m_00475	Protein_length		174aa		
2572232119	t3m_00475	GC			0.63	
2572232120	t3m_00476	Locus_type		CDS		
2572232120	t3m_00476	Product_name		hypothetical protein		
2572232120	t3m_00476	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232120	t3m_00476	Coordinates		14257..14547(-)		
2572232120	t3m_00476	DNA_length		291bp		
2572232120	t3m_00476	Protein_length		96aa		
2572232120	t3m_00476	GC			0.6	

2572232121	t3m_00477	Locus_type		CDS	
2572232121	t3m_00477	Product_name		hypothetical protein	
2572232121	t3m_00477	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232121	t3m_00477	Coordinates		14544..14669(-)	
2572232121	t3m_00477	DNA_length		126bp	
2572232121	t3m_00477	Protein_length		41aa	
2572232121	t3m_00477	GC		0.6	
2572232122	t3m_00478	Locus_type		CDS	
2572232122	t3m_00478	Product_name		hypothetical protein	
2572232122	t3m_00478	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232122	t3m_00478	Coordinates		14666..14818(-)	
2572232122	t3m_00478	DNA_length		153bp	
2572232122	t3m_00478	Protein_length		50aa	
2572232122	t3m_00478	GC		0.58	
2572232123	t3m_00479	pfam00004	AAA		2.40E-16
2572232123	t3m_00479	KO:K04801	replication factor C small subunit		0.00E+00
2572232123	t3m_00479	ITERM:00096	replication factor C small subunit		
2572232123	t3m_00479	Locus_type		CDS	
2572232123	t3m_00479	Product_name		replication factor C small subunit	
2572232123	t3m_00479	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232123	t3m_00479	Coordinates		14832..15761(-)	
2572232123	t3m_00479	DNA_length		930bp	
2572232123	t3m_00479	Protein_length		309aa	
2572232123	t3m_00479	GC		0.65	
2572232124	t3m_00480	Locus_type		CDS	
2572232124	t3m_00480	Product_name		hypothetical protein	
2572232124	t3m_00480	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232124	t3m_00480	Coordinates		15904..16116(-)	
2572232124	t3m_00480	DNA_length		213bp	
2572232124	t3m_00480	Protein_length		70aa	
2572232124	t3m_00480	GC		0.57	

2572232125	t3m_00481	Locus_type		CDS	
2572232125	t3m_00481	Product_name		hypothetical protein	
2572232125	t3m_00481	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232125	t3m_00481	Coordinates		16106..16288(-)	
2572232125	t3m_00481	DNA_length		183bp	
2572232125	t3m_00481	Protein_length		60aa	
2572232125	t3m_00481	GC		0.67	
2572232126	t3m_00482	Locus_type		CDS	
2572232126	t3m_00482	Product_name		hypothetical protein	
2572232126	t3m_00482	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232126	t3m_00482	Coordinates		16279..16425(-)	
2572232126	t3m_00482	DNA_length		147bp	
2572232126	t3m_00482	Protein_length		48aa	
2572232126	t3m_00482	GC		0.66	
2572232127	t3m_00483	Locus_type		CDS	
2572232127	t3m_00483	Product_name		hypothetical protein	
2572232127	t3m_00483	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232127	t3m_00483	Coordinates		16422..17630(-)	
2572232127	t3m_00483	DNA_length		1209bp	
2572232127	t3m_00483	Protein_length		402aa	
2572232127	t3m_00483	GC		0.64	
2572232128	t3m_00484	Locus_type		CDS	
2572232128	t3m_00484	Product_name		hypothetical protein	
2572232128	t3m_00484	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232128	t3m_00484	Coordinates		17647..18591(-)	
2572232128	t3m_00484	DNA_length		945bp	
2572232128	t3m_00484	Protein_length		314aa	
2572232128	t3m_00484	GC		0.67	
2572232129	t3m_00485	pfam03837	RecT		1.60E-18

2572232129	t3m_00485	TIGR01913	phage recombination protein Bet			6.70E-22
2572232129	t3m_00485	Locus_type		CDS		
2572232129	t3m_00485	Product_name		RecT family		
2572232129	t3m_00485	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232129	t3m_00485	Coordinates		18588..19547(-)		
2572232129	t3m_00485	DNA_length		960bp		
2572232129	t3m_00485	Protein_length		319aa		
2572232129	t3m_00485	GC			0.67	
2572232130	t3m_00486	Locus_type		CDS		
2572232130	t3m_00486	Product_name		hypothetical protein		
2572232130	t3m_00486	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232130	t3m_00486	Coordinates		19552..20691(-)		
2572232130	t3m_00486	DNA_length		1140bp		
2572232130	t3m_00486	Protein_length		379aa		
2572232130	t3m_00486	GC			0.66	
2572232131	t3m_00487	Locus_type		CDS		
2572232131	t3m_00487	Product_name		hypothetical protein		
2572232131	t3m_00487	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232131	t3m_00487	Coordinates		20722..20889(-)		
2572232131	t3m_00487	DNA_length		168bp		
2572232131	t3m_00487	Protein_length		55aa		
2572232131	t3m_00487	GC			0.57	
2572232131	t3m_00487	Transmembrane		Yes		
2572232132	t3m_00488	Locus_type		CDS		
2572232132	t3m_00488	Product_name		hypothetical protein		
2572232132	t3m_00488	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232132	t3m_00488	Coordinates		21043..21339(+)		
2572232132	t3m_00488	DNA_length		297bp		
2572232132	t3m_00488	Protein_length		98aa		
2572232132	t3m_00488	GC			0.61	

2572232133	t3m_00489	Locus_type		CDS	
2572232133	t3m_00489	Product_name		hypothetical protein	
2572232133	t3m_00489	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232133	t3m_00489	Coordinates		21336..22733(-)	
2572232133	t3m_00489	DNA_length		1398bp	
2572232133	t3m_00489	Protein_length		465aa	
2572232133	t3m_00489	GC		0.66	
2572232134	t3m_00490	Locus_type		CDS	
2572232134	t3m_00490	Product_name		hypothetical protein	
2572232134	t3m_00490	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232134	t3m_00490	Coordinates		22735..23385(-)	
2572232134	t3m_00490	DNA_length		651bp	
2572232134	t3m_00490	Protein_length		216aa	
2572232134	t3m_00490	GC		0.66	
2572232135	t3m_00491	pfam00271	Helicase_C		7.00E-10
2572232135	t3m_00491	pfam00176	SNF2_N		2.00E-16
2572232135	t3m_00491	Locus_type		CDS	
2572232135	t3m_00491	Product_name		Helicase conserved C-terminal domain/SNF2 family N-terminal domain	
2572232135	t3m_00491	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232135	t3m_00491	Coordinates		23458..25407(-)	
2572232135	t3m_00491	DNA_length		1950bp	
2572232135	t3m_00491	Protein_length		649aa	
2572232135	t3m_00491	GC		0.66	
2572232136	t3m_00492	Locus_type		CDS	
2572232136	t3m_00492	Product_name		hypothetical protein	
2572232136	t3m_00492	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232136	t3m_00492	Coordinates		25556..26455(-)	
2572232136	t3m_00492	DNA_length		900bp	
2572232136	t3m_00492	Protein_length		299aa	
2572232136	t3m_00492	GC		0.64	

2572232137	t3m_00493	Locus_type	CDS	
2572232137	t3m_00493	Product_name	hypothetical protein	
2572232137	t3m_00493	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232137	t3m_00493	Coordinates	26551..26850(-)	
2572232137	t3m_00493	DNA_length	300bp	
2572232137	t3m_00493	Protein_length	99aa	
2572232137	t3m_00493	GC		0.67

2572232138	t3m_00494	Locus_type	CDS	
2572232138	t3m_00494	Product_name	hypothetical protein	
2572232138	t3m_00494	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232138	t3m_00494	Coordinates	26969..27604(-)	
2572232138	t3m_00494	DNA_length	636bp	
2572232138	t3m_00494	Protein_length	211aa	
2572232138	t3m_00494	GC		0.63

2572232139	t3m_00495	Locus_type	CDS	
2572232139	t3m_00495	Product_name	hypothetical protein	
2572232139	t3m_00495	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232139	t3m_00495	Coordinates	27633..27797(-)	
2572232139	t3m_00495	DNA_length	165bp	
2572232139	t3m_00495	Protein_length	54aa	
2572232139	t3m_00495	GC		0.61

2572232140	t3m_00496	Locus_type	CDS	
2572232140	t3m_00496	Product_name	hypothetical protein	
2572232140	t3m_00496	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232140	t3m_00496	Coordinates	28225..28380(+)	
2572232140	t3m_00496	DNA_length	156bp	
2572232140	t3m_00496	Protein_length	51aa	
2572232140	t3m_00496	GC		0.62
2572232140	t3m_00496	Transmembrane	Yes	

2572232141	t3m_00497	COG_category	[M] Cell wall/membrane/envelope biogenesis	

2572232141	t3m_00497	COG0438	Glycosyltransferase			3.00E-24
2572232141	t3m_00497	pfam13579	Glyco_trans_4_4			3.10E-22
2572232141	t3m_00497	pfam00534	Glycos_transf_1			4.90E-23
2572232141	t3m_00497	Locus_type		CDS		
2572232141	t3m_00497	Product_name		Glycosyltransferase		
2572232141	t3m_00497	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232141	t3m_00497	Coordinates		28377..29489(+)		
2572232141	t3m_00497	DNA_length		1113bp		
2572232141	t3m_00497	Protein_length		370aa		
2572232141	t3m_00497	GC			0.64	

2572232142	t3m_00498	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232142	t3m_00498	COG0438	Glycosyltransferase			3.00E-33
2572232142	t3m_00498	pfam00534	Glycos_transf_1			1.40E-19
2572232142	t3m_00498	pfam13579	Glyco_trans_4_4			4.70E-13
2572232142	t3m_00498	Locus_type		CDS		
2572232142	t3m_00498	Product_name		Glycosyltransferase		
2572232142	t3m_00498	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232142	t3m_00498	Coordinates		29486..30661(+)		
2572232142	t3m_00498	DNA_length		1176bp		
2572232142	t3m_00498	Protein_length		391aa		
2572232142	t3m_00498	GC			0.66	

2572232143	t3m_00499	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232143	t3m_00499	COG_category	[G] Carbohydrate transport and metabolism			
2572232143	t3m_00499	COG0451	Nucleoside-diphosphate-sugar epimerases			3.00E-29
2572232143	t3m_00499	pfam01370	Epimerase			1.60E-31
2572232143	t3m_00499	Locus_type		CDS		
2572232143	t3m_00499	Product_name		Nucleoside-diphosphate-sugar epimerases		
2572232143	t3m_00499	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232143	t3m_00499	Coordinates		30636..31598(-)		
2572232143	t3m_00499	DNA_length		963bp		
2572232143	t3m_00499	Protein_length		320aa		
2572232143	t3m_00499	GC			0.66	

2572232144	t3m_00500	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232144	t3m_00500	COG0438	Glycosyltransferase			1.00E-31
2572232144	t3m_00500	pfam13579	Glyco_trans_4_4			2.00E-07
2572232144	t3m_00500	pfam00534	Glycos_transf_1			2.10E-33
2572232144	t3m_00500	Locus_type		CDS		
2572232144	t3m_00500	Product_name		Glycosyltransferase		
2572232144	t3m_00500	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232144	t3m_00500	Coordinates		31595..32731(-)		
2572232144	t3m_00500	DNA_length		1137bp		
2572232144	t3m_00500	Protein_length		378aa		
2572232144	t3m_00500	GC			0.65	

2572232145	t3m_00501	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232145	t3m_00501	COG0438	Glycosyltransferase			2.00E-22
2572232145	t3m_00501	pfam13692	Glyco_trans_1_4			8.10E-11
2572232145	t3m_00501	pfam13439	Glyco_transf_4			2.60E-14
2572232145	t3m_00501	Locus_type		CDS		
2572232145	t3m_00501	Product_name		Glycosyltransferase		
2572232145	t3m_00501	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232145	t3m_00501	Coordinates		32820..33851(-)		
2572232145	t3m_00501	DNA_length		1032bp		
2572232145	t3m_00501	Protein_length		343aa		
2572232145	t3m_00501	GC			0.66	

2572232146	t3m_00502	pfam00535	Glycos_transf_2			7.70E-13
2572232146	t3m_00502	Locus_type		CDS		
2572232146	t3m_00502	Product_name		Glycosyl transferase family 2		
2572232146	t3m_00502	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232146	t3m_00502	Coordinates		33848..34780(-)		
2572232146	t3m_00502	DNA_length		933bp		
2572232146	t3m_00502	Protein_length		310aa		
2572232146	t3m_00502	GC			0.64	

2572232147	t3m_00503	pfam13578	Methyltransf_24			1.30E-10
2572232147	t3m_00503	Locus_type		CDS		
2572232147	t3m_00503	Product_name		Methyltransferase domain		
2572232147	t3m_00503	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232147	t3m_00503	Coordinates		34777..35508(-)		
2572232147	t3m_00503	DNA_length		732bp		
2572232147	t3m_00503	Protein_length		243aa		
2572232147	t3m_00503	GC			0.65	
2572232148	t3m_00504	Locus_type		CDS		
2572232148	t3m_00504	Product_name		hypothetical protein		
2572232148	t3m_00504	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232148	t3m_00504	Coordinates		35526..35675(-)		
2572232148	t3m_00504	DNA_length		150bp		
2572232148	t3m_00504	Protein_length		49aa		
2572232148	t3m_00504	GC			0.59	
2572232149	t3m_00505	Locus_type		CDS		
2572232149	t3m_00505	Product_name		hypothetical protein		
2572232149	t3m_00505	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232149	t3m_00505	Coordinates		35675..36070(-)		
2572232149	t3m_00505	DNA_length		396bp		
2572232149	t3m_00505	Protein_length		131aa		
2572232149	t3m_00505	GC			0.65	
2572232150	t3m_00506	Locus_type		CDS		
2572232150	t3m_00506	Product_name		hypothetical protein		
2572232150	t3m_00506	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232150	t3m_00506	Coordinates		36303..36548(-)		
2572232150	t3m_00506	DNA_length		246bp		
2572232150	t3m_00506	Protein_length		81aa		
2572232150	t3m_00506	GC			0.67	
2572232151	t3m_00507	Locus_type		CDS		

2572232151	t3m_00507	Product_name	hypothetical protein
2572232151	t3m_00507	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232151	t3m_00507	Coordinates	36706..36894(-)
2572232151	t3m_00507	DNA_length	189bp
2572232151	t3m_00507	Protein_length	62aa
2572232151	t3m_00507	GC	0.6

2572232152	t3m_00508	Locus_type	CDS
2572232152	t3m_00508	Product_name	hypothetical protein
2572232152	t3m_00508	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232152	t3m_00508	Coordinates	36891..37043(-)
2572232152	t3m_00508	DNA_length	153bp
2572232152	t3m_00508	Protein_length	50aa
2572232152	t3m_00508	GC	0.63

2572232153	t3m_00509	Locus_type	CDS
2572232153	t3m_00509	Product_name	hypothetical protein
2572232153	t3m_00509	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232153	t3m_00509	Coordinates	37040..37378(-)
2572232153	t3m_00509	DNA_length	339bp
2572232153	t3m_00509	Protein_length	112aa
2572232153	t3m_00509	GC	0.65

2572232154	t3m_00510	Locus_type	CDS
2572232154	t3m_00510	Product_name	hypothetical protein
2572232154	t3m_00510	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7
2572232154	t3m_00510	Coordinates	37375..37800(-)
2572232154	t3m_00510	DNA_length	426bp
2572232154	t3m_00510	Protein_length	141aa
2572232154	t3m_00510	GC	0.62
2572232154	t3m_00510	Transmembrane	Yes

2572232155	t3m_00511	Locus_type	CDS
2572232155	t3m_00511	Product_name	hypothetical protein

2572232155	t3m_00511	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232155	t3m_00511	Coordinates	37797..38546(-)	
2572232155	t3m_00511	DNA_length	750bp	
2572232155	t3m_00511	Protein_length	249aa	
2572232155	t3m_00511	GC		0.63
2572232155	t3m_00511	Transmembrane	Yes	
2572232156	t3m_00512	Locus_type	CDS	
2572232156	t3m_00512	Product_name	hypothetical protein	
2572232156	t3m_00512	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232156	t3m_00512	Coordinates	38676..39038(-)	
2572232156	t3m_00512	DNA_length	363bp	
2572232156	t3m_00512	Protein_length	120aa	
2572232156	t3m_00512	GC		0.65
2572232156	t3m_00512	Transmembrane	Yes	
2572232157	t3m_00513	Locus_type	CDS	
2572232157	t3m_00513	Product_name	hypothetical protein	
2572232157	t3m_00513	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232157	t3m_00513	Coordinates	39045..39407(-)	
2572232157	t3m_00513	DNA_length	363bp	
2572232157	t3m_00513	Protein_length	120aa	
2572232157	t3m_00513	GC		0.61
2572232157	t3m_00513	Transmembrane	Yes	
2572232158	t3m_00514	Locus_type	CDS	
2572232158	t3m_00514	Product_name	hypothetical protein	
2572232158	t3m_00514	Scaffold	t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232158	t3m_00514	Coordinates	39404..39574(-)	
2572232158	t3m_00514	DNA_length	171bp	
2572232158	t3m_00514	Protein_length	56aa	
2572232158	t3m_00514	GC		0.65
2572232158	t3m_00514	Transmembrane	Yes	

2572232159	t3m_00515	Locus_type		CDS	
2572232159	t3m_00515	Product_name		hypothetical protein	
2572232159	t3m_00515	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232159	t3m_00515	Coordinates		39643..40419(-)	
2572232159	t3m_00515	DNA_length		777bp	
2572232159	t3m_00515	Protein_length		258aa	
2572232159	t3m_00515	GC		0.6	
2572232159	t3m_00515	Transmembrane		Yes	
2572232160	t3m_00516	Locus_type		CDS	
2572232160	t3m_00516	Product_name		hypothetical protein	
2572232160	t3m_00516	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232160	t3m_00516	Coordinates		40425..41834(-)	
2572232160	t3m_00516	DNA_length		1410bp	
2572232160	t3m_00516	Protein_length		469aa	
2572232160	t3m_00516	GC		0.61	
2572232160	t3m_00516	Transmembrane		Yes	
2572232161	t3m_00517	Locus_type		CDS	
2572232161	t3m_00517	Product_name		hypothetical protein	
2572232161	t3m_00517	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232161	t3m_00517	Coordinates		41831..45124(-)	
2572232161	t3m_00517	DNA_length		3294bp	
2572232161	t3m_00517	Protein_length		1097aa	
2572232161	t3m_00517	GC		0.59	
2572232161	t3m_00517	Transmembrane		Yes	
2572232162	t3m_00518	pfam00041	fn3		8.60E-12
2572232162	t3m_00518	Locus_type		CDS	
2572232162	t3m_00518	Product_name		Fibronectin type III domain	
2572232162	t3m_00518	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7	
2572232162	t3m_00518	Coordinates		45121..48402(-)	
2572232162	t3m_00518	DNA_length		3282bp	
2572232162	t3m_00518	Protein_length		1093aa	

2572232162	t3m_00518	GC			0.62	
2572232162	t3m_00518	Transmembrane		Yes		
2572232163	t3m_00519	Locus_type		CDS		
2572232163	t3m_00519	Product_name		hypothetical protein		
2572232163	t3m_00519	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232163	t3m_00519	Coordinates		48477..49019(-)		
2572232163	t3m_00519	DNA_length		543bp		
2572232163	t3m_00519	Protein_length		180aa		
2572232163	t3m_00519	GC			0.66	
2572232164	t3m_00520	Locus_type		CDS		
2572232164	t3m_00520	Product_name		hypothetical protein		
2572232164	t3m_00520	Scaffold		t3m_contig_70_54_len_49701_read_count_4695079.7		
2572232164	t3m_00520	Coordinates		49091..49681(-)		
2572232164	t3m_00520	DNA_length		591bp		
2572232164	t3m_00520	Protein_length		196aa		
2572232164	t3m_00520	GC			0.62	
2572232164	t3m_00520	Transmembrane		Yes		
2572232165	t3m_00521	pfam01496	V_ATPase_I			4.50E-13
2572232165	t3m_00521	Locus_type		CDS		
2572232165	t3m_00521	Product_name		V-type ATPase 116kDa subunit family		
2572232165	t3m_00521	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232165	t3m_00521	Coordinates		2..952(-)		
2572232165	t3m_00521	DNA_length		951bp		
2572232165	t3m_00521	Protein_length		317aa		
2572232165	t3m_00521	GC			0.71	
2572232166	t3m_00522	Locus_type		CDS		
2572232166	t3m_00522	Product_name		hypothetical protein		
2572232166	t3m_00522	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232166	t3m_00522	Coordinates		983..1342(-)		
2572232166	t3m_00522	DNA_length		360bp		

2572232166	t3m_00522	Protein_length		119aa		
2572232166	t3m_00522	GC			0.74	
2572232167	t3m_00523	Locus_type		CDS		
2572232167	t3m_00523	Product_name		hypothetical protein		
2572232167	t3m_00523	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232167	t3m_00523	Coordinates		1345..1470(-)		
2572232167	t3m_00523	DNA_length		126bp		
2572232167	t3m_00523	Protein_length		41aa		
2572232167	t3m_00523	GC			0.68	
2572232167	t3m_00523	Transmembrane		Yes		
2572232168	t3m_00524	KEGG_module	M00159: V-type ATPase, prokaryotes			
2572232168	t3m_00524	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2572232168	t3m_00524	COG_category	[C] Energy production and conversion			
2572232168	t3m_00524	COG1394	Archaeal/vacuolar-type H+-ATPase subunit D			2.00E-39
2572232168	t3m_00524	pfam01813	ATP-synt_D			3.30E-48
2572232168	t3m_00524	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2572232168	t3m_00524	TIGR00309	H(+)-transporting ATP synthase, vacuolar type, subunit D			2.10E-47
2572232168	t3m_00524	KO:K02120	V-type H+-transporting ATPase subunit D [EC:3.6.3.14]			1.40E-45
2572232168	t3m_00524	Locus_type		CDS		
2572232168	t3m_00524	Product_name		H(+)-transporting ATP synthase, vacuolar type, subunit D		
2572232168	t3m_00524	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232168	t3m_00524	Coordinates		1454..2098(-)		
2572232168	t3m_00524	DNA_length		645bp		
2572232168	t3m_00524	Protein_length		214aa		
2572232168	t3m_00524	GC			0.66	
2572232169	t3m_00525	KEGG_module	M00159: V-type ATPase, prokaryotes			
2572232169	t3m_00525	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2572232169	t3m_00525	COG_category	[C] Energy production and conversion			
2572232169	t3m_00525	COG1156	Archaeal/vacuolar-type H+-ATPase subunit B			0.00E+00
2572232169	t3m_00525	pfam00306	ATP-synt_ab_C			6.00E-14
2572232169	t3m_00525	pfam02874	ATP-synt_ab_N			6.20E-08

2572232169	t3m_00525	pfam00006	ATP-synt_ab			1.70E-59
2572232169	t3m_00525	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2572232169	t3m_00525	TIGR01041	ATP synthase archaeal, B subunit			0.00E+00
2572232169	t3m_00525	KO:K02118	V-type H+-transporting ATPase subunit B [EC:3.6.3.14]			0.00E+00
2572232169	t3m_00525	Locus_type		CDS		
2572232169	t3m_00525	Product_name		Archaeal/vacuolar-type H+-ATPase subunit B		
2572232169	t3m_00525	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232169	t3m_00525	Coordinates		2116..3546(-)		
2572232169	t3m_00525	DNA_length		1431bp		
2572232169	t3m_00525	Protein_length		476aa		
2572232169	t3m_00525	GC			0.68	
2572232170	t3m_00526	KEGG_module	M00159: V-type ATPase, prokaryotes			
2572232170	t3m_00526	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2572232170	t3m_00526	COG_category	[C] Energy production and conversion			
2572232170	t3m_00526	COG1155	Archaeal/vacuolar-type H+-ATPase subunit A			0.00E+00
2572232170	t3m_00526	pfam00006	ATP-synt_ab			1.00E-96
2572232170	t3m_00526	pfam00306	ATP-synt_ab_C			1.20E-17
2572232170	t3m_00526	pfam02874	ATP-synt_ab_N			9.50E-12
2572232170	t3m_00526	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2572232170	t3m_00526	KO:K02117	V-type H+-transporting ATPase subunit A [EC:3.6.3.14]			0.00E+00
2572232170	t3m_00526	Locus_type		CDS		
2572232170	t3m_00526	Product_name		Archaeal/vacuolar-type H+-ATPase subunit A		
2572232170	t3m_00526	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232170	t3m_00526	Coordinates		3546..5309(-)		
2572232170	t3m_00526	DNA_length		1764bp		
2572232170	t3m_00526	Protein_length		587aa		
2572232170	t3m_00526	GC			0.67	
2572232171	t3m_00527	COG_category	[C] Energy production and conversion			
2572232171	t3m_00527	COG1436	Archaeal/vacuolar-type H+-ATPase subunit F			4.00E-08
2572232171	t3m_00527	pfam01990	ATP-synt_F			1.50E-11
2572232171	t3m_00527	Locus_type		CDS		
2572232171	t3m_00527	Product_name		Archaeal/vacuolar-type H+-ATPase subunit F		

2572232171	t3m_00527	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232171	t3m_00527	Coordinates		5323..5658(-)		
2572232171	t3m_00527	DNA_length		336bp		
2572232171	t3m_00527	Protein_length		111aa		
2572232171	t3m_00527	GC			0.67	

2572232172	t3m_00528	COG_category	[S] Function unknown			
2572232172	t3m_00528	COG4430	Uncharacterized protein conserved in bacteria			2.00E-13
2572232172	t3m_00528	pfam13376	OmdA			1.10E-13
2572232172	t3m_00528	Locus_type		CDS		
2572232172	t3m_00528	Product_name		Uncharacterized protein conserved in bacteria		
2572232172	t3m_00528	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232172	t3m_00528	Coordinates		5687..6361(-)		
2572232172	t3m_00528	DNA_length		675bp		
2572232172	t3m_00528	Protein_length		224aa		
2572232172	t3m_00528	GC			0.7	

2572232173	t3m_00529	pfam13187	Fer4_9			7.70E-09
2572232173	t3m_00529	Locus_type		CDS		
2572232173	t3m_00529	Product_name		4Fe-4S dicluster domain		
2572232173	t3m_00529	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232173	t3m_00529	Coordinates		6373..6651(-)		
2572232173	t3m_00529	DNA_length		279bp		
2572232173	t3m_00529	Protein_length		92aa		
2572232173	t3m_00529	GC			0.62	

2572232174	t3m_00530	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes
2572232174	t3m_00530	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes
2572232174	t3m_00530	Metacyc	PWY-6281: selenocysteine biosynthesis II (archaea and eukaryotes)
2572232174	t3m_00530	Metacyc	PWY0-901: selenocysteine biosynthesis I (bacteria)
2572232174	t3m_00530	Metacyc	TRNA-CHARGING-PWY: tRNA charging
2572232174	t3m_00530	IMG_pathway	352: Bacterial selenocysteine synthesis
2572232174	t3m_00530	IMG_pathway	467: Archaeal/eukaryotic selenocysteine synthesis
2572232174	t3m_00530	IMG_pathway	503: L-serine ligation to tRNA(Ser)

2572232174	t3m_00530	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232174	t3m_00530	COG0172	Seryl-tRNA synthetase			4.00E-130
2572232174	t3m_00530	pfam00587	tRNA-synt_2b			9.50E-36
2572232174	t3m_00530	pfam02403	Seryl_tRNA_N			3.00E-13
2572232174	t3m_00530	EC:6.1.1.11	Serine--tRNA ligase.			
2572232174	t3m_00530	TIGR00414	seryl-tRNA synthetase			0.00E+00
2572232174	t3m_00530	KO:K01875	seryl-tRNA synthetase [EC:6.1.1.11]			0.00E+00
2572232174	t3m_00530	ITERM:00388	seryl-tRNA synthetase (EC 6.1.1.11)			
2572232174	t3m_00530	Locus_type		CDS		
2572232174	t3m_00530	Product_name		seryl-tRNA synthetase (EC 6.1.1.11)		
2572232174	t3m_00530	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232174	t3m_00530	Coordinates		6688..8082(-)		
2572232174	t3m_00530	DNA_length		1395bp		
2572232174	t3m_00530	Protein_length		464aa		
2572232174	t3m_00530	GC			0.7	
2572232175	t3m_00531	COG_category	[S] Function unknown			
2572232175	t3m_00531	COG1801	Uncharacterized conserved protein			3.00E-47
2572232175	t3m_00531	pfam01904	DUF72			2.90E-66
2572232175	t3m_00531	Locus_type		CDS		
2572232175	t3m_00531	Product_name		Uncharacterized conserved protein		
2572232175	t3m_00531	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232175	t3m_00531	Coordinates		8181..8948(+)		
2572232175	t3m_00531	DNA_length		768bp		
2572232175	t3m_00531	Protein_length		255aa		
2572232175	t3m_00531	GC			0.68	
2572232176	t3m_00532	Locus_type		CDS		
2572232176	t3m_00532	Product_name		hypothetical protein		
2572232176	t3m_00532	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232176	t3m_00532	Coordinates		8961..9797(-)		
2572232176	t3m_00532	DNA_length		837bp		
2572232176	t3m_00532	Protein_length		278aa		
2572232176	t3m_00532	GC			0.68	

2572232176	t3m_00532	Transmembrane		Yes		

2572232177	t3m_00533	pfam08423	Rad51			2.80E-05
2572232177	t3m_00533	Locus_type		CDS		
2572232177	t3m_00533	Product_name		Rad51		
2572232177	t3m_00533	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232177	t3m_00533	Coordinates		10026..10922(+)		
2572232177	t3m_00533	DNA_length		897bp		
2572232177	t3m_00533	Protein_length		298aa		
2572232177	t3m_00533	GC			0.72	

2572232178	t3m_00534	Locus_type		CDS		
2572232178	t3m_00534	Product_name		hypothetical protein		
2572232178	t3m_00534	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232178	t3m_00534	Coordinates		10919..11128(+)		
2572232178	t3m_00534	DNA_length		210bp		
2572232178	t3m_00534	Protein_length		69aa		
2572232178	t3m_00534	GC			0.71	

2572232179	t3m_00535	COG_category	[L] Replication, recombination and repair			
2572232179	t3m_00535	COG0417	DNA polymerase elongation subunit (family B)			4.00E-78
2572232179	t3m_00535	pfam00136	DNA_pol_B			4.50E-18
2572232179	t3m_00535	pfam03104	DNA_pol_B_exo1			2.30E-05
2572232179	t3m_00535	EC:2.7.7.7	DNA-directed DNA polymerase.			
2572232179	t3m_00535	KO:K02319	DNA polymerase I [EC:2.7.7.7]			0.00E+00
2572232179	t3m_00535	Locus_type		CDS		
2572232179	t3m_00535	Product_name		DNA polymerase elongation subunit (family B)		
2572232179	t3m_00535	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232179	t3m_00535	Coordinates		11131..13470(+)		
2572232179	t3m_00535	DNA_length		2340bp		
2572232179	t3m_00535	Protein_length		779aa		
2572232179	t3m_00535	GC			0.71	

2572232180	t3m_00536	COG_category	[C] Energy production and conversion			

2572232180	t3m_00536	COG1413	FOG: HEAT repeat		5.00E-22
2572232180	t3m_00536	pfam13646	HEAT_2		9.50E-16
2572232180	t3m_00536	pfam13646	HEAT_2		1.00E-13
2572232180	t3m_00536	pfam03130	HEAT_PBS		2.60E-03
2572232180	t3m_00536	pfam02985	HEAT		2.40E-04
2572232180	t3m_00536	Locus_type		CDS	
2572232180	t3m_00536	Product_name		FOG: HEAT repeat	
2572232180	t3m_00536	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8	
2572232180	t3m_00536	Coordinates		13493..14986(+)	
2572232180	t3m_00536	DNA_length		1494bp	
2572232180	t3m_00536	Protein_length		497aa	
2572232180	t3m_00536	GC		0.74	
2572232181	t3m_00537	COG_category	[R] General function prediction only		
2572232181	t3m_00537	COG0456	Acetyltransferases		4.00E-08
2572232181	t3m_00537	pfam00583	Acetyltransf_1		9.70E-16
2572232181	t3m_00537	Locus_type		CDS	
2572232181	t3m_00537	Product_name		Acetyltransferases	
2572232181	t3m_00537	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8	
2572232181	t3m_00537	Coordinates		14983..15921(+)	
2572232181	t3m_00537	DNA_length		939bp	
2572232181	t3m_00537	Protein_length		312aa	
2572232181	t3m_00537	GC		0.7	
2572232182	t3m_00538	Locus_type		CDS	
2572232182	t3m_00538	Product_name		hypothetical protein	
2572232182	t3m_00538	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8	
2572232182	t3m_00538	Coordinates		15944..17206(+)	
2572232182	t3m_00538	DNA_length		1263bp	
2572232182	t3m_00538	Protein_length		420aa	
2572232182	t3m_00538	GC		0.72	
2572232183	t3m_00539	COG_category	[E] Amino acid transport and metabolism		
2572232183	t3m_00539	COG2309	Leucyl aminopeptidase (aminopeptidase T)		3.00E-15

2572232183	t3m_00539	pfam02073	Peptidase_M29			7.40E-09
2572232183	t3m_00539	Locus_type		CDS		
2572232183	t3m_00539	Product_name		Leucyl aminopeptidase (aminopeptidase T)		
2572232183	t3m_00539	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232183	t3m_00539	Coordinates		17236..18345(+)		
2572232183	t3m_00539	DNA_length		1110bp		
2572232183	t3m_00539	Protein_length		369aa		
2572232183	t3m_00539	GC			0.73	

2572232184	t3m_00540	COG_category	[L] Replication, recombination and repair			
2572232184	t3m_00540	COG2094	3-methyladenine DNA glycosylase			2.00E-33
2572232184	t3m_00540	pfam02245	Pur_DNA_glyco			2.10E-43
2572232184	t3m_00540	EC:3.2.2.21	DNA-3-methyladenine glycosylase II.			
2572232184	t3m_00540	TIGR00567	DNA-3-methyladenine glycosylase (3mg)			1.50E-38
2572232184	t3m_00540	KO:K03652	DNA-3-methyladenine glycosylase [EC:3.2.2.21]			6.10E-27
2572232184	t3m_00540	Locus_type		CDS		
2572232184	t3m_00540	Product_name		DNA-3-methyladenine glycosylase (3mg)		
2572232184	t3m_00540	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232184	t3m_00540	Coordinates		18305..18901(+)		
2572232184	t3m_00540	DNA_length		597bp		
2572232184	t3m_00540	Protein_length		198aa		
2572232184	t3m_00540	GC			0.73	

2572232185	t3m_00541	KEGG_module	M00179: Ribosome, archaea			
2572232185	t3m_00541	KEGG_module	M00177: Ribosome, eukaryotes			
2572232185	t3m_00541	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232185	t3m_00541	COG2126	Ribosomal protein L37E			8.00E-07
2572232185	t3m_00541	pfam01907	Ribosomal_L37e			9.00E-20
2572232185	t3m_00541	KO:K02922	large subunit ribosomal protein L37e			1.20E-12
2572232185	t3m_00541	Locus_type		CDS		
2572232185	t3m_00541	Product_name		LSU ribosomal protein L37E		
2572232185	t3m_00541	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232185	t3m_00541	Coordinates		18894..19055(-)		
2572232185	t3m_00541	DNA_length		162bp		

2572232185	t3m_00541	Protein_length		53aa		
2572232185	t3m_00541	GC			0.62	
2572232186	t3m_00542	COG_category	[K] Transcription			
2572232186	t3m_00542	COG1958	Small nuclear ribonucleoprotein (snRNP) homolog			9.00E-15
2572232186	t3m_00542	pfam01423	LSM			1.80E-21
2572232186	t3m_00542	KO:K04796	small nuclear ribonucleoprotein			1.90E-16
2572232186	t3m_00542	Locus_type		CDS		
2572232186	t3m_00542	Product_name		Small nuclear ribonucleoprotein, LSM family		
2572232186	t3m_00542	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232186	t3m_00542	Coordinates		19067..19279(-)		
2572232186	t3m_00542	DNA_length		213bp		
2572232186	t3m_00542	Protein_length		70aa		
2572232186	t3m_00542	GC			0.64	
2572232187	t3m_00543	COG_category	[F] Nucleotide transport and metabolism			
2572232187	t3m_00543	COG1428	Deoxynucleoside kinases			1.00E-06
2572232187	t3m_00543	Locus_type		CDS		
2572232187	t3m_00543	Product_name		Deoxynucleoside kinases		
2572232187	t3m_00543	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232187	t3m_00543	Coordinates		19312..20034(-)		
2572232187	t3m_00543	DNA_length		723bp		
2572232187	t3m_00543	Protein_length		240aa		
2572232187	t3m_00543	GC			0.72	
2572232188	t3m_00544	KEGG_module	M00126: Tetrahydrofolate biosynthesis, GTP => THF			
2572232188	t3m_00544	Metacyc	PWY-6614: tetrahydrofolate biosynthesis			
2572232188	t3m_00544	COG_category	[H] Coenzyme transport and metabolism			
2572232188	t3m_00544	COG0294	Dihydropteroate synthase and related enzymes			2.00E-63
2572232188	t3m_00544	pfam00809	Pterin_bind			6.00E-69
2572232188	t3m_00544	EC:2.5.1.15	Dihydropteroate synthase.			
2572232188	t3m_00544	TIGR01496	dihydropteroate synthase			1.40E-91
2572232188	t3m_00544	KO:K00796	dihydropteroate synthase [EC:2.5.1.15]			0.00E+00
2572232188	t3m_00544	Locus_type		CDS		

2572232188	t3m_00544	Product_name		dihydropteroate synthase	
2572232188	t3m_00544	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8	
2572232188	t3m_00544	Coordinates		20188..21423(+)	
2572232188	t3m_00544	DNA_length		1236bp	
2572232188	t3m_00544	Protein_length		411aa	
2572232188	t3m_00544	GC		0.71	

2572232189	t3m_00545	Locus_type		CDS	
2572232189	t3m_00545	Product_name		hypothetical protein	
2572232189	t3m_00545	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8	
2572232189	t3m_00545	Coordinates		21470..21655(-)	
2572232189	t3m_00545	DNA_length		186bp	
2572232189	t3m_00545	Protein_length		61aa	
2572232189	t3m_00545	GC		0.67	

2572232190	t3m_00546	COG_category	[L] Replication, recombination and repair		
2572232190	t3m_00546	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subu		0.00E+00
2572232190	t3m_00546	pfam03989	DNA_gyraseA_C		1.70E-09
2572232190	t3m_00546	pfam03989	DNA_gyraseA_C		5.60E-08
2572232190	t3m_00546	pfam03989	DNA_gyraseA_C		1.50E-06
2572232190	t3m_00546	pfam00521	DNA_topoisoIV		0.00E+00
2572232190	t3m_00546	pfam03989	DNA_gyraseA_C		5.40E-06
2572232190	t3m_00546	pfam03989	DNA_gyraseA_C		3.20E-11
2572232190	t3m_00546	pfam03989	DNA_gyraseA_C		4.90E-10
2572232190	t3m_00546	EC:5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).		
2572232190	t3m_00546	TIGR01063	DNA gyrase, A subunit		0.00E+00
2572232190	t3m_00546	KO:K02469	DNA gyrase subunit A [EC:5.99.1.3]		0.00E+00
2572232190	t3m_00546	Locus_type		CDS	
2572232190	t3m_00546	Product_name		DNA gyrase subunit A (EC 5.99.1.3)	
2572232190	t3m_00546	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8	
2572232190	t3m_00546	Coordinates		21630..24275(-)	
2572232190	t3m_00546	DNA_length		2646bp	
2572232190	t3m_00546	Protein_length		881aa	
2572232190	t3m_00546	GC		0.68	

2572232191	t3m_00547	COG_category	[L] Replication, recombination and repair			
2572232191	t3m_00547	COG0608	Single-stranded DNA-specific exonuclease			9.00E-33
2572232191	t3m_00547	pfam02272	DHHA1			5.30E-07
2572232191	t3m_00547	pfam01368	DHH			9.20E-07
2572232191	t3m_00547	KO:K07463	archaea-specific RecJ-like exonuclease			0.00E+00
2572232191	t3m_00547	Locus_type		CDS		
2572232191	t3m_00547	Product_name		Single-stranded DNA-specific exonuclease		
2572232191	t3m_00547	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232191	t3m_00547	Coordinates		24272..25669(-)		
2572232191	t3m_00547	DNA_length		1398bp		
2572232191	t3m_00547	Protein_length		465aa		
2572232191	t3m_00547	GC			0.71	
2572232192	t3m_00548	KEGG_module	M00179: Ribosome, archaea			
2572232192	t3m_00548	KEGG_module	M00178: Ribosome, bacteria			
2572232192	t3m_00548	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232192	t3m_00548	COG0184	Ribosomal protein S15P/S13E			1.00E-14
2572232192	t3m_00548	pfam08069	Ribosomal_S13_N			1.00E-19
2572232192	t3m_00548	pfam00312	Ribosomal_S15			1.50E-20
2572232192	t3m_00548	KO:K02956	small subunit ribosomal protein S15			4.40E-39
2572232192	t3m_00548	Locus_type		CDS		
2572232192	t3m_00548	Product_name		Ribosomal protein S15P/S13E		
2572232192	t3m_00548	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232192	t3m_00548	Coordinates		25669..26124(-)		
2572232192	t3m_00548	DNA_length		456bp		
2572232192	t3m_00548	Protein_length		151aa		
2572232192	t3m_00548	GC			0.69	
2572232193	t3m_00549	Locus_type		CDS		
2572232193	t3m_00549	Product_name		hypothetical protein		
2572232193	t3m_00549	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232193	t3m_00549	Coordinates		26206..26550(-)		
2572232193	t3m_00549	DNA_length		345bp		

2572232193	t3m_00549	Protein_length		114aa		
2572232193	t3m_00549	GC			0.67	
2572232194	t3m_00550	Locus_type		CDS		
2572232194	t3m_00550	Product_name		hypothetical protein		
2572232194	t3m_00550	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232194	t3m_00550	Coordinates		26611..26949(-)		
2572232194	t3m_00550	DNA_length		339bp		
2572232194	t3m_00550	Protein_length		112aa		
2572232194	t3m_00550	GC			0.69	
2572232195	t3m_00551	Locus_type		CDS		
2572232195	t3m_00551	Product_name		hypothetical protein		
2572232195	t3m_00551	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232195	t3m_00551	Coordinates		27042..27350(+)		
2572232195	t3m_00551	DNA_length		309bp		
2572232195	t3m_00551	Protein_length		102aa		
2572232195	t3m_00551	GC			0.67	
2572232196	t3m_00552	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232196	t3m_00552	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232196	t3m_00552	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232196	t3m_00552	IMG_pathway	506: L-tryptophan ligation to tRNA(Trp)			
2572232196	t3m_00552	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232196	t3m_00552	COG0180	Tryptophanyl-tRNA synthetase			9.00E-66
2572232196	t3m_00552	pfam00579	tRNA-synt_1b			3.70E-22
2572232196	t3m_00552	EC:6.1.1.2	Tryptophan--tRNA ligase.			
2572232196	t3m_00552	TIGR00233	tryptophanyl-tRNA synthetase			9.60E-71
2572232196	t3m_00552	KO:K01867	tryptophanyl-tRNA synthetase [EC:6.1.1.2]			0.00E+00
2572232196	t3m_00552	ITERM:00401	tryptophanyl-tRNA synthetase (EC 6.1.1.2)			
2572232196	t3m_00552	Locus_type		CDS		
2572232196	t3m_00552	Product_name		tryptophanyl-tRNA synthetase (EC 6.1.1.2)		
2572232196	t3m_00552	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232196	t3m_00552	Coordinates		27362..28510(+)		

2572232196	t3m_00552	DNA_length		1149bp		
2572232196	t3m_00552	Protein_length		382aa		
2572232196	t3m_00552	GC			0.69	

2572232197	t3m_00553	pfam13414	TPR_11			3.00E-07
2572232197	t3m_00553	pfam13414	TPR_11			5.00E-09
2572232197	t3m_00553	pfam00515	TPR_1			5.80E-06
2572232197	t3m_00553	Locus_type		CDS		
2572232197	t3m_00553	Product_name		Tetratricopeptide repeat/TPR repeat		
2572232197	t3m_00553	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232197	t3m_00553	Coordinates		28536..29312(-)		
2572232197	t3m_00553	DNA_length		777bp		
2572232197	t3m_00553	Protein_length		258aa		
2572232197	t3m_00553	GC			0.72	

2572232198	t3m_00554	KEGG_module	M00288: RPA complex			
2572232198	t3m_00554	KO:K07466	replication factor A1			3.30E-35
2572232198	t3m_00554	Locus_type		CDS		
2572232198	t3m_00554	Product_name		hypothetical protein		
2572232198	t3m_00554	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232198	t3m_00554	Coordinates		29603..30109(+)		
2572232198	t3m_00554	DNA_length		507bp		
2572232198	t3m_00554	Protein_length		168aa		
2572232198	t3m_00554	GC			0.65	

2572232199	t3m_00555	pfam01037	AsnC_trans_reg			7.70E-09
2572232199	t3m_00555	Locus_type		CDS		
2572232199	t3m_00555	Product_name		AsnC family		
2572232199	t3m_00555	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232199	t3m_00555	Coordinates		30221..30892(+)		
2572232199	t3m_00555	DNA_length		672bp		
2572232199	t3m_00555	Protein_length		223aa		
2572232199	t3m_00555	GC			0.66	

2572232200	t3m_00556	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP			
2572232200	t3m_00556	Metacyc	PWY-5154: arginine biosynthesis III			
2572232200	t3m_00556	Metacyc	ARGSYNBSUB-PWY: arginine biosynthesis II (acetyl cycle)			
2572232200	t3m_00556	Metacyc	ARGSYN-PWY: arginine biosynthesis I			
2572232200	t3m_00556	Metacyc	PWY-5686: UMP biosynthesis			
2572232200	t3m_00556	COG_category	[F] Nucleotide transport and metabolism			
2572232200	t3m_00556	COG_category	[E] Amino acid transport and metabolism			
2572232200	t3m_00556	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)			3.00E-130
2572232200	t3m_00556	pfam00289	CPSase_L_chain			1.50E-11
2572232200	t3m_00556	pfam02786	CPSase_L_D2			7.90E-72
2572232200	t3m_00556	pfam02787	CPSase_L_D3			3.30E-33
2572232200	t3m_00556	pfam02142	MGS			3.40E-08
2572232200	t3m_00556	pfam00289	CPSase_L_chain			4.30E-10
2572232200	t3m_00556	pfam02786	CPSase_L_D2			5.50E-30
2572232200	t3m_00556	EC:6.3.5.5	Carbamoyl-phosphate synthase (glutamine-hydrolyzing).			
2572232200	t3m_00556	TIGR01369	carbamoyl-phosphate synthase, large subunit			0.00E+00
2572232200	t3m_00556	KO:K01955	carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]			0.00E+00
2572232200	t3m_00556	Locus_type		CDS		
2572232200	t3m_00556	Product_name		carbamoyl-phosphate synthase, large subunit		
2572232200	t3m_00556	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232200	t3m_00556	Coordinates		30855..34217(-)		
2572232200	t3m_00556	DNA_length		3363bp		
2572232200	t3m_00556	Protein_length		1120aa		
2572232200	t3m_00556	GC			0.7	

2572232201	t3m_00557	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP	
2572232201	t3m_00557	Metacyc	PWY-5154: arginine biosynthesis III	
2572232201	t3m_00557	Metacyc	ARGSYN-PWY: arginine biosynthesis I	
2572232201	t3m_00557	Metacyc	ARGSYNBSUB-PWY: arginine biosynthesis II (acetyl cycle)	
2572232201	t3m_00557	Metacyc	PWY-5686: UMP biosynthesis	
2572232201	t3m_00557	COG_category	[F] Nucleotide transport and metabolism	
2572232201	t3m_00557	COG_category	[E] Amino acid transport and metabolism	
2572232201	t3m_00557	COG0505	Carbamoylphosphate synthase small subunit	2.00E-103
2572232201	t3m_00557	pfam00988	CPSase_sm_chain	2.80E-47

2572232201	t3m_00557	pfam00117	GATase			1.20E-29
2572232201	t3m_00557	EC:6.3.5.5	Carbamoyl-phosphate synthase (glutamine-hydrolyzing).			
2572232201	t3m_00557	TIGR01368	carbamoyl-phosphate synthase, small subunit			4.20E-112
2572232201	t3m_00557	KO:K01956	carbamoyl-phosphate synthase small subunit [EC:6.3.5.5]			0.00E+00
2572232201	t3m_00557	Locus_type		CDS		
2572232201	t3m_00557	Product_name		carbamoyl-phosphate synthase, small subunit		
2572232201	t3m_00557	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232201	t3m_00557	Coordinates		34214..35359(-)		
2572232201	t3m_00557	DNA_length		1146bp		
2572232201	t3m_00557	Protein_length		381aa		
2572232201	t3m_00557	GC			0.71	
2572232202	t3m_00558	Metacyc	THIOREDOX-PWY: thioredoxin pathway			
2572232202	t3m_00558	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232202	t3m_00558	COG0492	Thioredoxin reductase			1.00E-19
2572232202	t3m_00558	pfam07992	Pyr_redox_2			2.30E-11
2572232202	t3m_00558	EC:1.8.1.9	Thioredoxin-disulfide reductase.			
2572232202	t3m_00558	KO:K00384	thioredoxin reductase (NADPH) [EC:1.8.1.9]			1.80E-29
2572232202	t3m_00558	Locus_type		CDS		
2572232202	t3m_00558	Product_name		Thioredoxin reductase		
2572232202	t3m_00558	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232202	t3m_00558	Coordinates		35491..36486(+)		
2572232202	t3m_00558	DNA_length		996bp		
2572232202	t3m_00558	Protein_length		331aa		
2572232202	t3m_00558	GC			0.68	
2572232203	t3m_00559	KEGG_module	M00532: Photorespiration			
2572232203	t3m_00559	Metacyc	PWY-181: photorespiration			
2572232203	t3m_00559	COG_category	[R] General function prediction only			
2572232203	t3m_00559	COG0546	Predicted phosphatases			9.00E-22
2572232203	t3m_00559	pfam13419	HAD_2			4.70E-20
2572232203	t3m_00559	EC:3.1.3.18	Phosphoglycolate phosphatase.			
2572232203	t3m_00559	TIGR01549	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m			2.90E-13
2572232203	t3m_00559	KO:K01091	phosphoglycolate phosphatase [EC:3.1.3.18]			3.20E-14

2572232203	t3m_00559	Locus_type		CDS		
2572232203	t3m_00559	Product_name		haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m		
2572232203	t3m_00559	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232203	t3m_00559	Coordinates		36493..37242(-)		
2572232203	t3m_00559	DNA_length		750bp		
2572232203	t3m_00559	Protein_length		249aa		
2572232203	t3m_00559	GC			0.68	
2572232204	t3m_00560	Locus_type		CDS		
2572232204	t3m_00560	Product_name		hypothetical protein		
2572232204	t3m_00560	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232204	t3m_00560	Coordinates		37323..37628(-)		
2572232204	t3m_00560	DNA_length		306bp		
2572232204	t3m_00560	Protein_length		101aa		
2572232204	t3m_00560	GC			0.66	
2572232205	t3m_00561	pfam13659	Methyltransf_26			4.80E-09
2572232205	t3m_00561	Locus_type		CDS		
2572232205	t3m_00561	Product_name		Methyltransferase domain		
2572232205	t3m_00561	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232205	t3m_00561	Coordinates		37654..39168(-)		
2572232205	t3m_00561	DNA_length		1515bp		
2572232205	t3m_00561	Protein_length		504aa		
2572232205	t3m_00561	GC			0.71	
2572232206	t3m_00562	COG_category	[S] Function unknown			
2572232206	t3m_00562	COG5607	Uncharacterized conserved protein			1.00E-08
2572232206	t3m_00562	pfam05235	CHAD			7.40E-20
2572232206	t3m_00562	Locus_type		CDS		
2572232206	t3m_00562	Product_name		Uncharacterized conserved protein		
2572232206	t3m_00562	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232206	t3m_00562	Coordinates		39213..40100(-)		
2572232206	t3m_00562	DNA_length		888bp		
2572232206	t3m_00562	Protein_length		295aa		

2572232206	t3m_00562	GC			0.7	
2572232207	t3m_00563	Metacyc	PPGPPMET-PWY: ppGpp biosynthesis			
2572232207	t3m_00563	COG_category	[P] Inorganic ion transport and metabolism			
2572232207	t3m_00563	COG_category	[F] Nucleotide transport and metabolism			
2572232207	t3m_00563	COG0248	Exopolyphosphatase			1.00E-76
2572232207	t3m_00563	pfam02541	Ppx-GppA			7.40E-55
2572232207	t3m_00563	EC:3.6.1.11	Exopolyphosphatase.			
2572232207	t3m_00563	EC:3.6.1.40	Guanosine-5'-triphosphate,3'-diphosphate diphosphatase.			
2572232207	t3m_00563	TIGR03706	exopolyphosphatase			7.20E-85
2572232207	t3m_00563	KO:K01524	exopolyphosphatase / guanosine-5'-triphosphate,3'-diphosphate pyrop			0.00E+00
2572232207	t3m_00563	Locus_type		CDS		
2572232207	t3m_00563	Product_name		Exopolyphosphatase		
2572232207	t3m_00563	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232207	t3m_00563	Coordinates		40213..41772(+)		
2572232207	t3m_00563	DNA_length		1560bp		
2572232207	t3m_00563	Protein_length		519aa		
2572232207	t3m_00563	GC			0.68	
2572232208	t3m_00564	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP			
2572232208	t3m_00564	COG_category	[F] Nucleotide transport and metabolism			
2572232208	t3m_00564	COG0125	Thymidylate kinase			6.00E-36
2572232208	t3m_00564	pfam02223	Thymidylate_kin			3.50E-28
2572232208	t3m_00564	EC:2.7.4.9	dTMP kinase.			
2572232208	t3m_00564	TIGR00041	thymidylate kinase			7.60E-32
2572232208	t3m_00564	KO:K00943	dTMP kinase [EC:2.7.4.9]			0.00E+00
2572232208	t3m_00564	Locus_type		CDS		
2572232208	t3m_00564	Product_name		thymidylate kinase		
2572232208	t3m_00564	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232208	t3m_00564	Coordinates		41765..42463(+)		
2572232208	t3m_00564	DNA_length		699bp		
2572232208	t3m_00564	Protein_length		232aa		
2572232208	t3m_00564	GC			0.64	

2572232209	t3m_00565	IMG_pathway	331: dTDP synthesis			
2572232209	t3m_00565	COG_category	[F] Nucleotide transport and metabolism			
2572232209	t3m_00565	COG0125	Thymidylate kinase			3.00E-28
2572232209	t3m_00565	pfam02223	Thymidylate_kin			8.00E-20
2572232209	t3m_00565	TIGR00041	thymidylate kinase			9.50E-27
2572232209	t3m_00565	ITERM:01406	thymidylate kinase (EC 2.7.4.9)			
2572232209	t3m_00565	Locus_type		CDS		
2572232209	t3m_00565	Product_name		thymidylate kinase (EC 2.7.4.9)		
2572232209	t3m_00565	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232209	t3m_00565	Coordinates		42453..43217(+)		
2572232209	t3m_00565	DNA_length		765bp		
2572232209	t3m_00565	Protein_length		254aa		
2572232209	t3m_00565	GC			0.68	
2572232210	t3m_00566	Metacyc	PWY-6366: D-<i>myo</i>-inositol (1,4,5,6)-tetrakisphosphate biosynthesis			
2572232210	t3m_00566	Metacyc	NADPHOS-DEPHOS-PWY: NAD phosphorylation and dephosphorylation			
2572232210	t3m_00566	Metacyc	PWY-6365: D-<i>myo</i>-inositol (3,4,5,6)-tetrakisphosphate biosynthesis			
2572232210	t3m_00566	Metacyc	PWY-6724: starch degradation II			
2572232210	t3m_00566	Metacyc	PWY-6456: serinol biosynthesis			
2572232210	t3m_00566	Metacyc	PWY-6367: D-<i>myo</i>-inositol-5-phosphate metabolism			
2572232210	t3m_00566	Metacyc	PWY-6991: (-)-camphor biosynthesis			
2572232210	t3m_00566	Metacyc	PWY-6352: 3-phosphoinositide biosynthesis			
2572232210	t3m_00566	Metacyc	NAD-BIOSYNTHESIS-II: NAD salvage pathway II			
2572232210	t3m_00566	Metacyc	PWY-6575: juvenile hormone III biosynthesis I			
2572232210	t3m_00566	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)			
2572232210	t3m_00566	Metacyc	PWY-6368: 3-phosphoinositide degradation			
2572232210	t3m_00566	Metacyc	PWY-6627: salinosporamide A biosynthesis			
2572232210	t3m_00566	Metacyc	PWY-5491: diethylphosphate degradation			
2572232210	t3m_00566	Metacyc	PWY-6990: (+)-camphor biosynthesis			
2572232210	t3m_00566	Metacyc	PWY-6686: mannosylglucosylglycerate biosynthesis I			
2572232210	t3m_00566	Metacyc	PWY-7119: sphingolipid recycling and degradation (yeast)			
2572232210	t3m_00566	Metacyc	PWY-7018: paromomycin biosynthesis			
2572232210	t3m_00566	Metacyc	PWY-6720: toyocamycin biosynthesis			
2572232210	t3m_00566	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			

2572232210	t3m_00566	COG_category	[T] Signal transduction mechanisms			
2572232210	t3m_00566	COG2062	Phosphohistidine phosphatase SixA			3.00E-19
2572232210	t3m_00566	pfam00300	His_Phos_1			4.20E-09
2572232210	t3m_00566	EC:3.1.3.-	Hydrolases. Acting on ester bonds. Phosphoric monoester hydrolases.			
2572232210	t3m_00566	TIGR00249	phosphohistidine phosphatase SixA			1.80E-24
2572232210	t3m_00566	KO:K08296	phosphohistidine phosphatase [EC:3.1.3.-]			1.00E-17
2572232210	t3m_00566	ITERM:02457	phosphohistidine phosphatase, SixA			
2572232210	t3m_00566	Locus_type		CDS		
2572232210	t3m_00566	Product_name		phosphohistidine phosphatase, SixA		
2572232210	t3m_00566	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232210	t3m_00566	Coordinates		43183..43719(-)		
2572232210	t3m_00566	DNA_length		537bp		
2572232210	t3m_00566	Protein_length		178aa		
2572232210	t3m_00566	GC			0.71	
2572232211	t3m_00567	COG_category	[P] Inorganic ion transport and metabolism			
2572232211	t3m_00567	COG0704	Phosphate uptake regulator			4.00E-05
2572232211	t3m_00567	Locus_type		CDS		
2572232211	t3m_00567	Product_name		Phosphate uptake regulator		
2572232211	t3m_00567	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232211	t3m_00567	Coordinates		43773..44819(-)		
2572232211	t3m_00567	DNA_length		1047bp		
2572232211	t3m_00567	Protein_length		348aa		
2572232211	t3m_00567	GC			0.69	
2572232212	t3m_00568	Locus_type		CDS		
2572232212	t3m_00568	Product_name		hypothetical protein		
2572232212	t3m_00568	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232212	t3m_00568	Coordinates		45029..45598(+)		
2572232212	t3m_00568	DNA_length		570bp		
2572232212	t3m_00568	Protein_length		189aa		
2572232212	t3m_00568	GC			0.69	
2572232213	t3m_00569	COG_category	[R] General function prediction only			

2572232213	t3m_00569	COG0456	Acetyltransferases			6.00E-09
2572232213	t3m_00569	pfam06906	DUF1272			1.90E-12
2572232213	t3m_00569	pfam00583	Acetyltransf_1			4.00E-16
2572232213	t3m_00569	Locus_type		CDS		
2572232213	t3m_00569	Product_name		Acetyltransferases		
2572232213	t3m_00569	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232213	t3m_00569	Coordinates		45747..46418(+)		
2572232213	t3m_00569	DNA_length		672bp		
2572232213	t3m_00569	Protein_length		223aa		
2572232213	t3m_00569	GC			0.67	
2572232213	t3m_00569	Fused_gene		Yes		
2572232214	t3m_00570	COG_category	[S] Function unknown			
2572232214	t3m_00570	COG3374	Predicted membrane protein			5.00E-25
2572232214	t3m_00570	pfam06168	DUF981			7.40E-40
2572232214	t3m_00570	KO:K08980	putative membrane protein			2.10E-37
2572232214	t3m_00570	Locus_type		CDS		
2572232214	t3m_00570	Product_name		Predicted membrane protein		
2572232214	t3m_00570	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232214	t3m_00570	Coordinates		46547..47227(-)		
2572232214	t3m_00570	DNA_length		681bp		
2572232214	t3m_00570	Protein_length		226aa		
2572232214	t3m_00570	GC			0.61	
2572232214	t3m_00570	Transmembrane		Yes		
2572232215	t3m_00571	Locus_type		tRNA		
2572232215	t3m_00571	Product_name		tRNA_Val_TAC		
2572232215	t3m_00571	Scaffold		t3m_contig_70_62_len_47528_read_count_3866024.8		
2572232215	t3m_00571	Coordinates		47382..47454(-)		
2572232215	t3m_00571	DNA_length		73bp		
2572232215	t3m_00571	GC			0.64	
2572232216	t3m_00572	Locus_type		CDS		
2572232216	t3m_00572	Product_name		hypothetical protein		

2572232216	t3m_00572	Scaffold	t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232216	t3m_00572	Coordinates	43..243(+)	
2572232216	t3m_00572	DNA_length	201bp	
2572232216	t3m_00572	Protein_length	66aa	
2572232216	t3m_00572	GC		0.69

2572232217	t3m_00573	Locus_type	CDS	
2572232217	t3m_00573	Product_name	hypothetical protein	
2572232217	t3m_00573	Scaffold	t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232217	t3m_00573	Coordinates	309..509(-)	
2572232217	t3m_00573	DNA_length	201bp	
2572232217	t3m_00573	Protein_length	66aa	
2572232217	t3m_00573	GC		0.64
2572232217	t3m_00573	Transmembrane	Yes	

2572232218	t3m_00574	Locus_type	CDS	
2572232218	t3m_00574	Product_name	hypothetical protein	
2572232218	t3m_00574	Scaffold	t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232218	t3m_00574	Coordinates	706..1086(-)	
2572232218	t3m_00574	DNA_length	381bp	
2572232218	t3m_00574	Protein_length	126aa	
2572232218	t3m_00574	GC		0.64
2572232218	t3m_00574	Transmembrane	Yes	

2572232219	t3m_00575	KEGG_module	M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate	
2572232219	t3m_00575	Metacyc	HISHP-PWY: histidine degradation VI	
2572232219	t3m_00575	Metacyc	PWY-5028: histidine degradation II	
2572232219	t3m_00575	Metacyc	PWY-5030: histidine degradation III	
2572232219	t3m_00575	Metacyc	HISDEG-PWY: histidine degradation I	
2572232219	t3m_00575	IMG_pathway	189: L-histidine degradation to L-glutamate and formamide	
2572232219	t3m_00575	IMG_pathway	190: L-histidine degradation to L-glutamate and formiminotetrahydrofolate	
2572232219	t3m_00575	COG_category	[E] Amino acid transport and metabolism	
2572232219	t3m_00575	COG2987	Urocanate hydratase	0.00E+00
2572232219	t3m_00575	pfam01175	Urocanase	0.00E+00

2572232219	t3m_00575	EC:4.2.1.49	Urocanate hydratase.			
2572232219	t3m_00575	TIGR01228	urocanate hydratase			0.00E+00
2572232219	t3m_00575	KO:K01712	urocanate hydratase [EC:4.2.1.49]			0.00E+00
2572232219	t3m_00575	ITERM:00501	urocanate hydratase (EC 4.2.1.49)			
2572232219	t3m_00575	Locus_type		CDS		
2572232219	t3m_00575	Product_name		urocanate hydratase (EC 4.2.1.49)		
2572232219	t3m_00575	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232219	t3m_00575	Coordinates		1342..3042(+)		
2572232219	t3m_00575	DNA_length		1701bp		
2572232219	t3m_00575	Protein_length		566aa		
2572232219	t3m_00575	GC			0.68	
2572232220	t3m_00576	COG_category	[E] Amino acid transport and metabolism			
2572232220	t3m_00576	COG2309	Leucyl aminopeptidase (aminopeptidase T)			1.00E-18
2572232220	t3m_00576	pfam02073	Peptidase_M29			9.10E-13
2572232220	t3m_00576	Locus_type		CDS		
2572232220	t3m_00576	Product_name		Leucyl aminopeptidase (aminopeptidase T)		
2572232220	t3m_00576	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232220	t3m_00576	Coordinates		3112..4173(+)		
2572232220	t3m_00576	DNA_length		1062bp		
2572232220	t3m_00576	Protein_length		353aa		
2572232220	t3m_00576	GC			0.69	
2572232221	t3m_00577	Locus_type		CDS		
2572232221	t3m_00577	Product_name		hypothetical protein		
2572232221	t3m_00577	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232221	t3m_00577	Coordinates		4275..5720(+)		
2572232221	t3m_00577	DNA_length		1446bp		
2572232221	t3m_00577	Protein_length		481aa		
2572232221	t3m_00577	GC			0.68	
2572232221	t3m_00577	Transmembrane		Yes		
2572232222	t3m_00578	COG_category	[F] Nucleotide transport and metabolism			
2572232222	t3m_00578	COG1051	ADP-ribose pyrophosphatase			9.00E-08

2572232222	t3m_00578	pfam00293	NUDIX			4.60E-22
2572232222	t3m_00578	Locus_type		CDS		
2572232222	t3m_00578	Product_name		ADP-ribose pyrophosphatase		
2572232222	t3m_00578	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232222	t3m_00578	Coordinates		5797..6273(-)		
2572232222	t3m_00578	DNA_length		477bp		
2572232222	t3m_00578	Protein_length		158aa		
2572232222	t3m_00578	GC			0.67	
2572232223	t3m_00579	Metacyc	PWY-7064: 3-amino-3-phenylpropanoyl-CoA formation (Taxol 13C-side chain biosynthesis)			
2572232223	t3m_00579	Metacyc	PWY66-388: fatty acid α-oxidation III			
2572232223	t3m_00579	Metacyc	PWY-6948: sitosterol degradation to androstenedione			
2572232223	t3m_00579	Metacyc	PWY-735: jasmonic acid biosynthesis			
2572232223	t3m_00579	Metacyc	PWYG-321: mycolate biosynthesis			
2572232223	t3m_00579	Metacyc	PWY-6799: fatty acid biosynthesis (plant mitochondria)			
2572232223	t3m_00579	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			
2572232223	t3m_00579	Metacyc	CARNMET-PWY: carnitine degradation I			
2572232223	t3m_00579	Metacyc	PWY-5958: acridone alkaloid biosynthesis			
2572232223	t3m_00579	Metacyc	PWY-6048: methylthiopropionate degradation I (cleavage)			
2572232223	t3m_00579	Metacyc	PWY-5140: cannabinoid biosynthesis			
2572232223	t3m_00579	Metacyc	PWY-6670: citronellol degradation			
2572232223	t3m_00579	Metacyc	PWY-6733: sporopollenin precursor biosynthesis			
2572232223	t3m_00579	Metacyc	PWY-6457: <i>trans</i>-cinnamoyl-CoA biosynthesis			
2572232223	t3m_00579	Metacyc	PWY-6593: sulfoacetate degradation			
2572232223	t3m_00579	COG_category	[I] Lipid transport and metabolism			
2572232223	t3m_00579	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2572232223	t3m_00579	COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II			2.00E-97
2572232223	t3m_00579	pfam13193	AMP-binding_C			5.50E-14
2572232223	t3m_00579	pfam00501	AMP-binding			6.50E-87
2572232223	t3m_00579	EC:6.2.1.-	Ligases. Forming carbon-sulfur bonds. Acid--thiol ligases.			
2572232223	t3m_00579	KO:K02182	crotonobetaine/carnitine-CoA ligase [EC:6.2.1.-]			0.00E+00
2572232223	t3m_00579	Locus_type		CDS		
2572232223	t3m_00579	Product_name		Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II		
2572232223	t3m_00579	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		

2572232223	t3m_00579	Coordinates		6352..7944(+)		
2572232223	t3m_00579	DNA_length		1593bp		
2572232223	t3m_00579	Protein_length		530aa		
2572232223	t3m_00579	GC			0.67	
2572232224	t3m_00580	COG_category	[R] General function prediction only			
2572232224	t3m_00580	COG1412	Uncharacterized proteins of PilT N-term./Vapc superfamily			4.00E-15
2572232224	t3m_00580	Locus_type		CDS		
2572232224	t3m_00580	Product_name		Uncharacterized proteins of PilT N-term./Vapc superfamily		
2572232224	t3m_00580	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232224	t3m_00580	Coordinates		7973..8398(+)		
2572232224	t3m_00580	DNA_length		426bp		
2572232224	t3m_00580	Protein_length		141aa		
2572232224	t3m_00580	GC			0.77	
2572232225	t3m_00581	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2572232225	t3m_00581	COG0412	Dienelactone hydrolase and related enzymes			3.00E-18
2572232225	t3m_00581	pfam01738	DLH			1.00E-24
2572232225	t3m_00581	Locus_type		CDS		
2572232225	t3m_00581	Product_name		Dienelactone hydrolase and related enzymes		
2572232225	t3m_00581	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232225	t3m_00581	Coordinates		8438..9484(+)		
2572232225	t3m_00581	DNA_length		1047bp		
2572232225	t3m_00581	Protein_length		348aa		
2572232225	t3m_00581	GC			0.69	
2572232226	t3m_00582	Locus_type		CDS		
2572232226	t3m_00582	Product_name		hypothetical protein		
2572232226	t3m_00582	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232226	t3m_00582	Coordinates		9651..10280(+)		
2572232226	t3m_00582	DNA_length		630bp		
2572232226	t3m_00582	Protein_length		209aa		
2572232226	t3m_00582	GC			0.67	
2572232226	t3m_00582	Transmembrane		Yes		

2572232227	t3m_00583	IMG_pathway	1014: Dicarboxylate/4-hydroxybutyrate cycle		
2572232227	t3m_00583	IMG_pathway	222: L-isoleucine degradation to propionyl-CoA and acetyl-CoA		
2572232227	t3m_00583	IMG_pathway	369: Pyruvate conversion to butyrate		
2572232227	t3m_00583	IMG_pathway	389: Crotonyl-CoA conversion to acetate		
2572232227	t3m_00583	IMG_pathway	596: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2572232227	t3m_00583	IMG_pathway	962: Glyoxylate from acetyl-CoA via ethylmalonyl-CoA pathway		
2572232227	t3m_00583	COG_category	[I] Lipid transport and metabolism		
2572232227	t3m_00583	COG1250	3-hydroxyacyl-CoA dehydrogenase		1.00E-73
2572232227	t3m_00583	pfam02737	3HCDH_N		2.40E-36
2572232227	t3m_00583	pfam02737	3HCDH_N		3.80E-11
2572232227	t3m_00583	pfam00725	3HCDH		2.10E-32
2572232227	t3m_00583	EC:1.1.1.157	3-hydroxybutyryl-CoA dehydrogenase.		
2572232227	t3m_00583	KO:K00074	3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]		0.00E+00
2572232227	t3m_00583	ITERM:00577	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)		
2572232227	t3m_00583	Locus_type		CDS	
2572232227	t3m_00583	Product_name		3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	
2572232227	t3m_00583	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232227	t3m_00583	Coordinates		10358..11323(-)	
2572232227	t3m_00583	DNA_length		966bp	
2572232227	t3m_00583	Protein_length		321aa	
2572232227	t3m_00583	GC		0.67	
2572232228	t3m_00584	Locus_type		CDS	
2572232228	t3m_00584	Product_name		hypothetical protein	
2572232228	t3m_00584	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232228	t3m_00584	Coordinates		11670..11993(-)	
2572232228	t3m_00584	DNA_length		324bp	
2572232228	t3m_00584	Protein_length		107aa	
2572232228	t3m_00584	GC		0.71	
2572232229	t3m_00585	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone		
2572232229	t3m_00585	KEGG_module	M00373: Ethylmalonyl pathway		
2572232229	t3m_00585	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		

2572232229	t3m_00585	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			
2572232229	t3m_00585	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle			
2572232229	t3m_00585	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			
2572232229	t3m_00585	Metacyc	PWY-5741: ethylmalonyl pathway			
2572232229	t3m_00585	Metacyc	PWY-6588: pyruvate fermentation to acetone			
2572232229	t3m_00585	Metacyc	PWY66-368: ketolysis			
2572232229	t3m_00585	Metacyc	PWY-5177: glutaryl-CoA degradation			
2572232229	t3m_00585	Metacyc	PWY-922: mevalonate pathway I			
2572232229	t3m_00585	Metacyc	PWY-6876: isopropanol biosynthesis			
2572232229	t3m_00585	Metacyc	PWY-7003: glycerol degradation to butanol			
2572232229	t3m_00585	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)			
2572232229	t3m_00585	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate			
2572232229	t3m_00585	Metacyc	PWY66-367: ketogenesis			
2572232229	t3m_00585	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis			
2572232229	t3m_00585	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate			
2572232229	t3m_00585	Metacyc	PWY-6863: pyruvate fermentation to hexanol			
2572232229	t3m_00585	Metacyc	PWY-6583: pyruvate fermentation to butanol I			
2572232229	t3m_00585	Metacyc	PWY-6174: mevalonate pathway II (archaea)			
2572232229	t3m_00585	Metacyc	PWY-6883: pyruvate fermentation to butanol II			
2572232229	t3m_00585	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II			
2572232229	t3m_00585	Metacyc	ILEUDEG-PWY: isoleucine degradation I			
2572232229	t3m_00585	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis			
2572232229	t3m_00585	COG_category	[I] Lipid transport and metabolism			
2572232229	t3m_00585	COG0183	Acetyl-CoA acetyltransferase			5.00E-43
2572232229	t3m_00585	pfam02803	Thiolase_C			3.80E-09
2572232229	t3m_00585	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.			
2572232229	t3m_00585	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]			0.00E+00
2572232229	t3m_00585	Locus_type		CDS		
2572232229	t3m_00585	Product_name		Acetyl-CoA acetyltransferase		
2572232229	t3m_00585	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232229	t3m_00585	Coordinates		11990..13123(-)		
2572232229	t3m_00585	DNA_length		1134bp		
2572232229	t3m_00585	Protein_length		377aa		
2572232229	t3m_00585	GC			0.69	

2572232230	t3m_00586	pfam01870	Hjc			4.10E-11
2572232230	t3m_00586	Locus_type		CDS		
2572232230	t3m_00586	Product_name		Archaeal holliday junction resolvase (hjc)		
2572232230	t3m_00586	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232230	t3m_00586	Coordinates		13128..13673(-)		
2572232230	t3m_00586	DNA_length		546bp		
2572232230	t3m_00586	Protein_length		181aa		
2572232230	t3m_00586	GC			0.64	
2572232231	t3m_00587	Locus_type		CDS		
2572232231	t3m_00587	Product_name		hypothetical protein		
2572232231	t3m_00587	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232231	t3m_00587	Coordinates		13731..15185(+)		
2572232231	t3m_00587	DNA_length		1455bp		
2572232231	t3m_00587	Protein_length		484aa		
2572232231	t3m_00587	GC			0.67	
2572232232	t3m_00588	Locus_type		CDS		
2572232232	t3m_00588	Product_name		hypothetical protein		
2572232232	t3m_00588	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232232	t3m_00588	Coordinates		15148..15663(+)		
2572232232	t3m_00588	DNA_length		516bp		
2572232232	t3m_00588	Protein_length		171aa		
2572232232	t3m_00588	GC			0.72	
2572232233	t3m_00589	COG_category	[S] Function unknown			
2572232233	t3m_00589	COG3391	Uncharacterized conserved protein			7.00E-09
2572232233	t3m_00589	pfam00801	PKD			1.00E-07
2572232233	t3m_00589	pfam00801	PKD			9.40E-11
2572232233	t3m_00589	TIGR02276	40-residue YVTN family beta-propeller repeat			5.80E-09
2572232233	t3m_00589	Locus_type		CDS		
2572232233	t3m_00589	Product_name		Uncharacterized conserved protein		
2572232233	t3m_00589	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		

2572232233	t3m_00589	Coordinates		15648..18695(-)		
2572232233	t3m_00589	DNA_length		3048bp		
2572232233	t3m_00589	Protein_length		1015aa		
2572232233	t3m_00589	GC			0.62	
2572232233	t3m_00589	Transmembrane		Yes		
2572232234	t3m_00590	Locus_type		CDS		
2572232234	t3m_00590	Product_name		hypothetical protein		
2572232234	t3m_00590	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232234	t3m_00590	Coordinates		19060..19890(-)		
2572232234	t3m_00590	DNA_length		831bp		
2572232234	t3m_00590	Protein_length		276aa		
2572232234	t3m_00590	GC			0.66	
2572232235	t3m_00591	COG_category	[S] Function unknown			
2572232235	t3m_00591	COG4260	Putative virion core protein (lumpy skin disease virus)			3.00E-33
2572232235	t3m_00591	pfam13421	Band_7_1			2.20E-35
2572232235	t3m_00591	pfam13240	zinc_ribbon_2			1.40E-06
2572232235	t3m_00591	pfam12773	DZR			2.40E-11
2572232235	t3m_00591	Locus_type		CDS		
2572232235	t3m_00591	Product_name		Putative virion core protein (lumpy skin disease virus)		
2572232235	t3m_00591	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232235	t3m_00591	Coordinates		20095..21252(-)		
2572232235	t3m_00591	DNA_length		1158bp		
2572232235	t3m_00591	Protein_length		385aa		
2572232235	t3m_00591	GC			0.67	
2572232235	t3m_00591	Fused_gene		Yes		
2572232236	t3m_00592	Locus_type		CDS		
2572232236	t3m_00592	Product_name		hypothetical protein		
2572232236	t3m_00592	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232236	t3m_00592	Coordinates		21279..21809(-)		
2572232236	t3m_00592	DNA_length		531bp		
2572232236	t3m_00592	Protein_length		176aa		

2572232236	t3m_00592	GC			0.67	
2572232237	t3m_00593	Locus_type		CDS		
2572232237	t3m_00593	Product_name		hypothetical protein		
2572232237	t3m_00593	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232237	t3m_00593	Coordinates		21985..22530(-)		
2572232237	t3m_00593	DNA_length		546bp		
2572232237	t3m_00593	Protein_length		181aa		
2572232237	t3m_00593	GC			0.68	
2572232237	t3m_00593	Transmembrane		Yes		
2572232238	t3m_00594	pfam14559	TPR_19			1.30E-05
2572232238	t3m_00594	pfam13414	TPR_11			9.70E-10
2572232238	t3m_00594	pfam13432	TPR_16			3.00E-08
2572232238	t3m_00594	pfam14559	TPR_19			1.90E-11
2572232238	t3m_00594	pfam13432	TPR_16			1.90E-06
2572232238	t3m_00594	pfam07719	TPR_2			5.50E-02
2572232238	t3m_00594	pfam13432	TPR_16			2.70E-07
2572232238	t3m_00594	Locus_type		CDS		
2572232238	t3m_00594	Product_name		Tetratricopeptide repeat/TPR repeat		
2572232238	t3m_00594	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232238	t3m_00594	Coordinates		22613..27202(-)		
2572232238	t3m_00594	DNA_length		4590bp		
2572232238	t3m_00594	Protein_length		1529aa		
2572232238	t3m_00594	GC			0.71	
2572232239	t3m_00595	COG_category	[R] General function prediction only			
2572232239	t3m_00595	COG1078	HD superfamily phosphohydrolases			8.00E-73
2572232239	t3m_00595	pfam01966	HD			4.00E-11
2572232239	t3m_00595	Locus_type		CDS		
2572232239	t3m_00595	Product_name		HD superfamily phosphohydrolases		
2572232239	t3m_00595	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232239	t3m_00595	Coordinates		27321..28577(+)		
2572232239	t3m_00595	DNA_length		1257bp		

2572232239	t3m_00595	Protein_length		418aa		
2572232239	t3m_00595	GC			0.72	
2572232240	t3m_00596	COG_category	[T] Signal transduction mechanisms			
2572232240	t3m_00596	COG0467	RecA-superfamily ATPases implicated in signal transduction			8.00E-24
2572232240	t3m_00596	pfam06745	KaiC			6.60E-38
2572232240	t3m_00596	KO:K08482	circadian clock protein KaiC			7.50E-25
2572232240	t3m_00596	Locus_type		CDS		
2572232240	t3m_00596	Product_name		RecA-superfamily ATPases implicated in signal transduction		
2572232240	t3m_00596	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232240	t3m_00596	Coordinates		28636..29352(-)		
2572232240	t3m_00596	DNA_length		717bp		
2572232240	t3m_00596	Protein_length		238aa		
2572232240	t3m_00596	GC			0.68	
2572232241	t3m_00597	COG_category	[T] Signal transduction mechanisms			
2572232241	t3m_00597	COG0467	RecA-superfamily ATPases implicated in signal transduction			3.00E-26
2572232241	t3m_00597	pfam06745	KaiC			4.60E-31
2572232241	t3m_00597	Locus_type		CDS		
2572232241	t3m_00597	Product_name		RecA-superfamily ATPases implicated in signal transduction		
2572232241	t3m_00597	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232241	t3m_00597	Coordinates		29413..31569(-)		
2572232241	t3m_00597	DNA_length		2157bp		
2572232241	t3m_00597	Protein_length		718aa		
2572232241	t3m_00597	GC			0.72	
2572232242	t3m_00598	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)			
2572232242	t3m_00598	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2572232242	t3m_00598	KEGG_module	M00114: Ascorbate biosynthesis, plants, glucose-6P => ascorbate			
2572232242	t3m_00598	Metacyc	PWY-3861: mannitol degradation II			
2572232242	t3m_00598	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2572232242	t3m_00598	Metacyc	PWY-5659: GDP-mannose biosynthesis			
2572232242	t3m_00598	Metacyc	PWY-5384: sucrose degradation IV			
2572232242	t3m_00598	Metacyc	PWY-5054: sorbitol biosynthesis I			

2572232242	t3m_00598	Metacyc	PWY-6981: chitin biosynthesis			
2572232242	t3m_00598	Metacyc	RUMP-PWY: formaldehyde oxidation I			
2572232242	t3m_00598	Metacyc	GLYCOLYSIS: glycolysis I			
2572232242	t3m_00598	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2572232242	t3m_00598	Metacyc	P341-PWY: glycolysis V (Pyrococcus)			
2572232242	t3m_00598	Metacyc	PWY-3801: sucrose degradation VI (anaerobic)			
2572232242	t3m_00598	Metacyc	MANNCAT-PWY: D-mannose degradation			
2572232242	t3m_00598	Metacyc	PWY-621: sucrose degradation III			
2572232242	t3m_00598	Metacyc	SUCSYN-PWY: sucrose biosynthesis			
2572232242	t3m_00598	Metacyc	PWY-6531: mannitol cycle			
2572232242	t3m_00598	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)			
2572232242	t3m_00598	Metacyc	PWY-3881: mannitol biosynthesis			
2572232242	t3m_00598	Metacyc	PWY-5514: UDP-<i>N</i>-acetyl-D-galactosamine biosynthesis II			
2572232242	t3m_00598	Metacyc	P124-PWY: Bifidobacterium shunt			
2572232242	t3m_00598	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)			
2572232242	t3m_00598	Metacyc	PWY-622: starch biosynthesis			
2572232242	t3m_00598	Metacyc	P122-PWY: heterolactic fermentation			
2572232242	t3m_00598	Metacyc	ANAEROFRUCAT-PWY: homolactic fermentation			
2572232242	t3m_00598	COG_category	[G] Carbohydrate transport and metabolism			
2572232242	t3m_00598	COG0166	Glucose-6-phosphate isomerase			2.00E-14
2572232242	t3m_00598	pfam10432	bact-PGI_C			2.60E-28
2572232242	t3m_00598	EC:5.3.1.8	Mannose-6-phosphate isomerase.			
2572232242	t3m_00598	EC:5.3.1.9	Glucose-6-phosphate isomerase.			
2572232242	t3m_00598	TIGR02128	bifunctional phosphoglucose/phosphomannose isomerase			1.60E-57
2572232242	t3m_00598	KO:K15916	glucose/mannose-6-phosphate isomerase [EC:5.3.1.9 5.3.1.8]			1.00E-42
2572232242	t3m_00598	Locus_type		CDS		
2572232242	t3m_00598	Product_name		Glucose-6-phosphate isomerase		
2572232242	t3m_00598	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232242	t3m_00598	Coordinates		31745..32758(+)		
2572232242	t3m_00598	DNA_length		1014bp		
2572232242	t3m_00598	Protein_length		337aa		
2572232242	t3m_00598	GC			0.72	
2572232243	t3m_00599	Locus_type		CDS		

2572232243	t3m_00599	Product_name		hypothetical protein	
2572232243	t3m_00599	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232243	t3m_00599	Coordinates		33036..33242(+)	
2572232243	t3m_00599	DNA_length		207bp	
2572232243	t3m_00599	Protein_length		68aa	
2572232243	t3m_00599	GC			0.75
2572232244	t3m_00600	Locus_type		CDS	
2572232244	t3m_00600	Product_name		hypothetical protein	
2572232244	t3m_00600	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232244	t3m_00600	Coordinates		33396..34568(+)	
2572232244	t3m_00600	DNA_length		1173bp	
2572232244	t3m_00600	Protein_length		390aa	
2572232244	t3m_00600	GC			0.71
2572232245	t3m_00601	Locus_type		CDS	
2572232245	t3m_00601	Product_name		hypothetical protein	
2572232245	t3m_00601	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232245	t3m_00601	Coordinates		34572..35657(+)	
2572232245	t3m_00601	DNA_length		1086bp	
2572232245	t3m_00601	Protein_length		361aa	
2572232245	t3m_00601	GC			0.72
2572232246	t3m_00602	Locus_type		CDS	
2572232246	t3m_00602	Product_name		hypothetical protein	
2572232246	t3m_00602	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232246	t3m_00602	Coordinates		35737..35958(+)	
2572232246	t3m_00602	DNA_length		222bp	
2572232246	t3m_00602	Protein_length		73aa	
2572232246	t3m_00602	GC			0.75
2572232247	t3m_00603	COG_category	[K] Transcription		
2572232247	t3m_00603	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatio		2.00E-99
2572232247	t3m_00603	pfam00382	TFIIB		3.70E-19

2572232247	t3m_00603	pfam00382	TFIIB			6.80E-23
2572232247	t3m_00603	pfam08271	TF_Zn_Ribbon			4.80E-17
2572232247	t3m_00603	KO:K03124	transcription initiation factor TFIIB			0.00E+00
2572232247	t3m_00603	Locus_type		CDS		
2572232247	t3m_00603	Product_name		Transcription initiation factor IIB (TFIIB)		
2572232247	t3m_00603	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232247	t3m_00603	Coordinates		35973..36941(+)		
2572232247	t3m_00603	DNA_length		969bp		
2572232247	t3m_00603	Protein_length		322aa		
2572232247	t3m_00603	GC			0.67	

2572232248	t3m_00604	COG_category	[R] General function prediction only			
2572232248	t3m_00604	COG0312	Predicted Zn-dependent proteases and their inactivated homologs			6.00E-67
2572232248	t3m_00604	pfam01523	PmbA_TldD			2.60E-55
2572232248	t3m_00604	KO:K03568	TldD protein			0.00E+00
2572232248	t3m_00604	Locus_type		CDS		
2572232248	t3m_00604	Product_name		Predicted Zn-dependent proteases and their inactivated homologs		
2572232248	t3m_00604	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232248	t3m_00604	Coordinates		37028..38476(+)		
2572232248	t3m_00604	DNA_length		1449bp		
2572232248	t3m_00604	Protein_length		482aa		
2572232248	t3m_00604	GC			0.71	

2572232249	t3m_00605	COG_category	[R] General function prediction only			
2572232249	t3m_00605	COG0312	Predicted Zn-dependent proteases and their inactivated homologs			5.00E-44
2572232249	t3m_00605	pfam01523	PmbA_TldD			2.10E-40
2572232249	t3m_00605	Locus_type		CDS		
2572232249	t3m_00605	Product_name		Predicted Zn-dependent proteases and their inactivated homologs		
2572232249	t3m_00605	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232249	t3m_00605	Coordinates		38479..39852(+)		
2572232249	t3m_00605	DNA_length		1374bp		
2572232249	t3m_00605	Protein_length		457aa		
2572232249	t3m_00605	GC			0.71	

2572232250	t3m_00606	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP			
2572232250	t3m_00606	Metacyc	PWY-6613: tetrahydrofolate salvage from 5,10-methenyltetrahydrofolate			
2572232250	t3m_00606	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I			
2572232250	t3m_00606	COG_category	[F] Nucleotide transport and metabolism			
2572232250	t3m_00606	COG0299	Folate-dependent phosphoribosylglycinamide formyltransferase PurN			5.00E-51
2572232250	t3m_00606	pfam00551	Formyl_trans_N			9.20E-42
2572232250	t3m_00606	EC:2.1.2.2	Phosphoribosylglycinamide formyltransferase.			
2572232250	t3m_00606	TIGR00639	phosphoribosylglycinamide formyltransferase, formyltetrahydrofolate-			2.80E-49
2572232250	t3m_00606	KO:K11175	phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]			1.40E-45
2572232250	t3m_00606	Locus_type		CDS		
2572232250	t3m_00606	Product_name		phosphoribosylglycinamide formyltransferase, formyltetrahydrofolate-d		
2572232250	t3m_00606	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232250	t3m_00606	Coordinates		39874..40533(+)		
2572232250	t3m_00606	DNA_length		660bp		
2572232250	t3m_00606	Protein_length		219aa		
2572232250	t3m_00606	GC			0.73	

2572232251	t3m_00607	pfam02195	ParBc			5.90E-09
2572232251	t3m_00607	Locus_type		CDS		
2572232251	t3m_00607	Product_name		ParB-like nuclease domain		
2572232251	t3m_00607	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232251	t3m_00607	Coordinates		40506..40955(-)		
2572232251	t3m_00607	DNA_length		450bp		
2572232251	t3m_00607	Protein_length		149aa		
2572232251	t3m_00607	GC			0.69	

2572232252	t3m_00608	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232252	t3m_00608	COG1975	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family			2.00E-28
2572232252	t3m_00608	pfam02625	XdhC_CoxI			1.00E-19
2572232252	t3m_00608	pfam13478	XdhC_C			2.20E-31
2572232252	t3m_00608	KO:K07402	xanthine dehydrogenase accessory factor			2.90E-35
2572232252	t3m_00608	Locus_type		CDS		
2572232252	t3m_00608	Product_name		Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family		
2572232252	t3m_00608	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		

2572232252	t3m_00608	Coordinates		41058..41903(-)		
2572232252	t3m_00608	DNA_length		846bp		
2572232252	t3m_00608	Protein_length		281aa		
2572232252	t3m_00608	GC			0.69	
2572232253	t3m_00609	COG_category	[R] General function prediction only			
2572232253	t3m_00609	COG2068	Uncharacterized MobA-related protein			1.00E-24
2572232253	t3m_00609	pfam12804	NTP_transf_3			5.80E-32
2572232253	t3m_00609	Locus_type		CDS		
2572232253	t3m_00609	Product_name		Uncharacterized MobA-related protein		
2572232253	t3m_00609	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232253	t3m_00609	Coordinates		41903..42511(-)		
2572232253	t3m_00609	DNA_length		609bp		
2572232253	t3m_00609	Protein_length		202aa		
2572232253	t3m_00609	GC			0.71	
2572232254	t3m_00610	KEGG_module	M00177: Ribosome, eukaryotes			
2572232254	t3m_00610	KEGG_module	M00179: Ribosome, archaea			
2572232254	t3m_00610	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232254	t3m_00610	COG2238	Ribosomal protein S19E (S16A)			1.00E-43
2572232254	t3m_00610	pfam01090	Ribosomal_S19e			4.90E-49
2572232254	t3m_00610	KO:K02966	small subunit ribosomal protein S19e			1.40E-37
2572232254	t3m_00610	ITERM:00336	SSU ribosomal protein S19E			
2572232254	t3m_00610	Locus_type		CDS		
2572232254	t3m_00610	Product_name		SSU ribosomal protein S19E		
2572232254	t3m_00610	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232254	t3m_00610	Coordinates		42710..43165(+)		
2572232254	t3m_00610	DNA_length		456bp		
2572232254	t3m_00610	Protein_length		151aa		
2572232254	t3m_00610	GC			0.66	
2572232255	t3m_00611	COG_category	[R] General function prediction only			
2572232255	t3m_00611	COG2118	DNA-binding protein			3.00E-11
2572232255	t3m_00611	pfam01984	dsDNA_bind			3.60E-28

2572232255	t3m_00611	KO:K06875	programmed cell death protein 5		4.90E-25
2572232255	t3m_00611	ITERM:01948	DNA-binding TFAR19-related protein		
2572232255	t3m_00611	Locus_type		CDS	
2572232255	t3m_00611	Product_name		DNA-binding TFAR19-related protein	
2572232255	t3m_00611	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232255	t3m_00611	Coordinates		43195..43554(+)	
2572232255	t3m_00611	DNA_length		360bp	
2572232255	t3m_00611	Protein_length		119aa	
2572232255	t3m_00611	GC		0.7	
2572232256	t3m_00612	KEGG_module	M00177: Ribosome, eukaryotes		
2572232256	t3m_00612	KEGG_module	M00179: Ribosome, archaea		
2572232256	t3m_00612	pfam00832	Ribosomal_L39		6.70E-13
2572232256	t3m_00612	KO:K02924	large subunit ribosomal protein L39e		5.70E-10
2572232256	t3m_00612	ITERM:00272	LSU ribosomal protein L39E		
2572232256	t3m_00612	Locus_type		CDS	
2572232256	t3m_00612	Product_name		LSU ribosomal protein L39E	
2572232256	t3m_00612	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232256	t3m_00612	Coordinates		43567..43725(+)	
2572232256	t3m_00612	DNA_length		159bp	
2572232256	t3m_00612	Protein_length		52aa	
2572232256	t3m_00612	GC		0.65	
2572232257	t3m_00613	KEGG_module	M00179: Ribosome, archaea		
2572232257	t3m_00613	KEGG_module	M00177: Ribosome, eukaryotes		
2572232257	t3m_00613	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232257	t3m_00613	COG2097	Ribosomal protein L31E		9.00E-18
2572232257	t3m_00613	pfam01198	Ribosomal_L31e		2.30E-26
2572232257	t3m_00613	KO:K02910	large subunit ribosomal protein L31e		1.30E-15
2572232257	t3m_00613	Locus_type		CDS	
2572232257	t3m_00613	Product_name		Ribosomal protein L31E	
2572232257	t3m_00613	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9	
2572232257	t3m_00613	Coordinates		43757..44053(+)	
2572232257	t3m_00613	DNA_length		297bp	

2572232257	t3m_00613	Protein_length		98aa		
2572232257	t3m_00613	GC			0.67	

2572232258	t3m_00614	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232258	t3m_00614	COG1976	Translation initiation factor 6 (eIF-6)			3.00E-51
2572232258	t3m_00614	pfam01912	eIF-6			1.00E-58
2572232258	t3m_00614	TIGR00323	translation initiation factor eIF-6, putative			3.60E-61
2572232258	t3m_00614	KO:K03264	translation initiation factor 6			3.90E-41
2572232258	t3m_00614	ITERM:01949	translation initiation factor 6 (aeIF-6)			
2572232258	t3m_00614	Locus_type		CDS		
2572232258	t3m_00614	Product_name		translation initiation factor 6 (aeIF-6)		
2572232258	t3m_00614	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232258	t3m_00614	Coordinates		44099..44743(+)		
2572232258	t3m_00614	DNA_length		645bp		
2572232258	t3m_00614	Protein_length		214aa		
2572232258	t3m_00614	GC			0.69	

2572232259	t3m_00615	KEGG_module	M00177: Ribosome, eukaryotes			
2572232259	t3m_00615	KEGG_module	M00179: Ribosome, archaea			
2572232259	t3m_00615	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232259	t3m_00615	COG1383	Ribosomal protein S17E			1.00E-11
2572232259	t3m_00615	pfam00833	Ribosomal_S17e			2.80E-10
2572232259	t3m_00615	KO:K02962	small subunit ribosomal protein S17e			5.00E-12
2572232259	t3m_00615	ITERM:00327	SSU ribosomal protein S17E			
2572232259	t3m_00615	Locus_type		CDS		
2572232259	t3m_00615	Product_name		SSU ribosomal protein S17E		
2572232259	t3m_00615	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232259	t3m_00615	Coordinates		44799..45023(-)		
2572232259	t3m_00615	DNA_length		225bp		
2572232259	t3m_00615	Protein_length		74aa		
2572232259	t3m_00615	GC			0.62	

2572232260	t3m_00616	pfam13519	VWA_2			3.20E-12
2572232260	t3m_00616	Locus_type		CDS		

2572232260	t3m_00616	Product_name		von Willebrand factor type A domain		
2572232260	t3m_00616	Scaffold		t3m_contig_70_65_len_46776_read_count_3444312.9		
2572232260	t3m_00616	Coordinates		45230..46735(+)		
2572232260	t3m_00616	DNA_length		1506bp		
2572232260	t3m_00616	Protein_length		501aa		
2572232260	t3m_00616	GC			0.69	
2572232261	t3m_00617	Locus_type		CDS		
2572232261	t3m_00617	Product_name		hypothetical protein		
2572232261	t3m_00617	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232261	t3m_00617	Coordinates		112..333(-)		
2572232261	t3m_00617	DNA_length		222bp		
2572232261	t3m_00617	Protein_length		73aa		
2572232261	t3m_00617	GC			0.59	
2572232262	t3m_00618	Locus_type		CDS		
2572232262	t3m_00618	Product_name		hypothetical protein		
2572232262	t3m_00618	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232262	t3m_00618	Coordinates		1373..1585(-)		
2572232262	t3m_00618	DNA_length		213bp		
2572232262	t3m_00618	Protein_length		70aa		
2572232262	t3m_00618	GC			0.54	
2572232262	t3m_00618	Transmembrane		Yes		
2572232263	t3m_00619	Locus_type		CDS		
2572232263	t3m_00619	Product_name		hypothetical protein		
2572232263	t3m_00619	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232263	t3m_00619	Coordinates		2117..2248(-)		
2572232263	t3m_00619	DNA_length		132bp		
2572232263	t3m_00619	Protein_length		43aa		
2572232263	t3m_00619	GC			0.67	
2572232264	t3m_00620	COG_category	[T] Signal transduction mechanisms			
2572232264	t3m_00620	COG0467	RecA-superfamily ATPases implicated in signal transduction			2.00E-08

2572232264	t3m_00620	pfam07088	GvpD		3.10E-23
2572232264	t3m_00620	Locus_type		CDS	
2572232264	t3m_00620	Product_name		RecA-superfamily ATPases implicated in signal transduction	
2572232264	t3m_00620	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232264	t3m_00620	Coordinates		2485..3936(+)	
2572232264	t3m_00620	DNA_length		1452bp	
2572232264	t3m_00620	Protein_length		483aa	
2572232264	t3m_00620	GC		0.63	
2572232265	t3m_00621	COG_category	[R] General function prediction only		
2572232265	t3m_00621	COG1011	Predicted hydrolase (HAD superfamily)		8.00E-15
2572232265	t3m_00621	pfam13419	HAD_2		4.10E-21
2572232265	t3m_00621	TIGR01493	Haloacid dehalogenase superfamily, subfamily IA, variant 2 with 3rd mc		9.10E-10
2572232265	t3m_00621	TIGR01549	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m		1.10E-09
2572232265	t3m_00621	TIGR01509	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third m		5.20E-10
2572232265	t3m_00621	KO:K07025	putative hydrolase of the HAD superfamily		3.40E-11
2572232265	t3m_00621	Locus_type		CDS	
2572232265	t3m_00621	Product_name		haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m	
2572232265	t3m_00621	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232265	t3m_00621	Coordinates		4159..4920(+)	
2572232265	t3m_00621	DNA_length		762bp	
2572232265	t3m_00621	Protein_length		253aa	
2572232265	t3m_00621	GC		0.61	
2572232266	t3m_00622	Locus_type		CDS	
2572232266	t3m_00622	Product_name		hypothetical protein	
2572232266	t3m_00622	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232266	t3m_00622	Coordinates		5235..5663(+)	
2572232266	t3m_00622	DNA_length		429bp	
2572232266	t3m_00622	Protein_length		142aa	
2572232266	t3m_00622	GC		0.6	
2572232267	t3m_00623	Locus_type		CDS	
2572232267	t3m_00623	Product_name		hypothetical protein	

2572232267	t3m_00623	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10
2572232267	t3m_00623	Coordinates		5808..6383(-)
2572232267	t3m_00623	DNA_length		576bp
2572232267	t3m_00623	Protein_length		191aa
2572232267	t3m_00623	GC		0.58
2572232267	t3m_00623	Transmembrane		Yes
2572232268	t3m_00624	Locus_type		CDS
2572232268	t3m_00624	Product_name		hypothetical protein
2572232268	t3m_00624	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10
2572232268	t3m_00624	Coordinates		6595..7044(-)
2572232268	t3m_00624	DNA_length		450bp
2572232268	t3m_00624	Protein_length		149aa
2572232268	t3m_00624	GC		0.58
2572232268	t3m_00624	Transmembrane		Yes
2572232269	t3m_00625	Locus_type		CDS
2572232269	t3m_00625	Product_name		hypothetical protein
2572232269	t3m_00625	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10
2572232269	t3m_00625	Coordinates		7204..7848(+)
2572232269	t3m_00625	DNA_length		645bp
2572232269	t3m_00625	Protein_length		214aa
2572232269	t3m_00625	GC		0.68
2572232270	t3m_00626	Locus_type		CDS
2572232270	t3m_00626	Product_name		hypothetical protein
2572232270	t3m_00626	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10
2572232270	t3m_00626	Coordinates		8279..8476(-)
2572232270	t3m_00626	DNA_length		198bp
2572232270	t3m_00626	Protein_length		65aa
2572232270	t3m_00626	GC		0.62
2572232271	t3m_00627	KEGG_module	M00254: ABC-2 type transport system	
2572232271	t3m_00627	COG_category	[V] Defense mechanisms	

2572232271	t3m_00627	COG1131	ABC-type multidrug transport system, ATPase component		2.00E-55
2572232271	t3m_00627	pfam00005	ABC_tran		1.40E-20
2572232271	t3m_00627	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2572232271	t3m_00627	Locus_type		CDS	
2572232271	t3m_00627	Product_name		ABC-type multidrug transport system, ATPase component	
2572232271	t3m_00627	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232271	t3m_00627	Coordinates		9794..10702(+)	
2572232271	t3m_00627	DNA_length		909bp	
2572232271	t3m_00627	Protein_length		302aa	
2572232271	t3m_00627	GC		0.58	
2572232272	t3m_00628	COG_category	[R] General function prediction only		
2572232272	t3m_00628	COG1277	ABC-type transport system involved in multi-copper enzyme maturatior		4.00E-03
2572232272	t3m_00628	pfam12679	ABC2_membrane_2		1.80E-06
2572232272	t3m_00628	Locus_type		CDS	
2572232272	t3m_00628	Product_name		ABC-2 family transporter protein	
2572232272	t3m_00628	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232272	t3m_00628	Coordinates		11431..12195(+)	
2572232272	t3m_00628	DNA_length		765bp	
2572232272	t3m_00628	Protein_length		254aa	
2572232272	t3m_00628	GC		0.6	
2572232272	t3m_00628	Transmembrane		Yes	
2572232273	t3m_00629	Locus_type		CDS	
2572232273	t3m_00629	Product_name		hypothetical protein	
2572232273	t3m_00629	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232273	t3m_00629	Coordinates		12211..12822(+)	
2572232273	t3m_00629	DNA_length		612bp	
2572232273	t3m_00629	Protein_length		203aa	
2572232273	t3m_00629	GC		0.69	
2572232274	t3m_00630	Locus_type		CDS	
2572232274	t3m_00630	Product_name		hypothetical protein	
2572232274	t3m_00630	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	

2572232274	t3m_00630	Coordinates		13566..13745(-)		
2572232274	t3m_00630	DNA_length		180bp		
2572232274	t3m_00630	Protein_length		59aa		
2572232274	t3m_00630	GC			0.61	
2572232275	t3m_00631	COG_category	[S] Function unknown			
2572232275	t3m_00631	COG3391	Uncharacterized conserved protein			8.00E-14
2572232275	t3m_00631	pfam01436	NHL			8.30E-05
2572232275	t3m_00631	TIGR02276	40-residue YVTN family beta-propeller repeat			6.20E-14
2572232275	t3m_00631	Locus_type		CDS		
2572232275	t3m_00631	Product_name		40-residue YVTN family beta-propeller repeat		
2572232275	t3m_00631	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232275	t3m_00631	Coordinates		15435..16739(+)		
2572232275	t3m_00631	DNA_length		1305bp		
2572232275	t3m_00631	Protein_length		434aa		
2572232275	t3m_00631	GC			0.61	
2572232275	t3m_00631	Transmembrane		Yes		
2572232276	t3m_00632	Locus_type		CDS		
2572232276	t3m_00632	Product_name		hypothetical protein		
2572232276	t3m_00632	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232276	t3m_00632	Coordinates		17035..17241(+)		
2572232276	t3m_00632	DNA_length		207bp		
2572232276	t3m_00632	Protein_length		68aa		
2572232276	t3m_00632	GC			0.61	
2572232277	t3m_00633	Locus_type		CDS		
2572232277	t3m_00633	Product_name		hypothetical protein		
2572232277	t3m_00633	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232277	t3m_00633	Coordinates		18031..18450(+)		
2572232277	t3m_00633	DNA_length		420bp		
2572232277	t3m_00633	Protein_length		139aa		
2572232277	t3m_00633	GC			0.57	
2572232277	t3m_00633	Transmembrane		Yes		

2572232278	t3m_00634	Locus_type		CDS		
2572232278	t3m_00634	Product_name		hypothetical protein		
2572232278	t3m_00634	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232278	t3m_00634	Coordinates		18460..18708(+)		
2572232278	t3m_00634	DNA_length		249bp		
2572232278	t3m_00634	Protein_length		82aa		
2572232278	t3m_00634	GC			0.63	
2572232278	t3m_00634	Transmembrane		Yes		
2572232279	t3m_00635	Locus_type		CDS		
2572232279	t3m_00635	Product_name		hypothetical protein		
2572232279	t3m_00635	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232279	t3m_00635	Coordinates		19342..19917(+)		
2572232279	t3m_00635	DNA_length		576bp		
2572232279	t3m_00635	Protein_length		191aa		
2572232279	t3m_00635	GC			0.64	
2572232280	t3m_00636	COG_category	[R] General function prediction only			
2572232280	t3m_00636	COG3413	Predicted DNA binding protein			3.00E-09
2572232280	t3m_00636	pfam04967	HTH_10			1.30E-09
2572232280	t3m_00636	Locus_type		CDS		
2572232280	t3m_00636	Product_name		Predicted DNA binding protein		
2572232280	t3m_00636	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232280	t3m_00636	Coordinates		19980..20603(+)		
2572232280	t3m_00636	DNA_length		624bp		
2572232280	t3m_00636	Protein_length		207aa		
2572232280	t3m_00636	GC			0.58	
2572232281	t3m_00637	COG_category	[T] Signal transduction mechanisms			
2572232281	t3m_00637	COG0467	RecA-superfamily ATPases implicated in signal transduction			3.00E-11
2572232281	t3m_00637	pfam07088	GvpD			5.60E-22
2572232281	t3m_00637	Locus_type		CDS		
2572232281	t3m_00637	Product_name		RecA-superfamily ATPases implicated in signal transduction		

2572232281	t3m_00637	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232281	t3m_00637	Coordinates		20695..22197(+)	
2572232281	t3m_00637	DNA_length		1503bp	
2572232281	t3m_00637	Protein_length		500aa	
2572232281	t3m_00637	GC			0.61
2572232282	t3m_00638	Locus_type		CDS	
2572232282	t3m_00638	Product_name		hypothetical protein	
2572232282	t3m_00638	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232282	t3m_00638	Coordinates		22493..22672(-)	
2572232282	t3m_00638	DNA_length		180bp	
2572232282	t3m_00638	Protein_length		59aa	
2572232282	t3m_00638	GC			0.56
2572232283	t3m_00639	Locus_type		tRNA	
2572232283	t3m_00639	Product_name		tRNA_Thr_TGT	
2572232283	t3m_00639	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232283	t3m_00639	Coordinates		22940..23012(+)	
2572232283	t3m_00639	DNA_length		73bp	
2572232283	t3m_00639	GC			0.58
2572232284	t3m_00640	Locus_type		CDS	
2572232284	t3m_00640	Product_name		hypothetical protein	
2572232284	t3m_00640	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232284	t3m_00640	Coordinates		23225..23449(+)	
2572232284	t3m_00640	DNA_length		225bp	
2572232284	t3m_00640	Protein_length		74aa	
2572232284	t3m_00640	GC			0.61
2572232284	t3m_00640	Transmembrane		Yes	
2572232285	t3m_00641	TIGR02537	archaeal flagellin N-terminal-like domain		3.60E-08
2572232285	t3m_00641	Locus_type		CDS	
2572232285	t3m_00641	Product_name		archaeal flagellin N-terminal-like domain	
2572232285	t3m_00641	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	

2572232285	t3m_00641	Coordinates		23579..24544(+)		
2572232285	t3m_00641	DNA_length		966bp		
2572232285	t3m_00641	Protein_length		321aa		
2572232285	t3m_00641	GC			0.62	
2572232285	t3m_00641	Transmembrane		Yes		
2572232286	t3m_00642	Locus_type		CDS		
2572232286	t3m_00642	Product_name		hypothetical protein		
2572232286	t3m_00642	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232286	t3m_00642	Coordinates		24599..25099(+)		
2572232286	t3m_00642	DNA_length		501bp		
2572232286	t3m_00642	Protein_length		166aa		
2572232286	t3m_00642	GC			0.62	
2572232286	t3m_00642	Transmembrane		Yes		
2572232287	t3m_00643	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232287	t3m_00643	COG1225	Peroxiredoxin			7.00E-39
2572232287	t3m_00643	pfam00578	AhpC-TSA			3.90E-35
2572232287	t3m_00643	EC:1.11.1.15	Peroxiredoxin.			
2572232287	t3m_00643	KO:K03564	peroxiredoxin Q/BCP [EC:1.11.1.15]			5.80E-31
2572232287	t3m_00643	Locus_type		CDS		
2572232287	t3m_00643	Product_name		Peroxiredoxin		
2572232287	t3m_00643	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232287	t3m_00643	Coordinates		25225..25677(-)		
2572232287	t3m_00643	DNA_length		453bp		
2572232287	t3m_00643	Protein_length		150aa		
2572232287	t3m_00643	GC			0.68	
2572232288	t3m_00644	COG_category	[C] Energy production and conversion			
2572232288	t3m_00644	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)			7.00E-14
2572232288	t3m_00644	Locus_type		CDS		
2572232288	t3m_00644	Product_name		Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)		
2572232288	t3m_00644	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232288	t3m_00644	Coordinates		25698..26654(-)		

2572232288	t3m_00644	DNA_length		957bp		
2572232288	t3m_00644	Protein_length		318aa		
2572232288	t3m_00644	GC			0.71	
2572232289	t3m_00645	pfam00004	AAA			2.70E-12
2572232289	t3m_00645	Locus_type		CDS		
2572232289	t3m_00645	Product_name		ATPase family associated with various cellular activities (AAA)		
2572232289	t3m_00645	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232289	t3m_00645	Coordinates		26750..28456(+)		
2572232289	t3m_00645	DNA_length		1707bp		
2572232289	t3m_00645	Protein_length		568aa		
2572232289	t3m_00645	GC			0.71	
2572232290	t3m_00646	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232290	t3m_00646	COG1764	Predicted redox protein, regulator of disulfide bond formation			3.00E-16
2572232290	t3m_00646	pfam02566	OsmC			8.60E-19
2572232290	t3m_00646	TIGR03562	peroxiredoxin, OsmC subfamily			3.40E-49
2572232290	t3m_00646	KO:K04063	osmotically inducible protein OsmC			2.20E-42
2572232290	t3m_00646	Locus_type		CDS		
2572232290	t3m_00646	Product_name		peroxiredoxin, OsmC subfamily		
2572232290	t3m_00646	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232290	t3m_00646	Coordinates		28478..28918(-)		
2572232290	t3m_00646	DNA_length		441bp		
2572232290	t3m_00646	Protein_length		146aa		
2572232290	t3m_00646	GC			0.68	
2572232291	t3m_00647	Locus_type		CDS		
2572232291	t3m_00647	Product_name		hypothetical protein		
2572232291	t3m_00647	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232291	t3m_00647	Coordinates		29008..29445(+)		
2572232291	t3m_00647	DNA_length		438bp		
2572232291	t3m_00647	Protein_length		145aa		
2572232291	t3m_00647	GC			0.7	

2572232292	t3m_00648	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2572232292	t3m_00648	COG2095	Multiple antibiotic transporter			1.00E-34
2572232292	t3m_00648	pfam01914	MarC			1.20E-58
2572232292	t3m_00648	TIGR00427	membrane protein, MarC family			2.00E-64
2572232292	t3m_00648	KO:K05595	multiple antibiotic resistance protein			5.40E-43
2572232292	t3m_00648	Locus_type		CDS		
2572232292	t3m_00648	Product_name		membrane protein, MarC family		
2572232292	t3m_00648	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232292	t3m_00648	Coordinates		29524..30159(+)		
2572232292	t3m_00648	DNA_length		636bp		
2572232292	t3m_00648	Protein_length		211aa		
2572232292	t3m_00648	GC			0.67	
2572232292	t3m_00648	Transmembrane		Yes		

2572232293	t3m_00649	pfam07920	DUF1684			1.50E-43
2572232293	t3m_00649	KO:K09164	hypothetical protein			8.70E-31
2572232293	t3m_00649	Locus_type		CDS		
2572232293	t3m_00649	Product_name		Protein of unknown function (DUF1684)		
2572232293	t3m_00649	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232293	t3m_00649	Coordinates		30125..30805(-)		
2572232293	t3m_00649	DNA_length		681bp		
2572232293	t3m_00649	Protein_length		226aa		
2572232293	t3m_00649	GC			0.68	

2572232294	t3m_00650	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232294	t3m_00650	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins			2.00E-10
2572232294	t3m_00650	pfam00583	Acetyltransf_1			1.10E-13
2572232294	t3m_00650	Locus_type		CDS		
2572232294	t3m_00650	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins		
2572232294	t3m_00650	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232294	t3m_00650	Coordinates		30831..31403(-)		
2572232294	t3m_00650	DNA_length		573bp		
2572232294	t3m_00650	Protein_length		190aa		
2572232294	t3m_00650	GC			0.65	

2572232295	t3m_00651	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232295	t3m_00651	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins		6.00E-11
2572232295	t3m_00651	pfam00583	Acetyltransf_1		7.80E-15
2572232295	t3m_00651	Locus_type		CDS	
2572232295	t3m_00651	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins	
2572232295	t3m_00651	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232295	t3m_00651	Coordinates		31429..32001(-)	
2572232295	t3m_00651	DNA_length		573bp	
2572232295	t3m_00651	Protein_length		190aa	
2572232295	t3m_00651	GC		0.65	
2572232296	t3m_00652	COG_category	[R] General function prediction only		
2572232296	t3m_00652	COG2151	Predicted metal-sulfur cluster biosynthetic enzyme		5.00E-26
2572232296	t3m_00652	pfam01883	DUF59		1.40E-12
2572232296	t3m_00652	Locus_type		CDS	
2572232296	t3m_00652	Product_name		Predicted metal-sulfur cluster biosynthetic enzyme	
2572232296	t3m_00652	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232296	t3m_00652	Coordinates		32029..32406(-)	
2572232296	t3m_00652	DNA_length		378bp	
2572232296	t3m_00652	Protein_length		125aa	
2572232296	t3m_00652	GC		0.66	
2572232297	t3m_00653	COG_category	[S] Function unknown		
2572232297	t3m_00653	COG1469	Uncharacterized conserved protein		1.00E-56
2572232297	t3m_00653	pfam02649	GCHY-1		1.50E-60
2572232297	t3m_00653	TIGR00294	GTP cyclohydrolase, MptA/FolE2 family		6.90E-64
2572232297	t3m_00653	KO:K09007	hypothetical protein		0.00E+00
2572232297	t3m_00653	Locus_type		CDS	
2572232297	t3m_00653	Product_name		GTP cyclohydrolase, MptA/FolE2 family	
2572232297	t3m_00653	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10	
2572232297	t3m_00653	Coordinates		32510..33418(+)	
2572232297	t3m_00653	DNA_length		909bp	
2572232297	t3m_00653	Protein_length		302aa	

2572232297	t3m_00653	GC			0.68	
2572232298	t3m_00654	pfam02687	FtsX			1.80E-15
2572232298	t3m_00654	pfam12704	MacB_PCD			1.10E-08
2572232298	t3m_00654	Locus_type		CDS		
2572232298	t3m_00654	Product_name		MacB-like periplasmic core domain/FtsX-like permease family		
2572232298	t3m_00654	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232298	t3m_00654	Coordinates		33485..34732(+)		
2572232298	t3m_00654	DNA_length		1248bp		
2572232298	t3m_00654	Protein_length		415aa		
2572232298	t3m_00654	GC			0.68	
2572232298	t3m_00654	Transmembrane		Yes		
2572232299	t3m_00655	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232299	t3m_00655	COG4591	ABC-type transport system, involved in lipoprotein release, permease c			5.00E-15
2572232299	t3m_00655	pfam12704	MacB_PCD			1.10E-12
2572232299	t3m_00655	pfam02687	FtsX			1.30E-12
2572232299	t3m_00655	Locus_type		CDS		
2572232299	t3m_00655	Product_name		ABC-type transport system, involved in lipoprotein release, permease cc		
2572232299	t3m_00655	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232299	t3m_00655	Coordinates		34732..35970(+)		
2572232299	t3m_00655	DNA_length		1239bp		
2572232299	t3m_00655	Protein_length		412aa		
2572232299	t3m_00655	GC			0.7	
2572232299	t3m_00655	Transmembrane		Yes		
2572232300	t3m_00656	KEGG_module	M00258: Putative ABC transport system			
2572232300	t3m_00656	COG_category	[V] Defense mechanisms			
2572232300	t3m_00656	COG1136	ABC-type antimicrobial peptide transport system, ATPase component			3.00E-74
2572232300	t3m_00656	pfam00005	ABC_tran			2.80E-31
2572232300	t3m_00656	KO:K02003	putative ABC transport system ATP-binding protein			0.00E+00
2572232300	t3m_00656	Locus_type		CDS		
2572232300	t3m_00656	Product_name		ABC-type antimicrobial peptide transport system, ATPase component		
2572232300	t3m_00656	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		

2572232300	t3m_00656	Coordinates		35967..36671(+)		
2572232300	t3m_00656	DNA_length		705bp		
2572232300	t3m_00656	Protein_length		234aa		
2572232300	t3m_00656	GC			0.72	
2572232301	t3m_00657	COG_category	[R] General function prediction only			
2572232301	t3m_00657	COG1245	Predicted ATPase, RNase L inhibitor (RLI) homolog			0.00E+00
2572232301	t3m_00657	pfam04068	RLI			4.70E-08
2572232301	t3m_00657	pfam00037	Fer4			1.30E-08
2572232301	t3m_00657	pfam00005	ABC_tran			3.50E-13
2572232301	t3m_00657	pfam00005	ABC_tran			1.30E-15
2572232301	t3m_00657	KO:K06174	ATP-binding cassette, sub-family E, member 1			0.00E+00
2572232301	t3m_00657	Locus_type		CDS		
2572232301	t3m_00657	Product_name		Predicted ATPase, RNase L inhibitor (RLI) homolog		
2572232301	t3m_00657	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232301	t3m_00657	Coordinates		36682..38460(+)		
2572232301	t3m_00657	DNA_length		1779bp		
2572232301	t3m_00657	Protein_length		592aa		
2572232301	t3m_00657	GC			0.68	
2572232302	t3m_00658	pfam10882	bPH_5			2.50E-06
2572232302	t3m_00658	Locus_type		CDS		
2572232302	t3m_00658	Product_name		Bacterial PH domain		
2572232302	t3m_00658	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232302	t3m_00658	Coordinates		38513..39055(+)		
2572232302	t3m_00658	DNA_length		543bp		
2572232302	t3m_00658	Protein_length		180aa		
2572232302	t3m_00658	GC			0.64	
2572232302	t3m_00658	Transmembrane		Yes		
2572232303	t3m_00659	COG_category	[H] Coenzyme transport and metabolism			
2572232303	t3m_00659	COG0476	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine			4.00E-75
2572232303	t3m_00659	pfam02597	ThiS			1.40E-07
2572232303	t3m_00659	pfam05237	MoeZ_MoeB			8.20E-31

2572232303	t3m_00659	pfam00899	ThiF			4.50E-43
2572232303	t3m_00659	pfam00581	Rhodanese			6.30E-16
2572232303	t3m_00659	KO:K11996	adenylyltransferase and sulfurtransferase			0.00E+00
2572232303	t3m_00659	Locus_type		CDS		
2572232303	t3m_00659	Product_name		Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine		
2572232303	t3m_00659	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232303	t3m_00659	Coordinates		39079..40473(-)		
2572232303	t3m_00659	DNA_length		1395bp		
2572232303	t3m_00659	Protein_length		464aa		
2572232303	t3m_00659	GC			0.69	
2572232303	t3m_00659	Transmembrane		Yes		

2572232304	t3m_00660	Locus_type		CDS		
2572232304	t3m_00660	Product_name		hypothetical protein		
2572232304	t3m_00660	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232304	t3m_00660	Coordinates		40429..41079(+)		
2572232304	t3m_00660	DNA_length		651bp		
2572232304	t3m_00660	Protein_length		216aa		
2572232304	t3m_00660	GC			0.67	

2572232305	t3m_00661	COG_category	[K] Transcription			
2572232305	t3m_00661	COG2345	Predicted transcriptional regulator			7.00E-25
2572232305	t3m_00661	pfam12802	MarR_2			1.80E-06
2572232305	t3m_00661	ITERM:02250	transcriptional regulator			
2572232305	t3m_00661	Locus_type		CDS		
2572232305	t3m_00661	Product_name		transcriptional regulator		
2572232305	t3m_00661	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232305	t3m_00661	Coordinates		41154..41795(-)		
2572232305	t3m_00661	DNA_length		642bp		
2572232305	t3m_00661	Protein_length		213aa		
2572232305	t3m_00661	GC			0.69	

2572232306	t3m_00662	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232306	t3m_00662	COG0396	ABC-type transport system involved in Fe-S cluster assembly, ATPase co			2.00E-92

2572232306	t3m_00662	pfam00005	ABC_tran			2.60E-21
2572232306	t3m_00662	TIGR01978	FeS assembly ATPase SufC			2.50E-101
2572232306	t3m_00662	KO:K09013	Fe-S cluster assembly ATP-binding protein			0.00E+00
2572232306	t3m_00662	Locus_type		CDS		
2572232306	t3m_00662	Product_name		FeS assembly ATPase SufC		
2572232306	t3m_00662	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232306	t3m_00662	Coordinates		41878..42660(+)		
2572232306	t3m_00662	DNA_length		783bp		
2572232306	t3m_00662	Protein_length		260aa		
2572232306	t3m_00662	GC			0.64	
2572232307	t3m_00663	Metacyc	PWY-6891: thiazole biosynthesis II (Bacillus)			
2572232307	t3m_00663	Metacyc	PWY-6823: molybdenum cofactor biosynthesis			
2572232307	t3m_00663	Metacyc	PWY0-1021: alanine biosynthesis III			
2572232307	t3m_00663	Metacyc	PWY-6892: thiazole biosynthesis I (E. coli)			
2572232307	t3m_00663	COG_category	[E] Amino acid transport and metabolism			
2572232307	t3m_00663	COG0520	Selenocysteine lyase			5.00E-129
2572232307	t3m_00663	pfam00266	Aminotran_5			0.00E+00
2572232307	t3m_00663	EC:2.8.1.7	Cysteine desulfurase.			
2572232307	t3m_00663	EC:4.4.1.16	Selenocysteine lyase.			
2572232307	t3m_00663	TIGR01979	cysteine desulfurases, SufSfamily			0.00E+00
2572232307	t3m_00663	KO:K11717	cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]			0.00E+00
2572232307	t3m_00663	Locus_type		CDS		
2572232307	t3m_00663	Product_name		cysteine desulfurases, SufSfamily		
2572232307	t3m_00663	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232307	t3m_00663	Coordinates		42690..43943(+)		
2572232307	t3m_00663	DNA_length		1254bp		
2572232307	t3m_00663	Protein_length		417aa		
2572232307	t3m_00663	GC			0.68	
2572232308	t3m_00664	Locus_type		CDS		
2572232308	t3m_00664	Product_name		hypothetical protein		
2572232308	t3m_00664	Scaffold		t3m_contig_70_75_len_44364_read_count_3757474.10		
2572232308	t3m_00664	Coordinates		44104..44361(+)		

2572232308	t3m_00664	DNA_length		258bp		
2572232308	t3m_00664	Protein_length		86aa		
2572232308	t3m_00664	GC			0.61	
2572232309	t3m_00665	Locus_type		CDS		
2572232309	t3m_00665	Product_name		hypothetical protein		
2572232309	t3m_00665	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232309	t3m_00665	Coordinates		3..353(-)		
2572232309	t3m_00665	DNA_length		351bp		
2572232309	t3m_00665	Protein_length		117aa		
2572232309	t3m_00665	GC			0.65	
2572232309	t3m_00665	Transmembrane		Yes		
2572232310	t3m_00666	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP			
2572232310	t3m_00666	Metacyc	PWY-6123: inosine-5'-phosphate biosynthesis I			
2572232310	t3m_00666	Metacyc	PWY-6124: inosine-5'-phosphate biosynthesis II			
2572232310	t3m_00666	COG_category	[F] Nucleotide transport and metabolism			
2572232310	t3m_00666	COG0138	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrola			0.00E+00
2572232310	t3m_00666	pfam01808	AICARFT_IMPCHas			2.40E-76
2572232310	t3m_00666	pfam02142	MGS			5.90E-10
2572232310	t3m_00666	EC:3.5.4.10	IMP cyclohydrolase.			
2572232310	t3m_00666	EC:2.1.2.3	Phosphoribosylaminoimidazolecarboxamide formyltransferase.			
2572232310	t3m_00666	KO:K00602	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cy			0.00E+00
2572232310	t3m_00666	Locus_type		CDS		
2572232310	t3m_00666	Product_name		AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolas		
2572232310	t3m_00666	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232310	t3m_00666	Coordinates		629..2197(+)		
2572232310	t3m_00666	DNA_length		1569bp		
2572232310	t3m_00666	Protein_length		522aa		
2572232310	t3m_00666	GC			0.71	
2572232311	t3m_00667	IMG_pathway	964: DsbC-DsbD disulfide-isomerizing reductive system			
2572232311	t3m_00667	pfam00085	Thioredoxin			8.20E-23
2572232311	t3m_00667	TIGR01068	thioredoxin			2.20E-30

2572232311	t3m_00667	KO:K03671	thioredoxin 1			1.40E-21
2572232311	t3m_00667	ITERM:01894	thioredoxin			
2572232311	t3m_00667	Locus_type		CDS		
2572232311	t3m_00667	Product_name		thioredoxin		
2572232311	t3m_00667	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232311	t3m_00667	Coordinates		2169..2540(-)		
2572232311	t3m_00667	DNA_length		372bp		
2572232311	t3m_00667	Protein_length		123aa		
2572232311	t3m_00667	GC			0.68	
2572232312	t3m_00668	Locus_type		CDS		
2572232312	t3m_00668	Product_name		hypothetical protein		
2572232312	t3m_00668	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232312	t3m_00668	Coordinates		2568..3257(-)		
2572232312	t3m_00668	DNA_length		690bp		
2572232312	t3m_00668	Protein_length		229aa		
2572232312	t3m_00668	GC			0.74	
2572232313	t3m_00669	Locus_type		CDS		
2572232313	t3m_00669	Product_name		hypothetical protein		
2572232313	t3m_00669	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232313	t3m_00669	Coordinates		3390..3569(-)		
2572232313	t3m_00669	DNA_length		180bp		
2572232313	t3m_00669	Protein_length		59aa		
2572232313	t3m_00669	GC			0.71	
2572232314	t3m_00670	KEGG_module	M00532: Photorespiration			
2572232314	t3m_00670	COG_category	[C] Energy production and conversion			
2572232314	t3m_00670	COG0277	FAD/FMN-containing dehydrogenases			2.00E-73
2572232314	t3m_00670	pfam02913	FAD-oxidase_C			1.10E-39
2572232314	t3m_00670	pfam01565	FAD_binding_4			3.00E-40
2572232314	t3m_00670	EC:1.1.3.15	(S)-2-hydroxy-acid oxidase.			
2572232314	t3m_00670	KO:K00104	glycolate oxidase [EC:1.1.3.15]			0.00E+00
2572232314	t3m_00670	Locus_type		CDS		

2572232314	t3m_00670	Product_name		FAD/FMN-containing dehydrogenases	
2572232314	t3m_00670	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232314	t3m_00670	Coordinates		3538..5064(-)	
2572232314	t3m_00670	DNA_length		1527bp	
2572232314	t3m_00670	Protein_length		508aa	
2572232314	t3m_00670	GC		0.72	
2572232315	t3m_00671	Locus_type		CDS	
2572232315	t3m_00671	Product_name		hypothetical protein	
2572232315	t3m_00671	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232315	t3m_00671	Coordinates		5088..5549(-)	
2572232315	t3m_00671	DNA_length		462bp	
2572232315	t3m_00671	Protein_length		153aa	
2572232315	t3m_00671	GC		0.69	
2572232316	t3m_00672	Locus_type		CDS	
2572232316	t3m_00672	Product_name		hypothetical protein	
2572232316	t3m_00672	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232316	t3m_00672	Coordinates		5843..6514(+)	
2572232316	t3m_00672	DNA_length		672bp	
2572232316	t3m_00672	Protein_length		223aa	
2572232316	t3m_00672	GC		0.73	
2572232317	t3m_00673	Metacyc	PWY-6854: ethylene biosynthesis III (microbes)		
2572232317	t3m_00673	Metacyc	DETOX1-PWY: superoxide radicals degradation		
2572232317	t3m_00673	pfam09055	Sod_Ni		1.10E-44
2572232317	t3m_00673	EC:1.15.1.1	Superoxide dismutase.		
2572232317	t3m_00673	TIGR02753	superoxide dismutase, Ni		1.60E-49
2572232317	t3m_00673	KO:K00518	nickel superoxide dismutase [EC:1.15.1.1]		4.70E-33
2572232317	t3m_00673	Locus_type		CDS	
2572232317	t3m_00673	Product_name		superoxide dismutase, Ni	
2572232317	t3m_00673	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232317	t3m_00673	Coordinates		6568..7071(-)	
2572232317	t3m_00673	DNA_length		504bp	

2572232317	t3m_00673	Protein_length		167aa		
2572232317	t3m_00673	GC			0.65	
2572232318	t3m_00674	pfam00717	Peptidase_S24			6.20E-11
2572232318	t3m_00674	TIGR02754	nickel-type superoxide dismutase maturation protease			6.00E-23
2572232318	t3m_00674	Locus_type		CDS		
2572232318	t3m_00674	Product_name		nickel-type superoxide dismutase maturation protease		
2572232318	t3m_00674	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232318	t3m_00674	Coordinates		7212..7520(+)		
2572232318	t3m_00674	DNA_length		309bp		
2572232318	t3m_00674	Protein_length		102aa		
2572232318	t3m_00674	GC			0.72	
2572232319	t3m_00675	COG_category	[P] Inorganic ion transport and metabolism			
2572232319	t3m_00675	COG0725	ABC-type molybdate transport system, periplasmic component			4.00E-08
2572232319	t3m_00675	pfam13531	SBP_bac_11			3.00E-17
2572232319	t3m_00675	Locus_type		CDS		
2572232319	t3m_00675	Product_name		ABC-type molybdate transport system, periplasmic component		
2572232319	t3m_00675	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232319	t3m_00675	Coordinates		7600..8679(+)		
2572232319	t3m_00675	DNA_length		1080bp		
2572232319	t3m_00675	Protein_length		359aa		
2572232319	t3m_00675	GC			0.68	
2572232319	t3m_00675	Transmembrane		Yes		
2572232320	t3m_00676	KEGG_module	M00423: Molybdate/tungstate transport system			
2572232320	t3m_00676	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232320	t3m_00676	COG0555	ABC-type sulfate transport system, permease component			9.00E-40
2572232320	t3m_00676	pfam00528	BPD_transp_1			1.80E-13
2572232320	t3m_00676	KO:K15496	molybdate/tungstate transport system permease protein			2.60E-42
2572232320	t3m_00676	Locus_type		CDS		
2572232320	t3m_00676	Product_name		ABC-type sulfate transport system, permease component		
2572232320	t3m_00676	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232320	t3m_00676	Coordinates		8676..9551(+)		

2572232320	t3m_00676	DNA_length		876bp	
2572232320	t3m_00676	Protein_length		291aa	
2572232320	t3m_00676	GC		0.71	
2572232320	t3m_00676	Transmembrane		Yes	
2572232321	t3m_00677	KEGG_module	M00189: Molybdate transport system		
2572232321	t3m_00677	COG_category	[E] Amino acid transport and metabolism		
2572232321	t3m_00677	COG3842	ABC-type spermidine/putrescine transport systems, ATPase componen		2.00E-58
2572232321	t3m_00677	pfam00005	ABC_tran		1.80E-28
2572232321	t3m_00677	EC:3.6.3.29	Molybdate-transporting ATPase.		
2572232321	t3m_00677	KO:K02017	molybdate transport system ATP-binding protein [EC:3.6.3.29]		0.00E+00
2572232321	t3m_00677	Locus_type		CDS	
2572232321	t3m_00677	Product_name		ABC-type spermidine/putrescine transport systems, ATPase component	
2572232321	t3m_00677	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232321	t3m_00677	Coordinates		9515..10594(+)	
2572232321	t3m_00677	DNA_length		1080bp	
2572232321	t3m_00677	Protein_length		359aa	
2572232321	t3m_00677	GC		0.73	
2572232322	t3m_00678	pfam03459	TOBE		2.10E-10
2572232322	t3m_00678	pfam00126	HTH_1		2.50E-05
2572232322	t3m_00678	TIGR00638	molybdenum-pterin binding domain		2.80E-13
2572232322	t3m_00678	TIGR00637	ModE molybdate transport repressor domain		5.40E-14
2572232322	t3m_00678	KO:K02019	molybdate transport system regulatory protein		4.80E-13
2572232322	t3m_00678	Locus_type		CDS	
2572232322	t3m_00678	Product_name		Bacterial regulatory helix-turn-helix protein, lysR family/TOBE domain	
2572232322	t3m_00678	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232322	t3m_00678	Coordinates		10591..11274(+)	
2572232322	t3m_00678	DNA_length		684bp	
2572232322	t3m_00678	Protein_length		227aa	
2572232322	t3m_00678	GC		0.73	
2572232323	t3m_00679	COG_category	[L] Replication, recombination and repair		
2572232323	t3m_00679	COG0468	RecA/RadA recombinase		8.00E-69

2572232323	t3m_00679	pfam08423	Rad51		6.80E-92
2572232323	t3m_00679	pfam14520	HHH_5		4.10E-07
2572232323	t3m_00679	TIGR02236	DNA repair and recombination protein RadA		0.00E+00
2572232323	t3m_00679	KO:K04483	DNA repair protein RadA		0.00E+00
2572232323	t3m_00679	Locus_type		CDS	
2572232323	t3m_00679	Product_name		DNA repair and recombination protein RadA	
2572232323	t3m_00679	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232323	t3m_00679	Coordinates		11249..12247(-)	
2572232323	t3m_00679	DNA_length		999bp	
2572232323	t3m_00679	Protein_length		332aa	
2572232323	t3m_00679	GC		0.69	
2572232324	t3m_00680	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572232324	t3m_00680	Metacyc	PWY-6124: inosine-5'-phosphate biosynthesis II		
2572232324	t3m_00680	Metacyc	PWY-6123: inosine-5'-phosphate biosynthesis I		
2572232324	t3m_00680	COG_category	[F] Nucleotide transport and metabolism		
2572232324	t3m_00680	COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase		7.00E-47
2572232324	t3m_00680	pfam01259	SAICAR_synt		3.30E-34
2572232324	t3m_00680	EC:6.3.2.6	Phosphoribosylaminoimidazolesuccinocarboxamide synthase.		
2572232324	t3m_00680	TIGR00081	phosphoribosylaminoimidazole-succinocarboxamide synthase		1.20E-57
2572232324	t3m_00680	KO:K01923	phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2		0.00E+00
2572232324	t3m_00680	Locus_type		CDS	
2572232324	t3m_00680	Product_name		phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.	
2572232324	t3m_00680	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232324	t3m_00680	Coordinates		12315..13274(-)	
2572232324	t3m_00680	DNA_length		960bp	
2572232324	t3m_00680	Protein_length		319aa	
2572232324	t3m_00680	GC		0.68	
2572232325	t3m_00681	COG_category	[R] General function prediction only		
2572232325	t3m_00681	COG0456	Acetyltransferases		9.00E-08
2572232325	t3m_00681	pfam00583	Acetyltransf_1		6.30E-10
2572232325	t3m_00681	Locus_type		CDS	
2572232325	t3m_00681	Product_name		Acetyltransferases	

2572232325	t3m_00681	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232325	t3m_00681	Coordinates		13345..13881(-)		
2572232325	t3m_00681	DNA_length		537bp		
2572232325	t3m_00681	Protein_length		178aa		
2572232325	t3m_00681	GC			0.71	

2572232326	t3m_00682	Metacyc	PWY-7118: chitin degradation to ethanol			
2572232326	t3m_00682	Metacyc	GLUCONEO-PWY: gluconeogenesis I			
2572232326	t3m_00682	COG_category	[C] Energy production and conversion			
2572232326	t3m_00682	COG0281	Malic enzyme			0.00E+00
2572232326	t3m_00682	pfam03949	Malic_M			6.50E-61
2572232326	t3m_00682	pfam00390	malic			4.10E-18
2572232326	t3m_00682	pfam00390	malic			7.30E-05
2572232326	t3m_00682	EC:1.1.1.38	Malate dehydrogenase (oxaloacetate-decarboxylating).			
2572232326	t3m_00682	KO:K00027	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]			0.00E+00
2572232326	t3m_00682	Locus_type		CDS		
2572232326	t3m_00682	Product_name		Malic enzyme		
2572232326	t3m_00682	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232326	t3m_00682	Coordinates		13878..15314(-)		
2572232326	t3m_00682	DNA_length		1437bp		
2572232326	t3m_00682	Protein_length		478aa		
2572232326	t3m_00682	GC			0.71	

2572232327	t3m_00683	COG_category	[R] General function prediction only			
2572232327	t3m_00683	COG0491	Zn-dependent hydrolases, including glyoxylases			5.00E-19
2572232327	t3m_00683	pfam00753	Lactamase_B			7.50E-23
2572232327	t3m_00683	pfam00581	Rhodanese			1.80E-08
2572232327	t3m_00683	Locus_type		CDS		
2572232327	t3m_00683	Product_name		Zn-dependent hydrolases, including glyoxylases		
2572232327	t3m_00683	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232327	t3m_00683	Coordinates		15472..16557(+)		
2572232327	t3m_00683	DNA_length		1086bp		
2572232327	t3m_00683	Protein_length		361aa		
2572232327	t3m_00683	GC			0.7	

2572232327	t3m_00683	Fused_gene		Yes		
2572232328	t3m_00684	COG_category	[E] Amino acid transport and metabolism			
2572232328	t3m_00684	COG0620	Methionine synthase II (cobalamin-independent)			3.00E-29
2572232328	t3m_00684	pfam08267	Meth_synt_1			5.40E-17
2572232328	t3m_00684	Locus_type		CDS		
2572232328	t3m_00684	Product_name		Methionine synthase II (cobalamin-independent)		
2572232328	t3m_00684	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232328	t3m_00684	Coordinates		16653..17621(+)		
2572232328	t3m_00684	DNA_length		969bp		
2572232328	t3m_00684	Protein_length		322aa		
2572232328	t3m_00684	GC			0.74	
2572232329	t3m_00685	KEGG_module	M00017: Methionine biosynthesis, apartate => homoserine => methionine			
2572232329	t3m_00685	Metacyc	HOMOSER-METSYN-PWY: methionine biosynthesis I			
2572232329	t3m_00685	Metacyc	HSERMETANA-PWY: methionine biosynthesis III			
2572232329	t3m_00685	Metacyc	PWY-5041: <i>S</i>-adenosyl-L-methionine cycle II			
2572232329	t3m_00685	Metacyc	PWY-6151: <i>S</i>-adenosyl-L-methionine cycle I			
2572232329	t3m_00685	Metacyc	PWY-6936: seleno-amino acid biosynthesis			
2572232329	t3m_00685	Metacyc	PWY-702: methionine biosynthesis II			
2572232329	t3m_00685	COG_category	[E] Amino acid transport and metabolism			
2572232329	t3m_00685	COG0620	Methionine synthase II (cobalamin-independent)			1.00E-57
2572232329	t3m_00685	pfam01717	Meth_synt_2			3.30E-46
2572232329	t3m_00685	EC:2.1.1.14	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase.			
2572232329	t3m_00685	KO:K00549	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransfera			0.00E+00
2572232329	t3m_00685	Locus_type		CDS		
2572232329	t3m_00685	Product_name		Methionine synthase II (cobalamin-independent)		
2572232329	t3m_00685	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232329	t3m_00685	Coordinates		17618..18760(+)		
2572232329	t3m_00685	DNA_length		1143bp		
2572232329	t3m_00685	Protein_length		380aa		
2572232329	t3m_00685	GC			0.71	
2572232330	t3m_00686	COG_category	[J] Translation, ribosomal structure and biogenesis			

2572232330	t3m_00686	COG0024	Methionine aminopeptidase			1.00E-49
2572232330	t3m_00686	pfam00557	Peptidase_M24			1.10E-40
2572232330	t3m_00686	EC:3.4.11.18	Methionyl aminopeptidase.			
2572232330	t3m_00686	TIGR00501	methionine aminopeptidase, type II			1.80E-79
2572232330	t3m_00686	KO:K01265	methionyl aminopeptidase [EC:3.4.11.18]			0.00E+00
2572232330	t3m_00686	ITERM:02546	methionine aminopeptidase, type II (EC 3.4.11.18)			
2572232330	t3m_00686	Locus_type		CDS		
2572232330	t3m_00686	Product_name		methionine aminopeptidase, type II (EC 3.4.11.18)		
2572232330	t3m_00686	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232330	t3m_00686	Coordinates		18765..19643(-)		
2572232330	t3m_00686	DNA_length		879bp		
2572232330	t3m_00686	Protein_length		292aa		
2572232330	t3m_00686	GC			0.72	
2572232331	t3m_00687	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232331	t3m_00687	COG0009	Putative translation factor (SUA5)			6.00E-42
2572232331	t3m_00687	pfam01300	Sua5_yciO_yrdC			1.00E-42
2572232331	t3m_00687	TIGR00057	tRNA threonylcarbamoyl adenosine modification protein, Sua5/YciO/Yr			1.70E-49
2572232331	t3m_00687	KO:K07566	tRNA threonylcarbamoyladenosine biosynthesis protein			6.50E-32
2572232331	t3m_00687	ITERM:02777	translation factor SUA5			
2572232331	t3m_00687	Locus_type		CDS		
2572232331	t3m_00687	Product_name		translation factor SUA5		
2572232331	t3m_00687	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232331	t3m_00687	Coordinates		19653..20216(-)		
2572232331	t3m_00687	DNA_length		564bp		
2572232331	t3m_00687	Protein_length		187aa		
2572232331	t3m_00687	GC			0.72	
2572232332	t3m_00688	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP			
2572232332	t3m_00688	KEGG_module	M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP			
2572232332	t3m_00688	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP			
2572232332	t3m_00688	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP			
2572232332	t3m_00688	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2572232332	t3m_00688	Metacyc	PWY-6545: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis III			

2572232332	t3m_00688	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2572232332	t3m_00688	Metacyc	PWY-7197: pyrimidine deoxyribonucleotide phosphorylation			
2572232332	t3m_00688	Metacyc	PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP			
2572232332	t3m_00688	Metacyc	PWY-7184: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis I			
2572232332	t3m_00688	Metacyc	PWY-7187: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis II			
2572232332	t3m_00688	Metacyc	PWY0-166: superpathway of pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis (E. coli			
2572232332	t3m_00688	Metacyc	PWY-7198: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis IV			
2572232332	t3m_00688	Metacyc	PWY-7205: CMP phosphorylation			
2572232332	t3m_00688	Metacyc	PWY-7176: UTP and CTP <i>de novo</i> biosynthesis			
2572232332	t3m_00688	Metacyc	PPGPPMET-PWY: ppGpp biosynthesis			
2572232332	t3m_00688	IMG_pathway	296: GTP biosynthesis			
2572232332	t3m_00688	IMG_pathway	323: UTP synthesis			
2572232332	t3m_00688	IMG_pathway	332: dTTP synthesis			
2572232332	t3m_00688	IMG_pathway	476: Cytidine conversion to CTP			
2572232332	t3m_00688	COG_category	[F] Nucleotide transport and metabolism			
2572232332	t3m_00688	COG0105	Nucleoside diphosphate kinase			1.00E-51
2572232332	t3m_00688	pfam00334	NDK			2.00E-52
2572232332	t3m_00688	EC:2.7.4.6	Nucleoside-diphosphate kinase.			
2572232332	t3m_00688	KO:K00940	nucleoside-diphosphate kinase [EC:2.7.4.6]			0.00E+00
2572232332	t3m_00688	ITERM:01287	nucleoside diphosphate kinase (EC 2.7.4.6)			
2572232332	t3m_00688	Locus_type		CDS		
2572232332	t3m_00688	Product_name		nucleoside diphosphate kinase (EC 2.7.4.6)		
2572232332	t3m_00688	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232332	t3m_00688	Coordinates		20223..20681(-)		
2572232332	t3m_00688	DNA_length		459bp		
2572232332	t3m_00688	Protein_length		152aa		
2572232332	t3m_00688	GC			0.69	
2572232333	t3m_00689	pfam12705	PDDEXK_1			8.60E-06
2572232333	t3m_00689	KO:K07464	putative RecB family exonuclease			3.00E-22
2572232333	t3m_00689	ITERM:05077	CRISPR-associated exonuclease, Cas4 family			
2572232333	t3m_00689	Locus_type		CDS		
2572232333	t3m_00689	Product_name		CRISPR-associated exonuclease, Cas4 family		
2572232333	t3m_00689	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		

2572232333	t3m_00689	Coordinates		20782..21309(-)		
2572232333	t3m_00689	DNA_length		528bp		
2572232333	t3m_00689	Protein_length		175aa		
2572232333	t3m_00689	GC			0.75	
2572232333	t3m_00689	Transmembrane		Yes		

2572232334	t3m_00690	Locus_type		CDS		
2572232334	t3m_00690	Product_name		hypothetical protein		
2572232334	t3m_00690	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232334	t3m_00690	Coordinates		21288..21551(-)		
2572232334	t3m_00690	DNA_length		264bp		
2572232334	t3m_00690	Protein_length		87aa		
2572232334	t3m_00690	GC			0.7	
2572232334	t3m_00690	Transmembrane		Yes		

2572232335	t3m_00691	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232335	t3m_00691	COG2075	Ribosomal protein L24E			3.00E-13
2572232335	t3m_00691	pfam01246	Ribosomal_L24e			6.30E-18
2572232335	t3m_00691	Locus_type		CDS		
2572232335	t3m_00691	Product_name		Ribosomal protein L24E		
2572232335	t3m_00691	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232335	t3m_00691	Coordinates		21620..22036(-)		
2572232335	t3m_00691	DNA_length		417bp		
2572232335	t3m_00691	Protein_length		138aa		
2572232335	t3m_00691	GC			0.72	

2572232336	t3m_00692	KEGG_module	M00179: Ribosome, archaea			
2572232336	t3m_00692	KEGG_module	M00177: Ribosome, eukaryotes			
2572232336	t3m_00692	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232336	t3m_00692	COG2053	Ribosomal protein S28E/S33			2.00E-17
2572232336	t3m_00692	pfam01200	Ribosomal_S28e			1.50E-27
2572232336	t3m_00692	KO:K02979	small subunit ribosomal protein S28e			1.30E-22
2572232336	t3m_00692	Locus_type		CDS		
2572232336	t3m_00692	Product_name		SSU ribosomal protein S28E		

2572232336	t3m_00692	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232336	t3m_00692	Coordinates		22050..22262(-)	
2572232336	t3m_00692	DNA_length		213bp	
2572232336	t3m_00692	Protein_length		70aa	
2572232336	t3m_00692	GC		0.7	
2572232337	t3m_00693	KEGG_module	M00179: Ribosome, archaea		
2572232337	t3m_00693	KEGG_module	M00177: Ribosome, eukaryotes		
2572232337	t3m_00693	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232337	t3m_00693	COG1358	Ribosomal protein HS6-type (S12/L30/L7a)		9.00E-23
2572232337	t3m_00693	pfam01248	Ribosomal_L7Ae		6.50E-28
2572232337	t3m_00693	TIGR03677	50S ribosomal protein L7Ae		5.10E-48
2572232337	t3m_00693	KO:K02936	large subunit ribosomal protein L7Ae		1.60E-38
2572232337	t3m_00693	ITERM:00224	LSU ribosomal protein L7AE		
2572232337	t3m_00693	Locus_type		CDS	
2572232337	t3m_00693	Product_name		LSU ribosomal protein L7AE	
2572232337	t3m_00693	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232337	t3m_00693	Coordinates		22299..22721(-)	
2572232337	t3m_00693	DNA_length		423bp	
2572232337	t3m_00693	Protein_length		140aa	
2572232337	t3m_00693	GC		0.66	
2572232338	t3m_00694	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2572232338	t3m_00694	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2572232338	t3m_00694	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2572232338	t3m_00694	IMG_pathway	507: L-tyrosine ligation to tRNA(Tyr)		
2572232338	t3m_00694	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232338	t3m_00694	COG0162	Tyrosyl-tRNA synthetase		2.00E-60
2572232338	t3m_00694	pfam00579	tRNA-synt_1b		3.80E-36
2572232338	t3m_00694	EC:6.1.1.1	Tyrosine--tRNA ligase.		
2572232338	t3m_00694	TIGR00234	tyrosyl-tRNA synthetase		4.80E-35
2572232338	t3m_00694	KO:K01866	tyrosyl-tRNA synthetase [EC:6.1.1.1]		0.00E+00
2572232338	t3m_00694	ITERM:00400	tyrosyl-tRNA synthetase (EC 6.1.1.1)		
2572232338	t3m_00694	Locus_type		CDS	

2572232338	t3m_00694	Product_name		tyrosyl-tRNA synthetase (EC 6.1.1.1)		
2572232338	t3m_00694	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232338	t3m_00694	Coordinates		22775..23842(-)		
2572232338	t3m_00694	DNA_length		1068bp		
2572232338	t3m_00694	Protein_length		355aa		
2572232338	t3m_00694	GC			0.7	
2572232339	t3m_00695	COG_category	[T] Signal transduction mechanisms			
2572232339	t3m_00695	COG0467	RecA-superfamily ATPases implicated in signal transduction			2.00E-21
2572232339	t3m_00695	pfam06745	KaiC			7.40E-18
2572232339	t3m_00695	Locus_type		CDS		
2572232339	t3m_00695	Product_name		RecA-superfamily ATPases implicated in signal transduction		
2572232339	t3m_00695	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232339	t3m_00695	Coordinates		23968..26382(+)		
2572232339	t3m_00695	DNA_length		2415bp		
2572232339	t3m_00695	Protein_length		804aa		
2572232339	t3m_00695	GC			0.7	
2572232340	t3m_00696	Locus_type		miscRNA		
2572232340	t3m_00696	Product_name		Archaeal signal recognition particle RNA		
2572232340	t3m_00696	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232340	t3m_00696	Coordinates		26466..26778(+)		
2572232340	t3m_00696	DNA_length		313bp		
2572232340	t3m_00696	GC			0.71	
2572232341	t3m_00697	Locus_type		CDS		
2572232341	t3m_00697	Product_name		hypothetical protein		
2572232341	t3m_00697	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232341	t3m_00697	Coordinates		26854..27147(+)		
2572232341	t3m_00697	DNA_length		294bp		
2572232341	t3m_00697	Protein_length		97aa		
2572232341	t3m_00697	GC			0.65	
2572232342	t3m_00698	Metacyc	PWY-6951: docosahexanoate biosynthesis II			

2572232342	t3m_00698	Metacyc	PWY0-1337: oleate β-oxidation		
2572232342	t3m_00698	Metacyc	PWY-361: phenylpropanoid biosynthesis		
2572232342	t3m_00698	Metacyc	PWY-6320: phaselate biosynthesis		
2572232342	t3m_00698	Metacyc	PWY-6944: androstenedione degradation		
2572232342	t3m_00698	Metacyc	PWY-6673: caffeoylglucarate biosynthesis		
2572232342	t3m_00698	Metacyc	PWY-6048: methylthiopropionate degradation I (cleavage)		
2572232342	t3m_00698	Metacyc	PWY-7027: hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosynthesis		
2572232342	t3m_00698	Metacyc	PWY-6039: chlorogenic acid biosynthesis I		
2572232342	t3m_00698	Metacyc	PWY-981: salicylate biosynthesis II		
2572232342	t3m_00698	Metacyc	PWY-7053: docosahexanoate biosynthesis I		
2572232342	t3m_00698	Metacyc	PWY-6948: sitosterol degradation to androstenedione		
2572232342	t3m_00698	Metacyc	PWY-5996: oleate biosynthesis II (animals and fungi)		
2572232342	t3m_00698	Metacyc	PWY-7007: methyl ketone biosynthesis		
2572232342	t3m_00698	Metacyc	PWY-6453: stigma estolide biosynthesis		
2572232342	t3m_00698	Metacyc	PWY-6585: 2-tridecanone biosynthesis		
2572232342	t3m_00698	COG_category	[R] General function prediction only		
2572232342	t3m_00698	COG0824	Predicted thioesterase		1.00E-16
2572232342	t3m_00698	pfam13279	4HBT_2		2.30E-14
2572232342	t3m_00698	EC:3.1.2.-	Hydrolases. Acting on ester bonds. Thiolester hydrolases.		
2572232342	t3m_00698	TIGR00051	acyl-CoA thioester hydrolase, YbgC/YbaW family		8.80E-13
2572232342	t3m_00698	KO:K07107	acyl-CoA thioester hydrolase [EC:3.1.2.-]		1.90E-10
2572232342	t3m_00698	Locus_type		CDS	
2572232342	t3m_00698	Product_name		Predicted thioesterase	
2572232342	t3m_00698	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232342	t3m_00698	Coordinates		27185..27640(-)	
2572232342	t3m_00698	DNA_length		456bp	
2572232342	t3m_00698	Protein_length		151aa	
2572232342	t3m_00698	GC		0.65	
2572232343	t3m_00699	KEGG_module	M00346: Formaldehyde assimilation, serine pathway		
2572232343	t3m_00699	KEGG_module	M00532: Photorespiration		
2572232343	t3m_00699	KEGG_module	M00141: C1-unit interconversion, eukaryotes		
2572232343	t3m_00699	KEGG_module	M00140: C1-unit interconversion, prokaryotes		
2572232343	t3m_00699	Metacyc	PWY-2161: folate polyglutamylation		

2572232343	t3m_00699	Metacyc	1CMET2-PWY: formylTHF biosynthesis I		
2572232343	t3m_00699	Metacyc	PWY-3841: folate transformations II		
2572232343	t3m_00699	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2572232343	t3m_00699	Metacyc	GLYSYN-PWY: glycine biosynthesis I		
2572232343	t3m_00699	Metacyc	PWY-2201: folate transformations I		
2572232343	t3m_00699	Metacyc	PWY-3661: glycine betaine degradation		
2572232343	t3m_00699	Metacyc	PWY-181: photorespiration		
2572232343	t3m_00699	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)		
2572232343	t3m_00699	IMG_pathway	1029: 5,10-methylenetetrahydrofolate polyglutamination		
2572232343	t3m_00699	IMG_pathway	127: L-serine conversion to glycine and methylene-THF		
2572232343	t3m_00699	IMG_pathway	959: Serine cycle		
2572232343	t3m_00699	COG_category	[E] Amino acid transport and metabolism		
2572232343	t3m_00699	COG0112	Glycine/serine hydroxymethyltransferase		7.00E-112
2572232343	t3m_00699	pfam00464	SHMT		1.20E-69
2572232343	t3m_00699	EC:2.1.2.1	Glycine hydroxymethyltransferase.		
2572232343	t3m_00699	KO:K00600	glycine hydroxymethyltransferase [EC:2.1.2.1]		0.00E+00
2572232343	t3m_00699	ITERM:00210	serine hydroxymethyltransferase (EC 2.1.2.1)		
2572232343	t3m_00699	Locus_type		CDS	
2572232343	t3m_00699	Product_name		serine hydroxymethyltransferase (EC 2.1.2.1)	
2572232343	t3m_00699	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232343	t3m_00699	Coordinates		27764..29095(+)	
2572232343	t3m_00699	DNA_length		1332bp	
2572232343	t3m_00699	Protein_length		443aa	
2572232343	t3m_00699	GC		0.7	
2572232344	t3m_00700	Locus_type		CDS	
2572232344	t3m_00700	Product_name		hypothetical protein	
2572232344	t3m_00700	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232344	t3m_00700	Coordinates		29116..30435(-)	
2572232344	t3m_00700	DNA_length		1320bp	
2572232344	t3m_00700	Protein_length		439aa	
2572232344	t3m_00700	GC		0.73	
2572232344	t3m_00700	Transmembrane		Yes	

2572232345	t3m_00701	COG_category	[L] Replication, recombination and repair			
2572232345	t3m_00701	COG0122	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase			8.00E-34
2572232345	t3m_00701	pfam00730	HhH-GPD			1.60E-13
2572232345	t3m_00701	EC:3.2.2.21	DNA-3-methyladenine glycosylase II.			
2572232345	t3m_00701	KO:K01247	DNA-3-methyladenine glycosylase II [EC:3.2.2.21]			9.50E-29
2572232345	t3m_00701	Locus_type		CDS		
2572232345	t3m_00701	Product_name		3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase		
2572232345	t3m_00701	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232345	t3m_00701	Coordinates		30578..31486(+)		
2572232345	t3m_00701	DNA_length		909bp		
2572232345	t3m_00701	Protein_length		302aa		
2572232345	t3m_00701	GC			0.72	
2572232346	t3m_00702	Metacyc	PWY-6689: tRNA splicing			
2572232346	t3m_00702	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232346	t3m_00702	COG1514	2'-5' RNA ligase			3.00E-23
2572232346	t3m_00702	pfam13563	2_5_RNA_ligase2			2.50E-16
2572232346	t3m_00702	EC:6.5.1.-	Ligases. Forming phosphoric ester bonds. Ligases that form phosphoric-ester bonds.			
2572232346	t3m_00702	TIGR02258	2'-5' RNA ligase			7.00E-35
2572232346	t3m_00702	KO:K01975	2'-5' RNA ligase [EC:6.5.1.-]			4.50E-22
2572232346	t3m_00702	Locus_type		CDS		
2572232346	t3m_00702	Product_name		2'-5' RNA ligase		
2572232346	t3m_00702	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232346	t3m_00702	Coordinates		31518..32057(-)		
2572232346	t3m_00702	DNA_length		540bp		
2572232346	t3m_00702	Protein_length		179aa		
2572232346	t3m_00702	GC			0.74	
2572232347	t3m_00703	pfam12846	AAA_10			4.00E-18
2572232347	t3m_00703	Locus_type		CDS		
2572232347	t3m_00703	Product_name		AAA-like domain		
2572232347	t3m_00703	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232347	t3m_00703	Coordinates		32083..34038(-)		
2572232347	t3m_00703	DNA_length		1956bp		

2572232347	t3m_00703	Protein_length		651aa		
2572232347	t3m_00703	GC			0.73	
2572232348	t3m_00704	Locus_type		CDS		
2572232348	t3m_00704	Product_name		hypothetical protein		
2572232348	t3m_00704	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232348	t3m_00704	Coordinates		34088..34615(+)		
2572232348	t3m_00704	DNA_length		528bp		
2572232348	t3m_00704	Protein_length		175aa		
2572232348	t3m_00704	GC			0.72	
2572232349	t3m_00705	Locus_type		CDS		
2572232349	t3m_00705	Product_name		hypothetical protein		
2572232349	t3m_00705	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232349	t3m_00705	Coordinates		34657..34899(-)		
2572232349	t3m_00705	DNA_length		243bp		
2572232349	t3m_00705	Protein_length		80aa		
2572232349	t3m_00705	GC			0.72	
2572232350	t3m_00706	pfam00583	Acetyltransf_1			2.90E-11
2572232350	t3m_00706	Locus_type		CDS		
2572232350	t3m_00706	Product_name		Acetyltransferase (GNAT) family		
2572232350	t3m_00706	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232350	t3m_00706	Coordinates		35620..36582(+)		
2572232350	t3m_00706	DNA_length		963bp		
2572232350	t3m_00706	Protein_length		320aa		
2572232350	t3m_00706	GC			0.65	
2572232351	t3m_00707	COG_category	[K] Transcription			
2572232351	t3m_00707	COG1733	Predicted transcriptional regulators			2.00E-22
2572232351	t3m_00707	pfam01638	HxlR			3.90E-22
2572232351	t3m_00707	ITERM:02284	transcriptional regulator, HxlR family			
2572232351	t3m_00707	Locus_type		CDS		
2572232351	t3m_00707	Product_name		transcriptional regulator, HxlR family		

2572232351	t3m_00707	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232351	t3m_00707	Coordinates		36857..37345(-)	
2572232351	t3m_00707	DNA_length		489bp	
2572232351	t3m_00707	Protein_length		162aa	
2572232351	t3m_00707	GC		0.72	
2572232352	t3m_00708	Locus_type		CDS	
2572232352	t3m_00708	Product_name		hypothetical protein	
2572232352	t3m_00708	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232352	t3m_00708	Coordinates		37488..38102(+)	
2572232352	t3m_00708	DNA_length		615bp	
2572232352	t3m_00708	Protein_length		204aa	
2572232352	t3m_00708	GC		0.72	
2572232353	t3m_00709	pfam13660	DUF4147		1.90E-24
2572232353	t3m_00709	Locus_type		CDS	
2572232353	t3m_00709	Product_name		Domain of unknown function (DUF4147)	
2572232353	t3m_00709	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	
2572232353	t3m_00709	Coordinates		38099..39448(-)	
2572232353	t3m_00709	DNA_length		1350bp	
2572232353	t3m_00709	Protein_length		449aa	
2572232353	t3m_00709	GC		0.73	
2572232354	t3m_00710	Metacyc	PWY-4722: creatinine degradation II		
2572232354	t3m_00710	Metacyc	CRNFORCAT-PWY: creatinine degradation I		
2572232354	t3m_00710	Metacyc	PWY-3661: glycine betaine degradation		
2572232354	t3m_00710	COG_category	[E] Amino acid transport and metabolism		
2572232354	t3m_00710	COG0665	Glycine/D-amino acid oxidases (deaminating)		1.00E-48
2572232354	t3m_00710	pfam01266	DAO		9.20E-77
2572232354	t3m_00710	EC:1.5.3.1	Sarcosine oxidase.		
2572232354	t3m_00710	KO:K00303	sarcosine oxidase, subunit beta [EC:1.5.3.1]		0.00E+00
2572232354	t3m_00710	Locus_type		CDS	
2572232354	t3m_00710	Product_name		Glycine/D-amino acid oxidases (deaminating)	
2572232354	t3m_00710	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11	

2572232354	t3m_00710	Coordinates		39501..40664(-)		
2572232354	t3m_00710	DNA_length		1164bp		
2572232354	t3m_00710	Protein_length		387aa		
2572232354	t3m_00710	GC			0.71	
2572232354	t3m_00710	Transmembrane		Yes		
2572232355	t3m_00711	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232355	t3m_00711	COG0492	Thioredoxin reductase			1.00E-10
2572232355	t3m_00711	pfam13510	Fer2_4			2.30E-19
2572232355	t3m_00711	Locus_type		CDS		
2572232355	t3m_00711	Product_name		Thioredoxin reductase		
2572232355	t3m_00711	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232355	t3m_00711	Coordinates		40661..42328(-)		
2572232355	t3m_00711	DNA_length		1668bp		
2572232355	t3m_00711	Protein_length		555aa		
2572232355	t3m_00711	GC			0.72	
2572232355	t3m_00711	Fused_gene		Yes		
2572232356	t3m_00712	COG_category	[P] Inorganic ion transport and metabolism			
2572232356	t3m_00712	COG0704	Phosphate uptake regulator			5.00E-28
2572232356	t3m_00712	pfam04014	Antitoxin-MazE			1.40E-04
2572232356	t3m_00712	pfam01895	PhoU			3.90E-06
2572232356	t3m_00712	pfam01895	PhoU			2.90E-19
2572232356	t3m_00712	Locus_type		CDS		
2572232356	t3m_00712	Product_name		Phosphate uptake regulator		
2572232356	t3m_00712	Scaffold		t3m_contig_70_80_len_43488_read_count_3312166.11		
2572232356	t3m_00712	Coordinates		42469..43485(+)		
2572232356	t3m_00712	DNA_length		1017bp		
2572232356	t3m_00712	Protein_length		339aa		
2572232356	t3m_00712	GC			0.67	
2572232357	t3m_00713	Locus_type		tRNA		
2572232357	t3m_00713	Product_name		tRNA_Pro_TGG		
2572232357	t3m_00713	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		

2572232357	t3m_00713	Coordinates		7..51(+)		
2572232357	t3m_00713	DNA_length		45bp		
2572232357	t3m_00713	GC			0.58	
2572232358	t3m_00714	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232358	t3m_00714	COG0438	Glycosyltransferase			7.00E-25
2572232358	t3m_00714	pfam00534	Glycos_transf_1			2.80E-22
2572232358	t3m_00714	pfam13579	Glyco_trans_4_4			2.80E-18
2572232358	t3m_00714	EC:2.4.1.57	Phosphatidylinositol alpha-mannosyltransferase.			
2572232358	t3m_00714	KO:K08256	phosphatidylinositol alpha-mannosyltransferase [EC:2.4.1.57]			2.70E-17
2572232358	t3m_00714	Locus_type		CDS		
2572232358	t3m_00714	Product_name		Glycosyltransferase		
2572232358	t3m_00714	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232358	t3m_00714	Coordinates		73..1176(-)		
2572232358	t3m_00714	DNA_length		1104bp		
2572232358	t3m_00714	Protein_length		367aa		
2572232358	t3m_00714	GC			0.69	
2572232359	t3m_00715	Locus_type		CDS		
2572232359	t3m_00715	Product_name		hypothetical protein		
2572232359	t3m_00715	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232359	t3m_00715	Coordinates		1242..1463(-)		
2572232359	t3m_00715	DNA_length		222bp		
2572232359	t3m_00715	Protein_length		73aa		
2572232359	t3m_00715	GC			0.69	
2572232360	t3m_00716	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232360	t3m_00716	COG0438	Glycosyltransferase			9.00E-29
2572232360	t3m_00716	pfam13692	Glyco_trans_1_4			1.90E-19
2572232360	t3m_00716	pfam13579	Glyco_trans_4_4			2.40E-10
2572232360	t3m_00716	Locus_type		CDS		
2572232360	t3m_00716	Product_name		Glycosyltransferase		
2572232360	t3m_00716	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232360	t3m_00716	Coordinates		1510..2640(+)		

2572232360	t3m_00716	DNA_length		1131bp		
2572232360	t3m_00716	Protein_length		376aa		
2572232360	t3m_00716	GC			0.68	

2572232361	t3m_00717	pfam05050	Methyltransf_21			1.50E-16
2572232361	t3m_00717	TIGR01444	methyltransferase, FkbM family			1.30E-24
2572232361	t3m_00717	Locus_type		CDS		
2572232361	t3m_00717	Product_name		methyltransferase, FkbM family		
2572232361	t3m_00717	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232361	t3m_00717	Coordinates		2759..3640(+)		
2572232361	t3m_00717	DNA_length		882bp		
2572232361	t3m_00717	Protein_length		293aa		
2572232361	t3m_00717	GC			0.67	

2572232362	t3m_00718	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232362	t3m_00718	COG0463	Glycosyltransferases involved in cell wall biogenesis			2.00E-06
2572232362	t3m_00718	pfam00535	Glycos_transf_2			4.00E-12
2572232362	t3m_00718	Locus_type		CDS		
2572232362	t3m_00718	Product_name		Glycosyltransferases involved in cell wall biogenesis		
2572232362	t3m_00718	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232362	t3m_00718	Coordinates		3734..4684(-)		
2572232362	t3m_00718	DNA_length		951bp		
2572232362	t3m_00718	Protein_length		316aa		
2572232362	t3m_00718	GC			0.67	

2572232363	t3m_00719	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2572232363	t3m_00719	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2572232363	t3m_00719	Metacyc	PWY-6397: mycolyl-arabinogalactan-peptidoglycan complex biosynthesis			
2572232363	t3m_00719	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			
2572232363	t3m_00719	Metacyc	PWY-6527: stachyose degradation			
2572232363	t3m_00719	Metacyc	PWY-3821: galactose degradation III			
2572232363	t3m_00719	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2572232363	t3m_00719	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232363	t3m_00719	COG_category	[G] Carbohydrate transport and metabolism			

2572232363	t3m_00719	COG0451	Nucleoside-diphosphate-sugar epimerases			8.00E-31
2572232363	t3m_00719	pfam01370	Epimerase			7.80E-37
2572232363	t3m_00719	EC:5.1.3.2	UDP-glucose 4-epimerase.			
2572232363	t3m_00719	KO:K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]			3.30E-39
2572232363	t3m_00719	Locus_type		CDS		
2572232363	t3m_00719	Product_name		Nucleoside-diphosphate-sugar epimerases		
2572232363	t3m_00719	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232363	t3m_00719	Coordinates		4907..5878(+)		
2572232363	t3m_00719	DNA_length		972bp		
2572232363	t3m_00719	Protein_length		323aa		
2572232363	t3m_00719	GC			0.68	
2572232364	t3m_00720	pfam13578	Methyltransf_24			1.30E-15
2572232364	t3m_00720	Locus_type		CDS		
2572232364	t3m_00720	Product_name		Methyltransferase domain		
2572232364	t3m_00720	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232364	t3m_00720	Coordinates		5920..6639(+)		
2572232364	t3m_00720	DNA_length		720bp		
2572232364	t3m_00720	Protein_length		239aa		
2572232364	t3m_00720	GC			0.71	
2572232365	t3m_00721	Locus_type		CDS		
2572232365	t3m_00721	Product_name		hypothetical protein		
2572232365	t3m_00721	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232365	t3m_00721	Coordinates		6932..7300(-)		
2572232365	t3m_00721	DNA_length		369bp		
2572232365	t3m_00721	Protein_length		122aa		
2572232365	t3m_00721	GC			0.7	
2572232366	t3m_00722	COG_category	[K] Transcription			
2572232366	t3m_00722	COG1293	Predicted RNA-binding protein homologous to eukaryotic snRNP			1.00E-70
2572232366	t3m_00722	pfam05670	DUF814			5.10E-19
2572232366	t3m_00722	pfam05833	FbpA			3.40E-34
2572232366	t3m_00722	Locus_type		CDS		

2572232366	t3m_00722	Product_name		Predicted RNA-binding protein homologous to eukaryotic snRNP	
2572232366	t3m_00722	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232366	t3m_00722	Coordinates		7328..9238(-)	
2572232366	t3m_00722	DNA_length		1911bp	
2572232366	t3m_00722	Protein_length		636aa	
2572232366	t3m_00722	GC		0.71	
2572232367	t3m_00723	COG_category	[I] Lipid transport and metabolism		
2572232367	t3m_00723	COG1960	Acyl-CoA dehydrogenases		2.00E-65
2572232367	t3m_00723	pfam02770	Acyl-CoA_dh_M		5.70E-18
2572232367	t3m_00723	pfam02771	Acyl-CoA_dh_N		6.60E-29
2572232367	t3m_00723	pfam00441	Acyl-CoA_dh_1		1.40E-27
2572232367	t3m_00723	Locus_type		CDS	
2572232367	t3m_00723	Product_name		Acyl-CoA dehydrogenases	
2572232367	t3m_00723	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232367	t3m_00723	Coordinates		9310..10449(+)	
2572232367	t3m_00723	DNA_length		1140bp	
2572232367	t3m_00723	Protein_length		379aa	
2572232367	t3m_00723	GC		0.71	
2572232368	t3m_00724	COG_category	[R] General function prediction only		
2572232368	t3m_00724	COG1204	Superfamily II helicase		0.00E+00
2572232368	t3m_00724	pfam00270	DEAD		1.90E-25
2572232368	t3m_00724	pfam00271	Helicase_C		4.20E-10
2572232368	t3m_00724	EC:3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; involved in cellular and subcellul		
2572232368	t3m_00724	KO:K03726	helicase [EC:3.6.4.-]		0.00E+00
2572232368	t3m_00724	Locus_type		CDS	
2572232368	t3m_00724	Product_name		Superfamily II helicase	
2572232368	t3m_00724	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232368	t3m_00724	Coordinates		10471..12774(+)	
2572232368	t3m_00724	DNA_length		2304bp	
2572232368	t3m_00724	Protein_length		767aa	
2572232368	t3m_00724	GC		0.71	

2572232369	t3m_00725	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232369	t3m_00725	COG_category	[L] Replication, recombination and repair			
2572232369	t3m_00725	COG1474	Cdc6-related protein, AAA superfamily ATPase			2.00E-12
2572232369	t3m_00725	Locus_type		CDS		
2572232369	t3m_00725	Product_name		Cdc6-related protein, AAA superfamily ATPase		
2572232369	t3m_00725	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232369	t3m_00725	Coordinates		12647..13849(-)		
2572232369	t3m_00725	DNA_length		1203bp		
2572232369	t3m_00725	Protein_length		400aa		
2572232369	t3m_00725	GC			0.71	
2572232370	t3m_00726	KEGG_module	M00010: Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate			
2572232370	t3m_00726	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)			
2572232370	t3m_00726	Metacyc	PWY-6549: glutamine biosynthesis III			
2572232370	t3m_00726	Metacyc	PWY-5690: TCA cycle II (eukaryotic)			
2572232370	t3m_00726	COG_category	[E] Amino acid transport and metabolism			
2572232370	t3m_00726	COG_category	[C] Energy production and conversion			
2572232370	t3m_00726	COG0473	Isocitrate/isopropylmalate dehydrogenase			6.00E-106
2572232370	t3m_00726	pfam00180	Iso_dh			9.20E-102
2572232370	t3m_00726	EC:1.1.1.41	Isocitrate dehydrogenase (NAD(+)).			
2572232370	t3m_00726	TIGR00175	isocitrate dehydrogenase, NAD-dependent, mitochondrial type			2.20E-107
2572232370	t3m_00726	KO:K00030	isocitrate dehydrogenase (NAD+) [EC:1.1.1.41]			0.00E+00
2572232370	t3m_00726	Locus_type		CDS		
2572232370	t3m_00726	Product_name		Isocitrate/isopropylmalate dehydrogenase		
2572232370	t3m_00726	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232370	t3m_00726	Coordinates		14059..15165(+)		
2572232370	t3m_00726	DNA_length		1107bp		
2572232370	t3m_00726	Protein_length		368aa		
2572232370	t3m_00726	GC			0.69	
2572232371	t3m_00727	COG_category	[S] Function unknown			
2572232371	t3m_00727	COG0432	Uncharacterized conserved protein			3.00E-39
2572232371	t3m_00727	pfam01894	UPF0047			1.10E-37
2572232371	t3m_00727	TIGR00149	secondary thiamine-phosphate synthase enzyme			1.50E-36

2572232371	t3m_00727	Locus_type	CDS
2572232371	t3m_00727	Product_name	secondary thiamine-phosphate synthase enzyme
2572232371	t3m_00727	Scaffold	t3m_contig_70_84_len_42953_read_count_3343224.12
2572232371	t3m_00727	Coordinates	15217..15627(-)
2572232371	t3m_00727	DNA_length	411bp
2572232371	t3m_00727	Protein_length	136aa
2572232371	t3m_00727	GC	0.65

2572232372	t3m_00728	Locus_type	CDS
2572232372	t3m_00728	Product_name	hypothetical protein
2572232372	t3m_00728	Scaffold	t3m_contig_70_84_len_42953_read_count_3343224.12
2572232372	t3m_00728	Coordinates	15695..16255(+)
2572232372	t3m_00728	DNA_length	561bp
2572232372	t3m_00728	Protein_length	186aa
2572232372	t3m_00728	GC	0.7
2572232372	t3m_00728	Transmembrane	Yes

2572232373	t3m_00729	Locus_type	CDS
2572232373	t3m_00729	Product_name	hypothetical protein
2572232373	t3m_00729	Scaffold	t3m_contig_70_84_len_42953_read_count_3343224.12
2572232373	t3m_00729	Coordinates	16264..16608(-)
2572232373	t3m_00729	DNA_length	345bp
2572232373	t3m_00729	Protein_length	114aa
2572232373	t3m_00729	GC	0.7

2572232374	t3m_00730	Locus_type	CDS
2572232374	t3m_00730	Product_name	hypothetical protein
2572232374	t3m_00730	Scaffold	t3m_contig_70_84_len_42953_read_count_3343224.12
2572232374	t3m_00730	Coordinates	16761..18593(+)
2572232374	t3m_00730	DNA_length	1833bp
2572232374	t3m_00730	Protein_length	610aa
2572232374	t3m_00730	GC	0.71
2572232374	t3m_00730	Transmembrane	Yes

2572232375	t3m_00731	COG_category	[R] General function prediction only			
2572232375	t3m_00731	COG1634	Uncharacterized Rossmann fold enzyme			3.00E-45
2572232375	t3m_00731	pfam01973	MAF_flag10			3.20E-19
2572232375	t3m_00731	Locus_type		CDS		
2572232375	t3m_00731	Product_name		Uncharacterized Rossmann fold enzyme		
2572232375	t3m_00731	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232375	t3m_00731	Coordinates		18557..19306(-)		
2572232375	t3m_00731	DNA_length		750bp		
2572232375	t3m_00731	Protein_length		249aa		
2572232375	t3m_00731	GC			0.73	
2572232376	t3m_00732	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2572232376	t3m_00732	COG0206	Cell division GTPase			2.00E-97
2572232376	t3m_00732	pfam00091	Tubulin			6.00E-35
2572232376	t3m_00732	pfam12327	FtsZ_C			1.10E-33
2572232376	t3m_00732	TIGR00065	cell division protein FtsZ			1.40E-128
2572232376	t3m_00732	KO:K03531	cell division protein FtsZ			0.00E+00
2572232376	t3m_00732	Locus_type		CDS		
2572232376	t3m_00732	Product_name		cell division protein FtsZ		
2572232376	t3m_00732	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232376	t3m_00732	Coordinates		19372..20490(+)		
2572232376	t3m_00732	DNA_length		1119bp		
2572232376	t3m_00732	Protein_length		372aa		
2572232376	t3m_00732	GC			0.69	
2572232377	t3m_00733	KEGG_module	M00401: Sec61 complex			
2572232377	t3m_00733	TIGR00327	protein translocase SEC61 complex gamma subunit, archaeal and eukar			1.90E-14
2572232377	t3m_00733	KO:K07342	protein transport protein SEC61 subunit gamma and related proteins			1.40E-10
2572232377	t3m_00733	Locus_type		CDS		
2572232377	t3m_00733	Product_name		protein translocase SEC61 complex gamma subunit, archaeal and eukary		
2572232377	t3m_00733	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232377	t3m_00733	Coordinates		20499..20744(+)		
2572232377	t3m_00733	DNA_length		246bp		
2572232377	t3m_00733	Protein_length		81aa		

2572232377	t3m_00733	GC			0.64	
2572232377	t3m_00733	Transmembrane		Yes		
2572232378	t3m_00734	COG_category	[K] Transcription			
2572232378	t3m_00734	COG0250	Transcription antiterminator			5.00E-19
2572232378	t3m_00734	pfam00467	KOW			6.90E-07
2572232378	t3m_00734	pfam03439	Spt5-NGN			1.60E-13
2572232378	t3m_00734	TIGR00405	ribosomal protein L24p/L26e, archaeal			5.80E-49
2572232378	t3m_00734	KO:K02601	transcriptional antiterminator NusG			4.20E-34
2572232378	t3m_00734	Locus_type		CDS		
2572232378	t3m_00734	Product_name		ribosomal protein L24p/L26e, archaeal		
2572232378	t3m_00734	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232378	t3m_00734	Coordinates		20765..21763(+)		
2572232378	t3m_00734	DNA_length		999bp		
2572232378	t3m_00734	Protein_length		332aa		
2572232378	t3m_00734	GC			0.7	
2572232379	t3m_00735	KEGG_module	M00179: Ribosome, archaea			
2572232379	t3m_00735	KEGG_module	M00178: Ribosome, bacteria			
2572232379	t3m_00735	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232379	t3m_00735	COG0080	Ribosomal protein L11			8.00E-33
2572232379	t3m_00735	pfam03946	Ribosomal_L11_N			7.80E-19
2572232379	t3m_00735	pfam00298	Ribosomal_L11			4.70E-21
2572232379	t3m_00735	KO:K02867	large subunit ribosomal protein L11			1.10E-37
2572232379	t3m_00735	ITERM:00227	LSU ribosomal protein L11P			
2572232379	t3m_00735	Locus_type		CDS		
2572232379	t3m_00735	Product_name		LSU ribosomal protein L11P		
2572232379	t3m_00735	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232379	t3m_00735	Coordinates		21765..22220(+)		
2572232379	t3m_00735	DNA_length		456bp		
2572232379	t3m_00735	Protein_length		151aa		
2572232379	t3m_00735	GC			0.69	
2572232380	t3m_00736	Locus_type		CDS		

2572232380	t3m_00736	Product_name		hypothetical protein		
2572232380	t3m_00736	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232380	t3m_00736	Coordinates		22220..22516(+)		
2572232380	t3m_00736	DNA_length		297bp		
2572232380	t3m_00736	Protein_length		98aa		
2572232380	t3m_00736	GC			0.67	
2572232381	t3m_00737	pfam13746	Fer4_18			5.70E-17
2572232381	t3m_00737	Locus_type		CDS		
2572232381	t3m_00737	Product_name		4Fe-4S dicluster domain		
2572232381	t3m_00737	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232381	t3m_00737	Coordinates		22859..24013(+)		
2572232381	t3m_00737	DNA_length		1155bp		
2572232381	t3m_00737	Protein_length		384aa		
2572232381	t3m_00737	GC			0.68	
2572232382	t3m_00738	pfam00027	cNMP_binding			1.70E-12
2572232382	t3m_00738	Locus_type		CDS		
2572232382	t3m_00738	Product_name		Cyclic nucleotide-binding domain		
2572232382	t3m_00738	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232382	t3m_00738	Coordinates		24010..24480(+)		
2572232382	t3m_00738	DNA_length		471bp		
2572232382	t3m_00738	Protein_length		156aa		
2572232382	t3m_00738	GC			0.65	
2572232383	t3m_00739	COG_category	[H] Coenzyme transport and metabolism			
2572232383	t3m_00739	COG_category	[C] Energy production and conversion			
2572232383	t3m_00739	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductase			8.00E-40
2572232383	t3m_00739	pfam10418	DHODB_Fe-S_bind			1.20E-09
2572232383	t3m_00739	pfam00175	NAD_binding_1			4.00E-17
2572232383	t3m_00739	pfam00970	FAD_binding_6			4.00E-08
2572232383	t3m_00739	Locus_type		CDS		
2572232383	t3m_00739	Product_name		2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases		
2572232383	t3m_00739	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		

2572232383	t3m_00739	Coordinates		24470..25351(+)		
2572232383	t3m_00739	DNA_length		882bp		
2572232383	t3m_00739	Protein_length		293aa		
2572232383	t3m_00739	GC			0.69	

2572232384	t3m_00740	COG_category	[C] Energy production and conversion			
2572232384	t3m_00740	COG1941	Coenzyme F420-reducing hydrogenase, gamma subunit			2.00E-36
2572232384	t3m_00740	pfam01058	Oxidored_q6			1.40E-22
2572232384	t3m_00740	Locus_type		CDS		
2572232384	t3m_00740	Product_name		Coenzyme F420-reducing hydrogenase, gamma subunit		
2572232384	t3m_00740	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232384	t3m_00740	Coordinates		25357..26151(+)		
2572232384	t3m_00740	DNA_length		795bp		
2572232384	t3m_00740	Protein_length		264aa		
2572232384	t3m_00740	GC			0.7	

2572232385	t3m_00741	COG_category	[C] Energy production and conversion			
2572232385	t3m_00741	COG3259	Coenzyme F420-reducing hydrogenase, alpha subunit			1.00E-77
2572232385	t3m_00741	pfam00374	NiFeSe_Hases			2.80E-15
2572232385	t3m_00741	pfam00374	NiFeSe_Hases			5.40E-10
2572232385	t3m_00741	Locus_type		CDS		
2572232385	t3m_00741	Product_name		Coenzyme F420-reducing hydrogenase, alpha subunit		
2572232385	t3m_00741	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232385	t3m_00741	Coordinates		26148..27446(+)		
2572232385	t3m_00741	DNA_length		1299bp		
2572232385	t3m_00741	Protein_length		432aa		
2572232385	t3m_00741	GC			0.67	

2572232386	t3m_00742	COG_category	[C] Energy production and conversion			
2572232386	t3m_00742	COG0680	Ni,Fe-hydrogenase maturation factor			4.00E-18
2572232386	t3m_00742	pfam01750	HycI			2.50E-14
2572232386	t3m_00742	TIGR00072	hydrogenase maturation protease			2.70E-36
2572232386	t3m_00742	Locus_type		CDS		
2572232386	t3m_00742	Product_name		hydrogenase maturation protease		

2572232386	t3m_00742	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232386	t3m_00742	Coordinates		27457..27975(+)	
2572232386	t3m_00742	DNA_length		519bp	
2572232386	t3m_00742	Protein_length		172aa	
2572232386	t3m_00742	GC		0.72	
2572232387	t3m_00743	pfam01155	HypA		6.40E-11
2572232387	t3m_00743	Locus_type		CDS	
2572232387	t3m_00743	Product_name		Hydrogenase expression/synthesis hypA family	
2572232387	t3m_00743	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232387	t3m_00743	Coordinates		27968..28246(+)	
2572232387	t3m_00743	DNA_length		279bp	
2572232387	t3m_00743	Protein_length		92aa	
2572232387	t3m_00743	GC		0.7	
2572232388	t3m_00744	Locus_type		CDS	
2572232388	t3m_00744	Product_name		hypothetical protein	
2572232388	t3m_00744	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232388	t3m_00744	Coordinates		28307..28624(+)	
2572232388	t3m_00744	DNA_length		318bp	
2572232388	t3m_00744	Protein_length		105aa	
2572232388	t3m_00744	GC		0.69	
2572232388	t3m_00744	Transmembrane		Yes	
2572232389	t3m_00745	Locus_type		CDS	
2572232389	t3m_00745	Product_name		hypothetical protein	
2572232389	t3m_00745	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232389	t3m_00745	Coordinates		28618..28779(-)	
2572232389	t3m_00745	DNA_length		162bp	
2572232389	t3m_00745	Protein_length		53aa	
2572232389	t3m_00745	GC		0.69	
2572232390	t3m_00746	COG_category	[R] General function prediction only		
2572232390	t3m_00746	COG0561	Predicted hydrolases of the HAD superfamily		9.00E-32

2572232390	t3m_00746	pfam08282	Hydrolase_3			4.70E-12
2572232390	t3m_00746	pfam08282	Hydrolase_3			1.50E-14
2572232390	t3m_00746	TIGR01484	HAD-superfamily hydrolase, subfamily IIB			1.10E-16
2572232390	t3m_00746	TIGR01487	phosphoglycolate phosphatase, TA0175-type			1.80E-44
2572232390	t3m_00746	Locus_type		CDS		
2572232390	t3m_00746	Product_name		phosphoglycolate phosphatase, TA0175-type		
2572232390	t3m_00746	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232390	t3m_00746	Coordinates		28859..29587(-)		
2572232390	t3m_00746	DNA_length		729bp		
2572232390	t3m_00746	Protein_length		242aa		
2572232390	t3m_00746	GC			0.7	

2572232391	t3m_00747	Metacyc	PWY-5921: L-glutamine biosynthesis II (tRNA-dependent)			
2572232391	t3m_00747	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232391	t3m_00747	COG2511	Archaeal Glu-tRNAGln amidotransferase subunit E (contains GAD domai			0.00E+00
2572232391	t3m_00747	pfam02934	GatB_N			2.60E-65
2572232391	t3m_00747	pfam02637	GatB_Yqey			2.30E-12
2572232391	t3m_00747	EC:6.3.5.7	Glutaminyl-tRNA synthase (glutamine-hydrolyzing).			
2572232391	t3m_00747	TIGR00134	glutamyl-tRNA(Gln) amidotransferase, subunit E			0.00E+00
2572232391	t3m_00747	KO:K03330	glutamyl-tRNA(Gln) amidotransferase subunit E [EC:6.3.5.7]			0.00E+00
2572232391	t3m_00747	ITERM:01533	glutamyl-tRNA(Gln) amidotransferase subunit E (EC 6.3.5.7)			
2572232391	t3m_00747	Locus_type		CDS		
2572232391	t3m_00747	Product_name		glutamyl-tRNA(Gln) amidotransferase subunit E (EC 6.3.5.7)		
2572232391	t3m_00747	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232391	t3m_00747	Coordinates		29607..31478(-)		
2572232391	t3m_00747	DNA_length		1872bp		
2572232391	t3m_00747	Protein_length		623aa		
2572232391	t3m_00747	GC			0.7	

2572232392	t3m_00748	Metacyc	PWY-5921: L-glutamine biosynthesis II (tRNA-dependent)			
2572232392	t3m_00748	COG_category	[E] Amino acid transport and metabolism			
2572232392	t3m_00748	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232392	t3m_00748	COG0252	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D			8.00E-82
2572232392	t3m_00748	pfam00710	Asparaginase			1.30E-80

2572232392	t3m_00748	EC:6.3.5.7	Glutaminyl-tRNA synthase (glutamine-hydrolyzing).			
2572232392	t3m_00748	TIGR00519	L-asparaginase, type I			3.70E-96
2572232392	t3m_00748	TIGR02153	glutamyl-tRNA(Gln) amidotransferase, subunit D			7.70E-130
2572232392	t3m_00748	KO:K09482	glutamyl-tRNA(Gln) amidotransferase subunit D [EC:6.3.5.7]			0.00E+00
2572232392	t3m_00748	ITERM:01532	glutamyl-tRNA(Gln) amidotransferase subunit D (EC 6.3.5.7)			
2572232392	t3m_00748	Locus_type		CDS		
2572232392	t3m_00748	Product_name		glutamyl-tRNA(Gln) amidotransferase subunit D (EC 6.3.5.7)		
2572232392	t3m_00748	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232392	t3m_00748	Coordinates		31475..32791(-)		
2572232392	t3m_00748	DNA_length		1317bp		
2572232392	t3m_00748	Protein_length		438aa		
2572232392	t3m_00748	GC			0.7	

2572232393	t3m_00749	Locus_type		tRNA		
2572232393	t3m_00749	Product_name		tRNA_Pseudo_GCG		
2572232393	t3m_00749	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232393	t3m_00749	Coordinates		32966..33038(+)		
2572232393	t3m_00749	DNA_length		73bp		
2572232393	t3m_00749	GC			0.63	

2572232394	t3m_00750	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP			
2572232394	t3m_00750	COG_category	[F] Nucleotide transport and metabolism			
2572232394	t3m_00750	COG0125	Thymidylate kinase			1.00E-26
2572232394	t3m_00750	pfam02223	Thymidylate_kin			1.20E-28
2572232394	t3m_00750	EC:2.7.4.9	dTMP kinase.			
2572232394	t3m_00750	TIGR00041	thymidylate kinase			5.10E-33
2572232394	t3m_00750	KO:K00943	dTMP kinase [EC:2.7.4.9]			2.30E-19
2572232394	t3m_00750	Locus_type		CDS		
2572232394	t3m_00750	Product_name		thymidylate kinase		
2572232394	t3m_00750	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232394	t3m_00750	Coordinates		33283..33873(+)		
2572232394	t3m_00750	DNA_length		591bp		
2572232394	t3m_00750	Protein_length		196aa		
2572232394	t3m_00750	GC			0.64	

2572232395	t3m_00751	pfam05368	NmrA		1.40E-23
2572232395	t3m_00751	Locus_type		CDS	
2572232395	t3m_00751	Product_name		NmrA-like family	
2572232395	t3m_00751	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232395	t3m_00751	Coordinates		34045..34773(-)	
2572232395	t3m_00751	DNA_length		729bp	
2572232395	t3m_00751	Protein_length		242aa	
2572232395	t3m_00751	GC		0.6	
2572232396	t3m_00752	COG_category	[C] Energy production and conversion		
2572232396	t3m_00752	COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family		2.00E-83
2572232396	t3m_00752	pfam00724	Oxidored_FMN		8.80E-64
2572232396	t3m_00752	pfam00724	Oxidored_FMN		5.20E-06
2572232396	t3m_00752	Locus_type		CDS	
2572232396	t3m_00752	Product_name		NADH:flavin oxidoreductases, Old Yellow Enzyme family	
2572232396	t3m_00752	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232396	t3m_00752	Coordinates		35239..36357(+)	
2572232396	t3m_00752	DNA_length		1119bp	
2572232396	t3m_00752	Protein_length		372aa	
2572232396	t3m_00752	GC		0.65	
2572232397	t3m_00753	Locus_type		CDS	
2572232397	t3m_00753	Product_name		hypothetical protein	
2572232397	t3m_00753	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	
2572232397	t3m_00753	Coordinates		36670..37068(+)	
2572232397	t3m_00753	DNA_length		399bp	
2572232397	t3m_00753	Protein_length		132aa	
2572232397	t3m_00753	GC		0.62	
2572232397	t3m_00753	Transmembrane		Yes	
2572232398	t3m_00754	Locus_type		CDS	
2572232398	t3m_00754	Product_name		hypothetical protein	
2572232398	t3m_00754	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12	

2572232398	t3m_00754	Coordinates		37257..38120(+)		
2572232398	t3m_00754	DNA_length		864bp		
2572232398	t3m_00754	Protein_length		287aa		
2572232398	t3m_00754	GC			0.65	
2572232398	t3m_00754	Transmembrane		Yes		
2572232399	t3m_00755	Locus_type		CDS		
2572232399	t3m_00755	Product_name		hypothetical protein		
2572232399	t3m_00755	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232399	t3m_00755	Coordinates		38307..38486(-)		
2572232399	t3m_00755	DNA_length		180bp		
2572232399	t3m_00755	Protein_length		59aa		
2572232399	t3m_00755	GC			0.58	
2572232399	t3m_00755	Transmembrane		Yes		
2572232400	t3m_00756	Locus_type		CDS		
2572232400	t3m_00756	Product_name		hypothetical protein		
2572232400	t3m_00756	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232400	t3m_00756	Coordinates		38738..38932(-)		
2572232400	t3m_00756	DNA_length		195bp		
2572232400	t3m_00756	Protein_length		64aa		
2572232400	t3m_00756	GC			0.59	
2572232401	t3m_00757	Locus_type		CDS		
2572232401	t3m_00757	Product_name		hypothetical protein		
2572232401	t3m_00757	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232401	t3m_00757	Coordinates		39245..39661(-)		
2572232401	t3m_00757	DNA_length		417bp		
2572232401	t3m_00757	Protein_length		138aa		
2572232401	t3m_00757	GC			0.61	
2572232401	t3m_00757	Transmembrane		Yes		
2572232402	t3m_00758	pfam00072	Response_reg			1.40E-20
2572232402	t3m_00758	pfam12840	HTH_20			3.40E-08

2572232402	t3m_00758	Locus_type		CDS		
2572232402	t3m_00758	Product_name		Response regulator receiver domain/Helix-turn-helix domain		
2572232402	t3m_00758	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232402	t3m_00758	Coordinates		39947..41005(+)		
2572232402	t3m_00758	DNA_length		1059bp		
2572232402	t3m_00758	Protein_length		352aa		
2572232402	t3m_00758	GC			0.65	

2572232403	t3m_00759	Locus_type		CDS		
2572232403	t3m_00759	Product_name		hypothetical protein		
2572232403	t3m_00759	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232403	t3m_00759	Coordinates		41158..41346(-)		
2572232403	t3m_00759	DNA_length		189bp		
2572232403	t3m_00759	Protein_length		62aa		
2572232403	t3m_00759	GC			0.62	

2572232404	t3m_00760	Locus_type		CDS		
2572232404	t3m_00760	Product_name		hypothetical protein		
2572232404	t3m_00760	Scaffold		t3m_contig_70_84_len_42953_read_count_3343224.12		
2572232404	t3m_00760	Coordinates		42272..42493(+)		
2572232404	t3m_00760	DNA_length		222bp		
2572232404	t3m_00760	Protein_length		73aa		
2572232404	t3m_00760	GC			0.61	

2572232405	t3m_00761	pfam02933	CDC48_2			1.50E-10
2572232405	t3m_00761	pfam02359	CDC48_N			9.50E-22
2572232405	t3m_00761	pfam00004	AAA			1.10E-25
2572232405	t3m_00761	Locus_type		CDS		
2572232405	t3m_00761	Product_name		Cell division protein 48 (CDC48), domain 2/Cell division protein 48 (CDC4		
2572232405	t3m_00761	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232405	t3m_00761	Coordinates		2..868(-)		
2572232405	t3m_00761	DNA_length		867bp		
2572232405	t3m_00761	Protein_length		289aa		
2572232405	t3m_00761	GC			0.68	

2572232406	t3m_00762	pfam05050	Methyltransf_21			8.40E-15
2572232406	t3m_00762	TIGR01444	methyltransferase, FkbM family			1.90E-26
2572232406	t3m_00762	Locus_type		CDS		
2572232406	t3m_00762	Product_name		methyltransferase, FkbM family		
2572232406	t3m_00762	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232406	t3m_00762	Coordinates		947..1903(-)		
2572232406	t3m_00762	DNA_length		957bp		
2572232406	t3m_00762	Protein_length		318aa		
2572232406	t3m_00762	GC			0.67	
2572232407	t3m_00763	Locus_type		CDS		
2572232407	t3m_00763	Product_name		hypothetical protein		
2572232407	t3m_00763	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232407	t3m_00763	Coordinates		1902..2060(+)		
2572232407	t3m_00763	DNA_length		159bp		
2572232407	t3m_00763	Protein_length		52aa		
2572232407	t3m_00763	GC			0.7	
2572232408	t3m_00764	Locus_type		CDS		
2572232408	t3m_00764	Product_name		hypothetical protein		
2572232408	t3m_00764	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232408	t3m_00764	Coordinates		2249..2461(-)		
2572232408	t3m_00764	DNA_length		213bp		
2572232408	t3m_00764	Protein_length		70aa		
2572232408	t3m_00764	GC			0.62	
2572232409	t3m_00765	pfam08241	Methyltransf_11			2.20E-15
2572232409	t3m_00765	Locus_type		CDS		
2572232409	t3m_00765	Product_name		Methyltransferase domain		
2572232409	t3m_00765	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232409	t3m_00765	Coordinates		2647..3378(+)		
2572232409	t3m_00765	DNA_length		732bp		
2572232409	t3m_00765	Protein_length		243aa		

2572232409	t3m_00765	GC			0.61	

2572232410	t3m_00766	pfam13302	Acetyltransf_3			1.90E-14
2572232410	t3m_00766	Locus_type		CDS		
2572232410	t3m_00766	Product_name		Acetyltransferase (GNAT) domain		
2572232410	t3m_00766	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232410	t3m_00766	Coordinates		3413..3712(-)		
2572232410	t3m_00766	DNA_length		300bp		
2572232410	t3m_00766	Protein_length		99aa		
2572232410	t3m_00766	GC			0.63	

2572232411	t3m_00767	COG_category	[S] Function unknown			
2572232411	t3m_00767	COG1801	Uncharacterized conserved protein			7.00E-43
2572232411	t3m_00767	pfam01904	DUF72			4.70E-51
2572232411	t3m_00767	Locus_type		CDS		
2572232411	t3m_00767	Product_name		Uncharacterized conserved protein		
2572232411	t3m_00767	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232411	t3m_00767	Coordinates		4781..5608(-)		
2572232411	t3m_00767	DNA_length		828bp		
2572232411	t3m_00767	Protein_length		275aa		
2572232411	t3m_00767	GC			0.69	

2572232412	t3m_00768	Locus_type		CDS		
2572232412	t3m_00768	Product_name		hypothetical protein		
2572232412	t3m_00768	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232412	t3m_00768	Coordinates		5746..6660(+)		
2572232412	t3m_00768	DNA_length		915bp		
2572232412	t3m_00768	Protein_length		304aa		
2572232412	t3m_00768	GC			0.73	

2572232413	t3m_00769	Metacyc	PWY-5386: methylglyoxal degradation I			
2572232413	t3m_00769	COG_category	[R] General function prediction only			
2572232413	t3m_00769	COG0491	Zn-dependent hydrolases, including glyoxylases			9.00E-23
2572232413	t3m_00769	pfam00753	Lactamase_B			8.50E-26

2572232413	t3m_00769	EC:3.1.2.6	Hydroxyacylglutathione hydrolase.			
2572232413	t3m_00769	KO:K01069	hydroxyacylglutathione hydrolase [EC:3.1.2.6]			7.00E-39
2572232413	t3m_00769	Locus_type		CDS		
2572232413	t3m_00769	Product_name		Zn-dependent hydrolases, including glyoxylases		
2572232413	t3m_00769	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232413	t3m_00769	Coordinates		6704..7315(+)		
2572232413	t3m_00769	DNA_length		612bp		
2572232413	t3m_00769	Protein_length		203aa		
2572232413	t3m_00769	GC			0.67	

2572232414	t3m_00770	COG_category	[S] Function unknown			
2572232414	t3m_00770	COG1617	Uncharacterized conserved protein			3.00E-08
2572232414	t3m_00770	pfam08617	CGI-121			3.20E-07
2572232414	t3m_00770	KO:K09119	hypothetical protein			2.50E-10
2572232414	t3m_00770	Locus_type		CDS		
2572232414	t3m_00770	Product_name		Uncharacterized conserved protein		
2572232414	t3m_00770	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232414	t3m_00770	Coordinates		7312..7890(+)		
2572232414	t3m_00770	DNA_length		579bp		
2572232414	t3m_00770	Protein_length		192aa		
2572232414	t3m_00770	GC			0.72	

2572232415	t3m_00771	Locus_type		tRNA		
2572232415	t3m_00771	Product_name		tRNA_Gly_TCC		
2572232415	t3m_00771	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232415	t3m_00771	Coordinates		7931..7999(+)		
2572232415	t3m_00771	DNA_length		69bp		
2572232415	t3m_00771	GC			0.58	

2572232416	t3m_00772	Locus_type		tRNA		
2572232416	t3m_00772	Product_name		tRNA_Ser_TGA		
2572232416	t3m_00772	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232416	t3m_00772	Coordinates		8098..8181(+)		
2572232416	t3m_00772	DNA_length		84bp		

2572232416	t3m_00772	GC			0.65	
2572232417	t3m_00773	IMG_pathway	241: Methyl-directed mismatch repair			
2572232417	t3m_00773	COG_category	[L] Replication, recombination and repair			
2572232417	t3m_00773	COG0249	Mismatch repair ATPase (MutS family)			0.00E+00
2572232417	t3m_00773	pfam01624	MutS_I			6.20E-38
2572232417	t3m_00773	pfam00488	MutS_V			1.40E-90
2572232417	t3m_00773	pfam05190	MutS_IV			1.20E-21
2572232417	t3m_00773	pfam05192	MutS_III			5.20E-34
2572232417	t3m_00773	TIGR01070	DNA mismatch repair protein MutS			0.00E+00
2572232417	t3m_00773	KO:K03555	DNA mismatch repair protein MutS			0.00E+00
2572232417	t3m_00773	ITERM:00607	DNA mismatch repair protein MutS			
2572232417	t3m_00773	Locus_type		CDS		
2572232417	t3m_00773	Product_name		DNA mismatch repair protein MutS		
2572232417	t3m_00773	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232417	t3m_00773	Coordinates		8237..10864(+)		
2572232417	t3m_00773	DNA_length		2628bp		
2572232417	t3m_00773	Protein_length		875aa		
2572232417	t3m_00773	GC			0.71	
2572232418	t3m_00774	IMG_pathway	241: Methyl-directed mismatch repair			
2572232418	t3m_00774	COG_category	[L] Replication, recombination and repair			
2572232418	t3m_00774	COG0323	DNA mismatch repair enzyme (predicted ATPase)			0.00E+00
2572232418	t3m_00774	pfam02518	HATPase_c			5.70E-09
2572232418	t3m_00774	pfam08676	MutL_C			9.00E-33
2572232418	t3m_00774	pfam01119	DNA_mis_repair			6.70E-28
2572232418	t3m_00774	TIGR00585	DNA mismatch repair protein MutL			2.90E-84
2572232418	t3m_00774	KO:K03572	DNA mismatch repair protein MutL			0.00E+00
2572232418	t3m_00774	ITERM:00608	DNA mismatch repair protein MutL			
2572232418	t3m_00774	Locus_type		CDS		
2572232418	t3m_00774	Product_name		DNA mismatch repair protein MutL		
2572232418	t3m_00774	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232418	t3m_00774	Coordinates		10861..12639(+)		
2572232418	t3m_00774	DNA_length		1779bp		

2572232418	t3m_00774	Protein_length		592aa		
2572232418	t3m_00774	GC			0.73	
2572232419	t3m_00775	Locus_type		CDS		
2572232419	t3m_00775	Product_name		hypothetical protein		
2572232419	t3m_00775	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232419	t3m_00775	Coordinates		12636..13196(+)		
2572232419	t3m_00775	DNA_length		561bp		
2572232419	t3m_00775	Protein_length		186aa		
2572232419	t3m_00775	GC			0.73	
2572232420	t3m_00776	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232420	t3m_00776	COG0438	Glycosyltransferase			2.00E-12
2572232420	t3m_00776	pfam13692	Glyco_trans_1_4			5.90E-11
2572232420	t3m_00776	pfam13579	Glyco_trans_4_4			1.50E-11
2572232420	t3m_00776	Locus_type		CDS		
2572232420	t3m_00776	Product_name		Glycosyltransferase		
2572232420	t3m_00776	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232420	t3m_00776	Coordinates		13215..14384(-)		
2572232420	t3m_00776	DNA_length		1170bp		
2572232420	t3m_00776	Protein_length		389aa		
2572232420	t3m_00776	GC			0.74	
2572232421	t3m_00777	COG_category	[S] Function unknown			
2572232421	t3m_00777	COG3379	Uncharacterized conserved protein			3.00E-40
2572232421	t3m_00777	pfam01663	Phosphodiest			2.80E-38
2572232421	t3m_00777	Locus_type		CDS		
2572232421	t3m_00777	Product_name		Uncharacterized conserved protein		
2572232421	t3m_00777	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232421	t3m_00777	Coordinates		14415..15917(-)		
2572232421	t3m_00777	DNA_length		1503bp		
2572232421	t3m_00777	Protein_length		500aa		
2572232421	t3m_00777	GC			0.69	

2572232422	t3m_00778	COG_category	[R] General function prediction only			
2572232422	t3m_00778	COG1782	Predicted metal-dependent RNase, consists of a metallo-beta-lactamas			0.00E+00
2572232422	t3m_00778	pfam10996	Beta-Casp			2.70E-33
2572232422	t3m_00778	pfam00753	Lactamase_B			3.90E-23
2572232422	t3m_00778	pfam07521	RMMBL			1.70E-12
2572232422	t3m_00778	TIGR03675	arCOG00543 universal archaeal KH-domain/beta-lactamase-domain pr			0.00E+00
2572232422	t3m_00778	Locus_type		CDS		
2572232422	t3m_00778	Product_name		arCOG00543 universal archaeal KH-domain/beta-lactamase-domain pro		
2572232422	t3m_00778	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232422	t3m_00778	Coordinates		16021..17925(-)		
2572232422	t3m_00778	DNA_length		1905bp		
2572232422	t3m_00778	Protein_length		634aa		
2572232422	t3m_00778	GC			0.66	
2572232423	t3m_00779	KEGG_module	M00342: Bacterial proteasome			
2572232423	t3m_00779	KEGG_module	M00343: Archaeal proteasome			
2572232423	t3m_00779	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232423	t3m_00779	COG0638	20S proteasome, alpha and beta subunits			1.00E-52
2572232423	t3m_00779	pfam00227	Proteasome			2.10E-52
2572232423	t3m_00779	EC:3.4.25.1	Proteasome endopeptidase complex.			
2572232423	t3m_00779	TIGR03634	proteasome endopeptidase complex, archaeal, beta subunit			2.00E-78
2572232423	t3m_00779	KO:K03433	proteasome beta subunit [EC:3.4.25.1]			0.00E+00
2572232423	t3m_00779	Locus_type		CDS		
2572232423	t3m_00779	Product_name		proteasome endopeptidase complex, beta component (EC 3.4.25.1). Thr		
2572232423	t3m_00779	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232423	t3m_00779	Coordinates		17990..18655(-)		
2572232423	t3m_00779	DNA_length		666bp		
2572232423	t3m_00779	Protein_length		221aa		
2572232423	t3m_00779	GC			0.65	
2572232424	t3m_00780	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)			
2572232424	t3m_00780	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2572232424	t3m_00780	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572232424	t3m_00780	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			

2572232424	t3m_00780	KEGG_module	M00376: 3-Hydroxypropionate bicycle		
2572232424	t3m_00780	KEGG_module	M00149: Succinate dehydrogenase, prokaryotes		
2572232424	t3m_00780	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2572232424	t3m_00780	Metacyc	PWY-5392: reductive TCA cycle II		
2572232424	t3m_00780	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2572232424	t3m_00780	Metacyc	P23-PWY: reductive TCA cycle I		
2572232424	t3m_00780	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)		
2572232424	t3m_00780	COG_category	[C] Energy production and conversion		
2572232424	t3m_00780	COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit		0.00E+00
2572232424	t3m_00780	pfam02910	Succ_DH_flav_C		2.20E-43
2572232424	t3m_00780	pfam00890	FAD_binding_2		3.30E-107
2572232424	t3m_00780	EC:1.3.99.1	Succinate dehydrogenase.		
2572232424	t3m_00780	TIGR01812	succinate dehydrogenase or fumarate reductase, flavoprotein subunitG		0.00E+00
2572232424	t3m_00780	KO:K00239	succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]		0.00E+00
2572232424	t3m_00780	ITERM:01372	succinate dehydrogenase subunit A (EC 1.3.5.1)		
2572232424	t3m_00780	Locus_type		CDS	
2572232424	t3m_00780	Product_name		succinate dehydrogenase subunit A (EC 1.3.5.1)	
2572232424	t3m_00780	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13	
2572232424	t3m_00780	Coordinates		18854..20536(+)	
2572232424	t3m_00780	DNA_length		1683bp	
2572232424	t3m_00780	Protein_length		560aa	
2572232424	t3m_00780	GC		0.68	

2572232425	t3m_00781	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate	
2572232425	t3m_00781	KEGG_module	M00149: Succinate dehydrogenase, prokaryotes	
2572232425	t3m_00781	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)	
2572232425	t3m_00781	Metacyc	PWY-5392: reductive TCA cycle II	
2572232425	t3m_00781	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)	
2572232425	t3m_00781	Metacyc	P42-PWY: incomplete reductive TCA cycle	
2572232425	t3m_00781	Metacyc	P23-PWY: reductive TCA cycle I	
2572232425	t3m_00781	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)	
2572232425	t3m_00781	COG_category	[C] Energy production and conversion	
2572232425	t3m_00781	COG0479	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	8.00E-60
2572232425	t3m_00781	pfam13085	Fer2_3	2.60E-30

2572232425	t3m_00781	pfam13183	Fer4_8			4.20E-11
2572232425	t3m_00781	EC:1.3.99.1	Succinate dehydrogenase.			
2572232425	t3m_00781	TIGR00384	succinate dehydrogenase and fumarate reductase iron-sulfur protein			1.80E-73
2572232425	t3m_00781	KO:K00240	succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]			0.00E+00
2572232425	t3m_00781	Locus_type		CDS		
2572232425	t3m_00781	Product_name		succinate dehydrogenase and fumarate reductase iron-sulfur protein		
2572232425	t3m_00781	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232425	t3m_00781	Coordinates		20536..21510(+)		
2572232425	t3m_00781	DNA_length		975bp		
2572232425	t3m_00781	Protein_length		324aa		
2572232425	t3m_00781	GC			0.67	
2572232426	t3m_00782	KEGG_module	M00561: Methanogenesis, trimethylamine => methane			
2572232426	t3m_00782	KEGG_module	M00567: Methanogenesis, CO2 => methane			
2572232426	t3m_00782	KEGG_module	M00562: Methanogenesis, dimethylamine => methane			
2572232426	t3m_00782	KEGG_module	M00347: Methanogenesis, formate => methane			
2572232426	t3m_00782	KEGG_module	M00563: Methanogenesis, methylamine => methane			
2572232426	t3m_00782	KEGG_module	M00357: Methanogenesis, acetate => methane			
2572232426	t3m_00782	KEGG_module	M00356: Methanogenesis, methanol => methane			
2572232426	t3m_00782	Metacyc	PWY-5207: coenzyme B/coenzyme M regeneration			
2572232426	t3m_00782	COG_category	[C] Energy production and conversion			
2572232426	t3m_00782	COG2048	Heterodisulfide reductase, subunit B			9.00E-76
2572232426	t3m_00782	pfam02754	CCG			2.40E-15
2572232426	t3m_00782	pfam02754	CCG			7.40E-13
2572232426	t3m_00782	EC:1.8.98.1	CoB--CoM heterodisulfide reductase.			
2572232426	t3m_00782	KO:K03389	heterodisulfide reductase subunit B [EC:1.8.98.1]			0.00E+00
2572232426	t3m_00782	Locus_type		CDS		
2572232426	t3m_00782	Product_name		Heterodisulfide reductase, subunit B		
2572232426	t3m_00782	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232426	t3m_00782	Coordinates		21507..22391(+)		
2572232426	t3m_00782	DNA_length		885bp		
2572232426	t3m_00782	Protein_length		294aa		
2572232426	t3m_00782	GC			0.68	

2572232427	t3m_00783	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232427	t3m_00783	COG0251	Putative translation initiation inhibitor, yjgF family			7.00E-25
2572232427	t3m_00783	pfam01042	Ribonuc_L-PSP			5.10E-29
2572232427	t3m_00783	Locus_type		CDS		
2572232427	t3m_00783	Product_name		Putative translation initiation inhibitor, yjgF family		
2572232427	t3m_00783	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232427	t3m_00783	Coordinates		22351..22797(+)		
2572232427	t3m_00783	DNA_length		447bp		
2572232427	t3m_00783	Protein_length		148aa		
2572232427	t3m_00783	GC			0.71	
2572232428	t3m_00784	Locus_type		CDS		
2572232428	t3m_00784	Product_name		hypothetical protein		
2572232428	t3m_00784	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232428	t3m_00784	Coordinates		22850..23149(-)		
2572232428	t3m_00784	DNA_length		300bp		
2572232428	t3m_00784	Protein_length		99aa		
2572232428	t3m_00784	GC			0.66	
2572232429	t3m_00785	Locus_type		CDS		
2572232429	t3m_00785	Product_name		hypothetical protein		
2572232429	t3m_00785	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232429	t3m_00785	Coordinates		23159..23356(-)		
2572232429	t3m_00785	DNA_length		198bp		
2572232429	t3m_00785	Protein_length		65aa		
2572232429	t3m_00785	GC			0.64	
2572232430	t3m_00786	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP			
2572232430	t3m_00786	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2572232430	t3m_00786	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2572232430	t3m_00786	IMG_pathway	295: Guanylate (GMP) biosynthesis via glutamine			
2572232430	t3m_00786	COG_category	[F] Nucleotide transport and metabolism			
2572232430	t3m_00786	COG0519	GMP synthase, PP-ATPase domain/subunit			9.00E-113
2572232430	t3m_00786	pfam00958	GMP_synt_C			7.10E-31

2572232430	t3m_00786	EC:6.3.5.2	GMP synthase (glutamine-hydrolyzing).		
2572232430	t3m_00786	TIGR00884	GMP synthase (glutamine-hydrolyzing), C-terminal domain or B subunit		9.50E-122
2572232430	t3m_00786	KO:K01951	GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]		0.00E+00
2572232430	t3m_00786	ITERM:01286	GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2)		
2572232430	t3m_00786	Locus_type		CDS	
2572232430	t3m_00786	Product_name		GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2)	
2572232430	t3m_00786	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13	
2572232430	t3m_00786	Coordinates		23446..24393(-)	
2572232430	t3m_00786	DNA_length		948bp	
2572232430	t3m_00786	Protein_length		315aa	
2572232430	t3m_00786	GC		0.71	

2572232431	t3m_00787	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572232431	t3m_00787	Metacyc	PWY-6123: inosine-5'-phosphate biosynthesis I		
2572232431	t3m_00787	COG_category	[F] Nucleotide transport and metabolism		
2572232431	t3m_00787	COG0041	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase		7.00E-38
2572232431	t3m_00787	pfam00731	AIRC		2.50E-47
2572232431	t3m_00787	EC:5.4.99.18	5-(carboxyamino)imidazole ribonucleotide mutase.		
2572232431	t3m_00787	TIGR01162	phosphoribosylaminoimidazole carboxylase, PurE protein		2.80E-53
2572232431	t3m_00787	KO:K01588	5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]		5.00E-38
2572232431	t3m_00787	Locus_type		CDS	
2572232431	t3m_00787	Product_name		phosphoribosylaminoimidazole carboxylase, PurE protein	
2572232431	t3m_00787	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13	
2572232431	t3m_00787	Coordinates		24390..24851(-)	
2572232431	t3m_00787	DNA_length		462bp	
2572232431	t3m_00787	Protein_length		153aa	
2572232431	t3m_00787	GC		0.71	

2572232432	t3m_00788	Locus_type		CDS	
2572232432	t3m_00788	Product_name		hypothetical protein	
2572232432	t3m_00788	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13	
2572232432	t3m_00788	Coordinates		24933..25586(+)	
2572232432	t3m_00788	DNA_length		654bp	
2572232432	t3m_00788	Protein_length		217aa	

2572232432	t3m_00788	GC			0.7	
2572232432	t3m_00788	Transmembrane		Yes		
2572232433	t3m_00789	COG_category	[T] Signal transduction mechanisms			
2572232433	t3m_00789	COG0467	RecA-superfamily ATPases implicated in signal transduction			6.00E-08
2572232433	t3m_00789	pfam07088	GvpD			8.50E-40
2572232433	t3m_00789	Locus_type		CDS		
2572232433	t3m_00789	Product_name		RecA-superfamily ATPases implicated in signal transduction		
2572232433	t3m_00789	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232433	t3m_00789	Coordinates		25603..27150(-)		
2572232433	t3m_00789	DNA_length		1548bp		
2572232433	t3m_00789	Protein_length		515aa		
2572232433	t3m_00789	GC			0.67	
2572232434	t3m_00790	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232434	t3m_00790	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232434	t3m_00790	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232434	t3m_00790	IMG_pathway	487: L-alanine ligation to tRNA(Ala)			
2572232434	t3m_00790	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232434	t3m_00790	COG0013	Alanyl-tRNA synthetase			0.00E+00
2572232434	t3m_00790	pfam01411	tRNA-synt_2c			1.90E-49
2572232434	t3m_00790	pfam01411	tRNA-synt_2c			7.70E-33
2572232434	t3m_00790	pfam07973	tRNA_SAD			8.40E-11
2572232434	t3m_00790	EC:6.1.1.7	Alanine--tRNA ligase.			
2572232434	t3m_00790	TIGR00344	alanine--tRNA ligase			0.00E+00
2572232434	t3m_00790	KO:K01872	alanyl-tRNA synthetase [EC:6.1.1.7]			0.00E+00
2572232434	t3m_00790	ITERM:00391	alanyl-tRNA synthetase (EC 6.1.1.7)			
2572232434	t3m_00790	Locus_type		CDS		
2572232434	t3m_00790	Product_name		alanyl-tRNA synthetase (EC 6.1.1.7)		
2572232434	t3m_00790	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232434	t3m_00790	Coordinates		27271..29838(-)		
2572232434	t3m_00790	DNA_length		2568bp		
2572232434	t3m_00790	Protein_length		855aa		
2572232434	t3m_00790	GC			0.69	

2572232435	t3m_00791	COG_category	[G] Carbohydrate transport and metabolism			
2572232435	t3m_00791	COG2814	Arabinose efflux permease			7.00E-22
2572232435	t3m_00791	pfam07690	MFS_1			2.40E-37
2572232435	t3m_00791	Locus_type		CDS		
2572232435	t3m_00791	Product_name		Arabinose efflux permease		
2572232435	t3m_00791	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232435	t3m_00791	Coordinates		29941..31182(+)		
2572232435	t3m_00791	DNA_length		1242bp		
2572232435	t3m_00791	Protein_length		413aa		
2572232435	t3m_00791	GC			0.72	
2572232435	t3m_00791	Transmembrane		Yes		

2572232436	t3m_00792	Locus_type		CDS		
2572232436	t3m_00792	Product_name		hypothetical protein		
2572232436	t3m_00792	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232436	t3m_00792	Coordinates		31262..31885(+)		
2572232436	t3m_00792	DNA_length		624bp		
2572232436	t3m_00792	Protein_length		207aa		
2572232436	t3m_00792	GC			0.71	

2572232437	t3m_00793	KEGG_module	M00126: Tetrahydrofolate biosynthesis, GTP => THF			
2572232437	t3m_00793	Metacyc	PWY-2161: folate polyglutamylation			
2572232437	t3m_00793	Metacyc	PWY-6614: tetrahydrofolate biosynthesis			
2572232437	t3m_00793	Metacyc	1CMET2-PWY: formylTHF biosynthesis I			
2572232437	t3m_00793	COG_category	[H] Coenzyme transport and metabolism			
2572232437	t3m_00793	COG0285	Folylpolyglutamate synthase			2.00E-97
2572232437	t3m_00793	pfam08245	Mur_ligase_M			3.00E-14
2572232437	t3m_00793	pfam02875	Mur_ligase_C			2.30E-07
2572232437	t3m_00793	EC:6.3.2.12	Dihydrofolate synthase.			
2572232437	t3m_00793	EC:6.3.2.17	Tetrahydrofolate synthase.			
2572232437	t3m_00793	TIGR01499	folylpolyglutamate synthase/dihydrofolate synthase			1.80E-108
2572232437	t3m_00793	KO:K11754	dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12 6.3.2			0.00E+00
2572232437	t3m_00793	Locus_type		CDS		

2572232437	t3m_00793	Product_name		folylpolyglutamate synthase/dihydrofolate synthase		
2572232437	t3m_00793	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232437	t3m_00793	Coordinates		31837..33240(-)		
2572232437	t3m_00793	DNA_length		1404bp		
2572232437	t3m_00793	Protein_length		467aa		
2572232437	t3m_00793	GC			0.72	

2572232438	t3m_00794	KEGG_module	M00376: 3-Hydroxypropionate bicycle			
2572232438	t3m_00794	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle			
2572232438	t3m_00794	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			
2572232438	t3m_00794	Metacyc	PWY0-43: conversion of succinate to propionate			
2572232438	t3m_00794	Metacyc	P108-PWY: pyruvate fermentation to propionate I			
2572232438	t3m_00794	Metacyc	PWY-5743: 3-hydroxypropionate cycle			
2572232438	t3m_00794	Metacyc	PWY-6728: methylaspartate cycle			
2572232438	t3m_00794	Metacyc	PROPIONMET-PWY: methylmalonyl pathway			
2572232438	t3m_00794	COG_category	[I] Lipid transport and metabolism			
2572232438	t3m_00794	COG1884	Methylmalonyl-CoA mutase, N-terminal domain/subunit			0.00E+00
2572232438	t3m_00794	pfam01642	MM_CoA_mutase			0.00E+00
2572232438	t3m_00794	EC:5.4.99.2	Methylmalonyl-CoA mutase.			
2572232438	t3m_00794	TIGR00641	methylmalonyl-CoA mutase N-terminal domain			0.00E+00
2572232438	t3m_00794	KO:K01848	methylmalonyl-CoA mutase, N-terminal domain [EC:5.4.99.2]			0.00E+00
2572232438	t3m_00794	Locus_type		CDS		
2572232438	t3m_00794	Product_name		methylmalonyl-CoA mutase (EC 5.4.99.2)		
2572232438	t3m_00794	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232438	t3m_00794	Coordinates		33257..34972(-)		
2572232438	t3m_00794	DNA_length		1716bp		
2572232438	t3m_00794	Protein_length		571aa		
2572232438	t3m_00794	GC			0.68	

2572232439	t3m_00795	COG_category	[R] General function prediction only			
2572232439	t3m_00795	COG2102	Predicted ATPases of PP-loop superfamily			2.00E-49
2572232439	t3m_00795	pfam01902	ATP_bind_4			6.90E-47
2572232439	t3m_00795	TIGR00289	TIGR00289 family protein			4.70E-49
2572232439	t3m_00795	TIGR00290	MJ0570-related uncharacterized domain			2.90E-49

2572232439	t3m_00795	Locus_type		CDS	
2572232439	t3m_00795	Product_name		Predicted ATPases of PP-loop superfamily	
2572232439	t3m_00795	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13	
2572232439	t3m_00795	Coordinates		35044..35748(-)	
2572232439	t3m_00795	DNA_length		705bp	
2572232439	t3m_00795	Protein_length		234aa	
2572232439	t3m_00795	GC		0.68	
2572232440	t3m_00796	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572232440	t3m_00796	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II		
2572232440	t3m_00796	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I		
2572232440	t3m_00796	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis		
2572232440	t3m_00796	COG_category	[F] Nucleotide transport and metabolism		
2572232440	t3m_00796	COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase doma		0.00E+00
2572232440	t3m_00796	pfam00586	AIRS		8.80E-19
2572232440	t3m_00796	pfam02769	AIRS_C		9.50E-25
2572232440	t3m_00796	pfam00586	AIRS		1.70E-08
2572232440	t3m_00796	pfam02769	AIRS_C		3.60E-17
2572232440	t3m_00796	EC:6.3.5.3	Phosphoribosylformylglycinamidine synthase.		
2572232440	t3m_00796	TIGR01736	phosphoribosylformylglycinamidine synthase II		0.00E+00
2572232440	t3m_00796	KO:K01952	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]		0.00E+00
2572232440	t3m_00796	Locus_type		CDS	
2572232440	t3m_00796	Product_name		phosphoribosylformylglycinamidine synthase II	
2572232440	t3m_00796	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13	
2572232440	t3m_00796	Coordinates		35758..38064(-)	
2572232440	t3m_00796	DNA_length		2307bp	
2572232440	t3m_00796	Protein_length		768aa	
2572232440	t3m_00796	GC		0.71	
2572232441	t3m_00797	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572232441	t3m_00797	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis		
2572232441	t3m_00797	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I		
2572232441	t3m_00797	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II		
2572232441	t3m_00797	COG_category	[F] Nucleotide transport and metabolism		

2572232441	t3m_00797	COG1828	Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component			5.00E-09
2572232441	t3m_00797	pfam02700	PurS			2.70E-11
2572232441	t3m_00797	EC:6.3.5.3	Phosphoribosylformylglycinamidine synthase.			
2572232441	t3m_00797	KO:K01952	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]			2.20E-06
2572232441	t3m_00797	Locus_type		CDS		
2572232441	t3m_00797	Product_name		Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component		
2572232441	t3m_00797	Scaffold		t3m_contig_70_104_len_38616_read_count_3010148.13		
2572232441	t3m_00797	Coordinates		38069..38275(-)		
2572232441	t3m_00797	DNA_length		207bp		
2572232441	t3m_00797	Protein_length		68aa		
2572232441	t3m_00797	GC			0.71	
2572232442	t3m_00798	Locus_type		CDS		
2572232442	t3m_00798	Product_name		hypothetical protein		
2572232442	t3m_00798	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232442	t3m_00798	Coordinates		3..1556(-)		
2572232442	t3m_00798	DNA_length		1554bp		
2572232442	t3m_00798	Protein_length		518aa		
2572232442	t3m_00798	GC			0.63	
2572232443	t3m_00799	COG_category	[E] Amino acid transport and metabolism			
2572232443	t3m_00799	COG1231	Monoamine oxidase			1.00E-36
2572232443	t3m_00799	pfam01593	Amino_oxidase			7.50E-16
2572232443	t3m_00799	pfam01593	Amino_oxidase			2.00E-41
2572232443	t3m_00799	Locus_type		CDS		
2572232443	t3m_00799	Product_name		Monoamine oxidase		
2572232443	t3m_00799	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232443	t3m_00799	Coordinates		1970..3310(-)		
2572232443	t3m_00799	DNA_length		1341bp		
2572232443	t3m_00799	Protein_length		446aa		
2572232443	t3m_00799	GC			0.69	
2572232444	t3m_00800	COG_category	[H] Coenzyme transport and metabolism			
2572232444	t3m_00800	COG0043	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxyl			6.00E-91

2572232444	t3m_00800	pfam01977	UbiD		5.70E-92
2572232444	t3m_00800	EC:4.1.1.61	4-hydroxybenzoate decarboxylase.		
2572232444	t3m_00800	TIGR00148	UbiD family decarboxylase		2.80E-99
2572232444	t3m_00800	KO:K01612	4-hydroxybenzoate decarboxylase [EC:4.1.1.61]		0.00E+00
2572232444	t3m_00800	Locus_type		CDS	
2572232444	t3m_00800	Product_name		UbiD family decarboxylase	
2572232444	t3m_00800	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232444	t3m_00800	Coordinates		3624..4913(+)	
2572232444	t3m_00800	DNA_length		1290bp	
2572232444	t3m_00800	Protein_length		429aa	
2572232444	t3m_00800	GC		0.62	
2572232445	t3m_00801	COG_category	[S] Function unknown		
2572232445	t3m_00801	COG1679	Uncharacterized conserved protein		7.00E-104
2572232445	t3m_00801	pfam04412	DUF521		3.30E-117
2572232445	t3m_00801	pfam01989	DUF126		3.40E-17
2572232445	t3m_00801	KO:K09123	hypothetical protein		0.00E+00
2572232445	t3m_00801	ITERM:01400	predicted aconitase subunit 1 (EC 4.2.1.3)		
2572232445	t3m_00801	Locus_type		CDS	
2572232445	t3m_00801	Product_name		predicted aconitase subunit 1 (EC 4.2.1.3)	
2572232445	t3m_00801	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232445	t3m_00801	Coordinates		4925..6403(+)	
2572232445	t3m_00801	DNA_length		1479bp	
2572232445	t3m_00801	Protein_length		492aa	
2572232445	t3m_00801	GC		0.63	
2572232445	t3m_00801	Fused_gene		Yes	
2572232446	t3m_00802	COG_category	[R] General function prediction only		
2572232446	t3m_00802	COG0535	Predicted Fe-S oxidoreductases		3.00E-34
2572232446	t3m_00802	pfam04055	Radical_SAM		1.50E-15
2572232446	t3m_00802	pfam11946	DUF3463		9.50E-20
2572232446	t3m_00802	pfam13353	Fer4_12		5.60E-05
2572232446	t3m_00802	TIGR03961	archaeal radical SAM protein, PTO1314 family		0.00E+00
2572232446	t3m_00802	Locus_type		CDS	

2572232446	t3m_00802	Product_name		archaeal radical SAM protein, PTO1314 family		
2572232446	t3m_00802	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232446	t3m_00802	Coordinates		6456..7490(-)		
2572232446	t3m_00802	DNA_length		1035bp		
2572232446	t3m_00802	Protein_length		344aa		
2572232446	t3m_00802	GC			0.63	
2572232447	t3m_00803	pfam00924	MS_channel			3.00E-19
2572232447	t3m_00803	Locus_type		CDS		
2572232447	t3m_00803	Product_name		Mechanosensitive ion channel		
2572232447	t3m_00803	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232447	t3m_00803	Coordinates		7588..8091(-)		
2572232447	t3m_00803	DNA_length		504bp		
2572232447	t3m_00803	Protein_length		167aa		
2572232447	t3m_00803	GC			0.65	
2572232447	t3m_00803	Transmembrane		Yes		
2572232448	t3m_00804	COG_category	[S] Function unknown			
2572232448	t3m_00804	COG4320	Uncharacterized protein conserved in bacteria			5.00E-30
2572232448	t3m_00804	pfam10009	DUF2252			8.80E-126
2572232448	t3m_00804	Locus_type		CDS		
2572232448	t3m_00804	Product_name		Uncharacterized protein conserved in bacteria		
2572232448	t3m_00804	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232448	t3m_00804	Coordinates		8582..9751(+)		
2572232448	t3m_00804	DNA_length		1170bp		
2572232448	t3m_00804	Protein_length		389aa		
2572232448	t3m_00804	GC			0.65	
2572232449	t3m_00805	Locus_type		CDS		
2572232449	t3m_00805	Product_name		hypothetical protein		
2572232449	t3m_00805	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232449	t3m_00805	Coordinates		9786..10367(-)		
2572232449	t3m_00805	DNA_length		582bp		
2572232449	t3m_00805	Protein_length		193aa		

2572232449	t3m_00805	GC			0.65	
2572232449	t3m_00805	Transmembrane		Yes		
2572232450	t3m_00806	pfam13527	Acetyltransf_9			2.80E-09
2572232450	t3m_00806	Locus_type		CDS		
2572232450	t3m_00806	Product_name		Acetyltransferase (GNAT) domain		
2572232450	t3m_00806	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232450	t3m_00806	Coordinates		10434..11393(-)		
2572232450	t3m_00806	DNA_length		960bp		
2572232450	t3m_00806	Protein_length		319aa		
2572232450	t3m_00806	GC			0.68	
2572232451	t3m_00807	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)			
2572232451	t3m_00807	KEGG_module	M00012: Glyoxylate cycle			
2572232451	t3m_00807	KEGG_module	M00010: Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate			
2572232451	t3m_00807	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572232451	t3m_00807	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)			
2572232451	t3m_00807	Metacyc	ANARESP1-PWY: respiration (anaerobic)			
2572232451	t3m_00807	Metacyc	FERMENTATION-PWY: mixed acid fermentation			
2572232451	t3m_00807	Metacyc	PWY-5750: itaconate biosynthesis			
2572232451	t3m_00807	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)			
2572232451	t3m_00807	Metacyc	PWY-6728: methylaspartate cycle			
2572232451	t3m_00807	Metacyc	GLYOXYLATE-BYPASS: glyoxylate cycle			
2572232451	t3m_00807	Metacyc	PWY-7124: ethylene biosynthesis V			
2572232451	t3m_00807	Metacyc	PWY-6549: glutamine biosynthesis III			
2572232451	t3m_00807	Metacyc	TCA: TCA cycle I (prokaryotic)			
2572232451	t3m_00807	Metacyc	PWY-5690: TCA cycle II (eukaryotic)			
2572232451	t3m_00807	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2572232451	t3m_00807	IMG_pathway	322: 2-oxoglutarate synthesis by partial TCA cycle			
2572232451	t3m_00807	IMG_pathway	334: Tricarboxylic acid cycle			
2572232451	t3m_00807	IMG_pathway	911: Acetyl-CoA assimilation via glyoxylate cycle			
2572232451	t3m_00807	IMG_pathway	913: Acetyl-CoA assimilation via methylaspartate cycle			
2572232451	t3m_00807	IMG_pathway	960: Glyoxalate from acetyl-CoA via isocitrate lyase cycle			
2572232451	t3m_00807	COG_category	[C] Energy production and conversion			

2572232451	t3m_00807	COG0372	Citrate synthase		5.00E-119
2572232451	t3m_00807	pfam00285	Citrate_synt		5.80E-129
2572232451	t3m_00807	EC:2.3.3.1	Citrate (Si)-synthase.		
2572232451	t3m_00807	TIGR01798	citrate synthase I (hexameric type)		0.00E+00
2572232451	t3m_00807	KO:K01647	citrate synthase [EC:2.3.3.1]		0.00E+00
2572232451	t3m_00807	ITERM:01395	citrate synthase (EC 2.3.3.1)		
2572232451	t3m_00807	Locus_type		CDS	
2572232451	t3m_00807	Product_name		citrate synthase (EC 2.3.3.1)	
2572232451	t3m_00807	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232451	t3m_00807	Coordinates		11463..12875(-)	
2572232451	t3m_00807	DNA_length		1413bp	
2572232451	t3m_00807	Protein_length		470aa	
2572232451	t3m_00807	GC		0.64	
2572232452	t3m_00808	pfam13489	Methyltransf_23		6.70E-18
2572232452	t3m_00808	Locus_type		CDS	
2572232452	t3m_00808	Product_name		Methyltransferase domain	
2572232452	t3m_00808	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232452	t3m_00808	Coordinates		13026..13742(+)	
2572232452	t3m_00808	DNA_length		717bp	
2572232452	t3m_00808	Protein_length		238aa	
2572232452	t3m_00808	GC		0.68	
2572232453	t3m_00809	KEGG_module	M00515: FlrB-FlrC (polar flagellar synthesis) two-component regulatory system		
2572232453	t3m_00809	pfam00072	Response_reg		5.60E-29
2572232453	t3m_00809	pfam12840	HTH_20		1.70E-12
2572232453	t3m_00809	KO:K10943	two component system, response regulator FlrC		2.20E-24
2572232453	t3m_00809	Locus_type		CDS	
2572232453	t3m_00809	Product_name		Response regulator receiver domain/Helix-turn-helix domain	
2572232453	t3m_00809	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232453	t3m_00809	Coordinates		13714..14763(-)	
2572232453	t3m_00809	DNA_length		1050bp	
2572232453	t3m_00809	Protein_length		349aa	
2572232453	t3m_00809	GC		0.68	

2572232454	t3m_00810	pfam08448	PAS_4			9.70E-09
2572232454	t3m_00810	pfam13426	PAS_9			6.20E-19
2572232454	t3m_00810	pfam02518	HATPase_c			4.80E-29
2572232454	t3m_00810	pfam00512	HisKA			9.60E-12
2572232454	t3m_00810	TIGR00229	PAS domain S-box			9.90E-10
2572232454	t3m_00810	Locus_type		CDS		
2572232454	t3m_00810	Product_name		PAS domain S-box		
2572232454	t3m_00810	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232454	t3m_00810	Coordinates		14843..16300(-)		
2572232454	t3m_00810	DNA_length		1458bp		
2572232454	t3m_00810	Protein_length		485aa		
2572232454	t3m_00810	GC			0.67	
2572232455	t3m_00811	Locus_type		CDS		
2572232455	t3m_00811	Product_name		hypothetical protein		
2572232455	t3m_00811	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232455	t3m_00811	Coordinates		16413..16811(+)		
2572232455	t3m_00811	DNA_length		399bp		
2572232455	t3m_00811	Protein_length		132aa		
2572232455	t3m_00811	GC			0.71	
2572232456	t3m_00812	COG_category	[R] General function prediction only			
2572232456	t3m_00812	COG2403	Predicted GTPase			1.00E-120
2572232456	t3m_00812	Locus_type		CDS		
2572232456	t3m_00812	Product_name		Predicted GTPase		
2572232456	t3m_00812	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232456	t3m_00812	Coordinates		16827..18149(-)		
2572232456	t3m_00812	DNA_length		1323bp		
2572232456	t3m_00812	Protein_length		440aa		
2572232456	t3m_00812	GC			0.67	
2572232457	t3m_00813	pfam07690	MFS_1			1.30E-43
2572232457	t3m_00813	TIGR00711	drug resistance transporter, EmrB/QacA subfamily			6.20E-71

2572232457	t3m_00813	Locus_type		CDS		
2572232457	t3m_00813	Product_name		Major Facilitator Superfamily		
2572232457	t3m_00813	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232457	t3m_00813	Coordinates		18206..19657(-)		
2572232457	t3m_00813	DNA_length		1452bp		
2572232457	t3m_00813	Protein_length		483aa		
2572232457	t3m_00813	GC			0.67	
2572232457	t3m_00813	Transmembrane		Yes		

2572232458	t3m_00814	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP			
2572232458	t3m_00814	Metacyc	PWY-6596: adenosine nucleotides degradation I			
2572232458	t3m_00814	Metacyc	PWY-5695: urate biosynthesis/inosine 5'-phosphate degradation			
2572232458	t3m_00814	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2572232458	t3m_00814	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2572232458	t3m_00814	pfam00571	CBS			2.80E-09
2572232458	t3m_00814	EC:1.1.1.205	IMP dehydrogenase.			
2572232458	t3m_00814	KO:K00088	IMP dehydrogenase [EC:1.1.1.205]			1.40E-18
2572232458	t3m_00814	Locus_type		CDS		
2572232458	t3m_00814	Product_name		CBS domain		
2572232458	t3m_00814	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232458	t3m_00814	Coordinates		19780..20223(-)		
2572232458	t3m_00814	DNA_length		444bp		
2572232458	t3m_00814	Protein_length		147aa		
2572232458	t3m_00814	GC			0.64	

2572232459	t3m_00815	COG_category	[R] General function prediction only			
2572232459	t3m_00815	COG0727	Predicted Fe-S-cluster oxidoreductase			1.00E-07
2572232459	t3m_00815	pfam03692	CxxCxxCC			2.30E-07
2572232459	t3m_00815	Locus_type		CDS		
2572232459	t3m_00815	Product_name		Predicted Fe-S-cluster oxidoreductase		
2572232459	t3m_00815	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232459	t3m_00815	Coordinates		20275..21384(+)		
2572232459	t3m_00815	DNA_length		1110bp		
2572232459	t3m_00815	Protein_length		369aa		

2572232459	t3m_00815	GC		0.7	
2572232460	t3m_00816	COG_category	[B] Chromatin structure and dynamics		
2572232460	t3m_00816	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism		
2572232460	t3m_00816	COG0123	Deacetylases, including yeast histone deacetylase and acetoin utilizatio		2.00E-65
2572232460	t3m_00816	pfam00850	Hist_deacetyl		8.30E-65
2572232460	t3m_00816	KO:K04768	acetoin utilization protein AcuC		0.00E+00
2572232460	t3m_00816	Locus_type		CDS	
2572232460	t3m_00816	Product_name		Deacetylases, including yeast histone deacetylase and acetoin utilization	
2572232460	t3m_00816	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232460	t3m_00816	Coordinates		21381..22529(-)	
2572232460	t3m_00816	DNA_length		1149bp	
2572232460	t3m_00816	Protein_length		382aa	
2572232460	t3m_00816	GC		0.69	
2572232461	t3m_00817	Locus_type		CDS	
2572232461	t3m_00817	Product_name		hypothetical protein	
2572232461	t3m_00817	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232461	t3m_00817	Coordinates		22746..22970(+)	
2572232461	t3m_00817	DNA_length		225bp	
2572232461	t3m_00817	Protein_length		74aa	
2572232461	t3m_00817	GC		0.59	
2572232462	t3m_00818	COG_category	[K] Transcription		
2572232462	t3m_00818	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatio		6.00E-44
2572232462	t3m_00818	pfam00382	TFIIB		7.70E-11
2572232462	t3m_00818	pfam00382	TFIIB		4.30E-12
2572232462	t3m_00818	KO:K03124	transcription initiation factor TFIIB		5.90E-35
2572232462	t3m_00818	Locus_type		CDS	
2572232462	t3m_00818	Product_name		Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatio	
2572232462	t3m_00818	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232462	t3m_00818	Coordinates		22975..23874(-)	
2572232462	t3m_00818	DNA_length		900bp	
2572232462	t3m_00818	Protein_length		299aa	

2572232462	t3m_00818	GC			0.71	

2572232463	t3m_00819	Locus_type		CDS		
2572232463	t3m_00819	Product_name		hypothetical protein		
2572232463	t3m_00819	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232463	t3m_00819	Coordinates		24035..24655(+)		
2572232463	t3m_00819	DNA_length		621bp		
2572232463	t3m_00819	Protein_length		206aa		
2572232463	t3m_00819	GC			0.67	
2572232463	t3m_00819	Transmembrane		Yes		

2572232464	t3m_00820	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232464	t3m_00820	COG0532	Translation initiation factor 2 (IF-2; GTPase)			6.00E-94
2572232464	t3m_00820	pfam03144	GTP_EFTU_D2			1.90E-06
2572232464	t3m_00820	pfam00009	GTP_EFTU			9.30E-29
2572232464	t3m_00820	pfam14578	GTP_EFTU_D4			1.50E-16
2572232464	t3m_00820	pfam11987	IF-2			2.00E-08
2572232464	t3m_00820	TIGR00491	translation initiation factor aIF-2/yIF-2			0.00E+00
2572232464	t3m_00820	TIGR00231	small GTP-binding protein domain			2.80E-19
2572232464	t3m_00820	KO:K03243	translation initiation factor 5B			0.00E+00
2572232464	t3m_00820	Locus_type		CDS		
2572232464	t3m_00820	Product_name		translation initiation factor aIF-2/yIF-2		
2572232464	t3m_00820	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232464	t3m_00820	Coordinates		24678..26441(-)		
2572232464	t3m_00820	DNA_length		1764bp		
2572232464	t3m_00820	Protein_length		587aa		
2572232464	t3m_00820	GC			0.69	

2572232465	t3m_00821	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2572232465	t3m_00821	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2572232465	t3m_00821	KEGG_module	M00549: Nucleotide sugar biosynthesis, glucose => UDP-glucose			
2572232465	t3m_00821	KEGG_module	M00554: Nucleotide sugar biosynthesis, galactose => UDP-galactose			
2572232465	t3m_00821	Metacyc	PWY-6527: stachyose degradation			
2572232465	t3m_00821	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			

2572232465	t3m_00821	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2572232465	t3m_00821	COG_category	[C] Energy production and conversion			
2572232465	t3m_00821	COG1085	Galactose-1-phosphate uridylyltransferase			2.00E-56
2572232465	t3m_00821	pfam01087	GalP_UDP_transf			1.30E-15
2572232465	t3m_00821	EC:2.7.7.12	UDP-glucose--hexose-1-phosphate uridylyltransferase.			
2572232465	t3m_00821	KO:K00965	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]			0.00E+00
2572232465	t3m_00821	Locus_type		CDS		
2572232465	t3m_00821	Product_name		Galactose-1-phosphate uridylyltransferase		
2572232465	t3m_00821	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232465	t3m_00821	Coordinates		26467..27486(-)		
2572232465	t3m_00821	DNA_length		1020bp		
2572232465	t3m_00821	Protein_length		339aa		
2572232465	t3m_00821	GC			0.71	
2572232466	t3m_00822	COG_category	[R] General function prediction only			
2572232466	t3m_00822	COG1524	Uncharacterized proteins of the AP superfamily			7.00E-19
2572232466	t3m_00822	pfam01663	Phosphodiest			3.40E-22
2572232466	t3m_00822	Locus_type		CDS		
2572232466	t3m_00822	Product_name		Uncharacterized proteins of the AP superfamily		
2572232466	t3m_00822	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232466	t3m_00822	Coordinates		27483..28844(-)		
2572232466	t3m_00822	DNA_length		1362bp		
2572232466	t3m_00822	Protein_length		453aa		
2572232466	t3m_00822	GC			0.71	
2572232467	t3m_00823	COG_category	[L] Replication, recombination and repair			
2572232467	t3m_00823	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair			2.00E-60
2572232467	t3m_00823	pfam11798	IMS_HHH			3.80E-08
2572232467	t3m_00823	pfam11799	IMS_C			1.50E-13
2572232467	t3m_00823	pfam00817	IMS			3.10E-38
2572232467	t3m_00823	EC:2.7.7.7	DNA-directed DNA polymerase.			
2572232467	t3m_00823	KO:K02346	DNA polymerase IV [EC:2.7.7.7]			0.00E+00
2572232467	t3m_00823	Locus_type		CDS		
2572232467	t3m_00823	Product_name		Nucleotidyltransferase/DNA polymerase involved in DNA repair		

2572232467	t3m_00823	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232467	t3m_00823	Coordinates		28907..30067(-)	
2572232467	t3m_00823	DNA_length		1161bp	
2572232467	t3m_00823	Protein_length		386aa	
2572232467	t3m_00823	GC		0.72	
2572232468	t3m_00824	COG_category	[T] Signal transduction mechanisms		
2572232468	t3m_00824	COG0467	RecA-superfamily ATPases implicated in signal transduction		6.00E-38
2572232468	t3m_00824	pfam06745	KaiC		4.10E-51
2572232468	t3m_00824	Locus_type		CDS	
2572232468	t3m_00824	Product_name		RecA-superfamily ATPases implicated in signal transduction	
2572232468	t3m_00824	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232468	t3m_00824	Coordinates		30143..30868(-)	
2572232468	t3m_00824	DNA_length		726bp	
2572232468	t3m_00824	Protein_length		241aa	
2572232468	t3m_00824	GC		0.68	
2572232469	t3m_00825	COG_category	[T] Signal transduction mechanisms		
2572232469	t3m_00825	COG0467	RecA-superfamily ATPases implicated in signal transduction		5.00E-11
2572232469	t3m_00825	pfam06745	KaiC		1.10E-05
2572232469	t3m_00825	Locus_type		CDS	
2572232469	t3m_00825	Product_name		RecA-superfamily ATPases implicated in signal transduction	
2572232469	t3m_00825	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14	
2572232469	t3m_00825	Coordinates		30855..31706(-)	
2572232469	t3m_00825	DNA_length		852bp	
2572232469	t3m_00825	Protein_length		283aa	
2572232469	t3m_00825	GC		0.68	
2572232470	t3m_00826	COG_category	[S] Function unknown		
2572232470	t3m_00826	COG0585	Uncharacterized conserved protein		2.00E-70
2572232470	t3m_00826	pfam01142	TruD		9.50E-80
2572232470	t3m_00826	EC:5.4.99.27	tRNA pseudouridine(13) synthase.		
2572232470	t3m_00826	TIGR00094	tRNA pseudouridine synthase, TruD family		2.00E-60
2572232470	t3m_00826	KO:K06176	tRNA pseudouridine13 synthase [EC:5.4.99.27]		0.00E+00

2572232470	t3m_00826	Locus_type		CDS		
2572232470	t3m_00826	Product_name		tRNA pseudouridine synthase, TruD family		
2572232470	t3m_00826	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232470	t3m_00826	Coordinates		31851..33104(-)		
2572232470	t3m_00826	DNA_length		1254bp		
2572232470	t3m_00826	Protein_length		417aa		
2572232470	t3m_00826	GC			0.71	
2572232471	t3m_00827	Locus_type		CDS		
2572232471	t3m_00827	Product_name		hypothetical protein		
2572232471	t3m_00827	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232471	t3m_00827	Coordinates		33185..33688(+)		
2572232471	t3m_00827	DNA_length		504bp		
2572232471	t3m_00827	Protein_length		167aa		
2572232471	t3m_00827	GC			0.64	
2572232472	t3m_00828	COG_category	[G] Carbohydrate transport and metabolism			
2572232472	t3m_00828	COG2814	Arabinose efflux permease			3.00E-04
2572232472	t3m_00828	pfam07690	MFS_1			7.60E-18
2572232472	t3m_00828	Locus_type		CDS		
2572232472	t3m_00828	Product_name		Arabinose efflux permease		
2572232472	t3m_00828	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232472	t3m_00828	Coordinates		33708..35171(-)		
2572232472	t3m_00828	DNA_length		1464bp		
2572232472	t3m_00828	Protein_length		487aa		
2572232472	t3m_00828	GC			0.68	
2572232472	t3m_00828	Transmembrane		Yes		
2572232473	t3m_00829	Locus_type		CDS		
2572232473	t3m_00829	Product_name		hypothetical protein		
2572232473	t3m_00829	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232473	t3m_00829	Coordinates		35226..35951(-)		
2572232473	t3m_00829	DNA_length		726bp		
2572232473	t3m_00829	Protein_length		241aa		

2572232473	t3m_00829	GC			0.68	
2572232474	t3m_00830	COG_category	[K] Transcription			
2572232474	t3m_00830	COG3620	Predicted transcriptional regulator with C-terminal CBS domains			5.00E-34
2572232474	t3m_00830	pfam01381	HTH_3			4.00E-11
2572232474	t3m_00830	pfam00571	CBS			5.70E-15
2572232474	t3m_00830	Locus_type		CDS		
2572232474	t3m_00830	Product_name		Predicted transcriptional regulator with C-terminal CBS domains		
2572232474	t3m_00830	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232474	t3m_00830	Coordinates		36051..36629(-)		
2572232474	t3m_00830	DNA_length		579bp		
2572232474	t3m_00830	Protein_length		192aa		
2572232474	t3m_00830	GC			0.71	
2572232475	t3m_00831	Locus_type		CDS		
2572232475	t3m_00831	Product_name		hypothetical protein		
2572232475	t3m_00831	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232475	t3m_00831	Coordinates		36744..36998(+)		
2572232475	t3m_00831	DNA_length		255bp		
2572232475	t3m_00831	Protein_length		84aa		
2572232475	t3m_00831	GC			0.67	
2572232476	t3m_00832	Locus_type		CDS		
2572232476	t3m_00832	Product_name		hypothetical protein		
2572232476	t3m_00832	Scaffold		t3m_contig_70_106_len_37820_read_count_3081661.14		
2572232476	t3m_00832	Coordinates		37086..37817(+)		
2572232476	t3m_00832	DNA_length		732bp		
2572232476	t3m_00832	Protein_length		244aa		
2572232476	t3m_00832	GC			0.64	
2572232477	t3m_00833	Locus_type		CDS		
2572232477	t3m_00833	Product_name		hypothetical protein		
2572232477	t3m_00833	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232477	t3m_00833	Coordinates		40..1200(+)		

2572232477	t3m_00833	DNA_length		1161bp		
2572232477	t3m_00833	Protein_length		386aa		
2572232477	t3m_00833	GC			0.67	
2572232478	t3m_00834	Locus_type		CDS		
2572232478	t3m_00834	Product_name		hypothetical protein		
2572232478	t3m_00834	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232478	t3m_00834	Coordinates		1200..4310(+)		
2572232478	t3m_00834	DNA_length		3111bp		
2572232478	t3m_00834	Protein_length		1036aa		
2572232478	t3m_00834	GC			0.71	
2572232479	t3m_00835	KEGG_module	M00222: Phosphate transport system			
2572232479	t3m_00835	COG_category	[P] Inorganic ion transport and metabolism			
2572232479	t3m_00835	COG1117	ABC-type phosphate transport system, ATPase component			6.00E-110
2572232479	t3m_00835	pfam00005	ABC_tran			1.10E-33
2572232479	t3m_00835	EC:3.6.3.27	Phosphate-transporting ATPase.			
2572232479	t3m_00835	TIGR00972	phosphate ABC transporter, ATP-binding protein			3.40E-108
2572232479	t3m_00835	KO:K02036	phosphate transport system ATP-binding protein [EC:3.6.3.27]			0.00E+00
2572232479	t3m_00835	ITERM:05785	phosphate ABC transporter ATP-binding protein, PhoT family (TC 3.A.1.7.1)			
2572232479	t3m_00835	Locus_type		CDS		
2572232479	t3m_00835	Product_name		phosphate ABC transporter ATP-binding protein, PhoT family (TC 3.A.1.7		
2572232479	t3m_00835	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232479	t3m_00835	Coordinates		4329..5084(-)		
2572232479	t3m_00835	DNA_length		756bp		
2572232479	t3m_00835	Protein_length		251aa		
2572232479	t3m_00835	GC			0.68	
2572232480	t3m_00836	KEGG_module	M00222: Phosphate transport system			
2572232480	t3m_00836	COG_category	[P] Inorganic ion transport and metabolism			
2572232480	t3m_00836	COG0573	ABC-type phosphate transport system, permease component			4.00E-67
2572232480	t3m_00836	pfam00528	BPD_transp_1			5.70E-16
2572232480	t3m_00836	pfam00528	BPD_transp_1			2.40E-14
2572232480	t3m_00836	TIGR00974	phosphate ABC transporter, permease protein PstA			1.10E-69

2572232480	t3m_00836	TIGR02138	phosphate ABC transporter, permease protein PstC		7.00E-90
2572232480	t3m_00836	KO:K02038	phosphate transport system permease protein		0.00E+00
2572232480	t3m_00836	ITERM:06114	phosphate ABC transporter membrane protein 2, PhoT family (TC 3.A.1.7.1)		
2572232480	t3m_00836	Locus_type		CDS	
2572232480	t3m_00836	Product_name		phosphate ABC transporter membrane protein 2, PhoT family (TC 3.A.1.	
2572232480	t3m_00836	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232480	t3m_00836	Coordinates		5091..7037(-)	
2572232480	t3m_00836	DNA_length		1947bp	
2572232480	t3m_00836	Protein_length		648aa	
2572232480	t3m_00836	GC		0.66	
2572232480	t3m_00836	Transmembrane		Yes	
2572232480	t3m_00836	Fused_gene		Yes	
2572232481	t3m_00837	KEGG_module	M00222: Phosphate transport system		
2572232481	t3m_00837	COG_category	[P] Inorganic ion transport and metabolism		
2572232481	t3m_00837	COG0226	ABC-type phosphate transport system, periplasmic component		3.00E-28
2572232481	t3m_00837	pfam12849	PBP_like_2		2.20E-37
2572232481	t3m_00837	TIGR00975	phosphate ABC transporter, phosphate-binding protein		6.40E-69
2572232481	t3m_00837	KO:K02040	phosphate transport system substrate-binding protein		0.00E+00
2572232481	t3m_00837	Locus_type		CDS	
2572232481	t3m_00837	Product_name		phosphate ABC transporter, phosphate-binding protein	
2572232481	t3m_00837	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232481	t3m_00837	Coordinates		7129..8310(-)	
2572232481	t3m_00837	DNA_length		1182bp	
2572232481	t3m_00837	Protein_length		393aa	
2572232481	t3m_00837	GC		0.63	
2572232481	t3m_00837	Transmembrane		Yes	
2572232482	t3m_00838	KEGG_module	M00176: Sulfur reduction, sulfate => H2S		
2572232482	t3m_00838	Metacyc	PWY-5340: sulfate activation for sulfonation		
2572232482	t3m_00838	COG_category	[P] Inorganic ion transport and metabolism		
2572232482	t3m_00838	COG0529	Adenylylsulfate kinase and related kinases		4.00E-52
2572232482	t3m_00838	pfam01583	APS_kinase		4.90E-52
2572232482	t3m_00838	EC:2.7.1.25	Adenylyl-sulfate kinase.		

2572232482	t3m_00838	TIGR00455	adenylylsulfate kinase (apsK)			5.80E-58
2572232482	t3m_00838	KO:K00860	adenylylsulfate kinase [EC:2.7.1.25]			0.00E+00
2572232482	t3m_00838	Locus_type		CDS		
2572232482	t3m_00838	Product_name		adenylylsulfate kinase (apsK)		
2572232482	t3m_00838	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232482	t3m_00838	Coordinates		8690..9256(+)		
2572232482	t3m_00838	DNA_length		567bp		
2572232482	t3m_00838	Protein_length		188aa		
2572232482	t3m_00838	GC			0.66	

2572232483	t3m_00839	COG_category	[S] Function unknown			
2572232483	t3m_00839	COG4068	Uncharacterized protein containing a Zn-ribbon			8.00E-05
2572232483	t3m_00839	pfam09889	DUF2116			3.90E-11
2572232483	t3m_00839	Locus_type		CDS		
2572232483	t3m_00839	Product_name		Uncharacterized protein containing a Zn-ribbon		
2572232483	t3m_00839	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232483	t3m_00839	Coordinates		9371..9562(+)		
2572232483	t3m_00839	DNA_length		192bp		
2572232483	t3m_00839	Protein_length		63aa		
2572232483	t3m_00839	GC			0.66	
2572232483	t3m_00839	Transmembrane		Yes		

2572232484	t3m_00840	COG_category	[R] General function prediction only			
2572232484	t3m_00840	COG1019	Predicted nucleotidyltransferase			9.00E-31
2572232484	t3m_00840	pfam01467	CTP_transf_2			4.70E-07
2572232484	t3m_00840	TIGR00125	cytidyltransferase-like domain			1.80E-14
2572232484	t3m_00840	Locus_type		CDS		
2572232484	t3m_00840	Product_name		cytidyltransferase-like domain		
2572232484	t3m_00840	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232484	t3m_00840	Coordinates		9576..10376(+)		
2572232484	t3m_00840	DNA_length		801bp		
2572232484	t3m_00840	Protein_length		266aa		
2572232484	t3m_00840	GC			0.72	

2572232485	t3m_00841	Locus_type		CDS		
2572232485	t3m_00841	Product_name		hypothetical protein		
2572232485	t3m_00841	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232485	t3m_00841	Coordinates		10415..10636(+)		
2572232485	t3m_00841	DNA_length		222bp		
2572232485	t3m_00841	Protein_length		73aa		
2572232485	t3m_00841	GC			0.67	

2572232486	t3m_00842	COG_category	[S] Function unknown			
2572232486	t3m_00842	COG4004	Uncharacterized protein conserved in archaea			6.00E-11
2572232486	t3m_00842	Locus_type		CDS		
2572232486	t3m_00842	Product_name		Uncharacterized protein conserved in archaea		
2572232486	t3m_00842	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232486	t3m_00842	Coordinates		10704..11030(+)		
2572232486	t3m_00842	DNA_length		327bp		
2572232486	t3m_00842	Protein_length		108aa		
2572232486	t3m_00842	GC			0.69	

2572232487	t3m_00843	pfam02163	Peptidase_M50			4.10E-12
2572232487	t3m_00843	Locus_type		CDS		
2572232487	t3m_00843	Product_name		Peptidase family M50		
2572232487	t3m_00843	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232487	t3m_00843	Coordinates		11034..12632(+)		
2572232487	t3m_00843	DNA_length		1599bp		
2572232487	t3m_00843	Protein_length		532aa		
2572232487	t3m_00843	GC			0.68	
2572232487	t3m_00843	Transmembrane		Yes		

2572232488	t3m_00844	COG_category	[L] Replication, recombination and repair			
2572232488	t3m_00844	COG1041	Predicted DNA modification methylase			7.00E-43
2572232488	t3m_00844	pfam01170	UPF0020			3.30E-26
2572232488	t3m_00844	EC:2.1.1.213	tRNA (guanine(10)-N(2))-dimethyltransferase.			
2572232488	t3m_00844	TIGR01177	TIGR01177 family protein			2.60E-55
2572232488	t3m_00844	KO:K07446	tRNA (guanine10-N2)-dimethyltransferase [EC:2.1.1.213]			5.30E-32

2572232488	t3m_00844	Locus_type		CDS		
2572232488	t3m_00844	Product_name		Predicted DNA modification methylase		
2572232488	t3m_00844	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232488	t3m_00844	Coordinates		12613..13638(-)		
2572232488	t3m_00844	DNA_length		1026bp		
2572232488	t3m_00844	Protein_length		341aa		
2572232488	t3m_00844	GC			0.71	
2572232489	t3m_00845	COG_category	[S] Function unknown			
2572232489	t3m_00845	COG1656	Uncharacterized conserved protein			9.00E-22
2572232489	t3m_00845	pfam01927	Mut7-C			2.50E-29
2572232489	t3m_00845	KO:K09122	hypothetical protein			1.50E-18
2572232489	t3m_00845	Locus_type		CDS		
2572232489	t3m_00845	Product_name		Uncharacterized conserved protein		
2572232489	t3m_00845	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232489	t3m_00845	Coordinates		13635..14081(-)		
2572232489	t3m_00845	DNA_length		447bp		
2572232489	t3m_00845	Protein_length		148aa		
2572232489	t3m_00845	GC			0.7	
2572232490	t3m_00846	KEGG_module	M00114: Ascorbate biosynthesis, plants, glucose-6P => ascorbate			
2572232490	t3m_00846	Metacyc	GLYCOCAT-PWY: glycogen degradation I			
2572232490	t3m_00846	Metacyc	PWY-622: starch biosynthesis			
2572232490	t3m_00846	Metacyc	GLUCOSE1PMETAB-PWY: glucose and glucose-1-phosphate degradation			
2572232490	t3m_00846	Metacyc	PWY-621: sucrose degradation III			
2572232490	t3m_00846	Metacyc	PWY-6737: starch degradation V			
2572232490	t3m_00846	Metacyc	PWY-5661: GDP-glucose biosynthesis			
2572232490	t3m_00846	Metacyc	PWY-5384: sucrose degradation IV			
2572232490	t3m_00846	Metacyc	PWY-5659: GDP-mannose biosynthesis			
2572232490	t3m_00846	Metacyc	PWY-5940: streptomycin biosynthesis			
2572232490	t3m_00846	Metacyc	PWY-5941: glycogen degradation II			
2572232490	t3m_00846	Metacyc	PWY-842: starch degradation I			
2572232490	t3m_00846	Metacyc	PWY-3801: sucrose degradation VI (anaerobic)			
2572232490	t3m_00846	Metacyc	SUCSYN-PWY: sucrose biosynthesis			

2572232490	t3m_00846	Metacyc	PWY-6731: starch degradation III			
2572232490	t3m_00846	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)			
2572232490	t3m_00846	COG_category	[G] Carbohydrate transport and metabolism			
2572232490	t3m_00846	COG1109	Phosphomannomutase			1.00E-107
2572232490	t3m_00846	pfam02879	PGM_PMM_II			4.40E-23
2572232490	t3m_00846	pfam02878	PGM_PMM_I			4.80E-36
2572232490	t3m_00846	pfam00408	PGM_PMM_IV			4.50E-09
2572232490	t3m_00846	pfam02880	PGM_PMM_III			1.10E-22
2572232490	t3m_00846	EC:5.4.2.2	Phosphoglucomutase.			
2572232490	t3m_00846	EC:5.4.2.8	Phosphomannomutase.			
2572232490	t3m_00846	TIGR03990	phosphoglucosamine mutase			0.00E+00
2572232490	t3m_00846	KO:K15778	phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]			0.00E+00
2572232490	t3m_00846	Locus_type		CDS		
2572232490	t3m_00846	Product_name		phosphoglucosamine mutase		
2572232490	t3m_00846	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232490	t3m_00846	Coordinates		14189..15565(+)		
2572232490	t3m_00846	DNA_length		1377bp		
2572232490	t3m_00846	Protein_length		458aa		
2572232490	t3m_00846	GC			0.69	

2572232491	t3m_00847	COG_category	[S] Function unknown			
2572232491	t3m_00847	COG4272	Predicted membrane protein			5.00E-06
2572232491	t3m_00847	pfam07843	DUF1634			1.70E-14
2572232491	t3m_00847	Locus_type		CDS		
2572232491	t3m_00847	Product_name		Predicted membrane protein		
2572232491	t3m_00847	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232491	t3m_00847	Coordinates		15594..16019(-)		
2572232491	t3m_00847	DNA_length		426bp		
2572232491	t3m_00847	Protein_length		141aa		
2572232491	t3m_00847	GC			0.69	
2572232491	t3m_00847	Transmembrane		Yes		

2572232492	t3m_00848	COG_category	[R] General function prediction only			
2572232492	t3m_00848	COG0730	Predicted permeases			2.00E-09

2572232492	t3m_00848	pfam01925	TauE			3.50E-39
2572232492	t3m_00848	Locus_type		CDS		
2572232492	t3m_00848	Product_name		Predicted permeases		
2572232492	t3m_00848	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232492	t3m_00848	Coordinates		16016..16891(-)		
2572232492	t3m_00848	DNA_length		876bp		
2572232492	t3m_00848	Protein_length		291aa		
2572232492	t3m_00848	GC			0.68	
2572232492	t3m_00848	Transmembrane		Yes		
2572232493	t3m_00849	Locus_type		CDS		
2572232493	t3m_00849	Product_name		hypothetical protein		
2572232493	t3m_00849	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232493	t3m_00849	Coordinates		17077..17643(+)		
2572232493	t3m_00849	DNA_length		567bp		
2572232493	t3m_00849	Protein_length		188aa		
2572232493	t3m_00849	GC			0.71	
2572232494	t3m_00850	KEGG_module	M00176: Sulfur reduction, sulfate => H2S			
2572232494	t3m_00850	Metacyc	PWY-6683: sulfate reduction III (assimilatory)			
2572232494	t3m_00850	Metacyc	SULFMETII-PWY: sulfate reduction II (assimilatory)			
2572232494	t3m_00850	Metacyc	PWY-5278: sulfite oxidation III			
2572232494	t3m_00850	Metacyc	PWY-6932: selenate reduction			
2572232494	t3m_00850	Metacyc	PWY-5340: sulfate activation for sulfonation			
2572232494	t3m_00850	Metacyc	P224-PWY: sulfate reduction V (dissimilatory)			
2572232494	t3m_00850	Metacyc	DISSULFRED-PWY: sulfate reduction IV (dissimilatory)			
2572232494	t3m_00850	IMG_pathway	870: Dissimilatory sulfate conversion to adenylylsulfate			
2572232494	t3m_00850	COG_category	[P] Inorganic ion transport and metabolism			
2572232494	t3m_00850	COG2046	ATP sulfurylase (sulfate adenylyltransferase)			2.00E-102
2572232494	t3m_00850	pfam14306	PUA_2			1.80E-36
2572232494	t3m_00850	pfam01747	ATP-sulfurylase			5.60E-74
2572232494	t3m_00850	EC:2.7.7.4	Sulfate adenylyltransferase.			
2572232494	t3m_00850	TIGR00339	ATP sulphurylase			1.80E-97
2572232494	t3m_00850	KO:K00958	sulfate adenylyltransferase [EC:2.7.7.4]			0.00E+00

2572232494	t3m_00850	ITERM:02082	sulfate adenylyltransferase (EC 2.7.7.4)			
2572232494	t3m_00850	Locus_type		CDS		
2572232494	t3m_00850	Product_name		sulfate adenylyltransferase (EC 2.7.7.4)		
2572232494	t3m_00850	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232494	t3m_00850	Coordinates		17663..18838(+)		
2572232494	t3m_00850	DNA_length		1176bp		
2572232494	t3m_00850	Protein_length		391aa		
2572232494	t3m_00850	GC			0.69	

2572232495	t3m_00851	KEGG_module	M00176: Sulfur reduction, sulfate => H2S			
2572232495	t3m_00851	Metacyc	PWY-5340: sulfate activation for sulfonation			
2572232495	t3m_00851	COG_category	[P] Inorganic ion transport and metabolism			
2572232495	t3m_00851	COG0529	Adenylylsulfate kinase and related kinases			3.00E-57
2572232495	t3m_00851	pfam01583	APS_kinase			7.40E-61
2572232495	t3m_00851	EC:2.7.1.25	Adenylyl-sulfate kinase.			
2572232495	t3m_00851	TIGR00455	adenylylsulfate kinase (apsK)			2.00E-63
2572232495	t3m_00851	KO:K00860	adenylylsulfate kinase [EC:2.7.1.25]			0.00E+00
2572232495	t3m_00851	Locus_type		CDS		
2572232495	t3m_00851	Product_name		adenylylsulfate kinase (apsK)		
2572232495	t3m_00851	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232495	t3m_00851	Coordinates		18898..19482(+)		
2572232495	t3m_00851	DNA_length		585bp		
2572232495	t3m_00851	Protein_length		194aa		
2572232495	t3m_00851	GC			0.69	

2572232496	t3m_00852	KEGG_module	M00248: Putative antibiotic transport system			
2572232496	t3m_00852	COG_category	[G] Carbohydrate transport and metabolism			
2572232496	t3m_00852	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232496	t3m_00852	COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease c			1.00E-07
2572232496	t3m_00852	pfam01061	ABC2_membrane			1.50E-28
2572232496	t3m_00852	TIGR01247	daunorubicin resistance ABC transporter membrane protein			1.50E-41
2572232496	t3m_00852	KO:K09686	antibiotic transport system permease protein			0.00E+00
2572232496	t3m_00852	Locus_type		CDS		
2572232496	t3m_00852	Product_name		ABC-type polysaccharide/polyol phosphate export systems, permease c		

2572232496	t3m_00852	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232496	t3m_00852	Coordinates		19543..20304(-)	
2572232496	t3m_00852	DNA_length		762bp	
2572232496	t3m_00852	Protein_length		253aa	
2572232496	t3m_00852	GC		0.64	
2572232496	t3m_00852	Transmembrane		Yes	
2572232497	t3m_00853	KEGG_module	M00248: Putative antibiotic transport system		
2572232497	t3m_00853	COG_category	[V] Defense mechanisms		
2572232497	t3m_00853	COG1131	ABC-type multidrug transport system, ATPase component		2.00E-71
2572232497	t3m_00853	pfam00005	ABC_tran		2.20E-28
2572232497	t3m_00853	pfam13732	DUF4162		4.80E-08
2572232497	t3m_00853	TIGR01188	daunorubicin resistance ABC transporter ATP-binding subunit		1.50E-95
2572232497	t3m_00853	KO:K09687	antibiotic transport system ATP-binding protein		0.00E+00
2572232497	t3m_00853	Locus_type		CDS	
2572232497	t3m_00853	Product_name		ABC-type multidrug transport system, ATPase component	
2572232497	t3m_00853	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232497	t3m_00853	Coordinates		20301..21290(-)	
2572232497	t3m_00853	DNA_length		990bp	
2572232497	t3m_00853	Protein_length		329aa	
2572232497	t3m_00853	GC		0.66	
2572232498	t3m_00854	pfam03551	PadR		8.70E-15
2572232498	t3m_00854	Locus_type		CDS	
2572232498	t3m_00854	Product_name		Transcriptional regulator PadR-like family	
2572232498	t3m_00854	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232498	t3m_00854	Coordinates		21287..21769(-)	
2572232498	t3m_00854	DNA_length		483bp	
2572232498	t3m_00854	Protein_length		160aa	
2572232498	t3m_00854	GC		0.72	
2572232499	t3m_00855	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2572232499	t3m_00855	COG0229	Conserved domain frequently associated with peptide methionine sulfc		2.00E-34
2572232499	t3m_00855	pfam01641	SelR		9.90E-39

2572232499	t3m_00855	EC:1.8.4.12	Peptide-methionine (R)-S-oxide reductase.		
2572232499	t3m_00855	TIGR00357	methionine-R-sulfoxide reductase		1.50E-35
2572232499	t3m_00855	KO:K07305	peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12]		1.40E-45
2572232499	t3m_00855	Locus_type		CDS	
2572232499	t3m_00855	Product_name		Conserved domain frequently associated with peptide methionine sulfo	
2572232499	t3m_00855	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232499	t3m_00855	Coordinates		22055..22378(+)	
2572232499	t3m_00855	DNA_length		324bp	
2572232499	t3m_00855	Protein_length		107aa	
2572232499	t3m_00855	GC		0.65	
2572232500	t3m_00856	pfam13620	CarboxypepD_reg		1.60E-07
2572232500	t3m_00856	Locus_type		CDS	
2572232500	t3m_00856	Product_name		Carboxypeptidase regulatory-like domain	
2572232500	t3m_00856	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232500	t3m_00856	Coordinates		22841..24142(+)	
2572232500	t3m_00856	DNA_length		1302bp	
2572232500	t3m_00856	Protein_length		433aa	
2572232500	t3m_00856	GC		0.65	
2572232500	t3m_00856	Transmembrane		Yes	
2572232501	t3m_00857	Locus_type		CDS	
2572232501	t3m_00857	Product_name		hypothetical protein	
2572232501	t3m_00857	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232501	t3m_00857	Coordinates		24420..24809(-)	
2572232501	t3m_00857	DNA_length		390bp	
2572232501	t3m_00857	Protein_length		129aa	
2572232501	t3m_00857	GC		0.58	
2572232502	t3m_00858	Locus_type		tRNA	
2572232502	t3m_00858	Product_name		tRNA_Arg_CCT	
2572232502	t3m_00858	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232502	t3m_00858	Coordinates		25050..25124(-)	
2572232502	t3m_00858	DNA_length		75bp	

2572232502	t3m_00858	GC			0.68	
2572232503	t3m_00859	Locus_type		CDS		
2572232503	t3m_00859	Product_name		hypothetical protein		
2572232503	t3m_00859	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232503	t3m_00859	Coordinates		25153..26226(-)		
2572232503	t3m_00859	DNA_length		1074bp		
2572232503	t3m_00859	Protein_length		357aa		
2572232503	t3m_00859	GC			0.72	
2572232504	t3m_00860	Locus_type		CDS		
2572232504	t3m_00860	Product_name		hypothetical protein		
2572232504	t3m_00860	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232504	t3m_00860	Coordinates		26315..27817(+)		
2572232504	t3m_00860	DNA_length		1503bp		
2572232504	t3m_00860	Protein_length		500aa		
2572232504	t3m_00860	GC			0.66	
2572232504	t3m_00860	Transmembrane		Yes		
2572232505	t3m_00861	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232505	t3m_00861	COG1503	Peptide chain release factor 1 (eRF1)			4.00E-114
2572232505	t3m_00861	pfam03465	eRF1_3			2.30E-25
2572232505	t3m_00861	pfam03463	eRF1_1			2.50E-13
2572232505	t3m_00861	pfam03464	eRF1_2			1.50E-35
2572232505	t3m_00861	TIGR03676	peptide chain release factor 1, archaeal and eukaryotic forms			0.00E+00
2572232505	t3m_00861	KO:K03265	peptide chain release factor subunit 1			0.00E+00
2572232505	t3m_00861	Locus_type		CDS		
2572232505	t3m_00861	Product_name		peptide chain release factor 1, archaeal and eukaryotic forms		
2572232505	t3m_00861	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232505	t3m_00861	Coordinates		27928..29223(-)		
2572232505	t3m_00861	DNA_length		1296bp		
2572232505	t3m_00861	Protein_length		431aa		
2572232505	t3m_00861	GC			0.66	

2572232506	t3m_00862	pfam00085	Thioredoxin		4.80E-12
2572232506	t3m_00862	Locus_type		CDS	
2572232506	t3m_00862	Product_name		Thioredoxin	
2572232506	t3m_00862	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232506	t3m_00862	Coordinates		29325..29540(-)	
2572232506	t3m_00862	DNA_length		216bp	
2572232506	t3m_00862	Protein_length		71aa	
2572232506	t3m_00862	GC		0.61	
2572232507	t3m_00863	COG_category	[R] General function prediction only		
2572232507	t3m_00863	COG4122	Predicted O-methyltransferase		3.00E-06
2572232507	t3m_00863	pfam13578	Methyltransf_24		7.60E-14
2572232507	t3m_00863	Locus_type		CDS	
2572232507	t3m_00863	Product_name		Predicted O-methyltransferase	
2572232507	t3m_00863	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232507	t3m_00863	Coordinates		29790..30602(+)	
2572232507	t3m_00863	DNA_length		813bp	
2572232507	t3m_00863	Protein_length		270aa	
2572232507	t3m_00863	GC		0.7	
2572232508	t3m_00864	COG_category	[H] Coenzyme transport and metabolism		
2572232508	t3m_00864	COG0521	Molybdopterin biosynthesis enzymes		3.00E-33
2572232508	t3m_00864	pfam00994	MoCF_biosynth		2.60E-27
2572232508	t3m_00864	TIGR00177	molybdenum cofactor synthesis domain		3.30E-32
2572232508	t3m_00864	KO:K03638	molybdenum cofactor biosynthesis protein B		2.50E-33
2572232508	t3m_00864	Locus_type		CDS	
2572232508	t3m_00864	Product_name		molybdenum cofactor synthesis domain	
2572232508	t3m_00864	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232508	t3m_00864	Coordinates		30613..31140(-)	
2572232508	t3m_00864	DNA_length		528bp	
2572232508	t3m_00864	Protein_length		175aa	
2572232508	t3m_00864	GC		0.67	
2572232509	t3m_00865	COG_category	[H] Coenzyme transport and metabolism		

2572232509	t3m_00865	COG0315	Molybdenum cofactor biosynthesis enzyme			3.00E-37
2572232509	t3m_00865	pfam01967	MoaC			3.10E-39
2572232509	t3m_00865	TIGR00581	molybdenum cofactor biosynthesis protein MoaC			9.80E-44
2572232509	t3m_00865	KO:K03637	molybdenum cofactor biosynthesis protein C			5.50E-34
2572232509	t3m_00865	ITERM:04711	cyclic pyranopterin monophosphate synthase subunit MoaC (EC 4.1.99.18)			
2572232509	t3m_00865	Locus_type		CDS		
2572232509	t3m_00865	Product_name		cyclic pyranopterin monophosphate synthase subunit MoaC (EC 4.1.99.1		
2572232509	t3m_00865	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232509	t3m_00865	Coordinates		31137..31586(-)		
2572232509	t3m_00865	DNA_length		450bp		
2572232509	t3m_00865	Protein_length		149aa		
2572232509	t3m_00865	GC			0.68	
2572232510	t3m_00866	pfam00004	AAA			6.40E-15
2572232510	t3m_00866	pfam08542	Rep_fac_C			1.00E-15
2572232510	t3m_00866	KO:K04801	replication factor C small subunit			0.00E+00
2572232510	t3m_00866	Locus_type		CDS		
2572232510	t3m_00866	Product_name		replication factor C small subunit		
2572232510	t3m_00866	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232510	t3m_00866	Coordinates		31590..32573(-)		
2572232510	t3m_00866	DNA_length		984bp		
2572232510	t3m_00866	Protein_length		327aa		
2572232510	t3m_00866	GC			0.68	
2572232511	t3m_00867	Locus_type		CDS		
2572232511	t3m_00867	Product_name		hypothetical protein		
2572232511	t3m_00867	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232511	t3m_00867	Coordinates		32623..33069(-)		
2572232511	t3m_00867	DNA_length		447bp		
2572232511	t3m_00867	Protein_length		148aa		
2572232511	t3m_00867	GC			0.67	
2572232512	t3m_00868	Locus_type		CDS		
2572232512	t3m_00868	Product_name		hypothetical protein		

2572232512	t3m_00868	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232512	t3m_00868	Coordinates		33322..34359(-)		
2572232512	t3m_00868	DNA_length		1038bp		
2572232512	t3m_00868	Protein_length		345aa		
2572232512	t3m_00868	GC			0.68	
2572232512	t3m_00868	Transmembrane		Yes		
2572232513	t3m_00869	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232513	t3m_00869	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2572232513	t3m_00869	COG0616	Periplasmic serine proteases (ClpP class)			2.00E-46
2572232513	t3m_00869	pfam01343	Peptidase_S49			1.40E-43
2572232513	t3m_00869	EC:3.4.21.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Serine endopeptidases.			
2572232513	t3m_00869	TIGR00706	signal peptide peptidase SppA, 36K type			3.60E-57
2572232513	t3m_00869	KO:K04773	protease IV [EC:3.4.21.-]			1.10E-31
2572232513	t3m_00869	Locus_type		CDS		
2572232513	t3m_00869	Product_name		signal peptide peptidase SppA, 36K type		
2572232513	t3m_00869	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232513	t3m_00869	Coordinates		34452..35246(+)		
2572232513	t3m_00869	DNA_length		795bp		
2572232513	t3m_00869	Protein_length		264aa		
2572232513	t3m_00869	GC			0.67	
2572232514	t3m_00870	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2572232514	t3m_00870	COG4023	Preprotein translocase subunit Sec61beta			1.00E-03
2572232514	t3m_00870	pfam03911	Sec61_beta			5.20E-04
2572232514	t3m_00870	Locus_type		CDS		
2572232514	t3m_00870	Product_name		Preprotein translocase subunit Sec61beta		
2572232514	t3m_00870	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15		
2572232514	t3m_00870	Coordinates		35294..35455(+)		
2572232514	t3m_00870	DNA_length		162bp		
2572232514	t3m_00870	Protein_length		53aa		
2572232514	t3m_00870	GC			0.62	
2572232514	t3m_00870	Transmembrane		Yes		

2572232515	t3m_00871	COG_category	[C] Energy production and conversion		
2572232515	t3m_00871	COG0731	Fe-S oxidoreductases		2.00E-59
2572232515	t3m_00871	pfam08608	Wyosine_form		1.40E-17
2572232515	t3m_00871	pfam13394	Fer4_14		3.40E-06
2572232515	t3m_00871	pfam04055	Radical_SAM		2.60E-19
2572232515	t3m_00871	Locus_type		CDS	
2572232515	t3m_00871	Product_name		Fe-S oxidoreductases	
2572232515	t3m_00871	Scaffold		t3m_contig_70_116_len_36300_read_count_2853038.15	
2572232515	t3m_00871	Coordinates		35468..36289(-)	
2572232515	t3m_00871	DNA_length		822bp	
2572232515	t3m_00871	Protein_length		273aa	
2572232515	t3m_00871	GC		0.67	

2572232516	t3m_00872	pfam00528	BPD_transp_1		5.00E-17
2572232516	t3m_00872	Locus_type		CDS	
2572232516	t3m_00872	Product_name		Binding-protein-dependent transport system inner membrane compone	
2572232516	t3m_00872	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232516	t3m_00872	Coordinates		3..581(+)	
2572232516	t3m_00872	DNA_length		579bp	
2572232516	t3m_00872	Protein_length		192aa	
2572232516	t3m_00872	GC		0.64	
2572232516	t3m_00872	Transmembrane		Yes	

2572232517	t3m_00873	pfam00005	ABC_tran		7.90E-16
2572232517	t3m_00873	pfam08352	oligo_HPY		8.60E-22
2572232517	t3m_00873	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termina		1.60E-33
2572232517	t3m_00873	Locus_type		CDS	
2572232517	t3m_00873	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termina	
2572232517	t3m_00873	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232517	t3m_00873	Coordinates		595..2229(+)	
2572232517	t3m_00873	DNA_length		1635bp	
2572232517	t3m_00873	Protein_length		544aa	
2572232517	t3m_00873	GC		0.68	

2572232518	t3m_00874	KEGG_module	M00239: Peptides/nickel transport system			
2572232518	t3m_00874	pfam08352	oligo_HPY			5.70E-20
2572232518	t3m_00874	pfam00005	ABC_tran			9.10E-27
2572232518	t3m_00874	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termina			2.10E-30
2572232518	t3m_00874	KO:K02032	peptide/nickel transport system ATP-binding protein			0.00E+00
2572232518	t3m_00874	Locus_type		CDS		
2572232518	t3m_00874	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termina		
2572232518	t3m_00874	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232518	t3m_00874	Coordinates		2234..3439(+)		
2572232518	t3m_00874	DNA_length		1206bp		
2572232518	t3m_00874	Protein_length		401aa		
2572232518	t3m_00874	GC			0.68	
2572232519	t3m_00875	Locus_type		CDS		
2572232519	t3m_00875	Product_name		hypothetical protein		
2572232519	t3m_00875	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232519	t3m_00875	Coordinates		3478..3924(+)		
2572232519	t3m_00875	DNA_length		447bp		
2572232519	t3m_00875	Protein_length		148aa		
2572232519	t3m_00875	GC			0.68	
2572232519	t3m_00875	Transmembrane		Yes		
2572232520	t3m_00876	Locus_type		CDS		
2572232520	t3m_00876	Product_name		hypothetical protein		
2572232520	t3m_00876	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232520	t3m_00876	Coordinates		4157..7207(-)		
2572232520	t3m_00876	DNA_length		3051bp		
2572232520	t3m_00876	Protein_length		1016aa		
2572232520	t3m_00876	GC			0.64	
2572232520	t3m_00876	Transmembrane		Yes		
2572232521	t3m_00877	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)			
2572232521	t3m_00877	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P			
2572232521	t3m_00877	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)			

2572232521	t3m_00877	Metacyc	PWY-5723: Rubisco shunt			
2572232521	t3m_00877	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)			
2572232521	t3m_00877	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			
2572232521	t3m_00877	Metacyc	P124-PWY: Bifidobacterium shunt			
2572232521	t3m_00877	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2572232521	t3m_00877	Metacyc	P122-PWY: heterolactic fermentation			
2572232521	t3m_00877	Metacyc	P21-PWY: pentose phosphate pathway (partial)			
2572232521	t3m_00877	Metacyc	RIBITOLUTIL-PWY: ribitol degradation			
2572232521	t3m_00877	Metacyc	DARABCAT-PWY: D-arabinose degradation II			
2572232521	t3m_00877	COG_category	[G] Carbohydrate transport and metabolism			
2572232521	t3m_00877	COG0036	Pentose-5-phosphate-3-epimerase			1.00E-69
2572232521	t3m_00877	pfam00834	Ribul_P_3_epim			2.10E-69
2572232521	t3m_00877	EC:5.1.3.1	Ribulose-phosphate 3-epimerase.			
2572232521	t3m_00877	TIGR01163	ribulose-phosphate 3-epimerase			1.50E-77
2572232521	t3m_00877	KO:K01783	ribulose-phosphate 3-epimerase [EC:5.1.3.1]			0.00E+00
2572232521	t3m_00877	Locus_type		CDS		
2572232521	t3m_00877	Product_name		ribulose-phosphate 3-epimerase		
2572232521	t3m_00877	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232521	t3m_00877	Coordinates		7332..8039(+)		
2572232521	t3m_00877	DNA_length		708bp		
2572232521	t3m_00877	Protein_length		235aa		
2572232521	t3m_00877	GC			0.69	
2572232522	t3m_00878	COG_category	[L] Replication, recombination and repair			
2572232522	t3m_00878	COG1793	ATP-dependent DNA ligase			7.00E-85
2572232522	t3m_00878	pfam04679	DNA_ligase_A_C			7.40E-25
2572232522	t3m_00878	pfam04675	DNA_ligase_A_N			1.70E-48
2572232522	t3m_00878	pfam01068	DNA_ligase_A_M			5.50E-47
2572232522	t3m_00878	EC:6.5.1.1	DNA ligase (ATP).			
2572232522	t3m_00878	TIGR00574	DNA ligase I, ATP-dependent (dnl1)			0.00E+00
2572232522	t3m_00878	KO:K10747	DNA ligase 1 [EC:6.5.1.1]			0.00E+00
2572232522	t3m_00878	Locus_type		CDS		
2572232522	t3m_00878	Product_name		DNA ligase I, ATP-dependent (dnl1)		
2572232522	t3m_00878	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		

2572232522	t3m_00878	Coordinates		8026..9813(+)		
2572232522	t3m_00878	DNA_length		1788bp		
2572232522	t3m_00878	Protein_length		595aa		
2572232522	t3m_00878	GC			0.69	

2572232523	t3m_00879	COG_category	[S] Function unknown			
2572232523	t3m_00879	COG1873	Uncharacterized conserved protein			5.00E-10
2572232523	t3m_00879	pfam05239	PRC			1.70E-09
2572232523	t3m_00879	Locus_type		CDS		
2572232523	t3m_00879	Product_name		Uncharacterized conserved protein		
2572232523	t3m_00879	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232523	t3m_00879	Coordinates		9914..10213(+)		
2572232523	t3m_00879	DNA_length		300bp		
2572232523	t3m_00879	Protein_length		99aa		
2572232523	t3m_00879	GC			0.63	

2572232524	t3m_00880	Locus_type		tRNA		
2572232524	t3m_00880	Product_name		tRNA_Leu_TAA		
2572232524	t3m_00880	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232524	t3m_00880	Coordinates		10218..10322(+)		
2572232524	t3m_00880	DNA_length		87bp		
2572232524	t3m_00880	GC			0.67	

2572232525	t3m_00881	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232525	t3m_00881	COG2263	Predicted RNA methylase			6.00E-42
2572232525	t3m_00881	pfam13659	Methyltransf_26			7.10E-16
2572232525	t3m_00881	KO:K07579	putative methylase			1.10E-29
2572232525	t3m_00881	Locus_type		CDS		
2572232525	t3m_00881	Product_name		Predicted RNA methylase		
2572232525	t3m_00881	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232525	t3m_00881	Coordinates		10380..10991(+)		
2572232525	t3m_00881	DNA_length		612bp		
2572232525	t3m_00881	Protein_length		203aa		
2572232525	t3m_00881	GC			0.71	

2572232526	t3m_00882	KEGG_module	M00390: Exosome, archaea			
2572232526	t3m_00882	KEGG_module	M00391: Exosome, eukaryotes			
2572232526	t3m_00882	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232526	t3m_00882	COG1096	Predicted RNA-binding protein (consists of S1 domain and a Zn-ribbon c			5.00E-38
2572232526	t3m_00882	pfam14382	ECR1_N			3.70E-15
2572232526	t3m_00882	KO:K07573	exosome complex component CSL4			5.60E-34
2572232526	t3m_00882	Locus_type		CDS		
2572232526	t3m_00882	Product_name		Predicted RNA-binding protein (consists of S1 domain and a Zn-ribbon d		
2572232526	t3m_00882	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232526	t3m_00882	Coordinates		10988..11584(+)		
2572232526	t3m_00882	DNA_length		597bp		
2572232526	t3m_00882	Protein_length		198aa		
2572232526	t3m_00882	GC			0.7	
2572232527	t3m_00883	KEGG_module	M00346: Formaldehyde assimilation, serine pathway			
2572232527	t3m_00883	KEGG_module	M00141: C1-unit interconversion, eukaryotes			
2572232527	t3m_00883	KEGG_module	M00140: C1-unit interconversion, prokaryotes			
2572232527	t3m_00883	KEGG_module	M00532: Photorespiration			
2572232527	t3m_00883	Metacyc	1CMET2-PWY: formylTHF biosynthesis I			
2572232527	t3m_00883	Metacyc	GLYSYN-PWY: glycine biosynthesis I			
2572232527	t3m_00883	Metacyc	PWY-3841: folate transformations II			
2572232527	t3m_00883	Metacyc	PWY-2201: folate transformations I			
2572232527	t3m_00883	Metacyc	PWY-2161: folate polyglutamylation			
2572232527	t3m_00883	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)			
2572232527	t3m_00883	Metacyc	PWY-181: photorespiration			
2572232527	t3m_00883	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)			
2572232527	t3m_00883	Metacyc	PWY-3661: glycine betaine degradation			
2572232527	t3m_00883	COG_category	[E] Amino acid transport and metabolism			
2572232527	t3m_00883	COG0112	Glycine/serine hydroxymethyltransferase			3.00E-70
2572232527	t3m_00883	pfam00464	SHMT			6.10E-24
2572232527	t3m_00883	EC:2.1.2.1	Glycine hydroxymethyltransferase.			
2572232527	t3m_00883	KO:K00600	glycine hydroxymethyltransferase [EC:2.1.2.1]			0.00E+00
2572232527	t3m_00883	Locus_type		CDS		

2572232527	t3m_00883	Product_name		Glycine/serine hydroxymethyltransferase	
2572232527	t3m_00883	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232527	t3m_00883	Coordinates		11574..12797(+)	
2572232527	t3m_00883	DNA_length		1224bp	
2572232527	t3m_00883	Protein_length		407aa	
2572232527	t3m_00883	GC		0.71	
2572232528	t3m_00884	Locus_type		CDS	
2572232528	t3m_00884	Product_name		hypothetical protein	
2572232528	t3m_00884	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232528	t3m_00884	Coordinates		12934..15363(-)	
2572232528	t3m_00884	DNA_length		2430bp	
2572232528	t3m_00884	Protein_length		809aa	
2572232528	t3m_00884	GC		0.64	
2572232528	t3m_00884	Transmembrane		Yes	
2572232529	t3m_00885	Locus_type		CDS	
2572232529	t3m_00885	Product_name		hypothetical protein	
2572232529	t3m_00885	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232529	t3m_00885	Coordinates		15796..15924(+)	
2572232529	t3m_00885	DNA_length		129bp	
2572232529	t3m_00885	Protein_length		42aa	
2572232529	t3m_00885	GC		0.68	
2572232530	t3m_00886	COG_category	[F] Nucleotide transport and metabolism		
2572232530	t3m_00886	COG1936	Predicted nucleotide kinase (related to CMP and AMP kinases)		2.00E-27
2572232530	t3m_00886	pfam13238	AAA_18		1.60E-10
2572232530	t3m_00886	Locus_type		CDS	
2572232530	t3m_00886	Product_name		Predicted nucleotide kinase (related to CMP and AMP kinases)	
2572232530	t3m_00886	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232530	t3m_00886	Coordinates		15986..16516(+)	
2572232530	t3m_00886	DNA_length		531bp	
2572232530	t3m_00886	Protein_length		176aa	
2572232530	t3m_00886	GC		0.67	

2572232531	t3m_00887	Metacyc	PWY4FS-7: phosphatidylglycerol biosynthesis I (plastidic)		
2572232531	t3m_00887	Metacyc	PWY-5269: cardiolipin biosynthesis II		
2572232531	t3m_00887	Metacyc	PWY4FS-8: phosphatidylglycerol biosynthesis II (non-plastidic)		
2572232531	t3m_00887	Metacyc	PWY0-1545: cardiolipin biosynthesis III		
2572232531	t3m_00887	Metacyc	PWY-5668: cardiolipin biosynthesis I		
2572232531	t3m_00887	COG_category	[I] Lipid transport and metabolism		
2572232531	t3m_00887	COG0558	Phosphatidylglycerophosphate synthase		9.00E-10
2572232531	t3m_00887	pfam01066	CDP-OH_P_transf		3.40E-11
2572232531	t3m_00887	EC:2.7.8.5	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase.		
2572232531	t3m_00887	KO:K00995	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [E		1.00E-39
2572232531	t3m_00887	Locus_type		CDS	
2572232531	t3m_00887	Product_name		Phosphatidylglycerophosphate synthase	
2572232531	t3m_00887	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232531	t3m_00887	Coordinates		16537..17199(+)	
2572232531	t3m_00887	DNA_length		663bp	
2572232531	t3m_00887	Protein_length		220aa	
2572232531	t3m_00887	GC		0.69	
2572232531	t3m_00887	Transmembrane		Yes	
2572232532	t3m_00888	KEGG_module	M00261: DNA polymerase alpha / primase complex		
2572232532	t3m_00888	Metacyc	PWY-6626: CDP-2-glycerol biosynthesis		
2572232532	t3m_00888	Metacyc	PWY4FS-4: phosphatidylcholine biosynthesis IV		
2572232532	t3m_00888	Metacyc	PWY-7127: CDP-D-mannitol biosynthesis		
2572232532	t3m_00888	Metacyc	PWY-6679: jadomycin biosynthesis		
2572232532	t3m_00888	Metacyc	PWY-6998: CDP-D-arabitol biosynthesis		
2572232532	t3m_00888	Metacyc	PWY-6749: CMP-legionaminate biosynthesis I		
2572232532	t3m_00888	COG_category	[L] Replication, recombination and repair		
2572232532	t3m_00888	COG2219	Eukaryotic-type DNA primase, large subunit		1.00E-35
2572232532	t3m_00888	pfam04104	DNA_primase_lrg		7.90E-26
2572232532	t3m_00888	EC:2.7.7.-	Transferases. Transferring phosphorous-containing groups. Nucleotidyltransferases.		
2572232532	t3m_00888	KO:K02685	DNA primase large subunit [EC:2.7.7.-]		2.70E-43
2572232532	t3m_00888	ITERM:00097	DNA primase large subunit (EC 2.7.7.-)		
2572232532	t3m_00888	Locus_type		CDS	

2572232532	t3m_00888	Product_name		DNA primase large subunit (EC 2.7.7.-)		
2572232532	t3m_00888	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232532	t3m_00888	Coordinates		17129..18316(-)		
2572232532	t3m_00888	DNA_length		1188bp		
2572232532	t3m_00888	Protein_length		395aa		
2572232532	t3m_00888	GC			0.73	

2572232533	t3m_00889	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232533	t3m_00889	COG0750	Predicted membrane-associated Zn-dependent proteases 1			1.00E-11
2572232533	t3m_00889	pfam02163	Peptidase_M50			9.30E-27
2572232533	t3m_00889	pfam13180	PDZ_2			6.50E-11
2572232533	t3m_00889	Locus_type		CDS		
2572232533	t3m_00889	Product_name		Predicted membrane-associated Zn-dependent proteases 1		
2572232533	t3m_00889	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232533	t3m_00889	Coordinates		18286..19623(-)		
2572232533	t3m_00889	DNA_length		1338bp		
2572232533	t3m_00889	Protein_length		445aa		
2572232533	t3m_00889	GC			0.67	
2572232533	t3m_00889	Transmembrane		Yes		

2572232534	t3m_00890	pfam00801	PKD			3.40E-13
2572232534	t3m_00890	pfam09286	Pro-kuma_activ			8.00E-16
2572232534	t3m_00890	pfam00801	PKD			2.00E-07
2572232534	t3m_00890	pfam00801	PKD			7.20E-06
2572232534	t3m_00890	Locus_type		CDS		
2572232534	t3m_00890	Product_name		PKD domain/Pro-kumamolisin, activation domain		
2572232534	t3m_00890	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232534	t3m_00890	Coordinates		19728..23612(+)		
2572232534	t3m_00890	DNA_length		3885bp		
2572232534	t3m_00890	Protein_length		1294aa		
2572232534	t3m_00890	GC			0.7	
2572232534	t3m_00890	Transmembrane		Yes		

2572232535	t3m_00891	COG_category	[S] Function unknown			

2572232535	t3m_00891	COG1690	Uncharacterized conserved protein			0.00E+00
2572232535	t3m_00891	pfam01139	RtcB			0.00E+00
2572232535	t3m_00891	EC:6.5.1.3	RNA ligase (ATP).			
2572232535	t3m_00891	KO:K14415	tRNA-splicing ligase RtcB [EC:6.5.1.3]			0.00E+00
2572232535	t3m_00891	Locus_type		CDS		
2572232535	t3m_00891	Product_name		Uncharacterized conserved protein		
2572232535	t3m_00891	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232535	t3m_00891	Coordinates		23602..25053(-)		
2572232535	t3m_00891	DNA_length		1452bp		
2572232535	t3m_00891	Protein_length		483aa		
2572232535	t3m_00891	GC			0.71	
2572232536	t3m_00892	Locus_type		CDS		
2572232536	t3m_00892	Product_name		hypothetical protein		
2572232536	t3m_00892	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232536	t3m_00892	Coordinates		25174..25521(+)		
2572232536	t3m_00892	DNA_length		348bp		
2572232536	t3m_00892	Protein_length		115aa		
2572232536	t3m_00892	GC			0.67	
2572232536	t3m_00892	Transmembrane		Yes		
2572232537	t3m_00893	Locus_type		CDS		
2572232537	t3m_00893	Product_name		hypothetical protein		
2572232537	t3m_00893	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232537	t3m_00893	Coordinates		25525..25905(+)		
2572232537	t3m_00893	DNA_length		381bp		
2572232537	t3m_00893	Protein_length		126aa		
2572232537	t3m_00893	GC			0.68	
2572232537	t3m_00893	Transmembrane		Yes		
2572232538	t3m_00894	pfam00364	Biotin_lipoyl			2.20E-15
2572232538	t3m_00894	Locus_type		CDS		
2572232538	t3m_00894	Product_name		Biotin-requiring enzyme		
2572232538	t3m_00894	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		

2572232538	t3m_00894	Coordinates		25910..26482(-)		
2572232538	t3m_00894	DNA_length		573bp		
2572232538	t3m_00894	Protein_length		190aa		
2572232538	t3m_00894	GC			0.69	
2572232539	t3m_00895	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2572232539	t3m_00895	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2572232539	t3m_00895	Metacyc	PWY-5750: itaconate biosynthesis			
2572232539	t3m_00895	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)			
2572232539	t3m_00895	Metacyc	PWY-6146: <i>Methanobacterium thermoautotrophicum</i> biosynthetic metabolism			
2572232539	t3m_00895	COG_category	[C] Energy production and conversion			
2572232539	t3m_00895	COG5016	Pyruvate/oxaloacetate carboxyltransferase			0.00E+00
2572232539	t3m_00895	pfam00682	HMGL-like			2.20E-36
2572232539	t3m_00895	pfam02436	PYC_OADA			4.40E-57
2572232539	t3m_00895	EC:6.4.1.1	Pyruvate carboxylase.			
2572232539	t3m_00895	KO:K01960	pyruvate carboxylase subunit B [EC:6.4.1.1]			0.00E+00
2572232539	t3m_00895	Locus_type		CDS		
2572232539	t3m_00895	Product_name		pyruvate carboxylase subunit B (EC 6.4.1.1)		
2572232539	t3m_00895	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232539	t3m_00895	Coordinates		26454..27986(-)		
2572232539	t3m_00895	DNA_length		1533bp		
2572232539	t3m_00895	Protein_length		510aa		
2572232539	t3m_00895	GC			0.71	
2572232540	t3m_00896	COG_category	[I] Lipid transport and metabolism			
2572232540	t3m_00896	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alph			0.00E+00
2572232540	t3m_00896	pfam01039	Carboxyl_trans			0.00E+00
2572232540	t3m_00896	Locus_type		CDS		
2572232540	t3m_00896	Product_name		Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha		
2572232540	t3m_00896	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232540	t3m_00896	Coordinates		28004..29554(-)		
2572232540	t3m_00896	DNA_length		1551bp		
2572232540	t3m_00896	Protein_length		516aa		
2572232540	t3m_00896	GC			0.71	

2572232541	t3m_00897	Metacyc	PWY0-1264: biotin-carboxyl carrier protein assembly			
2572232541	t3m_00897	COG_category	[H] Coenzyme transport and metabolism			
2572232541	t3m_00897	COG0340	Biotin-(acetyl-CoA carboxylase) ligase			3.00E-33
2572232541	t3m_00897	pfam03099	BPL_LplA_LipB			3.60E-16
2572232541	t3m_00897	EC:6.3.4.15	Biotin--[acetyl-CoA-carboxylase] ligase.			
2572232541	t3m_00897	TIGR00121	birA, biotin-[acetyl-CoA-carboxylase] ligase region			3.00E-37
2572232541	t3m_00897	KO:K03524	BirA family transcriptional regulator, biotin operon repressor / biotin-[a			5.50E-30
2572232541	t3m_00897	Locus_type		CDS		
2572232541	t3m_00897	Product_name		birA, biotin-[acetyl-CoA-carboxylase] ligase region		
2572232541	t3m_00897	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232541	t3m_00897	Coordinates		29551..30291(-)		
2572232541	t3m_00897	DNA_length		741bp		
2572232541	t3m_00897	Protein_length		246aa		
2572232541	t3m_00897	GC			0.73	

2572232542	t3m_00898	Locus_type		CDS		
2572232542	t3m_00898	Product_name		hypothetical protein		
2572232542	t3m_00898	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232542	t3m_00898	Coordinates		30445..30801(+)		
2572232542	t3m_00898	DNA_length		357bp		
2572232542	t3m_00898	Protein_length		118aa		
2572232542	t3m_00898	GC			0.69	

2572232543	t3m_00899	KEGG_module	M00125: Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD			
2572232543	t3m_00899	Metacyc	PWY-6168: flavin biosynthesis III (fungi)			
2572232543	t3m_00899	Metacyc	PWY-6167: flavin biosynthesis II (archaea)			
2572232543	t3m_00899	Metacyc	RIBOSYN2-PWY: flavin biosynthesis I (bacteria and plants)			
2572232543	t3m_00899	IMG_pathway	293: riboflavin biosynthesis			
2572232543	t3m_00899	COG_category	[H] Coenzyme transport and metabolism			
2572232543	t3m_00899	COG0054	Riboflavin synthase beta-chain			3.00E-29
2572232543	t3m_00899	pfam00885	DMRL_synthase			4.70E-35
2572232543	t3m_00899	EC:2.5.1.78	6,7-dimethyl-8-ribityllumazine synthase.			
2572232543	t3m_00899	TIGR00114	6,7-dimethyl-8-ribityllumazine synthase			2.00E-41

2572232543	t3m_00899	KO:K00794	6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]		3.40E-44
2572232543	t3m_00899	ITERM:00568	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)		
2572232543	t3m_00899	Locus_type		CDS	
2572232543	t3m_00899	Product_name		6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)	
2572232543	t3m_00899	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232543	t3m_00899	Coordinates		30820..31260(-)	
2572232543	t3m_00899	DNA_length		441bp	
2572232543	t3m_00899	Protein_length		146aa	
2572232543	t3m_00899	GC		0.68	

2572232544	t3m_00900	KEGG_module	M00125: Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD		
2572232544	t3m_00900	Metacyc	PWY-6167: flavin biosynthesis II (archaea)		
2572232544	t3m_00900	Metacyc	RIBOSYN2-PWY: flavin biosynthesis I (bacteria and plants)		
2572232544	t3m_00900	Metacyc	PWY-6168: flavin biosynthesis III (fungi)		
2572232544	t3m_00900	IMG_pathway	293: riboflavin biosynthesis		
2572232544	t3m_00900	COG_category	[H] Coenzyme transport and metabolism		
2572232544	t3m_00900	COG1731	Archaeal riboflavin synthase		1.00E-45
2572232544	t3m_00900	pfam00885	DMRL_synthase		2.10E-10
2572232544	t3m_00900	EC:2.5.1.9	Riboflavin synthase.		
2572232544	t3m_00900	TIGR01506	riboflavin synthase		3.00E-53
2572232544	t3m_00900	KO:K00793	riboflavin synthase [EC:2.5.1.9]		0.00E+00
2572232544	t3m_00900	ITERM:01278	riboflavin synthase alpha chain (EC 2.5.1.9)		
2572232544	t3m_00900	Locus_type		CDS	
2572232544	t3m_00900	Product_name		riboflavin synthase alpha chain (EC 2.5.1.9)	
2572232544	t3m_00900	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16	
2572232544	t3m_00900	Coordinates		31305..31775(-)	
2572232544	t3m_00900	DNA_length		471bp	
2572232544	t3m_00900	Protein_length		156aa	
2572232544	t3m_00900	GC		0.72	

2572232545	t3m_00901	COG_category	[I] Lipid transport and metabolism		
2572232545	t3m_00901	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572232545	t3m_00901	COG0615	Cytidylyltransferase		2.00E-28
2572232545	t3m_00901	pfam01467	CTP_transf_2		1.20E-12

2572232545	t3m_00901	TIGR00125	cytidyltransferase-like domain			2.50E-23
2572232545	t3m_00901	KO:K14656	FAD synthetase			9.10E-39
2572232545	t3m_00901	Locus_type		CDS		
2572232545	t3m_00901	Product_name		cytidyltransferase-like domain		
2572232545	t3m_00901	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232545	t3m_00901	Coordinates		31772..32191(-)		
2572232545	t3m_00901	DNA_length		420bp		
2572232545	t3m_00901	Protein_length		139aa		
2572232545	t3m_00901	GC			0.69	
2572232546	t3m_00902	KEGG_module	M00125: Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD			
2572232546	t3m_00902	Metacyc	PWY-6167: flavin biosynthesis II (archaea)			
2572232546	t3m_00902	Metacyc	RIBOSYN2-PWY: flavin biosynthesis I (bacteria and plants)			
2572232546	t3m_00902	Metacyc	PWY-6168: flavin biosynthesis III (fungi)			
2572232546	t3m_00902	COG_category	[H] Coenzyme transport and metabolism			
2572232546	t3m_00902	COG0108	3,4-dihydroxy-2-butanone 4-phosphate synthase			7.00E-49
2572232546	t3m_00902	pfam00926	DHBP_synthase			3.80E-53
2572232546	t3m_00902	EC:4.1.99.12	3,4-dihydroxy-2-butanone-4-phosphate synthase.			
2572232546	t3m_00902	TIGR00506	3,4-dihydroxy-2-butanone 4-phosphate synthase			1.00E-62
2572232546	t3m_00902	KO:K02858	3,4-dihydroxy 2-butanone 4-phosphate synthase [EC:4.1.99.12]			0.00E+00
2572232546	t3m_00902	Locus_type		CDS		
2572232546	t3m_00902	Product_name		3,4-dihydroxy-2-butanone 4-phosphate synthase		
2572232546	t3m_00902	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232546	t3m_00902	Coordinates		32191..32895(-)		
2572232546	t3m_00902	DNA_length		705bp		
2572232546	t3m_00902	Protein_length		234aa		
2572232546	t3m_00902	GC			0.71	
2572232547	t3m_00903	Locus_type		rRNA		
2572232547	t3m_00903	Gene_symbol		16S		
2572232547	t3m_00903	Product_name		16S rRNA. Archaeal SSU		
2572232547	t3m_00903	Scaffold		t3m_contig_70_133_len_34754_read_count_2944360.16		
2572232547	t3m_00903	Coordinates		33224..34515(-)		
2572232547	t3m_00903	DNA_length		1292bp		

2572232547	t3m_00903	GC		0.59
2572232548	t3m_00904	Locus_type		tRNA
2572232548	t3m_00904	Product_name		tRNA_Gly_GCC
2572232548	t3m_00904	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17
2572232548	t3m_00904	Coordinates		1..74(+)
2572232548	t3m_00904	DNA_length		74bp
2572232548	t3m_00904	GC		0.54
2572232549	t3m_00905	Locus_type		CDS
2572232549	t3m_00905	Product_name		hypothetical protein
2572232549	t3m_00905	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17
2572232549	t3m_00905	Coordinates		126..815(-)
2572232549	t3m_00905	DNA_length		690bp
2572232549	t3m_00905	Protein_length		229aa
2572232549	t3m_00905	GC		0.67
2572232549	t3m_00905	Transmembrane		Yes
2572232550	t3m_00906	Locus_type		CDS
2572232550	t3m_00906	Product_name		hypothetical protein
2572232550	t3m_00906	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17
2572232550	t3m_00906	Coordinates		842..2458(-)
2572232550	t3m_00906	DNA_length		1617bp
2572232550	t3m_00906	Protein_length		538aa
2572232550	t3m_00906	GC		0.63
2572232550	t3m_00906	Transmembrane		Yes
2572232551	t3m_00907	Metacyc	PWY-5770: phenazine-1-carboxylate biosynthesis	
2572232551	t3m_00907	Metacyc	PWY-5365: linear furanocoumarin biosynthesis	
2572232551	t3m_00907	Metacyc	PWY-5133: cohumulone biosynthesis	
2572232551	t3m_00907	Metacyc	PWY-6262: demethylmenaquinol-8 biosynthesis II	
2572232551	t3m_00907	Metacyc	PWY-5802: alizarin biosynthesis	
2572232551	t3m_00907	Metacyc	PWY-5816: all <i>trans</i> undecaprenyl diphosphate biosynthesis	
2572232551	t3m_00907	Metacyc	PWY-4681: kievitone biosynthesis	

2572232551	t3m_00907	Metacyc	PWY-5068: chlorophyll cycle		
2572232551	t3m_00907	Metacyc	PWY-5893: tridecaprenyl diphosphate biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-5817: dodecaprenyl diphosphate biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-2681: <i>trans</i>-zeatin biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-5132: humulone biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-5808: hyperforin and adhyperforin biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-5135: xanthohumol biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-6681: neurosporaxanthin biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-5064: chlorophyll <i>a</i> biosynthesis II		
2572232551	t3m_00907	Metacyc	PWY-6403: carrageenan biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-6834: spermidine biosynthesis III		
2572232551	t3m_00907	Metacyc	PWY-702: methionine biosynthesis II		
2572232551	t3m_00907	Metacyc	PWY-4502: wighteone and luteone biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-7169: hyperxanthone E biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-6936: seleno-amino acid biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-5027: phylloquinol biosynthesis		
2572232551	t3m_00907	Metacyc	PWY-6793: demethylmenaquinol-8 biosynthesis III		
2572232551	t3m_00907	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2572232551	t3m_00907	COG0109	Polyprenyltransferase (cytochrome oxidase assembly factor)		7.00E-62
2572232551	t3m_00907	pfam01040	UbiA		4.60E-29
2572232551	t3m_00907	EC:2.5.1.-	Transferases. Transferring alkyl or aryl groups, other than methyl groups. Transferring alkyl or aryl		
2572232551	t3m_00907	TIGR01473	protoheme IX farnesyltransferase		1.80E-78
2572232551	t3m_00907	KO:K02301	protoheme IX farnesyltransferase [EC:2.5.1.-]		0.00E+00
2572232551	t3m_00907	Locus_type		CDS	
2572232551	t3m_00907	Product_name		protoheme IX farnesyltransferase	
2572232551	t3m_00907	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232551	t3m_00907	Coordinates		2765..3715(+)	
2572232551	t3m_00907	DNA_length		951bp	
2572232551	t3m_00907	Protein_length		316aa	
2572232551	t3m_00907	GC		0.67	
2572232551	t3m_00907	Transmembrane		Yes	
2572232552	t3m_00908	COG_category	[F] Nucleotide transport and metabolism		
2572232552	t3m_00908	COG1051	ADP-ribose pyrophosphatase		6.00E-12

2572232552	t3m_00908	pfam00293	NUDIX			2.90E-14
2572232552	t3m_00908	Locus_type		CDS		
2572232552	t3m_00908	Product_name		ADP-ribose pyrophosphatase		
2572232552	t3m_00908	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232552	t3m_00908	Coordinates		3980..4483(-)		
2572232552	t3m_00908	DNA_length		504bp		
2572232552	t3m_00908	Protein_length		167aa		
2572232552	t3m_00908	GC			0.68	
2572232553	t3m_00909	COG_category	[S] Function unknown			
2572232553	t3m_00909	COG4805	Uncharacterized protein conserved in bacteria			1.00E-23
2572232553	t3m_00909	pfam05960	DUF885			2.20E-61
2572232553	t3m_00909	Locus_type		CDS		
2572232553	t3m_00909	Product_name		Uncharacterized protein conserved in bacteria		
2572232553	t3m_00909	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232553	t3m_00909	Coordinates		4502..6127(-)		
2572232553	t3m_00909	DNA_length		1626bp		
2572232553	t3m_00909	Protein_length		541aa		
2572232553	t3m_00909	GC			0.67	
2572232554	t3m_00910	KEGG_module	M00532: Photorespiration			
2572232554	t3m_00910	COG_category	[C] Energy production and conversion			
2572232554	t3m_00910	COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy a			7.00E-74
2572232554	t3m_00910	pfam01070	FMN_dh			4.40E-118
2572232554	t3m_00910	EC:1.1.3.15	(S)-2-hydroxy-acid oxidase.			
2572232554	t3m_00910	KO:K00104	glycolate oxidase [EC:1.1.3.15]			0.00E+00
2572232554	t3m_00910	Locus_type		CDS		
2572232554	t3m_00910	Product_name		L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy a		
2572232554	t3m_00910	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232554	t3m_00910	Coordinates		6186..7277(-)		
2572232554	t3m_00910	DNA_length		1092bp		
2572232554	t3m_00910	Protein_length		363aa		
2572232554	t3m_00910	GC			0.71	

2572232555	t3m_00911	COG_category	[R] General function prediction only		
2572232555	t3m_00911	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa		5.00E-23
2572232555	t3m_00911	pfam12697	Abhydrolase_6		3.70E-31
2572232555	t3m_00911	EC:3.4.11.5	Prolyl aminopeptidase.		
2572232555	t3m_00911	TIGR01250	proline-specific peptidase, Bacillus coagulans-type subfamily		1.10E-45
2572232555	t3m_00911	KO:K01259	proline iminopeptidase [EC:3.4.11.5]		4.40E-23
2572232555	t3m_00911	Locus_type		CDS	
2572232555	t3m_00911	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfan	
2572232555	t3m_00911	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232555	t3m_00911	Coordinates		7461..8315(+)	
2572232555	t3m_00911	DNA_length		855bp	
2572232555	t3m_00911	Protein_length		284aa	
2572232555	t3m_00911	GC		0.66	

2572232556	t3m_00912	COG_category	[R] General function prediction only		
2572232556	t3m_00912	COG2151	Predicted metal-sulfur cluster biosynthetic enzyme		2.00E-26
2572232556	t3m_00912	pfam01883	DUF59		7.70E-15
2572232556	t3m_00912	Locus_type		CDS	
2572232556	t3m_00912	Product_name		Predicted metal-sulfur cluster biosynthetic enzyme	
2572232556	t3m_00912	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232556	t3m_00912	Coordinates		8379..9104(+)	
2572232556	t3m_00912	DNA_length		726bp	
2572232556	t3m_00912	Protein_length		241aa	
2572232556	t3m_00912	GC		0.71	

2572232557	t3m_00913	pfam12847	Methyltransf_18		1.40E-10
2572232557	t3m_00913	Locus_type		CDS	
2572232557	t3m_00913	Product_name		Methyltransferase domain	
2572232557	t3m_00913	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232557	t3m_00913	Coordinates		9116..9886(-)	
2572232557	t3m_00913	DNA_length		771bp	
2572232557	t3m_00913	Protein_length		256aa	
2572232557	t3m_00913	GC		0.69	

2572232558	t3m_00914	Locus_type		CDS		
2572232558	t3m_00914	Product_name		hypothetical protein		
2572232558	t3m_00914	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232558	t3m_00914	Coordinates		10046..10762(+)		
2572232558	t3m_00914	DNA_length		717bp		
2572232558	t3m_00914	Protein_length		238aa		
2572232558	t3m_00914	GC			0.69	

2572232559	t3m_00915	COG_category	[K] Transcription			
2572232559	t3m_00915	COG1758	DNA-directed RNA polymerase, subunit K/omega			7.00E-09
2572232559	t3m_00915	pfam01192	RNA_pol_Rpb6			6.80E-14
2572232559	t3m_00915	Locus_type		CDS		
2572232559	t3m_00915	Product_name		DNA-directed RNA polymerase, subunit K/omega		
2572232559	t3m_00915	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232559	t3m_00915	Coordinates		10862..11119(+)		
2572232559	t3m_00915	DNA_length		258bp		
2572232559	t3m_00915	Protein_length		85aa		
2572232559	t3m_00915	GC			0.71	

2572232560	t3m_00916	KEGG_module	M00034: Methionine salvage pathway			
2572232560	t3m_00916	Metacyc	PWY-6756: <i>S</i>-methyl-5'-thioadenosine degradation II			
2572232560	t3m_00916	COG_category	[F] Nucleotide transport and metabolism			
2572232560	t3m_00916	COG0005	Purine nucleoside phosphorylase			2.00E-66
2572232560	t3m_00916	pfam01048	PNP_UDP_1			1.50E-45
2572232560	t3m_00916	EC:2.4.2.28	S-methyl-5'-thioadenosine phosphorylase.			
2572232560	t3m_00916	TIGR01694	5'-deoxy-5'-methylthioadenosine phosphorylase			3.20E-93
2572232560	t3m_00916	KO:K00772	5'-methylthioadenosine phosphorylase [EC:2.4.2.28]			0.00E+00
2572232560	t3m_00916	Locus_type		CDS		
2572232560	t3m_00916	Product_name		methylthioadenosine phosphorylase (EC 2.4.2.28)		
2572232560	t3m_00916	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232560	t3m_00916	Coordinates		11129..11920(-)		
2572232560	t3m_00916	DNA_length		792bp		
2572232560	t3m_00916	Protein_length		263aa		
2572232560	t3m_00916	GC			0.7	

2572232561	t3m_00917	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232561	t3m_00917	COG2178	Predicted RNA-binding protein of the translin family			7.00E-25
2572232561	t3m_00917	pfam01997	Translin			9.00E-17
2572232561	t3m_00917	KO:K07477	translin			6.30E-26
2572232561	t3m_00917	Locus_type		CDS		
2572232561	t3m_00917	Product_name		Predicted RNA-binding protein of the translin family		
2572232561	t3m_00917	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232561	t3m_00917	Coordinates		11917..12582(-)		
2572232561	t3m_00917	DNA_length		666bp		
2572232561	t3m_00917	Protein_length		221aa		
2572232561	t3m_00917	GC			0.73	

2572232562	t3m_00918	COG_category	[S] Function unknown			
2572232562	t3m_00918	COG1849	Uncharacterized protein conserved in archaea			5.00E-18
2572232562	t3m_00918	pfam04010	DUF357			7.90E-27
2572232562	t3m_00918	KO:K09728	hypothetical protein			1.80E-17
2572232562	t3m_00918	Locus_type		CDS		
2572232562	t3m_00918	Product_name		Uncharacterized protein conserved in archaea		
2572232562	t3m_00918	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232562	t3m_00918	Coordinates		12554..12850(-)		
2572232562	t3m_00918	DNA_length		297bp		
2572232562	t3m_00918	Protein_length		98aa		
2572232562	t3m_00918	GC			0.72	

2572232563	t3m_00919	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P
2572232563	t3m_00919	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)
2572232563	t3m_00919	Metacyc	P124-PWY: Bifidobacterium shunt
2572232563	t3m_00919	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)
2572232563	t3m_00919	Metacyc	PWY-5723: Rubisco shunt
2572232563	t3m_00919	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)
2572232563	t3m_00919	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)
2572232563	t3m_00919	IMG_pathway	342: Nonoxidative pentose phosphate pathway
2572232563	t3m_00919	IMG_pathway	953: RuMP cycle rearrangement pathway - transaldolase variant

2572232563	t3m_00919	COG_category	[G] Carbohydrate transport and metabolism			
2572232563	t3m_00919	COG0176	Transaldolase			2.00E-63
2572232563	t3m_00919	pfam00923	Transaldolase			4.10E-55
2572232563	t3m_00919	EC:2.2.1.2	Transaldolase.			
2572232563	t3m_00919	TIGR00875	fructose-6-phosphate aldolase, TalC/MipB family			1.50E-96
2572232563	t3m_00919	KO:K00616	transaldolase [EC:2.2.1.2]			0.00E+00
2572232563	t3m_00919	ITERM:01500	transaldolase (EC 2.2.1.2)			
2572232563	t3m_00919	Locus_type		CDS		
2572232563	t3m_00919	Product_name		transaldolase (EC 2.2.1.2)		
2572232563	t3m_00919	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232563	t3m_00919	Coordinates		12899..13546(-)		
2572232563	t3m_00919	DNA_length		648bp		
2572232563	t3m_00919	Protein_length		215aa		
2572232563	t3m_00919	GC			0.66	

2572232564	t3m_00920	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)	
2572232564	t3m_00920	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P	
2572232564	t3m_00920	KEGG_module	M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP	
2572232564	t3m_00920	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)	
2572232564	t3m_00920	Metacyc	P21-PWY: pentose phosphate pathway (partial)	
2572232564	t3m_00920	Metacyc	P124-PWY: Bifidobacterium shunt	
2572232564	t3m_00920	Metacyc	PWY-5723: Rubisco shunt	
2572232564	t3m_00920	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)	
2572232564	t3m_00920	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle	
2572232564	t3m_00920	Metacyc	PWY-6901: xylose degradation IV	
2572232564	t3m_00920	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)	
2572232564	t3m_00920	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)	
2572232564	t3m_00920	COG_category	[G] Carbohydrate transport and metabolism	
2572232564	t3m_00920	COG3958	Transketolase, C-terminal subunit	1.00E-98
2572232564	t3m_00920	pfam02780	Transketolase_C	1.90E-30
2572232564	t3m_00920	pfam02779	Transket_pyr	5.90E-35
2572232564	t3m_00920	EC:2.2.1.1	Transketolase.	
2572232564	t3m_00920	KO:K00615	transketolase [EC:2.2.1.1]	0.00E+00
2572232564	t3m_00920	ITERM:01499	transketolase subunit B (EC 2.2.1.1)	

2572232564	t3m_00920	Locus_type		CDS		
2572232564	t3m_00920	Product_name		transketolase subunit B (EC 2.2.1.1)		
2572232564	t3m_00920	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232564	t3m_00920	Coordinates		13572..14528(-)		
2572232564	t3m_00920	DNA_length		957bp		
2572232564	t3m_00920	Protein_length		318aa		
2572232564	t3m_00920	GC			0.7	

2572232565	t3m_00921	KEGG_module	M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP			
2572232565	t3m_00921	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P			
2572232565	t3m_00921	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)			
2572232565	t3m_00921	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)			
2572232565	t3m_00921	Metacyc	PWY-5723: Rubisco shunt			
2572232565	t3m_00921	Metacyc	P124-PWY: Bifidobacterium shunt			
2572232565	t3m_00921	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)			
2572232565	t3m_00921	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)			
2572232565	t3m_00921	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2572232565	t3m_00921	Metacyc	PWY-6901: xylose degradation IV			
2572232565	t3m_00921	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			
2572232565	t3m_00921	Metacyc	P21-PWY: pentose phosphate pathway (partial)			
2572232565	t3m_00921	COG_category	[G] Carbohydrate transport and metabolism			
2572232565	t3m_00921	COG3959	Transketolase, N-terminal subunit			5.00E-87
2572232565	t3m_00921	pfam00456	Transketolase_N			1.60E-69
2572232565	t3m_00921	EC:2.2.1.1	Transketolase.			
2572232565	t3m_00921	KO:K00615	transketolase [EC:2.2.1.1]			0.00E+00
2572232565	t3m_00921	Locus_type		CDS		
2572232565	t3m_00921	Product_name		transketolase subunit A (EC 2.2.1.1)		
2572232565	t3m_00921	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232565	t3m_00921	Coordinates		14525..15376(-)		
2572232565	t3m_00921	DNA_length		852bp		
2572232565	t3m_00921	Protein_length		283aa		
2572232565	t3m_00921	GC			0.69	

2572232566	t3m_00922	IMG_pathway	224: Nucleotide incision repair			

2572232566	t3m_00922	IMG_pathway	225: Abasic site processing by AP lyase activity		
2572232566	t3m_00922	IMG_pathway	616: Abasic site processing by AP endonuclease activity		
2572232566	t3m_00922	COG_category	[L] Replication, recombination and repair		
2572232566	t3m_00922	COG0648	Endonuclease IV		2.00E-69
2572232566	t3m_00922	pfam01261	AP_endonuc_2		1.40E-32
2572232566	t3m_00922	EC:3.1.21.2	Deoxyribonuclease IV (phage-T(4)-induced).		
2572232566	t3m_00922	TIGR00587	apurinic endonuclease (APN1)		8.10E-82
2572232566	t3m_00922	KO:K01151	deoxyribonuclease IV [EC:3.1.21.2]		0.00E+00
2572232566	t3m_00922	ITERM:00591	Endonuclease IV (EC 3.1.21.-)		
2572232566	t3m_00922	Locus_type		CDS	
2572232566	t3m_00922	Product_name		Endonuclease IV (EC 3.1.21.-)	
2572232566	t3m_00922	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232566	t3m_00922	Coordinates		15402..16319(-)	
2572232566	t3m_00922	DNA_length		918bp	
2572232566	t3m_00922	Protein_length		305aa	
2572232566	t3m_00922	GC		0.7	
2572232567	t3m_00923	Locus_type		rRNA	
2572232567	t3m_00923	Gene_symbol		5S	
2572232567	t3m_00923	Product_name		5S rRNA. Archaeal TSU	
2572232567	t3m_00923	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232567	t3m_00923	Coordinates		16384..16505(-)	
2572232567	t3m_00923	DNA_length		122bp	
2572232567	t3m_00923	GC		0.63	
2572232568	t3m_00924	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism		
2572232568	t3m_00924	COG2050	Uncharacterized protein, possibly involved in aromatic compounds cata		3.00E-17
2572232568	t3m_00924	pfam03061	4HBT		4.50E-17
2572232568	t3m_00924	TIGR00369	uncharacterized domain 1		1.00E-23
2572232568	t3m_00924	Locus_type		CDS	
2572232568	t3m_00924	Product_name		uncharacterized domain 1	
2572232568	t3m_00924	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232568	t3m_00924	Coordinates		16532..17056(-)	
2572232568	t3m_00924	DNA_length		525bp	

2572232568	t3m_00924	Protein_length		174aa		
2572232568	t3m_00924	GC			0.72	
2572232569	t3m_00925	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			
2572232569	t3m_00925	Metacyc	PWY-922: mevalonate pathway I			
2572232569	t3m_00925	IMG_pathway	178: Mevalonate pathway for isopentenyl pyrophopsphate synthesis			
2572232569	t3m_00925	COG_category	[I] Lipid transport and metabolism			
2572232569	t3m_00925	COG3407	Mevalonate pyrophosphate decarboxylase			2.00E-61
2572232569	t3m_00925	pfam00288	GHMP_kinases_N			3.60E-07
2572232569	t3m_00925	EC:4.1.1.33	Diphosphomevalonate decarboxylase.			
2572232569	t3m_00925	TIGR01240	diphosphomevalonate decarboxylase			4.80E-74
2572232569	t3m_00925	KO:K01597	diphosphomevalonate decarboxylase [EC:4.1.1.33]			0.00E+00
2572232569	t3m_00925	ITERM:00468	diphosphomevalonate decarboxylase (EC 4.1.1.33)			
2572232569	t3m_00925	Locus_type		CDS		
2572232569	t3m_00925	Product_name		diphosphomevalonate decarboxylase (EC 4.1.1.33)		
2572232569	t3m_00925	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232569	t3m_00925	Coordinates		17116..18123(+)		
2572232569	t3m_00925	DNA_length		1008bp		
2572232569	t3m_00925	Protein_length		335aa		
2572232569	t3m_00925	GC			0.72	
2572232570	t3m_00926	KEGG_module	M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P			
2572232570	t3m_00926	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)			
2572232570	t3m_00926	KEGG_module	M00004: Pentose phosphate pathway (Pentose phosphate cycle)			
2572232570	t3m_00926	KEGG_module	M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP			
2572232570	t3m_00926	Metacyc	PWY-5723: Rubisco shunt			
2572232570	t3m_00926	Metacyc	NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)			
2572232570	t3m_00926	Metacyc	P124-PWY: Bifidobacterium shunt			
2572232570	t3m_00926	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)			
2572232570	t3m_00926	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			
2572232570	t3m_00926	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)			
2572232570	t3m_00926	IMG_pathway	341: Oxidative pentose phosphate pathway			
2572232570	t3m_00926	IMG_pathway	342: Nonoxidative pentose phosphate pathway			
2572232570	t3m_00926	IMG_pathway	343: Reverse ribulose monophosphate pathway			

2572232570	t3m_00926	IMG_pathway	527: Calvin cycle			
2572232570	t3m_00926	IMG_pathway	535: D-allose conversion to D-fructose 6-phosphate			
2572232570	t3m_00926	COG_category	[G] Carbohydrate transport and metabolism			
2572232570	t3m_00926	COG0120	Ribose 5-phosphate isomerase			6.00E-51
2572232570	t3m_00926	pfam06026	Rib_5-P_isom_A			8.50E-49
2572232570	t3m_00926	EC:5.3.1.6	Ribose-5-phosphate isomerase.			
2572232570	t3m_00926	TIGR00021	ribose 5-phosphate isomerase			4.20E-63
2572232570	t3m_00926	KO:K01807	ribose 5-phosphate isomerase A [EC:5.3.1.6]			1.60E-42
2572232570	t3m_00926	ITERM:01495	ribose-5-phosphate isomerase (EC 5.3.1.6)			
2572232570	t3m_00926	Locus_type		CDS		
2572232570	t3m_00926	Product_name		ribose-5-phosphate isomerase (EC 5.3.1.6)		
2572232570	t3m_00926	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232570	t3m_00926	Coordinates		18138..18848(-)		
2572232570	t3m_00926	DNA_length		711bp		
2572232570	t3m_00926	Protein_length		236aa		
2572232570	t3m_00926	GC			0.72	
2572232571	t3m_00927	COG_category	[F] Nucleotide transport and metabolism			
2572232571	t3m_00927	COG0528	Uridylate kinase			2.00E-32
2572232571	t3m_00927	pfam00696	AA_kinase			4.20E-24
2572232571	t3m_00927	EC:2.7.4.22	UMP kinase.			
2572232571	t3m_00927	TIGR02076	uridylate kinase, putative			1.40E-62
2572232571	t3m_00927	KO:K09903	uridylate kinase [EC:2.7.4.22]			3.00E-37
2572232571	t3m_00927	Locus_type		CDS		
2572232571	t3m_00927	Product_name		uridylate kinase, putative		
2572232571	t3m_00927	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232571	t3m_00927	Coordinates		18933..19664(+)		
2572232571	t3m_00927	DNA_length		732bp		
2572232571	t3m_00927	Protein_length		243aa		
2572232571	t3m_00927	GC			0.73	
2572232572	t3m_00928	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP			
2572232572	t3m_00928	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2572232572	t3m_00928	COG_category	[F] Nucleotide transport and metabolism			

2572232572	t3m_00928	COG0563	Adenylate kinase and related kinases			3.00E-42
2572232572	t3m_00928	pfam05191	ADK_lid			3.80E-14
2572232572	t3m_00928	pfam00406	ADK			5.90E-48
2572232572	t3m_00928	EC:2.7.4.3	Adenylate kinase.			
2572232572	t3m_00928	TIGR01351	adenylate kinase			7.70E-75
2572232572	t3m_00928	KO:K00939	adenylate kinase [EC:2.7.4.3]			0.00E+00
2572232572	t3m_00928	ITERM:00632	Adenylate kinase (EC 2.7.4.3)			
2572232572	t3m_00928	Locus_type		CDS		
2572232572	t3m_00928	Product_name		Adenylate kinase (EC 2.7.4.3)		
2572232572	t3m_00928	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232572	t3m_00928	Coordinates		19689..20321(+)		
2572232572	t3m_00928	DNA_length		633bp		
2572232572	t3m_00928	Protein_length		210aa		
2572232572	t3m_00928	GC			0.71	
2572232573	t3m_00929	pfam00300	His_Phos_1			9.20E-10
2572232573	t3m_00929	Locus_type		CDS		
2572232573	t3m_00929	Product_name		Histidine phosphatase superfamily (branch 1)		
2572232573	t3m_00929	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232573	t3m_00929	Coordinates		20335..20862(-)		
2572232573	t3m_00929	DNA_length		528bp		
2572232573	t3m_00929	Protein_length		175aa		
2572232573	t3m_00929	GC			0.69	
2572232574	t3m_00930	Locus_type		tRNA		
2572232574	t3m_00930	Product_name		tRNA_Tyr_GTA		
2572232574	t3m_00930	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232574	t3m_00930	Coordinates		20927..21033(+)		
2572232574	t3m_00930	DNA_length		74bp		
2572232574	t3m_00930	GC			0.65	
2572232575	t3m_00931	Locus_type		tRNA		
2572232575	t3m_00931	Product_name		tRNA_Gly_CCC		
2572232575	t3m_00931	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		

2572232575	t3m_00931	Coordinates		21132..21203(-)		
2572232575	t3m_00931	DNA_length		72bp		
2572232575	t3m_00931	GC			0.57	
2572232576	t3m_00932	Locus_type		CDS		
2572232576	t3m_00932	Product_name		hypothetical protein		
2572232576	t3m_00932	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232576	t3m_00932	Coordinates		21452..22576(+)		
2572232576	t3m_00932	DNA_length		1125bp		
2572232576	t3m_00932	Protein_length		374aa		
2572232576	t3m_00932	GC			0.64	
2572232576	t3m_00932	Transmembrane		Yes		
2572232577	t3m_00933	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2572232577	t3m_00933	COG_category	[N] Cell motility			
2572232577	t3m_00933	COG0630	Type IV secretory pathway, VirB11 components, and related ATPases in			3.00E-87
2572232577	t3m_00933	pfam00437	T2SE			1.10E-42
2572232577	t3m_00933	KO:K07332	archaeal flagellar protein FlaI			0.00E+00
2572232577	t3m_00933	Locus_type		CDS		
2572232577	t3m_00933	Product_name		Type IV secretory pathway, VirB11 components, and related ATPases inv		
2572232577	t3m_00933	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232577	t3m_00933	Coordinates		22581..24245(+)		
2572232577	t3m_00933	DNA_length		1665bp		
2572232577	t3m_00933	Protein_length		554aa		
2572232577	t3m_00933	GC			0.65	
2572232578	t3m_00934	pfam00482	T2SF			2.40E-12
2572232578	t3m_00934	KO:K07333	archaeal flagellar protein FlaJ			0.00E+00
2572232578	t3m_00934	Locus_type		CDS		
2572232578	t3m_00934	Product_name		Type II secretion system (T2SS), protein F		
2572232578	t3m_00934	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232578	t3m_00934	Coordinates		24242..25231(+)		
2572232578	t3m_00934	DNA_length		990bp		
2572232578	t3m_00934	Protein_length		329aa		

2572232578	t3m_00934	GC		0.67	
2572232578	t3m_00934	Transmembrane		Yes	
2572232579	t3m_00935	pfam00482	T2SF		1.80E-17
2572232579	t3m_00935	KO:K07333	archaeal flagellar protein FlaJ		0.00E+00
2572232579	t3m_00935	Locus_type		CDS	
2572232579	t3m_00935	Product_name		Type II secretion system (T2SS), protein F	
2572232579	t3m_00935	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232579	t3m_00935	Coordinates		25233..26207(+)	
2572232579	t3m_00935	DNA_length		975bp	
2572232579	t3m_00935	Protein_length		324aa	
2572232579	t3m_00935	GC		0.68	
2572232579	t3m_00935	Transmembrane		Yes	
2572232580	t3m_00936	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport		
2572232580	t3m_00936	COG_category	[N] Cell motility		
2572232580	t3m_00936	COG0630	Type IV secretory pathway, VirB11 components, and related ATPases in		6.00E-89
2572232580	t3m_00936	pfam00437	T2SE		1.20E-42
2572232580	t3m_00936	KO:K07332	archaeal flagellar protein FlaI		0.00E+00
2572232580	t3m_00936	Locus_type		CDS	
2572232580	t3m_00936	Product_name		Type IV secretory pathway, VirB11 components, and related ATPases inv	
2572232580	t3m_00936	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17	
2572232580	t3m_00936	Coordinates		26224..27987(+)	
2572232580	t3m_00936	DNA_length		1764bp	
2572232580	t3m_00936	Protein_length		587aa	
2572232580	t3m_00936	GC		0.66	
2572232581	t3m_00937	COG_category	[L] Replication, recombination and repair		
2572232581	t3m_00937	COG0863	DNA modification methylase		7.00E-17
2572232581	t3m_00937	pfam01555	N6_N4_Mtase		3.30E-30
2572232581	t3m_00937	EC:2.1.1.113	Site-specific DNA-methyltransferase (cytosine-N(4)-specific).		
2572232581	t3m_00937	KO:K00590	site-specific DNA-methyltransferase (cytosine-N4-specific) [EC:2.1.1.11		0.00E+00
2572232581	t3m_00937	Locus_type		CDS	
2572232581	t3m_00937	Product_name		DNA modification methylase	

2572232581	t3m_00937	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232581	t3m_00937	Coordinates		28048..28989(+)		
2572232581	t3m_00937	DNA_length		942bp		
2572232581	t3m_00937	Protein_length		313aa		
2572232581	t3m_00937	GC			0.73	
2572232582	t3m_00938	Locus_type		CDS		
2572232582	t3m_00938	Product_name		hypothetical protein		
2572232582	t3m_00938	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232582	t3m_00938	Coordinates		28952..29389(-)		
2572232582	t3m_00938	DNA_length		438bp		
2572232582	t3m_00938	Protein_length		145aa		
2572232582	t3m_00938	GC			0.69	
2572232583	t3m_00939	pfam13519	VWA_2			2.70E-07
2572232583	t3m_00939	Locus_type		CDS		
2572232583	t3m_00939	Product_name		von Willebrand factor type A domain		
2572232583	t3m_00939	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232583	t3m_00939	Coordinates		29452..30885(-)		
2572232583	t3m_00939	DNA_length		1434bp		
2572232583	t3m_00939	Protein_length		477aa		
2572232583	t3m_00939	GC			0.71	
2572232584	t3m_00940	COG_category	[H] Coenzyme transport and metabolism			
2572232584	t3m_00940	COG1239	Mg-chelatase subunit ChlI			2.00E-14
2572232584	t3m_00940	pfam08298	AAA_PrkA			8.90E-12
2572232584	t3m_00940	Locus_type		CDS		
2572232584	t3m_00940	Product_name		Mg-chelatase subunit ChlI		
2572232584	t3m_00940	Scaffold		t3m_contig_70_148_len_32708_read_count_2644530.17		
2572232584	t3m_00940	Coordinates		31247..32707(-)		
2572232584	t3m_00940	DNA_length		1461bp		
2572232584	t3m_00940	Protein_length		486aa		
2572232584	t3m_00940	GC			0.69	

2572232585	t3m_00941	pfam02775	TPP_enzyme_C			4.70E-21
2572232585	t3m_00941	Locus_type		CDS		
2572232585	t3m_00941	Product_name		Thiamine pyrophosphate enzyme, C-terminal TPP binding domain		
2572232585	t3m_00941	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232585	t3m_00941	Coordinates		2..451(-)		
2572232585	t3m_00941	DNA_length		450bp		
2572232585	t3m_00941	Protein_length		150aa		
2572232585	t3m_00941	GC			0.66	

2572232586	t3m_00942	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			
2572232586	t3m_00942	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2572232586	t3m_00942	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572232586	t3m_00942	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2572232586	t3m_00942	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572232586	t3m_00942	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2572232586	t3m_00942	Metacyc	P23-PWY: reductive TCA cycle I			
2572232586	t3m_00942	Metacyc	PWY-5392: reductive TCA cycle II			
2572232586	t3m_00942	COG_category	[C] Energy production and conversion			
2572232586	t3m_00942	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o			2.00E-74
2572232586	t3m_00942	pfam01855	POR_N			1.50E-70
2572232586	t3m_00942	EC:1.2.7.3	2-oxoglutarate synthase.			
2572232586	t3m_00942	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]			0.00E+00
2572232586	t3m_00942	ITERM:01389	2-oxoglutarate ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.3)			
2572232586	t3m_00942	Locus_type		CDS		
2572232586	t3m_00942	Product_name		2-oxoglutarate ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.3)		
2572232586	t3m_00942	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232586	t3m_00942	Coordinates		421..1626(-)		
2572232586	t3m_00942	DNA_length		1206bp		
2572232586	t3m_00942	Protein_length		401aa		
2572232586	t3m_00942	GC			0.67	

2572232587	t3m_00943	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572232587	t3m_00943	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			
2572232587	t3m_00943	Metacyc	PWY-5392: reductive TCA cycle II			

2572232587	t3m_00943	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572232587	t3m_00943	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2572232587	t3m_00943	Metacyc	P23-PWY: reductive TCA cycle I			
2572232587	t3m_00943	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2572232587	t3m_00943	pfam12838	Fer4_7			5.10E-08
2572232587	t3m_00943	EC:1.2.7.3	2-oxoglutarate synthase.			
2572232587	t3m_00943	KO:K00176	2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7.3]			1.10E-18
2572232587	t3m_00943	Locus_type		CDS		
2572232587	t3m_00943	Product_name		4Fe-4S dicluster domain		
2572232587	t3m_00943	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232587	t3m_00943	Coordinates		1623..1910(-)		
2572232587	t3m_00943	DNA_length		288bp		
2572232587	t3m_00943	Protein_length		95aa		
2572232587	t3m_00943	GC			0.62	
2572232588	t3m_00944	pfam07690	MFS_1			1.10E-35
2572232588	t3m_00944	Locus_type		CDS		
2572232588	t3m_00944	Product_name		Major Facilitator Superfamily		
2572232588	t3m_00944	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232588	t3m_00944	Coordinates		2131..3756(+)		
2572232588	t3m_00944	DNA_length		1626bp		
2572232588	t3m_00944	Protein_length		541aa		
2572232588	t3m_00944	GC			0.64	
2572232588	t3m_00944	Transmembrane		Yes		
2572232589	t3m_00945	COG_category	[R] General function prediction only			
2572232589	t3m_00945	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa			3.00E-24
2572232589	t3m_00945	pfam12697	Abhydrolase_6			2.80E-34
2572232589	t3m_00945	EC:3.4.11.5	Prolyl aminopeptidase.			
2572232589	t3m_00945	TIGR01250	proline-specific peptidase, Bacillus coagulans-type subfamily			1.80E-87
2572232589	t3m_00945	KO:K01259	proline iminopeptidase [EC:3.4.11.5]			0.00E+00
2572232589	t3m_00945	ITERM:04888	tricorn interacting aminopeptidase F1. Serine peptidase. MEROPS family S33			
2572232589	t3m_00945	Locus_type		CDS		
2572232589	t3m_00945	Product_name		tricorn interacting aminopeptidase F1. Serine peptidase. MEROPS family		

2572232589	t3m_00945	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232589	t3m_00945	Coordinates		3740..4651(-)		
2572232589	t3m_00945	DNA_length		912bp		
2572232589	t3m_00945	Protein_length		303aa		
2572232589	t3m_00945	GC			0.65	
2572232589	t3m_00945	Fused_gene		Yes		
2572232590	t3m_00946	pfam03061	4HBT			6.60E-10
2572232590	t3m_00946	Locus_type		CDS		
2572232590	t3m_00946	Product_name		Thioesterase superfamily		
2572232590	t3m_00946	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232590	t3m_00946	Coordinates		4658..5248(+)		
2572232590	t3m_00946	DNA_length		591bp		
2572232590	t3m_00946	Protein_length		196aa		
2572232590	t3m_00946	GC			0.68	
2572232591	t3m_00947	COG_category	[C] Energy production and conversion			
2572232591	t3m_00947	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)			2.00E-89
2572232591	t3m_00947	pfam00248	Aldo_ket_red			1.20E-79
2572232591	t3m_00947	Locus_type		CDS		
2572232591	t3m_00947	Product_name		Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)		
2572232591	t3m_00947	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232591	t3m_00947	Coordinates		5303..6289(+)		
2572232591	t3m_00947	DNA_length		987bp		
2572232591	t3m_00947	Protein_length		328aa		
2572232591	t3m_00947	GC			0.69	
2572232592	t3m_00948	pfam06157	DUF973			2.00E-13
2572232592	t3m_00948	Locus_type		CDS		
2572232592	t3m_00948	Product_name		Protein of unknown function (DUF973)		
2572232592	t3m_00948	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232592	t3m_00948	Coordinates		6601..7233(+)		
2572232592	t3m_00948	DNA_length		633bp		
2572232592	t3m_00948	Protein_length		210aa		

2572232592	t3m_00948	GC			0.62	
2572232592	t3m_00948	Transmembrane		Yes		
2572232593	t3m_00949	COG_category	[R] General function prediction only			
2572232593	t3m_00949	COG_category	[C] Energy production and conversion			
2572232593	t3m_00949	COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases			2.00E-32
2572232593	t3m_00949	pfam00107	ADH_zinc_N			2.30E-09
2572232593	t3m_00949	Locus_type		CDS		
2572232593	t3m_00949	Product_name		NADPH:quinone reductase and related Zn-dependent oxidoreductases		
2572232593	t3m_00949	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232593	t3m_00949	Coordinates		7362..8327(+)		
2572232593	t3m_00949	DNA_length		966bp		
2572232593	t3m_00949	Protein_length		321aa		
2572232593	t3m_00949	GC			0.71	
2572232594	t3m_00950	pfam01814	Hemerythrin			2.00E-08
2572232594	t3m_00950	Locus_type		CDS		
2572232594	t3m_00950	Product_name		Hemerythrin HHE cation binding domain		
2572232594	t3m_00950	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232594	t3m_00950	Coordinates		8429..9154(-)		
2572232594	t3m_00950	DNA_length		726bp		
2572232594	t3m_00950	Protein_length		241aa		
2572232594	t3m_00950	GC			0.63	
2572232595	t3m_00951	COG_category	[R] General function prediction only			
2572232595	t3m_00951	COG1033	Predicted exporters of the RND superfamily			3.00E-44
2572232595	t3m_00951	pfam03176	MMPL			2.20E-37
2572232595	t3m_00951	pfam03176	MMPL			3.00E-41
2572232595	t3m_00951	Locus_type		CDS		
2572232595	t3m_00951	Product_name		Predicted exporters of the RND superfamily		
2572232595	t3m_00951	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232595	t3m_00951	Coordinates		9346..12276(-)		
2572232595	t3m_00951	DNA_length		2931bp		
2572232595	t3m_00951	Protein_length		976aa		

2572232595	t3m_00951	GC			0.67	
2572232595	t3m_00951	Transmembrane		Yes		
2572232596	t3m_00952	Metacyc	PWY-6935: seleno-amino acid detoxification and volatilization II			
2572232596	t3m_00952	Metacyc	PWY1A0-6325: actinorhodin biosynthesis			
2572232596	t3m_00952	COG_category	[R] General function prediction only			
2572232596	t3m_00952	COG0491	Zn-dependent hydrolases, including glyoxylases			4.00E-09
2572232596	t3m_00952	pfam00753	Lactamase_B			6.20E-21
2572232596	t3m_00952	EC:4.-	Lyases.			
2572232596	t3m_00952	KO:K05555	cyclase [EC:4.-.-.-]			1.50E-24
2572232596	t3m_00952	Locus_type		CDS		
2572232596	t3m_00952	Product_name		Zn-dependent hydrolases, including glyoxylases		
2572232596	t3m_00952	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232596	t3m_00952	Coordinates		12522..13457(+)		
2572232596	t3m_00952	DNA_length		936bp		
2572232596	t3m_00952	Protein_length		311aa		
2572232596	t3m_00952	GC			0.7	
2572232597	t3m_00953	COG_category	[S] Function unknown			
2572232597	t3m_00953	COG4805	Uncharacterized protein conserved in bacteria			5.00E-34
2572232597	t3m_00953	pfam05960	DUF885			1.10E-60
2572232597	t3m_00953	Locus_type		CDS		
2572232597	t3m_00953	Product_name		Uncharacterized protein conserved in bacteria		
2572232597	t3m_00953	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232597	t3m_00953	Coordinates		13490..15127(-)		
2572232597	t3m_00953	DNA_length		1638bp		
2572232597	t3m_00953	Protein_length		545aa		
2572232597	t3m_00953	GC			0.68	
2572232598	t3m_00954	Locus_type		CDS		
2572232598	t3m_00954	Product_name		hypothetical protein		
2572232598	t3m_00954	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232598	t3m_00954	Coordinates		15192..15515(-)		
2572232598	t3m_00954	DNA_length		324bp		

2572232598	t3m_00954	Protein_length		107aa		
2572232598	t3m_00954	GC			0.72	
2572232599	t3m_00955	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232599	t3m_00955	COG0251	Putative translation initiation inhibitor, yjgF family			1.00E-11
2572232599	t3m_00955	pfam14588	YjgF_endoribonc			6.00E-20
2572232599	t3m_00955	Locus_type		CDS		
2572232599	t3m_00955	Product_name		Putative translation initiation inhibitor, yjgF family		
2572232599	t3m_00955	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232599	t3m_00955	Coordinates		15600..16073(+)		
2572232599	t3m_00955	DNA_length		474bp		
2572232599	t3m_00955	Protein_length		157aa		
2572232599	t3m_00955	GC			0.71	
2572232600	t3m_00956	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232600	t3m_00956	COG1889	Fibrillarin-like rRNA methylase			2.00E-52
2572232600	t3m_00956	pfam01269	Fibrillarin			1.90E-54
2572232600	t3m_00956	KO:K04795	fibrillarin-like pre-rRNA processing protein			2.70E-37
2572232600	t3m_00956	Locus_type		CDS		
2572232600	t3m_00956	Product_name		Fibrillarin-like rRNA methylase		
2572232600	t3m_00956	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232600	t3m_00956	Coordinates		16070..16729(+)		
2572232600	t3m_00956	DNA_length		660bp		
2572232600	t3m_00956	Protein_length		219aa		
2572232600	t3m_00956	GC			0.7	
2572232601	t3m_00957	Locus_type		CDS		
2572232601	t3m_00957	Product_name		hypothetical protein		
2572232601	t3m_00957	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232601	t3m_00957	Coordinates		16809..19061(+)		
2572232601	t3m_00957	DNA_length		2253bp		
2572232601	t3m_00957	Protein_length		750aa		
2572232601	t3m_00957	GC			0.67	
2572232601	t3m_00957	Transmembrane		Yes		

2572232602	t3m_00958	Locus_type	CDS
2572232602	t3m_00958	Product_name	hypothetical protein
2572232602	t3m_00958	Scaffold	t3m_contig_70_149_len_32466_read_count_2958036.18
2572232602	t3m_00958	Coordinates	19208..19444(+)
2572232602	t3m_00958	DNA_length	237bp
2572232602	t3m_00958	Protein_length	78aa
2572232602	t3m_00958	GC	0.59
2572232602	t3m_00958	Transmembrane	Yes

2572232603	t3m_00959	Locus_type	CDS
2572232603	t3m_00959	Product_name	hypothetical protein
2572232603	t3m_00959	Scaffold	t3m_contig_70_149_len_32466_read_count_2958036.18
2572232603	t3m_00959	Coordinates	19455..20588(+)
2572232603	t3m_00959	DNA_length	1134bp
2572232603	t3m_00959	Protein_length	377aa
2572232603	t3m_00959	GC	0.66
2572232603	t3m_00959	Transmembrane	Yes

2572232604	t3m_00960	Locus_type	CDS
2572232604	t3m_00960	Product_name	hypothetical protein
2572232604	t3m_00960	Scaffold	t3m_contig_70_149_len_32466_read_count_2958036.18
2572232604	t3m_00960	Coordinates	20590..21372(+)
2572232604	t3m_00960	DNA_length	783bp
2572232604	t3m_00960	Protein_length	260aa
2572232604	t3m_00960	GC	0.68

2572232605	t3m_00961	Locus_type	CDS
2572232605	t3m_00961	Product_name	hypothetical protein
2572232605	t3m_00961	Scaffold	t3m_contig_70_149_len_32466_read_count_2958036.18
2572232605	t3m_00961	Coordinates	21369..21743(+)
2572232605	t3m_00961	DNA_length	375bp
2572232605	t3m_00961	Protein_length	124aa
2572232605	t3m_00961	GC	0.68

2572232605	t3m_00961	Transmembrane		Yes		
2572232606	t3m_00962	pfam12846	AAA_10			1.20E-45
2572232606	t3m_00962	Locus_type		CDS		
2572232606	t3m_00962	Product_name		AAA-like domain		
2572232606	t3m_00962	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232606	t3m_00962	Coordinates		21740..23434(+)		
2572232606	t3m_00962	DNA_length		1695bp		
2572232606	t3m_00962	Protein_length		564aa		
2572232606	t3m_00962	GC			0.67	
2572232607	t3m_00963	Locus_type		CDS		
2572232607	t3m_00963	Product_name		hypothetical protein		
2572232607	t3m_00963	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232607	t3m_00963	Coordinates		23429..23776(-)		
2572232607	t3m_00963	DNA_length		348bp		
2572232607	t3m_00963	Protein_length		115aa		
2572232607	t3m_00963	GC			0.68	
2572232608	t3m_00964	COG_category	[L] Replication, recombination and repair			
2572232608	t3m_00964	COG0863	DNA modification methylase			2.00E-27
2572232608	t3m_00964	pfam01555	N6_N4_Mtase			9.60E-34
2572232608	t3m_00964	EC:2.1.1.113	Site-specific DNA-methyltransferase (cytosine-N(4)-specific).			
2572232608	t3m_00964	KO:K00590	site-specific DNA-methyltransferase (cytosine-N4-specific) [EC:2.1.1.11			0.00E+00
2572232608	t3m_00964	Locus_type		CDS		
2572232608	t3m_00964	Product_name		DNA modification methylase		
2572232608	t3m_00964	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232608	t3m_00964	Coordinates		23868..24746(-)		
2572232608	t3m_00964	DNA_length		879bp		
2572232608	t3m_00964	Protein_length		292aa		
2572232608	t3m_00964	GC			0.7	
2572232609	t3m_00965	KEGG_module	M00345: Formaldehyde assimilation, ribulose monophosphate pathway			
2572232609	t3m_00965	Metacyc	RUMP-PWY: formaldehyde oxidation I			

2572232609	t3m_00965	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)			
2572232609	t3m_00965	IMG_pathway	343: Reverse ribulose monophosphate pathway			
2572232609	t3m_00965	IMG_pathway	950: RuMP cycle formaldehyde fixation pathway			
2572232609	t3m_00965	COG_category	[G] Carbohydrate transport and metabolism			
2572232609	t3m_00965	COG0269	3-hexulose-6-phosphate synthase and related proteins			7.00E-52
2572232609	t3m_00965	pfam03737	Methyltransf_6			1.60E-35
2572232609	t3m_00965	pfam00215	OMPdecase			2.90E-23
2572232609	t3m_00965	EC:5.3.1.27	6-phospho-3-hexuloisomerase.			
2572232609	t3m_00965	EC:4.1.2.43	3-hexulose-6-phosphate synthase.			
2572232609	t3m_00965	TIGR03128	3-hexulose-6-phosphate synthase			6.50E-67
2572232609	t3m_00965	KO:K13831	3-hexulose-6-phosphate synthase / 6-phospho-3-hexuloisomerase [EC:			0.00E+00
2572232609	t3m_00965	ITERM:01503	3-hexulose-6-phosphate synthase (EC 4.1.2.43)			
2572232609	t3m_00965	Locus_type		CDS		
2572232609	t3m_00965	Product_name		3-hexulose-6-phosphate synthase (EC 4.1.2.43)		
2572232609	t3m_00965	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232609	t3m_00965	Coordinates		24798..26102(+)		
2572232609	t3m_00965	DNA_length		1305bp		
2572232609	t3m_00965	Protein_length		434aa		
2572232609	t3m_00965	GC			0.69	
2572232609	t3m_00965	Fused_gene		Yes		
2572232610	t3m_00966	pfam01416	PseudoU_synth_1			1.70E-07
2572232610	t3m_00966	TIGR00071	tRNA pseudouridine(38-40) synthase			2.80E-17
2572232610	t3m_00966	Locus_type		CDS		
2572232610	t3m_00966	Product_name		tRNA pseudouridine synthase		
2572232610	t3m_00966	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232610	t3m_00966	Coordinates		26135..26734(-)		
2572232610	t3m_00966	DNA_length		600bp		
2572232610	t3m_00966	Protein_length		199aa		
2572232610	t3m_00966	GC			0.64	
2572232611	t3m_00967	KEGG_module	M00222: Phosphate transport system			
2572232611	t3m_00967	COG_category	[P] Inorganic ion transport and metabolism			
2572232611	t3m_00967	COG0226	ABC-type phosphate transport system, periplasmic component			3.00E-37

2572232611	t3m_00967	pfam12849	PBP_like_2		3.40E-38
2572232611	t3m_00967	TIGR00975	phosphate ABC transporter, phosphate-binding protein		7.30E-80
2572232611	t3m_00967	KO:K02040	phosphate transport system substrate-binding protein		0.00E+00
2572232611	t3m_00967	Locus_type		CDS	
2572232611	t3m_00967	Product_name		phosphate ABC transporter, phosphate-binding protein	
2572232611	t3m_00967	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18	
2572232611	t3m_00967	Coordinates		27268..28410(+)	
2572232611	t3m_00967	DNA_length		1143bp	
2572232611	t3m_00967	Protein_length		380aa	
2572232611	t3m_00967	GC		0.61	
2572232611	t3m_00967	Transmembrane		Yes	
2572232612	t3m_00968	KEGG_module	M00222: Phosphate transport system		
2572232612	t3m_00968	COG_category	[P] Inorganic ion transport and metabolism		
2572232612	t3m_00968	COG0573	ABC-type phosphate transport system, permease component		6.00E-63
2572232612	t3m_00968	pfam00528	BPD_transp_1		6.50E-18
2572232612	t3m_00968	TIGR02138	phosphate ABC transporter, permease protein PstC		6.90E-91
2572232612	t3m_00968	KO:K02037	phosphate transport system permease protein		0.00E+00
2572232612	t3m_00968	ITERM:05784	phosphate ABC transporter membrane protein 1, PhoT family (TC 3.A.1.7.1)		
2572232612	t3m_00968	Locus_type		CDS	
2572232612	t3m_00968	Product_name		phosphate ABC transporter membrane protein 1, PhoT family (TC 3.A.1.	
2572232612	t3m_00968	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18	
2572232612	t3m_00968	Coordinates		28548..29450(+)	
2572232612	t3m_00968	DNA_length		903bp	
2572232612	t3m_00968	Protein_length		300aa	
2572232612	t3m_00968	GC		0.64	
2572232612	t3m_00968	Transmembrane		Yes	
2572232613	t3m_00969	KEGG_module	M00222: Phosphate transport system		
2572232613	t3m_00969	COG_category	[P] Inorganic ion transport and metabolism		
2572232613	t3m_00969	COG0581	ABC-type phosphate transport system, permease component		9.00E-50
2572232613	t3m_00969	pfam00528	BPD_transp_1		1.70E-19
2572232613	t3m_00969	TIGR00974	phosphate ABC transporter, permease protein PstA		1.10E-74
2572232613	t3m_00969	KO:K02038	phosphate transport system permease protein		0.00E+00

2572232613	t3m_00969	ITERM:06114	phosphate ABC transporter membrane protein 2, PhoT family (TC 3.A.1.7.1)			
2572232613	t3m_00969	Locus_type		CDS		
2572232613	t3m_00969	Product_name		phosphate ABC transporter membrane protein 2, PhoT family (TC 3.A.1.		
2572232613	t3m_00969	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232613	t3m_00969	Coordinates		29447..30328(+)		
2572232613	t3m_00969	DNA_length		882bp		
2572232613	t3m_00969	Protein_length		293aa		
2572232613	t3m_00969	GC			0.63	
2572232613	t3m_00969	Transmembrane		Yes		
2572232614	t3m_00970	KEGG_module	M00222: Phosphate transport system			
2572232614	t3m_00970	COG_category	[P] Inorganic ion transport and metabolism			
2572232614	t3m_00970	COG1117	ABC-type phosphate transport system, ATPase component			2.00E-112
2572232614	t3m_00970	pfam00005	ABC_tran			1.90E-31
2572232614	t3m_00970	EC:3.6.3.27	Phosphate-transporting ATPase.			
2572232614	t3m_00970	TIGR00972	phosphate ABC transporter, ATP-binding protein			7.60E-116
2572232614	t3m_00970	KO:K02036	phosphate transport system ATP-binding protein [EC:3.6.3.27]			0.00E+00
2572232614	t3m_00970	ITERM:05785	phosphate ABC transporter ATP-binding protein, PhoT family (TC 3.A.1.7.1)			
2572232614	t3m_00970	Locus_type		CDS		
2572232614	t3m_00970	Product_name		phosphate ABC transporter ATP-binding protein, PhoT family (TC 3.A.1.7		
2572232614	t3m_00970	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232614	t3m_00970	Coordinates		30335..31090(+)		
2572232614	t3m_00970	DNA_length		756bp		
2572232614	t3m_00970	Protein_length		251aa		
2572232614	t3m_00970	GC			0.62	
2572232615	t3m_00971	COG_category	[P] Inorganic ion transport and metabolism			
2572232615	t3m_00971	COG0704	Phosphate uptake regulator			4.00E-27
2572232615	t3m_00971	pfam01895	PhoU			6.20E-15
2572232615	t3m_00971	pfam01895	PhoU			2.20E-10
2572232615	t3m_00971	TIGR02135	phosphate transport system regulatory protein PhoU			1.50E-41
2572232615	t3m_00971	KO:K02039	phosphate transport system protein			2.40E-23
2572232615	t3m_00971	Locus_type		CDS		
2572232615	t3m_00971	Product_name		Phosphate uptake regulator		

2572232615	t3m_00971	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232615	t3m_00971	Coordinates		31087..31848(+)		
2572232615	t3m_00971	DNA_length		762bp		
2572232615	t3m_00971	Protein_length		253aa		
2572232615	t3m_00971	GC			0.64	

2572232616	t3m_00972	Locus_type		tRNA		
2572232616	t3m_00972	Product_name		tRNA_Glu_TTC		
2572232616	t3m_00972	Scaffold		t3m_contig_70_149_len_32466_read_count_2958036.18		
2572232616	t3m_00972	Coordinates		32343..32442(+)		
2572232616	t3m_00972	DNA_length		77bp		
2572232616	t3m_00972	GC			0.62	

2572232617	t3m_00973	Metacyc	PWY-6891: thiazole biosynthesis II (Bacillus)			
2572232617	t3m_00973	Metacyc	PWY0-1021: alanine biosynthesis III			
2572232617	t3m_00973	Metacyc	PWY-6823: molybdenum cofactor biosynthesis			
2572232617	t3m_00973	Metacyc	PWY-6892: thiazole biosynthesis I (E. coli)			
2572232617	t3m_00973	COG_category	[E] Amino acid transport and metabolism			
2572232617	t3m_00973	COG0520	Selenocysteine lyase			5.00E-87
2572232617	t3m_00973	pfam00266	Aminotran_5			4.20E-90
2572232617	t3m_00973	EC:2.8.1.7	Cysteine desulfurase.			
2572232617	t3m_00973	EC:4.4.1.16	Selenocysteine lyase.			
2572232617	t3m_00973	KO:K11717	cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]			0.00E+00
2572232617	t3m_00973	Locus_type		CDS		
2572232617	t3m_00973	Product_name		Selenocysteine lyase		
2572232617	t3m_00973	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232617	t3m_00973	Coordinates		3..1049(-)		
2572232617	t3m_00973	DNA_length		1047bp		
2572232617	t3m_00973	Protein_length		349aa		
2572232617	t3m_00973	GC			0.71	

2572232618	t3m_00974	Metacyc	PWY-5665: vanilla biosynthesis			
2572232618	t3m_00974	Metacyc	PWY-5846: colchicine biosynthesis			
2572232618	t3m_00974	Metacyc	PWY-6984: lipoate salvage II			

2572232618	t3m_00974	Metacyc	PWY-6899: base-degraded thiamin salvage		
2572232618	t3m_00974	Metacyc	P621-PWY: nylon-6 oligomer degradation		
2572232618	t3m_00974	Metacyc	PWY-6431: 4-hydroxybenzoate biosynthesis IV		
2572232618	t3m_00974	Metacyc	PWY-1822: indole-3-acetate activation I		
2572232618	t3m_00974	Metacyc	PWY-5784: IAA conjugate biosynthesis II		
2572232618	t3m_00974	Metacyc	PWY-7018: paromomycin biosynthesis		
2572232618	t3m_00974	Metacyc	LYSDEGII-PWY: lysine degradation III		
2572232618	t3m_00974	Metacyc	PWY-6855: chitin degradation I (archaea)		
2572232618	t3m_00974	COG_category	[R] General function prediction only		
2572232618	t3m_00974	COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase		8.00E-103
2572232618	t3m_00974	pfam07687	M20_dimer		1.50E-13
2572232618	t3m_00974	pfam01546	Peptidase_M20		2.20E-22
2572232618	t3m_00974	EC:3.5.1.-	Hydrolases. Acting on carbon-nitrogen bonds, other than peptide bonds. In linear amides.		
2572232618	t3m_00974	TIGR01891	amidohydrolase		6.80E-107
2572232618	t3m_00974	KO:K01436	amidohydrolase [EC:3.5.1.-]		0.00E+00
2572232618	t3m_00974	Locus_type		CDS	
2572232618	t3m_00974	Product_name		amidohydrolase	
2572232618	t3m_00974	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232618	t3m_00974	Coordinates		1046..2242(-)	
2572232618	t3m_00974	DNA_length		1197bp	
2572232618	t3m_00974	Protein_length		398aa	
2572232618	t3m_00974	GC		0.7	

2572232619	t3m_00975	COG_category	[R] General function prediction only		
2572232619	t3m_00975	COG1011	Predicted hydrolase (HAD superfamily)		1.00E-29
2572232619	t3m_00975	pfam13419	HAD_2		2.00E-26
2572232619	t3m_00975	TIGR01509	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third m		5.70E-14
2572232619	t3m_00975	TIGR01549	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m		1.30E-17
2572232619	t3m_00975	KO:K07025	putative hydrolase of the HAD superfamily		2.70E-44
2572232619	t3m_00975	Locus_type		CDS	
2572232619	t3m_00975	Product_name		haloacid dehalogenase superfamily, subfamily IA, variant 3 with third m	
2572232619	t3m_00975	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232619	t3m_00975	Coordinates		2288..3061(-)	
2572232619	t3m_00975	DNA_length		774bp	

2572232619	t3m_00975	Protein_length		257aa	
2572232619	t3m_00975	GC		0.67	
2572232620	t3m_00976	Locus_type		CDS	
2572232620	t3m_00976	Product_name		hypothetical protein	
2572232620	t3m_00976	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232620	t3m_00976	Coordinates		4241..4807(-)	
2572232620	t3m_00976	DNA_length		567bp	
2572232620	t3m_00976	Protein_length		188aa	
2572232620	t3m_00976	GC		0.64	
2572232620	t3m_00976	Transmembrane		Yes	
2572232621	t3m_00977	Locus_type		CDS	
2572232621	t3m_00977	Product_name		hypothetical protein	
2572232621	t3m_00977	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232621	t3m_00977	Coordinates		5021..5758(-)	
2572232621	t3m_00977	DNA_length		738bp	
2572232621	t3m_00977	Protein_length		245aa	
2572232621	t3m_00977	GC		0.64	
2572232621	t3m_00977	Transmembrane		Yes	
2572232622	t3m_00978	Locus_type		CDS	
2572232622	t3m_00978	Product_name		hypothetical protein	
2572232622	t3m_00978	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232622	t3m_00978	Coordinates		6168..6809(-)	
2572232622	t3m_00978	DNA_length		642bp	
2572232622	t3m_00978	Protein_length		213aa	
2572232622	t3m_00978	GC		0.62	
2572232623	t3m_00979	COG_category	[R] General function prediction only		
2572232623	t3m_00979	COG_category	[C] Energy production and conversion		
2572232623	t3m_00979	COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases		5.00E-60
2572232623	t3m_00979	pfam13602	ADH_zinc_N_2		2.40E-27
2572232623	t3m_00979	pfam08240	ADH_N		1.00E-07

2572232623	t3m_00979	Locus_type		CDS	
2572232623	t3m_00979	Product_name		NADPH:quinone reductase and related Zn-dependent oxidoreductases	
2572232623	t3m_00979	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232623	t3m_00979	Coordinates		6860..7822(-)	
2572232623	t3m_00979	DNA_length		963bp	
2572232623	t3m_00979	Protein_length		320aa	
2572232623	t3m_00979	GC		0.6	
2572232624	t3m_00980	Locus_type		CDS	
2572232624	t3m_00980	Product_name		hypothetical protein	
2572232624	t3m_00980	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232624	t3m_00980	Coordinates		8151..8360(+)	
2572232624	t3m_00980	DNA_length		210bp	
2572232624	t3m_00980	Protein_length		69aa	
2572232624	t3m_00980	GC		0.61	
2572232624	t3m_00980	Transmembrane		Yes	
2572232625	t3m_00981	pfam01548	DEDD_Tnp_IS110		5.50E-11
2572232625	t3m_00981	Locus_type		CDS	
2572232625	t3m_00981	Product_name		Transposase	
2572232625	t3m_00981	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232625	t3m_00981	Coordinates		8517..8789(+)	
2572232625	t3m_00981	DNA_length		273bp	
2572232625	t3m_00981	Protein_length		90aa	
2572232625	t3m_00981	GC		0.63	
2572232626	t3m_00982	pfam02371	Transposase_20		2.40E-21
2572232626	t3m_00982	Locus_type		CDS	
2572232626	t3m_00982	Product_name		Transposase IS116/IS110/IS902 family	
2572232626	t3m_00982	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232626	t3m_00982	Coordinates		8802..9551(+)	
2572232626	t3m_00982	DNA_length		750bp	
2572232626	t3m_00982	Protein_length		249aa	
2572232626	t3m_00982	GC		0.63	

2572232627	t3m_00983	pfam13673	Acetyltransf_10			3.90E-12
2572232627	t3m_00983	Locus_type		CDS		
2572232627	t3m_00983	Product_name		Acetyltransferase (GNAT) domain		
2572232627	t3m_00983	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232627	t3m_00983	Coordinates		9769..10551(-)		
2572232627	t3m_00983	DNA_length		783bp		
2572232627	t3m_00983	Protein_length		260aa		
2572232627	t3m_00983	GC			0.65	
2572232628	t3m_00984	Locus_type		CDS		
2572232628	t3m_00984	Product_name		hypothetical protein		
2572232628	t3m_00984	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232628	t3m_00984	Coordinates		10703..10924(-)		
2572232628	t3m_00984	DNA_length		222bp		
2572232628	t3m_00984	Protein_length		73aa		
2572232628	t3m_00984	GC			0.64	
2572232628	t3m_00984	Transmembrane		Yes		
2572232629	t3m_00985	COG_category	[E] Amino acid transport and metabolism			
2572232629	t3m_00985	COG0308	Aminopeptidase N			1.00E-108
2572232629	t3m_00985	pfam11838	ERAP1_C			2.20E-27
2572232629	t3m_00985	pfam01433	Peptidase_M1			2.70E-86
2572232629	t3m_00985	EC:3.4.11.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Aminopeptidases.			
2572232629	t3m_00985	KO:K13722	tricorn protease interacting factor F2/3 [EC:3.4.11.-]			0.00E+00
2572232629	t3m_00985	Locus_type		CDS		
2572232629	t3m_00985	Product_name		Aminopeptidase N		
2572232629	t3m_00985	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232629	t3m_00985	Coordinates		11009..13423(-)		
2572232629	t3m_00985	DNA_length		2415bp		
2572232629	t3m_00985	Protein_length		804aa		
2572232629	t3m_00985	GC			0.66	
2572232630	t3m_00986	Locus_type		CDS		

2572232630	t3m_00986	Product_name		hypothetical protein		
2572232630	t3m_00986	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232630	t3m_00986	Coordinates		13444..13584(+)		
2572232630	t3m_00986	DNA_length		141bp		
2572232630	t3m_00986	Protein_length		46aa		
2572232630	t3m_00986	GC			0.67	
2572232631	t3m_00987	pfam02010	REJ			2.70E-05
2572232631	t3m_00987	Locus_type		CDS		
2572232631	t3m_00987	Product_name		REJ domain		
2572232631	t3m_00987	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232631	t3m_00987	Coordinates		13842..20969(+)		
2572232631	t3m_00987	DNA_length		7128bp		
2572232631	t3m_00987	Protein_length		2375aa		
2572232631	t3m_00987	GC			0.67	
2572232631	t3m_00987	Signal_peptide		Yes		
2572232631	t3m_00987	Transmembrane		Yes		
2572232632	t3m_00988	KEGG_module	M00248: Putative antibiotic transport system			
2572232632	t3m_00988	pfam01061	ABC2_membrane			1.90E-17
2572232632	t3m_00988	KO:K09686	antibiotic transport system permease protein			0.00E+00
2572232632	t3m_00988	Locus_type		CDS		
2572232632	t3m_00988	Product_name		ABC-2 type transporter		
2572232632	t3m_00988	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232632	t3m_00988	Coordinates		21033..21800(-)		
2572232632	t3m_00988	DNA_length		768bp		
2572232632	t3m_00988	Protein_length		255aa		
2572232632	t3m_00988	GC			0.64	
2572232632	t3m_00988	Transmembrane		Yes		
2572232633	t3m_00989	KEGG_module	M00254: ABC-2 type transport system			
2572232633	t3m_00989	COG_category	[V] Defense mechanisms			
2572232633	t3m_00989	COG1131	ABC-type multidrug transport system, ATPase component			2.00E-69
2572232633	t3m_00989	pfam00005	ABC_tran			1.00E-31

2572232633	t3m_00989	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2572232633	t3m_00989	Locus_type		CDS	
2572232633	t3m_00989	Product_name		ABC-type multidrug transport system, ATPase component	
2572232633	t3m_00989	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232633	t3m_00989	Coordinates		21787..22782(-)	
2572232633	t3m_00989	DNA_length		996bp	
2572232633	t3m_00989	Protein_length		331aa	
2572232633	t3m_00989	GC		0.66	
2572232634	t3m_00990	pfam00583	Acetyltransf_1		1.70E-14
2572232634	t3m_00990	Locus_type		CDS	
2572232634	t3m_00990	Product_name		Acetyltransferase (GNAT) family	
2572232634	t3m_00990	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232634	t3m_00990	Coordinates		22960..23403(-)	
2572232634	t3m_00990	DNA_length		444bp	
2572232634	t3m_00990	Protein_length		147aa	
2572232634	t3m_00990	GC		0.65	
2572232635	t3m_00991	COG_category	[G] Carbohydrate transport and metabolism		
2572232635	t3m_00991	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Prote		3.00E-33
2572232635	t3m_00991	pfam00230	MIP		8.20E-46
2572232635	t3m_00991	TIGR00861	MIP family channel proteins		1.60E-48
2572232635	t3m_00991	KO:K06188	aquaporin Z		0.00E+00
2572232635	t3m_00991	Locus_type		CDS	
2572232635	t3m_00991	Product_name		Glycerol uptake facilitator and related permeases (Major Intrinsic Protei	
2572232635	t3m_00991	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19	
2572232635	t3m_00991	Coordinates		23779..24675(+)	
2572232635	t3m_00991	DNA_length		897bp	
2572232635	t3m_00991	Protein_length		298aa	
2572232635	t3m_00991	GC		0.68	
2572232635	t3m_00991	Transmembrane		Yes	
2572232636	t3m_00992	COG_category	[S] Function unknown		
2572232636	t3m_00992	COG2326	Uncharacterized conserved protein		3.00E-67

2572232636	t3m_00992	pfam03976	PPK2			2.20E-75
2572232636	t3m_00992	TIGR03709	polyphosphate:nucleotide phosphotransferase, PPK2 family			3.70E-114
2572232636	t3m_00992	Locus_type		CDS		
2572232636	t3m_00992	Product_name		Polyphosphate:AMP phosphotransferase (EC 2.7.4.-)		
2572232636	t3m_00992	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232636	t3m_00992	Coordinates		24672..25487(+)		
2572232636	t3m_00992	DNA_length		816bp		
2572232636	t3m_00992	Protein_length		271aa		
2572232636	t3m_00992	GC			0.65	
2572232637	t3m_00993	Locus_type		CDS		
2572232637	t3m_00993	Product_name		hypothetical protein		
2572232637	t3m_00993	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232637	t3m_00993	Coordinates		25830..27041(-)		
2572232637	t3m_00993	DNA_length		1212bp		
2572232637	t3m_00993	Protein_length		403aa		
2572232637	t3m_00993	GC			0.66	
2572232638	t3m_00994	pfam04967	HTH_10			1.40E-11
2572232638	t3m_00994	Locus_type		CDS		
2572232638	t3m_00994	Product_name		HTH DNA binding domain		
2572232638	t3m_00994	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232638	t3m_00994	Coordinates		27127..27753(-)		
2572232638	t3m_00994	DNA_length		627bp		
2572232638	t3m_00994	Protein_length		208aa		
2572232638	t3m_00994	GC			0.59	
2572232639	t3m_00995	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232639	t3m_00995	COG0443	Molecular chaperone			0.00E+00
2572232639	t3m_00995	pfam00012	HSP70			0.00E+00
2572232639	t3m_00995	pfam00012	HSP70			6.50E-11
2572232639	t3m_00995	TIGR02350	chaperone protein DnaK			0.00E+00
2572232639	t3m_00995	KO:K04043	molecular chaperone DnaK			0.00E+00
2572232639	t3m_00995	Locus_type		CDS		

2572232639	t3m_00995	Product_name		chaperone protein DnaK		
2572232639	t3m_00995	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232639	t3m_00995	Coordinates		28285..30135(+)		
2572232639	t3m_00995	DNA_length		1851bp		
2572232639	t3m_00995	Protein_length		616aa		
2572232639	t3m_00995	GC			0.67	
2572232640	t3m_00996	KEGG_module	M00012: Glyoxylate cycle			
2572232640	t3m_00996	KEGG_module	M00010: Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate			
2572232640	t3m_00996	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)			
2572232640	t3m_00996	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)			
2572232640	t3m_00996	Metacyc	REDCITCYC: TCA cycle III (helicobacter)			
2572232640	t3m_00996	Metacyc	P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)			
2572232640	t3m_00996	Metacyc	ANARESP1-PWY: respiration (anaerobic)			
2572232640	t3m_00996	Metacyc	PWY-6549: glutamine biosynthesis III			
2572232640	t3m_00996	Metacyc	PWY-5690: TCA cycle II (eukaryotic)			
2572232640	t3m_00996	Metacyc	PWY-5750: itaconate biosynthesis			
2572232640	t3m_00996	Metacyc	FERMENTATION-PWY: mixed acid fermentation			
2572232640	t3m_00996	Metacyc	TCA: TCA cycle I (prokaryotic)			
2572232640	t3m_00996	Metacyc	PWY-6728: methylaspartate cycle			
2572232640	t3m_00996	Metacyc	GLYOXYLATE-BYPASS: glyoxylate cycle			
2572232640	t3m_00996	Metacyc	PWY-7124: ethylene biosynthesis V			
2572232640	t3m_00996	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572232640	t3m_00996	COG_category	[C] Energy production and conversion			
2572232640	t3m_00996	COG0372	Citrate synthase			2.00E-86
2572232640	t3m_00996	pfam00285	Citrate_synt			9.90E-104
2572232640	t3m_00996	EC:2.3.3.1	Citrate (Si)-synthase.			
2572232640	t3m_00996	KO:K01647	citrate synthase [EC:2.3.3.1]			0.00E+00
2572232640	t3m_00996	Locus_type		CDS		
2572232640	t3m_00996	Product_name		Citrate synthase		
2572232640	t3m_00996	Scaffold		t3m_contig_70_156_len_31387_read_count_2567722.19		
2572232640	t3m_00996	Coordinates		30148..31275(-)		
2572232640	t3m_00996	DNA_length		1128bp		
2572232640	t3m_00996	Protein_length		375aa		

2572232640	t3m_00996	GC			0.72	

2572232641	t3m_00997	pfam08241	Methyltransf_11			6.20E-23
2572232641	t3m_00997	Locus_type		CDS		
2572232641	t3m_00997	Product_name		Methyltransferase domain		
2572232641	t3m_00997	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232641	t3m_00997	Coordinates		807..1430(+)		
2572232641	t3m_00997	DNA_length		624bp		
2572232641	t3m_00997	Protein_length		207aa		
2572232641	t3m_00997	GC			0.65	

2572232642	t3m_00998	KEGG_module	M00264: DNA polymerase II complex, archaea			
2572232642	t3m_00998	COG_category	[L] Replication, recombination and repair			
2572232642	t3m_00998	COG1933	Archaeal DNA polymerase II, large subunit			9.00E-80
2572232642	t3m_00998	pfam03833	PolC_DP2			0.00E+00
2572232642	t3m_00998	EC:2.7.7.7	DNA-directed DNA polymerase.			
2572232642	t3m_00998	TIGR00354	DNA polymerase, archaeal type II, large subunit			0.00E+00
2572232642	t3m_00998	KO:K02322	DNA polymerase II large subunit [EC:2.7.7.7]			0.00E+00
2572232642	t3m_00998	ITERM:00108	DNA polymerase II large subunit (EC 2.7.7.7)			
2572232642	t3m_00998	Locus_type		CDS		
2572232642	t3m_00998	Product_name		DNA polymerase II large subunit (EC 2.7.7.7)		
2572232642	t3m_00998	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232642	t3m_00998	Coordinates		1539..4943(+)		
2572232642	t3m_00998	DNA_length		3405bp		
2572232642	t3m_00998	Protein_length		1134aa		
2572232642	t3m_00998	GC			0.69	

2572232643	t3m_00999	Locus_type		CDS		
2572232643	t3m_00999	Product_name		hypothetical protein		
2572232643	t3m_00999	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232643	t3m_00999	Coordinates		5088..5393(-)		
2572232643	t3m_00999	DNA_length		306bp		
2572232643	t3m_00999	Protein_length		101aa		
2572232643	t3m_00999	GC			0.7	

2572232644	t3m_01000	Locus_type		CDS	
2572232644	t3m_01000	Product_name		hypothetical protein	
2572232644	t3m_01000	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20	
2572232644	t3m_01000	Coordinates		5390..5911(-)	
2572232644	t3m_01000	DNA_length		522bp	
2572232644	t3m_01000	Protein_length		173aa	
2572232644	t3m_01000	GC		0.66	
2572232645	t3m_01001	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572232645	t3m_01001	Metacyc	PWY-6720: toyocamycin biosynthesis		
2572232645	t3m_01001	COG_category	[R] General function prediction only		
2572232645	t3m_01001	COG1759	ATP-utilizing enzymes of ATP-grasp superfamily (probably carboligases)		1.00E-110
2572232645	t3m_01001	pfam06849	DUF1246		4.70E-34
2572232645	t3m_01001	pfam06973	DUF1297		2.30E-70
2572232645	t3m_01001	EC:6.3.4.-	Ligases. Forming carbon-nitrogen bonds. Other carbon--nitrogen ligases.		
2572232645	t3m_01001	KO:K06863	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuranosyl 5'-mon		0.00E+00
2572232645	t3m_01001	Locus_type		CDS	
2572232645	t3m_01001	Product_name		ATP-utilizing enzymes of ATP-grasp superfamily (probably carboligases)	
2572232645	t3m_01001	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20	
2572232645	t3m_01001	Coordinates		6139..7296(+)	
2572232645	t3m_01001	DNA_length		1158bp	
2572232645	t3m_01001	Protein_length		385aa	
2572232645	t3m_01001	GC		0.68	
2572232646	t3m_01002	Metacyc	GLYCLEAV-PWY: glycine cleavage		
2572232646	t3m_01002	COG_category	[E] Amino acid transport and metabolism		
2572232646	t3m_01002	COG0404	Glycine cleavage system T protein (aminomethyltransferase)		9.00E-91
2572232646	t3m_01002	pfam01571	GCV_T		2.30E-57
2572232646	t3m_01002	pfam08669	GCV_T_C		3.90E-23
2572232646	t3m_01002	EC:2.1.2.10	Aminomethyltransferase.		
2572232646	t3m_01002	TIGR00528	glycine cleavage system T protein		2.20E-92
2572232646	t3m_01002	KO:K00605	aminomethyltransferase [EC:2.1.2.10]		0.00E+00
2572232646	t3m_01002	Locus_type		CDS	

2572232646	t3m_01002	Product_name		glycine cleavage system T protein		
2572232646	t3m_01002	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232646	t3m_01002	Coordinates		7293..8471(+)		
2572232646	t3m_01002	DNA_length		1179bp		
2572232646	t3m_01002	Protein_length		392aa		
2572232646	t3m_01002	GC			0.69	
2572232647	t3m_01003	pfam13191	AAA_16			1.60E-19
2572232647	t3m_01003	Locus_type		CDS		
2572232647	t3m_01003	Product_name		AAA ATPase domain		
2572232647	t3m_01003	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232647	t3m_01003	Coordinates		8506..10887(+)		
2572232647	t3m_01003	DNA_length		2382bp		
2572232647	t3m_01003	Protein_length		793aa		
2572232647	t3m_01003	GC			0.71	
2572232648	t3m_01004	KEGG_module	M00115: NAD biosynthesis, aspartate => NAD			
2572232648	t3m_01004	Metacyc	PYRIDNUCSYN-PWY: NAD biosynthesis I (from aspartate)			
2572232648	t3m_01004	Metacyc	PWY-5316: nicotine biosynthesis			
2572232648	t3m_01004	Metacyc	PWY-5653: NAD biosynthesis from 2-amino-3-carboxymuconate semialdehyde			
2572232648	t3m_01004	IMG_pathway	212: Deamido-NAD biosynthesis			
2572232648	t3m_01004	COG_category	[H] Coenzyme transport and metabolism			
2572232648	t3m_01004	COG0157	Nicotinate-nucleotide pyrophosphorylase			2.00E-63
2572232648	t3m_01004	pfam01729	QRPTase_C			4.20E-42
2572232648	t3m_01004	pfam02749	QRPTase_N			1.50E-20
2572232648	t3m_01004	EC:2.4.2.19	Nicotinate-nucleotide diphosphorylase (carboxylating).			
2572232648	t3m_01004	TIGR00078	nicotinate-nucleotide pyrophosphorylase			2.10E-79
2572232648	t3m_01004	KO:K00767	nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19]			0.00E+00
2572232648	t3m_01004	ITERM:00563	nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 2.4.2.19)			
2572232648	t3m_01004	Locus_type		CDS		
2572232648	t3m_01004	Product_name		nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 2.4.2.19)		
2572232648	t3m_01004	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232648	t3m_01004	Coordinates		10817..11761(+)		
2572232648	t3m_01004	DNA_length		945bp		

2572232648	t3m_01004	Protein_length		314aa		
2572232648	t3m_01004	GC			0.73	

2572232649	t3m_01005	KEGG_module	M00115: NAD biosynthesis, aspartate => NAD			
2572232649	t3m_01005	Metacyc	PWY-5316: nicotine biosynthesis			
2572232649	t3m_01005	Metacyc	PYRIDNUCSYN-PWY: NAD biosynthesis I (from aspartate)			
2572232649	t3m_01005	IMG_pathway	210: Quinolinate biosynthesis via aspartate			
2572232649	t3m_01005	COG_category	[H] Coenzyme transport and metabolism			
2572232649	t3m_01005	COG0379	Quinolinate synthase			6.00E-107
2572232649	t3m_01005	pfam02445	NadA			1.10E-113
2572232649	t3m_01005	EC:2.5.1.72	Quinolinate synthase.			
2572232649	t3m_01005	TIGR00550	quinolinate synthetase complex, A subunit			2.00E-100
2572232649	t3m_01005	KO:K03517	quinolinate synthase [EC:2.5.1.72]			0.00E+00
2572232649	t3m_01005	ITERM:00562	quinolinate synthetase (EC 2.5.1.72)			
2572232649	t3m_01005	Locus_type		CDS		
2572232649	t3m_01005	Product_name		quinolinate synthetase (EC 2.5.1.72)		
2572232649	t3m_01005	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232649	t3m_01005	Coordinates		11777..12682(+)		
2572232649	t3m_01005	DNA_length		906bp		
2572232649	t3m_01005	Protein_length		301aa		
2572232649	t3m_01005	GC			0.68	

2572232650	t3m_01006	Locus_type		CDS		
2572232650	t3m_01006	Product_name		hypothetical protein		
2572232650	t3m_01006	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232650	t3m_01006	Coordinates		12692..13057(-)		
2572232650	t3m_01006	DNA_length		366bp		
2572232650	t3m_01006	Protein_length		121aa		
2572232650	t3m_01006	GC			0.68	
2572232650	t3m_01006	Transmembrane		Yes		

2572232651	t3m_01007	COG_category	[L] Replication, recombination and repair			
2572232651	t3m_01007	COG1796	DNA polymerase IV (family X)			6.00E-87
2572232651	t3m_01007	pfam14792	DNA_pol_B_palm			1.40E-05

2572232651	t3m_01007	pfam14716	HHH_8			4.00E-18
2572232651	t3m_01007	pfam14520	HHH_5			2.20E-07
2572232651	t3m_01007	pfam14791	DNA_pol_B_thumb			1.60E-25
2572232651	t3m_01007	KO:K02347	DNA polymerase (family X)			0.00E+00
2572232651	t3m_01007	Locus_type		CDS		
2572232651	t3m_01007	Product_name		DNA polymerase IV (family X)		
2572232651	t3m_01007	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232651	t3m_01007	Coordinates		13430..15151(-)		
2572232651	t3m_01007	DNA_length		1722bp		
2572232651	t3m_01007	Protein_length		573aa		
2572232651	t3m_01007	GC			0.72	
2572232652	t3m_01008	pfam00583	Acetyltransf_1			1.20E-15
2572232652	t3m_01008	Locus_type		CDS		
2572232652	t3m_01008	Product_name		Acetyltransferase (GNAT) family		
2572232652	t3m_01008	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232652	t3m_01008	Coordinates		15207..15998(-)		
2572232652	t3m_01008	DNA_length		792bp		
2572232652	t3m_01008	Protein_length		263aa		
2572232652	t3m_01008	GC			0.7	
2572232653	t3m_01009	pfam09674	DUF2400			7.00E-46
2572232653	t3m_01009	TIGR02757	TIGR02757 family protein			6.40E-43
2572232653	t3m_01009	Locus_type		CDS		
2572232653	t3m_01009	Product_name		Protein of unknown function (DUF2400)		
2572232653	t3m_01009	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232653	t3m_01009	Coordinates		16099..16986(+)		
2572232653	t3m_01009	DNA_length		888bp		
2572232653	t3m_01009	Protein_length		295aa		
2572232653	t3m_01009	GC			0.7	
2572232654	t3m_01010	Locus_type		CDS		
2572232654	t3m_01010	Product_name		hypothetical protein		
2572232654	t3m_01010	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		

2572232654	t3m_01010	Coordinates		16983..17390(+)		
2572232654	t3m_01010	DNA_length		408bp		
2572232654	t3m_01010	Protein_length		135aa		
2572232654	t3m_01010	GC			0.74	

2572232655	t3m_01011	COG_category	[K] Transcription			
2572232655	t3m_01011	COG1846	Transcriptional regulators			6.00E-13
2572232655	t3m_01011	pfam01047	MarR			6.70E-12
2572232655	t3m_01011	Locus_type		CDS		
2572232655	t3m_01011	Product_name		Transcriptional regulators		
2572232655	t3m_01011	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232655	t3m_01011	Coordinates		17447..17935(+)		
2572232655	t3m_01011	DNA_length		489bp		
2572232655	t3m_01011	Protein_length		162aa		
2572232655	t3m_01011	GC			0.68	

2572232656	t3m_01012	pfam07690	MFS_1			2.30E-15
2572232656	t3m_01012	pfam07690	MFS_1			1.30E-27
2572232656	t3m_01012	Locus_type		CDS		
2572232656	t3m_01012	Product_name		Major Facilitator Superfamily		
2572232656	t3m_01012	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232656	t3m_01012	Coordinates		17932..19545(+)		
2572232656	t3m_01012	DNA_length		1614bp		
2572232656	t3m_01012	Protein_length		537aa		
2572232656	t3m_01012	GC			0.67	
2572232656	t3m_01012	Transmembrane		Yes		

2572232657	t3m_01013	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP
2572232657	t3m_01013	Metacyc	PWY-7198: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis IV
2572232657	t3m_01013	Metacyc	PWY0-166: superpathway of pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis (E. coli
2572232657	t3m_01013	Metacyc	PWY-7184: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis I
2572232657	t3m_01013	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis
2572232657	t3m_01013	Metacyc	PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP
2572232657	t3m_01013	Metacyc	PWY-6545: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis III

2572232657	t3m_01013	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis		
2572232657	t3m_01013	COG_category	[F] Nucleotide transport and metabolism		
2572232657	t3m_01013	COG0209	Ribonucleotide reductase, alpha subunit		3.00E-83
2572232657	t3m_01013	pfam08471	Ribonuc_red_2_N		2.10E-15
2572232657	t3m_01013	pfam00317	Ribonuc_red_lgN		3.20E-05
2572232657	t3m_01013	pfam12637	TSCPD		3.90E-20
2572232657	t3m_01013	pfam02867	Ribonuc_red_lgC		0.00E+00
2572232657	t3m_01013	EC:1.17.4.1	Ribonucleoside-diphosphate reductase.		
2572232657	t3m_01013	TIGR02504	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent		0.00E+00
2572232657	t3m_01013	KO:K00525	ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]		0.00E+00
2572232657	t3m_01013	ITERM:00726	ribonucleoside-diphosphate reductase class II (EC 1.17.4.-)		
2572232657	t3m_01013	Locus_type		CDS	
2572232657	t3m_01013	Product_name		ribonucleoside-diphosphate reductase class II (EC 1.17.4.-)	
2572232657	t3m_01013	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20	
2572232657	t3m_01013	Coordinates		19570..22359(-)	
2572232657	t3m_01013	DNA_length		2790bp	
2572232657	t3m_01013	Protein_length		929aa	
2572232657	t3m_01013	GC		0.68	
2572232658	t3m_01014	Locus_type		CDS	
2572232658	t3m_01014	Product_name		hypothetical protein	
2572232658	t3m_01014	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20	
2572232658	t3m_01014	Coordinates		22708..23730(+)	
2572232658	t3m_01014	DNA_length		1023bp	
2572232658	t3m_01014	Protein_length		340aa	
2572232658	t3m_01014	GC		0.69	
2572232658	t3m_01014	Transmembrane		Yes	
2572232659	t3m_01015	Locus_type		CDS	
2572232659	t3m_01015	Product_name		hypothetical protein	
2572232659	t3m_01015	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20	
2572232659	t3m_01015	Coordinates		23867..24082(-)	
2572232659	t3m_01015	DNA_length		216bp	
2572232659	t3m_01015	Protein_length		71aa	

2572232659	t3m_01015	GC			0.54	
2572232660	t3m_01016	KEGG_module	M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate			
2572232660	t3m_01016	Metacyc	PWY-5030: histidine degradation III			
2572232660	t3m_01016	Metacyc	PWY-5028: histidine degradation II			
2572232660	t3m_01016	Metacyc	HISDEG-PWY: histidine degradation I			
2572232660	t3m_01016	Metacyc	HISHP-PWY: histidine degradation VI			
2572232660	t3m_01016	IMG_pathway	189: L-histidine degradation to L-glutamate and formamide			
2572232660	t3m_01016	IMG_pathway	190: L-histidine degradation to L-glutamate and formiminotetrahydrofolate			
2572232660	t3m_01016	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2572232660	t3m_01016	COG1228	Imidazolonepropionase and related amidohydrolases			1.00E-67
2572232660	t3m_01016	pfam13147	Amidohydro_4			1.20E-18
2572232660	t3m_01016	EC:3.5.2.7	Imidazolonepropionase.			
2572232660	t3m_01016	TIGR01224	imidazolonepropionase			4.10E-120
2572232660	t3m_01016	KO:K01468	imidazolonepropionase [EC:3.5.2.7]			0.00E+00
2572232660	t3m_01016	ITERM:00502	imidazolonepropionase (EC 3.5.2.7)			
2572232660	t3m_01016	Locus_type		CDS		
2572232660	t3m_01016	Product_name		imidazolonepropionase (EC 3.5.2.7)		
2572232660	t3m_01016	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232660	t3m_01016	Coordinates		24121..25392(-)		
2572232660	t3m_01016	DNA_length		1272bp		
2572232660	t3m_01016	Protein_length		423aa		
2572232660	t3m_01016	GC			0.72	
2572232661	t3m_01017	COG_category	[R] General function prediction only			
2572232661	t3m_01017	COG1234	Metal-dependent hydrolases of the beta-lactamase superfamily III			6.00E-73
2572232661	t3m_01017	pfam12706	Lactamase_B_2			4.50E-30
2572232661	t3m_01017	EC:3.1.26.11	Ribonuclease Z.			
2572232661	t3m_01017	TIGR02651	ribonuclease Z			9.80E-101
2572232661	t3m_01017	KO:K00784	ribonuclease Z [EC:3.1.26.11]			0.00E+00
2572232661	t3m_01017	Locus_type		CDS		
2572232661	t3m_01017	Product_name		ribonuclease Z		
2572232661	t3m_01017	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232661	t3m_01017	Coordinates		25389..26291(-)		

2572232661	t3m_01017	DNA_length		903bp		
2572232661	t3m_01017	Protein_length		300aa		
2572232661	t3m_01017	GC			0.69	

2572232662	t3m_01018	pfam06053	DUF929			1.10E-08
2572232662	t3m_01018	Locus_type		CDS		
2572232662	t3m_01018	Product_name		Domain of unknown function (DUF929)		
2572232662	t3m_01018	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232662	t3m_01018	Coordinates		26403..27575(+)		
2572232662	t3m_01018	DNA_length		1173bp		
2572232662	t3m_01018	Protein_length		390aa		
2572232662	t3m_01018	GC			0.65	
2572232662	t3m_01018	Transmembrane		Yes		

2572232663	t3m_01019	COG_category	[S] Function unknown			
2572232663	t3m_01019	COG4243	Predicted membrane protein			4.00E-12
2572232663	t3m_01019	pfam07884	VKOR			4.70E-24
2572232663	t3m_01019	Locus_type		CDS		
2572232663	t3m_01019	Product_name		Predicted membrane protein		
2572232663	t3m_01019	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232663	t3m_01019	Coordinates		27585..28073(+)		
2572232663	t3m_01019	DNA_length		489bp		
2572232663	t3m_01019	Protein_length		162aa		
2572232663	t3m_01019	GC			0.66	
2572232663	t3m_01019	Transmembrane		Yes		

2572232664	t3m_01020	KEGG_module	M00159: V-type ATPase, prokaryotes			
2572232664	t3m_01020	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2572232664	t3m_01020	pfam00137	ATP-synt_C			2.60E-15
2572232664	t3m_01020	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2572232664	t3m_01020	KO:K02124	V-type H+-transporting ATPase subunit K [EC:3.6.3.14]			4.10E-27
2572232664	t3m_01020	Locus_type		CDS		
2572232664	t3m_01020	Product_name		ATP synthase subunit C		
2572232664	t3m_01020	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		

2572232664	t3m_01020	Coordinates		28153..28371(+)		
2572232664	t3m_01020	DNA_length		219bp		
2572232664	t3m_01020	Protein_length		72aa		
2572232664	t3m_01020	GC			0.62	
2572232664	t3m_01020	Transmembrane		Yes		
2572232665	t3m_01021	COG_category	[C] Energy production and conversion			
2572232665	t3m_01021	COG1390	Archaeal/vacuolar-type H+-ATPase subunit E			2.00E-11
2572232665	t3m_01021	pfam01991	vATP-synt_E			1.10E-12
2572232665	t3m_01021	Locus_type		CDS		
2572232665	t3m_01021	Product_name		Archaeal/vacuolar-type H+-ATPase subunit E		
2572232665	t3m_01021	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232665	t3m_01021	Coordinates		28389..28940(+)		
2572232665	t3m_01021	DNA_length		552bp		
2572232665	t3m_01021	Protein_length		183aa		
2572232665	t3m_01021	GC			0.7	
2572232666	t3m_01022	KEGG_module	M00159: V-type ATPase, prokaryotes			
2572232666	t3m_01022	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2572232666	t3m_01022	COG_category	[C] Energy production and conversion			
2572232666	t3m_01022	COG1527	Archaeal/vacuolar-type H+-ATPase subunit C			1.00E-44
2572232666	t3m_01022	pfam01992	vATP-synt_AC39			4.70E-31
2572232666	t3m_01022	EC:3.6.3.14	H(+)-transporting two-sector ATPase.			
2572232666	t3m_01022	KO:K02119	V-type H+-transporting ATPase subunit C [EC:3.6.3.14]			0.00E+00
2572232666	t3m_01022	Locus_type		CDS		
2572232666	t3m_01022	Product_name		Archaeal/vacuolar-type H+-ATPase subunit C		
2572232666	t3m_01022	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232666	t3m_01022	Coordinates		28950..30026(+)		
2572232666	t3m_01022	DNA_length		1077bp		
2572232666	t3m_01022	Protein_length		358aa		
2572232666	t3m_01022	GC			0.68	
2572232667	t3m_01023	pfam01496	V_ATPase_I			3.40E-20
2572232667	t3m_01023	pfam01496	V_ATPase_I			1.60E-21

2572232667	t3m_01023	Locus_type		CDS		
2572232667	t3m_01023	Product_name		V-type ATPase 116kDa subunit family		
2572232667	t3m_01023	Scaffold		t3m_contig_70_157_len_31137_read_count_2595890.20		
2572232667	t3m_01023	Coordinates		30047..31135(-)		
2572232667	t3m_01023	DNA_length		1089bp		
2572232667	t3m_01023	Protein_length		362aa		
2572232667	t3m_01023	GC			0.66	
2572232667	t3m_01023	Transmembrane		Yes		
2572232668	t3m_01024	COG_category	[K] Transcription			
2572232668	t3m_01024	COG1958	Small nuclear ribonucleoprotein (snRNP) homolog			2.00E-13
2572232668	t3m_01024	pfam01423	LSM			1.10E-18
2572232668	t3m_01024	KO:K04796	small nuclear ribonucleoprotein			1.30E-13
2572232668	t3m_01024	ITERM:05216	Small nuclear ribonucleoprotein, LSM family			
2572232668	t3m_01024	Locus_type		CDS		
2572232668	t3m_01024	Product_name		Small nuclear ribonucleoprotein, LSM family		
2572232668	t3m_01024	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232668	t3m_01024	Coordinates		279..521(+)		
2572232668	t3m_01024	DNA_length		243bp		
2572232668	t3m_01024	Protein_length		80aa		
2572232668	t3m_01024	GC			0.67	
2572232669	t3m_01025	Metacyc	PWY-6167: flavin biosynthesis II (archaea)			
2572232669	t3m_01025	COG_category	[H] Coenzyme transport and metabolism			
2572232669	t3m_01025	COG_category	[K] Transcription			
2572232669	t3m_01025	COG1339	Transcriptional regulator of a riboflavin/FAD biosynthetic operon			8.00E-50
2572232669	t3m_01025	pfam01982	CTP-dep_RFKase			2.90E-38
2572232669	t3m_01025	EC:2.7.1.161	CTP-dependent riboflavin kinase.			
2572232669	t3m_01025	KO:K07732	riboflavin kinase, archaea type [EC:2.7.1.161]			9.20E-44
2572232669	t3m_01025	Locus_type		CDS		
2572232669	t3m_01025	Product_name		Transcriptional regulator of a riboflavin/FAD biosynthetic operon		
2572232669	t3m_01025	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232669	t3m_01025	Coordinates		521..1225(+)		
2572232669	t3m_01025	DNA_length		705bp		

2572232669	t3m_01025	Protein_length		234aa		
2572232669	t3m_01025	GC			0.68	
2572232670	t3m_01026	COG_category	[R] General function prediction only			
2572232670	t3m_01026	COG1244	Predicted Fe-S oxidoreductase			8.00E-85
2572232670	t3m_01026	pfam04055	Radical_SAM			5.30E-07
2572232670	t3m_01026	TIGR01210	TIGR01210 family protein			2.70E-92
2572232670	t3m_01026	Locus_type		CDS		
2572232670	t3m_01026	Product_name		TIGR01210 family protein		
2572232670	t3m_01026	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232670	t3m_01026	Coordinates		1222..2244(+)		
2572232670	t3m_01026	DNA_length		1023bp		
2572232670	t3m_01026	Protein_length		340aa		
2572232670	t3m_01026	GC			0.71	
2572232671	t3m_01027	KEGG_module	M00115: NAD biosynthesis, aspartate => NAD			
2572232671	t3m_01027	Metacyc	PYRIDNUCSYN-PWY: NAD biosynthesis I (from aspartate)			
2572232671	t3m_01027	COG_category	[H] Coenzyme transport and metabolism			
2572232671	t3m_01027	COG0171	NAD synthase			3.00E-66
2572232671	t3m_01027	pfam02540	NAD_synthase			9.60E-77
2572232671	t3m_01027	EC:6.3.1.5	NAD(+) synthase.			
2572232671	t3m_01027	TIGR00552	NAD+ synthetase			4.40E-77
2572232671	t3m_01027	KO:K01916	NAD+ synthase [EC:6.3.1.5]			0.00E+00
2572232671	t3m_01027	Locus_type		CDS		
2572232671	t3m_01027	Product_name		NAD+ synthetase		
2572232671	t3m_01027	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232671	t3m_01027	Coordinates		2241..3050(+)		
2572232671	t3m_01027	DNA_length		810bp		
2572232671	t3m_01027	Protein_length		269aa		
2572232671	t3m_01027	GC			0.7	
2572232672	t3m_01028	Locus_type		CDS		
2572232672	t3m_01028	Product_name		hypothetical protein		
2572232672	t3m_01028	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		

2572232672	t3m_01028	Coordinates		3289..3516(-)		
2572232672	t3m_01028	DNA_length		228bp		
2572232672	t3m_01028	Protein_length		75aa		
2572232672	t3m_01028	GC			0.68	
2572232673	t3m_01029	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232673	t3m_01029	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232673	t3m_01029	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232673	t3m_01029	IMG_pathway	493: L-histidine ligation to tRNA(His)			
2572232673	t3m_01029	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232673	t3m_01029	COG0124	Histidyl-tRNA synthetase			9.00E-82
2572232673	t3m_01029	pfam03129	HGTP_anticodon			9.40E-08
2572232673	t3m_01029	pfam13393	tRNA-synt_His			2.20E-41
2572232673	t3m_01029	EC:6.1.1.21	Histidine--tRNA ligase.			
2572232673	t3m_01029	TIGR00442	histidyl-tRNA synthetase			4.80E-93
2572232673	t3m_01029	KO:K01892	histidyl-tRNA synthetase [EC:6.1.1.21]			0.00E+00
2572232673	t3m_01029	ITERM:00386	histidyl-tRNA synthetase (EC 6.1.1.21)			
2572232673	t3m_01029	Locus_type		CDS		
2572232673	t3m_01029	Product_name		histidyl-tRNA synthetase (EC 6.1.1.21)		
2572232673	t3m_01029	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232673	t3m_01029	Coordinates		3885..5186(-)		
2572232673	t3m_01029	DNA_length		1302bp		
2572232673	t3m_01029	Protein_length		433aa		
2572232673	t3m_01029	GC			0.72	
2572232674	t3m_01030	Locus_type		CDS		
2572232674	t3m_01030	Product_name		hypothetical protein		
2572232674	t3m_01030	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232674	t3m_01030	Coordinates		5216..5947(-)		
2572232674	t3m_01030	DNA_length		732bp		
2572232674	t3m_01030	Protein_length		243aa		
2572232674	t3m_01030	GC			0.71	
2572232675	t3m_01031	Locus_type		CDS		

2572232675	t3m_01031	Product_name		hypothetical protein		
2572232675	t3m_01031	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232675	t3m_01031	Coordinates		5950..6258(-)		
2572232675	t3m_01031	DNA_length		309bp		
2572232675	t3m_01031	Protein_length		102aa		
2572232675	t3m_01031	GC			0.7	
2572232676	t3m_01032	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232676	t3m_01032	COG0501	Zn-dependent protease with chaperone function			4.00E-36
2572232676	t3m_01032	pfam01435	Peptidase_M48			2.00E-37
2572232676	t3m_01032	EC:3.4.24.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Metalloendopeptidases.			
2572232676	t3m_01032	KO:K03799	heat shock protein HtpX [EC:3.4.24.-]			0.00E+00
2572232676	t3m_01032	Locus_type		CDS		
2572232676	t3m_01032	Product_name		Heat shock protein. Metallo peptidase. MEROPS family M48B		
2572232676	t3m_01032	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232676	t3m_01032	Coordinates		6343..7275(-)		
2572232676	t3m_01032	DNA_length		933bp		
2572232676	t3m_01032	Protein_length		310aa		
2572232676	t3m_01032	GC			0.68	
2572232676	t3m_01032	Transmembrane		Yes		
2572232677	t3m_01033	COG_category	[R] General function prediction only			
2572232677	t3m_01033	COG1571	Predicted DNA-binding protein containing a Zn-ribbon domain			4.00E-78
2572232677	t3m_01033	pfam08489	DUF1743			2.90E-26
2572232677	t3m_01033	Locus_type		CDS		
2572232677	t3m_01033	Product_name		Predicted DNA-binding protein containing a Zn-ribbon domain		
2572232677	t3m_01033	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232677	t3m_01033	Coordinates		7342..8661(-)		
2572232677	t3m_01033	DNA_length		1320bp		
2572232677	t3m_01033	Protein_length		439aa		
2572232677	t3m_01033	GC			0.72	
2572232678	t3m_01034	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572232678	t3m_01034	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase			

2572232678	t3m_01034	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2572232678	t3m_01034	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2572232678	t3m_01034	Metacyc	P23-PWY: reductive TCA cycle I		
2572232678	t3m_01034	Metacyc	PWY-5392: reductive TCA cycle II		
2572232678	t3m_01034	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2572232678	t3m_01034	COG_category	[C] Energy production and conversion		
2572232678	t3m_01034	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o		1.00E-57
2572232678	t3m_01034	pfam02775	TPP_enzyme_C		9.70E-22
2572232678	t3m_01034	pfam12367	PFO_beta_C		9.10E-06
2572232678	t3m_01034	EC:1.2.7.3	2-oxoglutarate synthase.		
2572232678	t3m_01034	KO:K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]		0.00E+00
2572232678	t3m_01034	Locus_type		CDS	
2572232678	t3m_01034	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin ox	
2572232678	t3m_01034	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232678	t3m_01034	Coordinates		8701..9567(-)	
2572232678	t3m_01034	DNA_length		867bp	
2572232678	t3m_01034	Protein_length		288aa	
2572232678	t3m_01034	GC		0.65	

2572232679	t3m_01035	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)	
2572232679	t3m_01035	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate	
2572232679	t3m_01035	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase	
2572232679	t3m_01035	Metacyc	P23-PWY: reductive TCA cycle I	
2572232679	t3m_01035	Metacyc	PWY-5392: reductive TCA cycle II	
2572232679	t3m_01035	Metacyc	P42-PWY: incomplete reductive TCA cycle	
2572232679	t3m_01035	Metacyc	REDCITCYC: TCA cycle III (helicobacter)	
2572232679	t3m_01035	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)	
2572232679	t3m_01035	COG_category	[C] Energy production and conversion	
2572232679	t3m_01035	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o	9.00E-66
2572232679	t3m_01035	pfam01558	POR	3.10E-29
2572232679	t3m_01035	pfam01855	POR_N	2.10E-57
2572232679	t3m_01035	EC:1.2.7.3	2-oxoglutarate synthase.	
2572232679	t3m_01035	TIGR03710	2-oxoacid:acceptor oxidoreductase, alpha subunit	0.00E+00
2572232679	t3m_01035	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]	0.00E+00

2572232679	t3m_01035	Locus_type		CDS	
2572232679	t3m_01035	Product_name		2-oxoacid:acceptor oxidoreductase, alpha subunit	
2572232679	t3m_01035	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232679	t3m_01035	Coordinates		9569..11362(-)	
2572232679	t3m_01035	DNA_length		1794bp	
2572232679	t3m_01035	Protein_length		597aa	
2572232679	t3m_01035	GC		0.67	
2572232680	t3m_01036	COG_category	[R] General function prediction only		
2572232680	t3m_01036	COG1287	Uncharacterized membrane protein, required for N-linked glycosylation		3.00E-49
2572232680	t3m_01036	pfam13620	CarboxypepD_reg		2.50E-07
2572232680	t3m_01036	pfam13620	CarboxypepD_reg		9.80E-10
2572232680	t3m_01036	pfam02516	STT3		8.70E-13
2572232680	t3m_01036	Locus_type		CDS	
2572232680	t3m_01036	Product_name		Uncharacterized membrane protein, required for N-linked glycosylation	
2572232680	t3m_01036	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232680	t3m_01036	Coordinates		11688..18272(+)	
2572232680	t3m_01036	DNA_length		6585bp	
2572232680	t3m_01036	Protein_length		2194aa	
2572232680	t3m_01036	GC		0.68	
2572232680	t3m_01036	Transmembrane		Yes	
2572232681	t3m_01037	Locus_type		CDS	
2572232681	t3m_01037	Product_name		hypothetical protein	
2572232681	t3m_01037	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232681	t3m_01037	Coordinates		18239..19084(+)	
2572232681	t3m_01037	DNA_length		846bp	
2572232681	t3m_01037	Protein_length		281aa	
2572232681	t3m_01037	GC		0.69	
2572232681	t3m_01037	Transmembrane		Yes	
2572232682	t3m_01038	KO:K07580	hypothetical protein		2.30E-09
2572232682	t3m_01038	Locus_type		CDS	
2572232682	t3m_01038	Product_name		hypothetical protein	

2572232682	t3m_01038	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232682	t3m_01038	Coordinates		19151..19279(+)	
2572232682	t3m_01038	DNA_length		129bp	
2572232682	t3m_01038	Protein_length		42aa	
2572232682	t3m_01038	GC		0.71	

2572232683	t3m_01039	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232683	t3m_01039	COG2092	Translation elongation factor EF-1beta		4.00E-14
2572232683	t3m_01039	pfam00736	EF1_GNE		2.00E-17
2572232683	t3m_01039	TIGR00489	translation elongation factor aEF-1 beta		2.00E-24
2572232683	t3m_01039	KO:K03232	elongation factor 1-beta		2.00E-15
2572232683	t3m_01039	Locus_type		CDS	
2572232683	t3m_01039	Product_name		translation elongation factor aEF-1 beta	
2572232683	t3m_01039	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232683	t3m_01039	Coordinates		19288..19554(+)	
2572232683	t3m_01039	DNA_length		267bp	
2572232683	t3m_01039	Protein_length		88aa	
2572232683	t3m_01039	GC		0.67	

2572232684	t3m_01040	pfam04307	DUF457		3.90E-16
2572232684	t3m_01040	Locus_type		CDS	
2572232684	t3m_01040	Product_name		Predicted membrane-bound metal-dependent hydrolase (DUF457)	
2572232684	t3m_01040	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232684	t3m_01040	Coordinates		19577..20560(+)	
2572232684	t3m_01040	DNA_length		984bp	
2572232684	t3m_01040	Protein_length		327aa	
2572232684	t3m_01040	GC		0.69	
2572232684	t3m_01040	Transmembrane		Yes	

2572232685	t3m_01041	Locus_type		CDS	
2572232685	t3m_01041	Product_name		hypothetical protein	
2572232685	t3m_01041	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232685	t3m_01041	Coordinates		20627..20839(-)	
2572232685	t3m_01041	DNA_length		213bp	

2572232685	t3m_01041	Protein_length		70aa		
2572232685	t3m_01041	GC			0.63	
2572232686	t3m_01042	Metacyc	PWY-7165: L-ascorbate biosynthesis VI (engineered pathway)			
2572232686	t3m_01042	Metacyc	KETOGLUCONMET-PWY: ketogluconate metabolism			
2572232686	t3m_01042	COG_category	[R] General function prediction only			
2572232686	t3m_01042	COG0656	Aldo/keto reductases, related to diketogulonate reductase			1.00E-90
2572232686	t3m_01042	pfam00248	Aldo_ket_red			5.70E-52
2572232686	t3m_01042	EC:1.1.1.274	2,5-didehydrogluconate reductase.			
2572232686	t3m_01042	KO:K05885	2,5-diketo-D-gluconate reductase [EC:1.1.1.274]			0.00E+00
2572232686	t3m_01042	Locus_type		CDS		
2572232686	t3m_01042	Product_name		Aldo/keto reductases, related to diketogulonate reductase		
2572232686	t3m_01042	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232686	t3m_01042	Coordinates		21010..21861(-)		
2572232686	t3m_01042	DNA_length		852bp		
2572232686	t3m_01042	Protein_length		283aa		
2572232686	t3m_01042	GC			0.7	
2572232687	t3m_01043	Locus_type		CDS		
2572232687	t3m_01043	Product_name		hypothetical protein		
2572232687	t3m_01043	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232687	t3m_01043	Coordinates		21886..22158(-)		
2572232687	t3m_01043	DNA_length		273bp		
2572232687	t3m_01043	Protein_length		90aa		
2572232687	t3m_01043	GC			0.7	
2572232688	t3m_01044	COG_category	[R] General function prediction only			
2572232688	t3m_01044	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa			2.00E-19
2572232688	t3m_01044	pfam12697	Abhydrolase_6			6.00E-39
2572232688	t3m_01044	Locus_type		CDS		
2572232688	t3m_01044	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfan		
2572232688	t3m_01044	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232688	t3m_01044	Coordinates		22345..23172(+)		
2572232688	t3m_01044	DNA_length		828bp		

2572232688	t3m_01044	Protein_length		275aa		
2572232688	t3m_01044	GC			0.68	
2572232689	t3m_01045	Locus_type		CDS		
2572232689	t3m_01045	Product_name		hypothetical protein		
2572232689	t3m_01045	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232689	t3m_01045	Coordinates		23193..23408(-)		
2572232689	t3m_01045	DNA_length		216bp		
2572232689	t3m_01045	Protein_length		71aa		
2572232689	t3m_01045	GC			0.67	
2572232690	t3m_01046	COG_category	[P] Inorganic ion transport and metabolism			
2572232690	t3m_01046	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)			6.00E-33
2572232690	t3m_01046	pfam00210	Ferritin			1.30E-28
2572232690	t3m_01046	KO:K04047	starvation-inducible DNA-binding protein			1.10E-28
2572232690	t3m_01046	Locus_type		CDS		
2572232690	t3m_01046	Product_name		DNA-binding ferritin-like protein (oxidative damage protectant)		
2572232690	t3m_01046	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232690	t3m_01046	Coordinates		23423..23899(+)		
2572232690	t3m_01046	DNA_length		477bp		
2572232690	t3m_01046	Protein_length		158aa		
2572232690	t3m_01046	GC			0.63	
2572232691	t3m_01047	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2572232691	t3m_01047	COG_category	[R] General function prediction only			
2572232691	t3m_01047	COG_category	[I] Lipid transport and metabolism			
2572232691	t3m_01047	COG1028	Dehydrogenases with different specificities (related to short-chain alco			2.00E-42
2572232691	t3m_01047	pfam13561	adh_short_C2			5.50E-30
2572232691	t3m_01047	Locus_type		CDS		
2572232691	t3m_01047	Product_name		Dehydrogenases with different specificities (related to short-chain alcoh		
2572232691	t3m_01047	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232691	t3m_01047	Coordinates		23907..24737(-)		
2572232691	t3m_01047	DNA_length		831bp		
2572232691	t3m_01047	Protein_length		276aa		

2572232691	t3m_01047	GC		0.7	
2572232692	t3m_01048	COG_category	[C] Energy production and conversion		
2572232692	t3m_01048	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2572232692	t3m_01048	COG0526	Thiol-disulfide isomerase and thioredoxins		1.00E-05
2572232692	t3m_01048	pfam00085	Thioredoxin		2.70E-11
2572232692	t3m_01048	KO:K03671	thioredoxin 1		1.40E-07
2572232692	t3m_01048	Locus_type		CDS	
2572232692	t3m_01048	Product_name		Thioredoxin	
2572232692	t3m_01048	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232692	t3m_01048	Coordinates		24830..25186(-)	
2572232692	t3m_01048	DNA_length		357bp	
2572232692	t3m_01048	Protein_length		118aa	
2572232692	t3m_01048	GC		0.67	
2572232693	t3m_01049	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232693	t3m_01049	COG1184	Translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family		1.00E-25
2572232693	t3m_01049	pfam01008	IF-2B		9.90E-23
2572232693	t3m_01049	Locus_type		CDS	
2572232693	t3m_01049	Product_name		Translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family	
2572232693	t3m_01049	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232693	t3m_01049	Coordinates		25227..26057(-)	
2572232693	t3m_01049	DNA_length		831bp	
2572232693	t3m_01049	Protein_length		276aa	
2572232693	t3m_01049	GC		0.72	
2572232694	t3m_01050	pfam00756	Esterase		4.30E-14
2572232694	t3m_01050	KO:K07214	enterochelin esterase and related enzymes		0.00E+00
2572232694	t3m_01050	Locus_type		CDS	
2572232694	t3m_01050	Product_name		Putative esterase	
2572232694	t3m_01050	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21	
2572232694	t3m_01050	Coordinates		26169..27230(+)	
2572232694	t3m_01050	DNA_length		1062bp	
2572232694	t3m_01050	Protein_length		353aa	

2572232694	t3m_01050	GC			0.69	
2572232695	t3m_01051	pfam13420	Acetyltransf_4			2.70E-16
2572232695	t3m_01051	Locus_type		CDS		
2572232695	t3m_01051	Product_name		Acetyltransferase (GNAT) domain		
2572232695	t3m_01051	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232695	t3m_01051	Coordinates		27544..27957(+)		
2572232695	t3m_01051	DNA_length		414bp		
2572232695	t3m_01051	Protein_length		137aa		
2572232695	t3m_01051	GC			0.64	
2572232696	t3m_01052	pfam07883	Cupin_2			3.50E-05
2572232696	t3m_01052	Locus_type		CDS		
2572232696	t3m_01052	Product_name		Cupin domain		
2572232696	t3m_01052	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232696	t3m_01052	Coordinates		27997..28407(-)		
2572232696	t3m_01052	DNA_length		411bp		
2572232696	t3m_01052	Protein_length		136aa		
2572232696	t3m_01052	GC			0.63	
2572232697	t3m_01053	Locus_type		CDS		
2572232697	t3m_01053	Product_name		hypothetical protein		
2572232697	t3m_01053	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232697	t3m_01053	Coordinates		28769..29338(-)		
2572232697	t3m_01053	DNA_length		570bp		
2572232697	t3m_01053	Protein_length		189aa		
2572232697	t3m_01053	GC			0.68	
2572232698	t3m_01054	Metacyc	PWY-6739: pinitol biosynthesis II			
2572232698	t3m_01054	Metacyc	PWY-6151: <i>S</i>-adenosyl-L-methionine cycle I			
2572232698	t3m_01054	Metacyc	PWY-5975: furaneol biosynthesis			
2572232698	t3m_01054	Metacyc	PWY-5882: epoxypseudoisoeugenol-2-methylbutyrate biosynthesis			
2572232698	t3m_01054	Metacyc	PWY-6835: 6-gingerol biosynthesis			
2572232698	t3m_01054	Metacyc	PWY-7150: polymethylated quercetin glucoside biosynthesis I - quercetin series (Chrysosplenium)			

2572232698	t3m_01054	Metacyc	PWY-7160: polymethylated myricetin biosynthesis (tomato)
2572232698	t3m_01054	Metacyc	PWY-6427: rot-2'-enonate biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5287: sanguinarine and macarpine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5290: secologanin and strictosidine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6424: sitosterol biosynthesis
2572232698	t3m_01054	Metacyc	PWY-3542: choline biosynthesis II
2572232698	t3m_01054	Metacyc	METH-ACETATE-PWY: methanogenesis from acetate
2572232698	t3m_01054	Metacyc	PWY-6477: gibberellin inactivation II (methylation)
2572232698	t3m_01054	Metacyc	PWY-5041: <i>S</i>-adenosyl-L-methionine cycle II
2572232698	t3m_01054	Metacyc	PWY-7076: 3,5-dimethoxytoluene biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5665: vanilla biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5135: xanthohumol biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7149: superpathway polymethylated quercetin/quercetagetin glucoside biosynthesis (Chrysc
2572232698	t3m_01054	Metacyc	PWY-5391: syringetin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5987: sorgoleone biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7058: esculetin modification
2572232698	t3m_01054	Metacyc	PWY-7138: noscapine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7135: emetine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6933: seleno-amino acid detoxification and volatilization III
2572232698	t3m_01054	Metacyc	PWY-6154: autoinducer AI-2 biosynthesis II (<i>Vibrio</i>)
2572232698	t3m_01054	Metacyc	PWY-6153: autoinducer AI-2 biosynthesis I
2572232698	t3m_01054	Metacyc	PWY-6978: plastoquinol-9 biosynthesis II
2572232698	t3m_01054	Metacyc	PWY-5209: methyl-coenzyme M oxidation to CO₂
2572232698	t3m_01054	Metacyc	PWY-6973: dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycarose biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6976: dTDP-L-mycarose biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6303: methyl indole-3-acetate interconversion
2572232698	t3m_01054	Metacyc	PWY-6955: lincomycin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7055: daphnetin modification
2572232698	t3m_01054	Metacyc	PWY-5479: podophyllotoxin and 6-methoxypodophyllotoxin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5748: γ-coniciene and coniine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5305: bixin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-1422: vitamin E biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7104: dTDP-L-megosamine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6650: juvenile hormone III biosynthesis II

2572232698	t3m_01054	Metacyc	PWY-6682: dehydrophos biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6442: spermidine hydroxycinnamic acid conjugates biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7097: vanillin and vanillate degradation I
2572232698	t3m_01054	Metacyc	PWY-4021: β-alanine betaine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7045: mithramycin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7161: polymethylated quercetin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7157: eupatolitin 3-<i>O</i>-glucoside biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5867: <i>t</i>-anethole biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5467: gramine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-1581: plastoquinol-9 biosynthesis I
2572232698	t3m_01054	Metacyc	PWY-6052: dimethylsulfoniopropionate degradation III (demethylation)
2572232698	t3m_01054	Metacyc	PWY-6736: sulfur volatiles biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6666: pyocyanin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5729: vestitol and sativan biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5846: colchicine biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6581: spirilloxanthin and 2,2'-diketo-spirilloxanthin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-4942: cyclopropane and cyclopropene fatty acid biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6339: syringate degradation
2572232698	t3m_01054	Metacyc	PWY-7186: superpathway of scopolin and esculin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5876: magnoflorine biosynthesis
2572232698	t3m_01054	Metacyc	PWYG-321: mycolate biosynthesis
2572232698	t3m_01054	Metacyc	PWY-5507: adenosylcobalamin biosynthesis I (early cobalt insertion)
2572232698	t3m_01054	Metacyc	METHIONINE-DEG1-PWY: methionine degradation I (to homocysteine)
2572232698	t3m_01054	Metacyc	PWY-6045: methylthiopropionate degradation II (demethylation)
2572232698	t3m_01054	Metacyc	PWY-1061: homogalacturonan biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6575: juvenile hormone III biosynthesis I
2572232698	t3m_01054	Metacyc	PWY-702: methionine biosynthesis II
2572232698	t3m_01054	Metacyc	PWY-5765: 1,3,5-trimethoxybenzene biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7025: gentamicin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-7151: polymethylated quercetin glucoside biosynthesis II - quercetagetin series (Chrysosplen
2572232698	t3m_01054	Metacyc	PWY-7163: polymethylated kaempferol biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6631: <i>O</i> -methylation of tricetin
2572232698	t3m_01054	Metacyc	PWY-7079: geodin biosynthesis
2572232698	t3m_01054	Metacyc	PWY-6286: spheroidene and spheroidenone biosynthesis

2572232698	t3m_01054	Metacyc	PWY-5773: gossypol biosynthesis			
2572232698	t3m_01054	COG_category	[H] Coenzyme transport and metabolism			
2572232698	t3m_01054	COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis			6.00E-16
2572232698	t3m_01054	pfam08242	Methyltransf_12			1.50E-16
2572232698	t3m_01054	EC:2.1.1.-	Transferases. Transferring one-carbon groups. Methyltransferases.			
2572232698	t3m_01054	KO:K15256	tRNA (cmo5U34)-methyltransferase [EC:2.1.1.-]			1.50E-27
2572232698	t3m_01054	Locus_type		CDS		
2572232698	t3m_01054	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2572232698	t3m_01054	Scaffold		t3m_contig_70_162_len_30467_read_count_2413924.21		
2572232698	t3m_01054	Coordinates		29579..30247(+)		
2572232698	t3m_01054	DNA_length		669bp		
2572232698	t3m_01054	Protein_length		222aa		
2572232698	t3m_01054	GC			0.7	

2572232699	t3m_01055	pfam03590	AsnA			4.60E-21
2572232699	t3m_01055	Locus_type		CDS		
2572232699	t3m_01055	Product_name		Aspartate-ammonia ligase		
2572232699	t3m_01055	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232699	t3m_01055	Coordinates		1..486(+)		
2572232699	t3m_01055	DNA_length		486bp		
2572232699	t3m_01055	Protein_length		161aa		
2572232699	t3m_01055	GC			0.66	

2572232700	t3m_01056	KEGG_module	M00125: Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD			
2572232700	t3m_01056	Metacyc	RIBOSYN2-PWY: flavin biosynthesis I (bacteria and plants)			
2572232700	t3m_01056	Metacyc	PWY-6167: flavin biosynthesis II (archaea)			
2572232700	t3m_01056	Metacyc	PWY-6168: flavin biosynthesis III (fungi)			
2572232700	t3m_01056	IMG_pathway	291: 5-amino-6-ribitylamino-2,4(1H,3H)-pyrimidinedione biosynthesis			
2572232700	t3m_01056	COG_category	[H] Coenzyme transport and metabolism			
2572232700	t3m_01056	COG0807	GTP cyclohydrolase II			3.00E-62
2572232700	t3m_01056	pfam00925	GTP_cyclohydro2			1.80E-64
2572232700	t3m_01056	EC:3.5.4.25	GTP cyclohydrolase II.			
2572232700	t3m_01056	EC:4.1.99.12	3,4-dihydroxy-2-butanone-4-phosphate synthase.			
2572232700	t3m_01056	TIGR00505	GTP cyclohydrolase II			7.50E-76

2572232700	t3m_01056	KO:K14652	3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase I			0.00E+00
2572232700	t3m_01056	ITERM:00567	GTP cyclohydrolase II (EC 3.5.4.25)			
2572232700	t3m_01056	Locus_type		CDS		
2572232700	t3m_01056	Product_name		GTP cyclohydrolase II (EC 3.5.4.25)		
2572232700	t3m_01056	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232700	t3m_01056	Coordinates		596..1300(+)		
2572232700	t3m_01056	DNA_length		705bp		
2572232700	t3m_01056	Protein_length		234aa		
2572232700	t3m_01056	GC			0.67	

2572232701	t3m_01057	pfam13229	Beta_helix			3.10E-11
2572232701	t3m_01057	pfam05317	Thermopsin			1.50E-60
2572232701	t3m_01057	Locus_type		CDS		
2572232701	t3m_01057	Product_name		Thermopsin/Right handed beta helix region		
2572232701	t3m_01057	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232701	t3m_01057	Coordinates		1429..6351(-)		
2572232701	t3m_01057	DNA_length		4923bp		
2572232701	t3m_01057	Protein_length		1640aa		
2572232701	t3m_01057	GC			0.63	
2572232701	t3m_01057	Transmembrane		Yes		

2572232702	t3m_01058	pfam03473	MOSC			2.80E-17
2572232702	t3m_01058	Locus_type		CDS		
2572232702	t3m_01058	Product_name		MOSC domain		
2572232702	t3m_01058	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232702	t3m_01058	Coordinates		6510..6983(-)		
2572232702	t3m_01058	DNA_length		474bp		
2572232702	t3m_01058	Protein_length		157aa		
2572232702	t3m_01058	GC			0.66	

2572232703	t3m_01059	Locus_type		CDS		
2572232703	t3m_01059	Product_name		hypothetical protein		
2572232703	t3m_01059	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232703	t3m_01059	Coordinates		7144..7521(+)		

2572232703	t3m_01059	DNA_length		378bp		
2572232703	t3m_01059	Protein_length		125aa		
2572232703	t3m_01059	GC			0.62	
2572232703	t3m_01059	Transmembrane		Yes		

2572232704	t3m_01060	COG_category	[E] Amino acid transport and metabolism			
2572232704	t3m_01060	COG1280	Putative threonine efflux protein			1.00E-07
2572232704	t3m_01060	pfam01810	LysE			1.40E-21
2572232704	t3m_01060	Locus_type		CDS		
2572232704	t3m_01060	Product_name		Putative threonine efflux protein		
2572232704	t3m_01060	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232704	t3m_01060	Coordinates		7591..8169(+)		
2572232704	t3m_01060	DNA_length		579bp		
2572232704	t3m_01060	Protein_length		192aa		
2572232704	t3m_01060	GC			0.67	
2572232704	t3m_01060	Transmembrane		Yes		

2572232705	t3m_01061	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232705	t3m_01061	COG0225	Peptide methionine sulfoxide reductase			1.00E-63
2572232705	t3m_01061	pfam01625	PMSR			4.40E-62
2572232705	t3m_01061	EC:1.8.4.11	Peptide-methionine (S)-S-oxide reductase.			
2572232705	t3m_01061	TIGR00401	methionine-S-sulfoxide reductase			2.90E-61
2572232705	t3m_01061	KO:K07304	peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]			0.00E+00
2572232705	t3m_01061	Locus_type		CDS		
2572232705	t3m_01061	Product_name		methionine-S-sulfoxide reductase		
2572232705	t3m_01061	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232705	t3m_01061	Coordinates		8194..8760(-)		
2572232705	t3m_01061	DNA_length		567bp		
2572232705	t3m_01061	Protein_length		188aa		
2572232705	t3m_01061	GC			0.65	

2572232706	t3m_01062	pfam06157	DUF973			9.10E-05
2572232706	t3m_01062	Locus_type		CDS		
2572232706	t3m_01062	Product_name		Protein of unknown function (DUF973)		

2572232706	t3m_01062	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232706	t3m_01062	Coordinates		8838..9608(-)	
2572232706	t3m_01062	DNA_length		771bp	
2572232706	t3m_01062	Protein_length		256aa	
2572232706	t3m_01062	GC		0.67	
2572232706	t3m_01062	Transmembrane		Yes	
2572232707	t3m_01063	COG_category	[T] Signal transduction mechanisms		
2572232707	t3m_01063	COG_category	[K] Transcription		
2572232707	t3m_01063	COG4978	Transcriptional regulator, effector-binding domain/component		3.00E-04
2572232707	t3m_01063	pfam06445	GyrI-like		1.30E-06
2572232707	t3m_01063	Locus_type		CDS	
2572232707	t3m_01063	Product_name		Transcriptional regulator, effector-binding domain/component	
2572232707	t3m_01063	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232707	t3m_01063	Coordinates		9687..10139(-)	
2572232707	t3m_01063	DNA_length		453bp	
2572232707	t3m_01063	Protein_length		150aa	
2572232707	t3m_01063	GC		0.64	
2572232708	t3m_01064	COG_category	[H] Coenzyme transport and metabolism		
2572232708	t3m_01064	COG2896	Molybdenum cofactor biosynthesis enzyme		1.00E-75
2572232708	t3m_01064	pfam06463	Mob_synth_C		2.90E-23
2572232708	t3m_01064	pfam04055	Radical_SAM		1.50E-23
2572232708	t3m_01064	pfam13394	Fer4_14		1.20E-08
2572232708	t3m_01064	TIGR02668	probable molybdenum cofactor biosynthesis protein A, archaeal		1.80E-107
2572232708	t3m_01064	KO:K03639	molybdenum cofactor biosynthesis protein		0.00E+00
2572232708	t3m_01064	Locus_type		CDS	
2572232708	t3m_01064	Product_name		probable molybdenum cofactor biosynthesis protein A, archaeal	
2572232708	t3m_01064	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232708	t3m_01064	Coordinates		10275..11261(-)	
2572232708	t3m_01064	DNA_length		987bp	
2572232708	t3m_01064	Protein_length		328aa	
2572232708	t3m_01064	GC		0.66	

2572232709	t3m_01065	KEGG_module	M00254: ABC-2 type transport system			
2572232709	t3m_01065	COG_category	[V] Defense mechanisms			
2572232709	t3m_01065	COG1131	ABC-type multidrug transport system, ATPase component			2.00E-70
2572232709	t3m_01065	pfam00005	ABC_tran			3.60E-29
2572232709	t3m_01065	KO:K01990	ABC-2 type transport system ATP-binding protein			0.00E+00
2572232709	t3m_01065	Locus_type		CDS		
2572232709	t3m_01065	Product_name		ABC-type multidrug transport system, ATPase component		
2572232709	t3m_01065	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232709	t3m_01065	Coordinates		11419..12264(+)		
2572232709	t3m_01065	DNA_length		846bp		
2572232709	t3m_01065	Protein_length		281aa		
2572232709	t3m_01065	GC			0.68	
2572232710	t3m_01066	Locus_type		CDS		
2572232710	t3m_01066	Product_name		hypothetical protein		
2572232710	t3m_01066	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232710	t3m_01066	Coordinates		12272..13870(+)		
2572232710	t3m_01066	DNA_length		1599bp		
2572232710	t3m_01066	Protein_length		532aa		
2572232710	t3m_01066	GC			0.69	
2572232710	t3m_01066	Transmembrane		Yes		
2572232711	t3m_01067	Locus_type		CDS		
2572232711	t3m_01067	Product_name		hypothetical protein		
2572232711	t3m_01067	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232711	t3m_01067	Coordinates		13886..14365(-)		
2572232711	t3m_01067	DNA_length		480bp		
2572232711	t3m_01067	Protein_length		159aa		
2572232711	t3m_01067	GC			0.7	
2572232712	t3m_01068	COG_category	[L] Replication, recombination and repair			
2572232712	t3m_01068	COG4912	Predicted DNA alkylation repair enzyme			1.00E-07
2572232712	t3m_01068	pfam08713	DNA_alkylation			3.10E-36
2572232712	t3m_01068	Locus_type		CDS		

2572232712	t3m_01068	Product_name		Predicted DNA alkylation repair enzyme		
2572232712	t3m_01068	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232712	t3m_01068	Coordinates		14390..15157(-)		
2572232712	t3m_01068	DNA_length		768bp		
2572232712	t3m_01068	Protein_length		255aa		
2572232712	t3m_01068	GC			0.71	
2572232713	t3m_01069	pfam01401	Peptidase_M2			0.00E+00
2572232713	t3m_01069	EC:3.4.15.1	Peptidyl-dipeptidase A.			
2572232713	t3m_01069	KO:K01283	peptidyl-dipeptidase A [EC:3.4.15.1]			0.00E+00
2572232713	t3m_01069	Locus_type		CDS		
2572232713	t3m_01069	Product_name		Angiotensin-converting enzyme		
2572232713	t3m_01069	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232713	t3m_01069	Coordinates		15151..16932(-)		
2572232713	t3m_01069	DNA_length		1782bp		
2572232713	t3m_01069	Protein_length		593aa		
2572232713	t3m_01069	GC			0.67	
2572232714	t3m_01070	Locus_type		CDS		
2572232714	t3m_01070	Product_name		hypothetical protein		
2572232714	t3m_01070	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232714	t3m_01070	Coordinates		17071..17223(+)		
2572232714	t3m_01070	DNA_length		153bp		
2572232714	t3m_01070	Protein_length		50aa		
2572232714	t3m_01070	GC			0.66	
2572232715	t3m_01071	Locus_type		CDS		
2572232715	t3m_01071	Product_name		hypothetical protein		
2572232715	t3m_01071	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232715	t3m_01071	Coordinates		17220..17441(+)		
2572232715	t3m_01071	DNA_length		222bp		
2572232715	t3m_01071	Protein_length		73aa		
2572232715	t3m_01071	GC			0.7	

2572232716	t3m_01072	COG_category	[L] Replication, recombination and repair			
2572232716	t3m_01072	COG0328	Ribonuclease HI			4.00E-16
2572232716	t3m_01072	pfam13456	RVT_3			1.10E-20
2572232716	t3m_01072	EC:3.1.26.4	Ribonuclease H.			
2572232716	t3m_01072	KO:K03469	ribonuclease HI [EC:3.1.26.4]			1.60E-27
2572232716	t3m_01072	Locus_type		CDS		
2572232716	t3m_01072	Product_name		Ribonuclease HI		
2572232716	t3m_01072	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232716	t3m_01072	Coordinates		17465..18016(-)		
2572232716	t3m_01072	DNA_length		552bp		
2572232716	t3m_01072	Protein_length		183aa		
2572232716	t3m_01072	GC			0.68	

2572232717	t3m_01073	Locus_type		CDS		
2572232717	t3m_01073	Product_name		hypothetical protein		
2572232717	t3m_01073	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232717	t3m_01073	Coordinates		18013..18528(-)		
2572232717	t3m_01073	DNA_length		516bp		
2572232717	t3m_01073	Protein_length		171aa		
2572232717	t3m_01073	GC			0.7	
2572232717	t3m_01073	Transmembrane		Yes		

2572232718	t3m_01074	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232718	t3m_01074	COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family			7.00E-51
2572232718	t3m_01074	pfam00160	Pro_isomerase			1.60E-53
2572232718	t3m_01074	EC:5.2.1.8	Peptidylprolyl isomerase.			
2572232718	t3m_01074	KO:K03767	peptidyl-prolyl cis-trans isomerase A (cyclophilin A) [EC:5.2.1.8]			0.00E+00
2572232718	t3m_01074	Locus_type		CDS		
2572232718	t3m_01074	Product_name		Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family		
2572232718	t3m_01074	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232718	t3m_01074	Coordinates		18640..19110(+)		
2572232718	t3m_01074	DNA_length		471bp		
2572232718	t3m_01074	Protein_length		156aa		
2572232718	t3m_01074	GC			0.67	

2572232719	t3m_01075	Locus_type		CDS	
2572232719	t3m_01075	Product_name		hypothetical protein	
2572232719	t3m_01075	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232719	t3m_01075	Coordinates		19122..19622(-)	
2572232719	t3m_01075	DNA_length		501bp	
2572232719	t3m_01075	Protein_length		166aa	
2572232719	t3m_01075	GC		0.65	
2572232719	t3m_01075	Transmembrane		Yes	
2572232720	t3m_01076	Locus_type		CDS	
2572232720	t3m_01076	Product_name		hypothetical protein	
2572232720	t3m_01076	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232720	t3m_01076	Coordinates		19619..20371(-)	
2572232720	t3m_01076	DNA_length		753bp	
2572232720	t3m_01076	Protein_length		250aa	
2572232720	t3m_01076	GC		0.67	
2572232720	t3m_01076	Transmembrane		Yes	
2572232721	t3m_01077	Locus_type		CDS	
2572232721	t3m_01077	Product_name		hypothetical protein	
2572232721	t3m_01077	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232721	t3m_01077	Coordinates		20722..20865(+)	
2572232721	t3m_01077	DNA_length		144bp	
2572232721	t3m_01077	Protein_length		47aa	
2572232721	t3m_01077	GC		0.69	
2572232722	t3m_01078	COG_category	[C] Energy production and conversion		
2572232722	t3m_01078	COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family		1.00E-82
2572232722	t3m_01078	pfam00724	Oxidored_FMN		6.60E-06
2572232722	t3m_01078	pfam00724	Oxidored_FMN		3.90E-64
2572232722	t3m_01078	Locus_type		CDS	
2572232722	t3m_01078	Product_name		NADH:flavin oxidoreductases, Old Yellow Enzyme family	
2572232722	t3m_01078	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	

2572232722	t3m_01078	Coordinates		21010..22128(-)	
2572232722	t3m_01078	DNA_length		1119bp	
2572232722	t3m_01078	Protein_length		372aa	
2572232722	t3m_01078	GC		0.69	
2572232723	t3m_01079	Locus_type		CDS	
2572232723	t3m_01079	Product_name		hypothetical protein	
2572232723	t3m_01079	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232723	t3m_01079	Coordinates		22482..24776(-)	
2572232723	t3m_01079	DNA_length		2295bp	
2572232723	t3m_01079	Protein_length		764aa	
2572232723	t3m_01079	GC		0.66	
2572232723	t3m_01079	Transmembrane		Yes	
2572232724	t3m_01080	Locus_type		tRNA	
2572232724	t3m_01080	Product_name		tRNA_Thr_CGT	
2572232724	t3m_01080	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232724	t3m_01080	Coordinates		24980..25053(-)	
2572232724	t3m_01080	DNA_length		74bp	
2572232724	t3m_01080	GC		0.59	
2572232725	t3m_01081	Metacyc	PWY-701: methionine degradation II		
2572232725	t3m_01081	COG_category	[E] Amino acid transport and metabolism		
2572232725	t3m_01081	COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases		3.00E-115
2572232725	t3m_01081	pfam01053	Cys_Met_Meta_PP		6.20E-119
2572232725	t3m_01081	EC:4.4.1.11	Methionine gamma-lyase.		
2572232725	t3m_01081	KO:K01761	methionine-gamma-lyase [EC:4.4.1.11]		0.00E+00
2572232725	t3m_01081	Locus_type		CDS	
2572232725	t3m_01081	Product_name		Cystathionine beta-lyases/cystathionine gamma-synthases	
2572232725	t3m_01081	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22	
2572232725	t3m_01081	Coordinates		25103..26332(-)	
2572232725	t3m_01081	DNA_length		1230bp	
2572232725	t3m_01081	Protein_length		409aa	
2572232725	t3m_01081	GC		0.69	

2572232726	t3m_01082	Metacyc	NAD-BIOSYNTHESIS-III: NAD biosynthesis III			
2572232726	t3m_01082	Metacyc	PWY3O-4106: NAD salvage pathway III			
2572232726	t3m_01082	COG_category	[H] Coenzyme transport and metabolism			
2572232726	t3m_01082	COG1056	Nicotinamide mononucleotide adenylyltransferase			2.00E-39
2572232726	t3m_01082	pfam01467	CTP_transf_2			2.40E-10
2572232726	t3m_01082	EC:2.7.7.1	Nicotinamide-nucleotide adenylyltransferase.			
2572232726	t3m_01082	TIGR01527	nicotinamide-nucleotide adenylyltransferase			6.30E-55
2572232726	t3m_01082	TIGR00125	cytidyltransferase-like domain			5.60E-12
2572232726	t3m_01082	KO:K00952	nicotinamide-nucleotide adenylyltransferase [EC:2.7.7.1]			4.90E-40
2572232726	t3m_01082	Locus_type		CDS		
2572232726	t3m_01082	Product_name		cytidyltransferase-like domain		
2572232726	t3m_01082	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232726	t3m_01082	Coordinates		26329..26880(-)		
2572232726	t3m_01082	DNA_length		552bp		
2572232726	t3m_01082	Protein_length		183aa		
2572232726	t3m_01082	GC			0.68	

2572232727	t3m_01083	Locus_type		CDS		
2572232727	t3m_01083	Product_name		hypothetical protein		
2572232727	t3m_01083	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232727	t3m_01083	Coordinates		26881..27126(-)		
2572232727	t3m_01083	DNA_length		246bp		
2572232727	t3m_01083	Protein_length		81aa		
2572232727	t3m_01083	GC			0.66	

2572232728	t3m_01084	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232728	t3m_01084	COG1067	Predicted ATP-dependent protease			0.00E+00
2572232728	t3m_01084	pfam13654	AAA_32			5.70E-20
2572232728	t3m_01084	pfam05362	Lon_C			1.20E-30
2572232728	t3m_01084	pfam01078	Mg_chelatase			5.30E-09
2572232728	t3m_01084	EC:3.4.21.-	Hydrolases. Acting on peptide bonds (peptide hydrolases). Serine endopeptidases.			
2572232728	t3m_01084	TIGR00764	lon-related putative ATP-dependent protease			0.00E+00
2572232728	t3m_01084	KO:K04076	Lon-like ATP-dependent protease [EC:3.4.21.-]			0.00E+00

2572232728	t3m_01084	Locus_type		CDS		
2572232728	t3m_01084	Product_name		lon-related putative ATP-dependent protease		
2572232728	t3m_01084	Scaffold		t3m_contig_70_173_len_29101_read_count_2611096.22		
2572232728	t3m_01084	Coordinates		27123..29099(-)		
2572232728	t3m_01084	DNA_length		1977bp		
2572232728	t3m_01084	Protein_length		658aa		
2572232728	t3m_01084	GC			0.67	
2572232728	t3m_01084	Transmembrane		Yes		

2572232729	t3m_01085	pfam00118	Cpn60_TCP1			3.10E-91
2572232729	t3m_01085	Locus_type		CDS		
2572232729	t3m_01085	Product_name		TCP-1/cpn60 chaperonin family		
2572232729	t3m_01085	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232729	t3m_01085	Coordinates		3..905(+)		
2572232729	t3m_01085	DNA_length		903bp		
2572232729	t3m_01085	Protein_length		300aa		
2572232729	t3m_01085	GC			0.65	

2572232730	t3m_01086	Locus_type		CDS		
2572232730	t3m_01086	Product_name		hypothetical protein		
2572232730	t3m_01086	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232730	t3m_01086	Coordinates		1008..1409(+)		
2572232730	t3m_01086	DNA_length		402bp		
2572232730	t3m_01086	Protein_length		133aa		
2572232730	t3m_01086	GC			0.73	

2572232731	t3m_01087	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232731	t3m_01087	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232731	t3m_01087	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232731	t3m_01087	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232731	t3m_01087	COG1190	Lysyl-tRNA synthetase (class II)			0.00E+00
2572232731	t3m_01087	pfam01336	tRNA_anti-codon			6.80E-11
2572232731	t3m_01087	pfam00152	tRNA-synt_2			1.00E-82
2572232731	t3m_01087	EC:6.1.1.6	Lysine--tRNA ligase.			

2572232731	t3m_01087	TIGR00499	lysyl-tRNA synthetase, eukaryotic and non-spirochete bacterial			0.00E+00
2572232731	t3m_01087	KO:K04567	lysyl-tRNA synthetase, class II [EC:6.1.1.6]			0.00E+00
2572232731	t3m_01087	ITERM:07335	lysyl-tRNA synthetase, class II (EC 6.1.1.6)			
2572232731	t3m_01087	Locus_type		CDS		
2572232731	t3m_01087	Product_name		lysyl-tRNA synthetase, class II (EC 6.1.1.6)		
2572232731	t3m_01087	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232731	t3m_01087	Coordinates		1464..2942(+)		
2572232731	t3m_01087	DNA_length		1479bp		
2572232731	t3m_01087	Protein_length		492aa		
2572232731	t3m_01087	GC			0.69	
2572232732	t3m_01088	KEGG_module	M00254: ABC-2 type transport system			
2572232732	t3m_01088	COG_category	[V] Defense mechanisms			
2572232732	t3m_01088	COG1131	ABC-type multidrug transport system, ATPase component			7.00E-61
2572232732	t3m_01088	pfam00005	ABC_tran			1.20E-26
2572232732	t3m_01088	KO:K01990	ABC-2 type transport system ATP-binding protein			0.00E+00
2572232732	t3m_01088	Locus_type		CDS		
2572232732	t3m_01088	Product_name		ABC-type multidrug transport system, ATPase component		
2572232732	t3m_01088	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232732	t3m_01088	Coordinates		2992..3798(+)		
2572232732	t3m_01088	DNA_length		807bp		
2572232732	t3m_01088	Protein_length		268aa		
2572232732	t3m_01088	GC			0.71	
2572232733	t3m_01089	COG_category	[R] General function prediction only			
2572232733	t3m_01089	COG3368	Predicted permease			6.00E-06
2572232733	t3m_01089	pfam09847	DUF2074			4.80E-13
2572232733	t3m_01089	Locus_type		CDS		
2572232733	t3m_01089	Product_name		Predicted permease (DUF2074)		
2572232733	t3m_01089	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232733	t3m_01089	Coordinates		3795..5459(+)		
2572232733	t3m_01089	DNA_length		1665bp		
2572232733	t3m_01089	Protein_length		554aa		
2572232733	t3m_01089	GC			0.7	

2572232733	t3m_01089	Transmembrane		Yes		

2572232734	t3m_01090	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232734	t3m_01090	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232734	t3m_01090	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232734	t3m_01090	IMG_pathway	505: L-valine ligation to tRNA(Val)			
2572232734	t3m_01090	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232734	t3m_01090	COG0525	Valyl-tRNA synthetase			0.00E+00
2572232734	t3m_01090	pfam00133	tRNA-synt_1			0.00E+00
2572232734	t3m_01090	pfam08264	Anticodon_1			3.70E-34
2572232734	t3m_01090	pfam10458	Val_tRNA-synt_C			5.10E-09
2572232734	t3m_01090	EC:6.1.1.9	Valine--tRNA ligase.			
2572232734	t3m_01090	TIGR00422	valyl-tRNA synthetase			0.00E+00
2572232734	t3m_01090	KO:K01873	valyl-tRNA synthetase [EC:6.1.1.9]			0.00E+00
2572232734	t3m_01090	ITERM:00407	valyl-tRNA synthetase (EC 6.1.1.9)			
2572232734	t3m_01090	Locus_type		CDS		
2572232734	t3m_01090	Product_name		valyl-tRNA synthetase (EC 6.1.1.9)		
2572232734	t3m_01090	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232734	t3m_01090	Coordinates		5627..8143(+)		
2572232734	t3m_01090	DNA_length		2517bp		
2572232734	t3m_01090	Protein_length		838aa		
2572232734	t3m_01090	GC			0.71	

2572232735	t3m_01091	COG_category	[C] Energy production and conversion			
2572232735	t3m_01091	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)			1.00E-54
2572232735	t3m_01091	pfam00248	Aldo_ket_red			4.10E-64
2572232735	t3m_01091	Locus_type		CDS		
2572232735	t3m_01091	Product_name		Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)		
2572232735	t3m_01091	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232735	t3m_01091	Coordinates		8140..9144(+)		
2572232735	t3m_01091	DNA_length		1005bp		
2572232735	t3m_01091	Protein_length		334aa		
2572232735	t3m_01091	GC			0.69	

2572232736	t3m_01092	KEGG_module	M00020: Serine biosynthesis, glycerate-3P => serine			
2572232736	t3m_01092	Metacyc	SERSYN-PWY: serine biosynthesis			
2572232736	t3m_01092	COG_category	[E] Amino acid transport and metabolism			
2572232736	t3m_01092	COG0560	Phosphoserine phosphatase			8.00E-25
2572232736	t3m_01092	pfam12710	HAD			3.00E-13
2572232736	t3m_01092	EC:3.1.3.3	Phosphoserine phosphatase.			
2572232736	t3m_01092	TIGR01488	Haloacid Dehalogenase superfamily, subfamily IB, phosphoserine phosp			8.10E-28
2572232736	t3m_01092	TIGR01491	HAD-superfamily, subfamily-IB PSPase-like hydrolase, archaeal			2.60E-47
2572232736	t3m_01092	KO:K01079	phosphoserine phosphatase [EC:3.1.3.3]			3.90E-27
2572232736	t3m_01092	Locus_type		CDS		
2572232736	t3m_01092	Product_name		Haloacid Dehalogenase superfamily, subfamily IB, phosphoserine phospl		
2572232736	t3m_01092	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232736	t3m_01092	Coordinates		9137..9796(+)		
2572232736	t3m_01092	DNA_length		660bp		
2572232736	t3m_01092	Protein_length		219aa		
2572232736	t3m_01092	GC			0.71	
2572232737	t3m_01093	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232737	t3m_01093	COG1601	Translation initiation factor 2, beta subunit (eIF-2beta)/eIF-5 N-terminal			3.00E-29
2572232737	t3m_01093	pfam01938	TRAM			7.60E-07
2572232737	t3m_01093	pfam01873	eIF-5_eIF-2B			3.50E-30
2572232737	t3m_01093	TIGR00311	translation initiation factor aIF-2, beta subunit, putative			2.50E-41
2572232737	t3m_01093	KO:K03238	translation initiation factor 2 subunit 2			4.90E-41
2572232737	t3m_01093	ITERM:01956	translation initiation factor 2 subunit beta (aeIF-2b)			
2572232737	t3m_01093	Locus_type		CDS		
2572232737	t3m_01093	Product_name		translation initiation factor 2 subunit beta (aeIF-2b)		
2572232737	t3m_01093	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232737	t3m_01093	Coordinates		9840..10457(+)		
2572232737	t3m_01093	DNA_length		618bp		
2572232737	t3m_01093	Protein_length		205aa		
2572232737	t3m_01093	GC			0.68	
2572232737	t3m_01093	Fused_gene		Yes		
2572232738	t3m_01094	COG_category	[S] Function unknown			

2572232738	t3m_01094	COG3389	Uncharacterized protein conserved in archaea			1.00E-36
2572232738	t3m_01094	pfam06550	DUF1119			8.80E-63
2572232738	t3m_01094	Locus_type		CDS		
2572232738	t3m_01094	Product_name		Uncharacterized protein conserved in archaea		
2572232738	t3m_01094	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232738	t3m_01094	Coordinates		10464..11432(+)		
2572232738	t3m_01094	DNA_length		969bp		
2572232738	t3m_01094	Protein_length		322aa		
2572232738	t3m_01094	GC			0.69	
2572232738	t3m_01094	Transmembrane		Yes		

2572232739	t3m_01095	Metacyc	PWY-5905: hypusine biosynthesis			
2572232739	t3m_01095	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232739	t3m_01095	COG1899	Deoxyhypusine synthase			3.00E-88
2572232739	t3m_01095	pfam01916	DS			3.90E-77
2572232739	t3m_01095	EC:2.5.1.46	Deoxyhypusine synthase.			
2572232739	t3m_01095	TIGR00321	deoxyhypusine synthase			5.00E-83
2572232739	t3m_01095	KO:K00809	deoxyhypusine synthase [EC:2.5.1.46]			0.00E+00
2572232739	t3m_01095	Locus_type		CDS		
2572232739	t3m_01095	Product_name		Deoxyhypusine synthase		
2572232739	t3m_01095	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232739	t3m_01095	Coordinates		11455..12393(+)		
2572232739	t3m_01095	DNA_length		939bp		
2572232739	t3m_01095	Protein_length		312aa		
2572232739	t3m_01095	GC			0.69	

2572232740	t3m_01096	KEGG_module	M00116: Menaquinone biosynthesis, chorismate => menaquinone			
2572232740	t3m_01096	Metacyc	PWY-5837: 1,4-dihydroxy-2-naphthoate biosynthesis I			
2572232740	t3m_01096	Metacyc	PWY-5791: 1,4-dihydroxy-2-naphthoate biosynthesis II (plants)			
2572232740	t3m_01096	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232740	t3m_01096	COG_category	[R] General function prediction only			
2572232740	t3m_01096	COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase supe			1.00E-47
2572232740	t3m_01096	pfam13378	MR_MLE_C			2.60E-15
2572232740	t3m_01096	pfam02746	MR_MLE_N			9.60E-13

2572232740	t3m_01096	EC:4.2.1.113	o-succinylbenzoate synthase.		
2572232740	t3m_01096	TIGR01928	o-succinylbenzoate synthase		2.80E-71
2572232740	t3m_01096	KO:K02549	O-succinylbenzoate synthase [EC:4.2.1.113]		0.00E+00
2572232740	t3m_01096	Locus_type		CDS	
2572232740	t3m_01096	Product_name		o-succinylbenzoate synthase	
2572232740	t3m_01096	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23	
2572232740	t3m_01096	Coordinates		12415..13530(-)	
2572232740	t3m_01096	DNA_length		1116bp	
2572232740	t3m_01096	Protein_length		371aa	
2572232740	t3m_01096	GC		0.7	
2572232741	t3m_01097	Locus_type		tRNA	
2572232741	t3m_01097	Product_name		tRNA_Lys_CTT	
2572232741	t3m_01097	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23	
2572232741	t3m_01097	Coordinates		13647..13720(+)	
2572232741	t3m_01097	DNA_length		74bp	
2572232741	t3m_01097	GC		0.68	
2572232742	t3m_01098	Locus_type		CDS	
2572232742	t3m_01098	Product_name		hypothetical protein	
2572232742	t3m_01098	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23	
2572232742	t3m_01098	Coordinates		13789..14763(+)	
2572232742	t3m_01098	DNA_length		975bp	
2572232742	t3m_01098	Protein_length		324aa	
2572232742	t3m_01098	GC		0.65	
2572232742	t3m_01098	Transmembrane		Yes	
2572232743	t3m_01099	COG_category	[S] Function unknown		
2572232743	t3m_01099	COG3247	Uncharacterized conserved protein		4.00E-04
2572232743	t3m_01099	Locus_type		CDS	
2572232743	t3m_01099	Product_name		Uncharacterized conserved protein	
2572232743	t3m_01099	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23	
2572232743	t3m_01099	Coordinates		14760..15935(-)	
2572232743	t3m_01099	DNA_length		1176bp	

2572232743	t3m_01099	Protein_length		391aa		
2572232743	t3m_01099	GC			0.66	
2572232743	t3m_01099	Transmembrane		Yes		
2572232744	t3m_01100	Locus_type		CDS		
2572232744	t3m_01100	Product_name		hypothetical protein		
2572232744	t3m_01100	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232744	t3m_01100	Coordinates		15939..16232(-)		
2572232744	t3m_01100	DNA_length		294bp		
2572232744	t3m_01100	Protein_length		97aa		
2572232744	t3m_01100	GC			0.65	
2572232745	t3m_01101	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232745	t3m_01101	COG1765	Predicted redox protein, regulator of disulfide bond formation			2.00E-09
2572232745	t3m_01101	pfam02566	OsmC			8.20E-14
2572232745	t3m_01101	KO:K07397	putative redox protein			1.60E-18
2572232745	t3m_01101	Locus_type		CDS		
2572232745	t3m_01101	Product_name		Predicted redox protein, regulator of disulfide bond formation		
2572232745	t3m_01101	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232745	t3m_01101	Coordinates		16415..16816(+)		
2572232745	t3m_01101	DNA_length		402bp		
2572232745	t3m_01101	Protein_length		133aa		
2572232745	t3m_01101	GC			0.63	
2572232745	t3m_01101	Transmembrane		Yes		
2572232746	t3m_01102	COG_category	[Q] Secondary metabolites biosynthesis, transport and catabolism			
2572232746	t3m_01102	COG2761	Predicted dithiol-disulfide isomerase involved in polyketide biosynthesi			2.00E-42
2572232746	t3m_01102	pfam01323	DSBA			4.50E-43
2572232746	t3m_01102	Locus_type		CDS		
2572232746	t3m_01102	Product_name		Predicted dithiol-disulfide isomerase involved in polyketide biosynthesis		
2572232746	t3m_01102	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23		
2572232746	t3m_01102	Coordinates		16834..17475(+)		
2572232746	t3m_01102	DNA_length		642bp		
2572232746	t3m_01102	Protein_length		213aa		

2572232746	t3m_01102	GC		0.66	
2572232747	t3m_01103	COG_category	[C] Energy production and conversion		
2572232747	t3m_01103	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)		1.00E-69
2572232747	t3m_01103	pfam00248	Aldo_ket_red		7.00E-71
2572232747	t3m_01103	Locus_type		CDS	
2572232747	t3m_01103	Product_name		Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	
2572232747	t3m_01103	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23	
2572232747	t3m_01103	Coordinates		17591..18562(+)	
2572232747	t3m_01103	DNA_length		972bp	
2572232747	t3m_01103	Protein_length		323aa	
2572232747	t3m_01103	GC		0.67	
2572232748	t3m_01104	Locus_type		CDS	
2572232748	t3m_01104	Product_name		hypothetical protein	
2572232748	t3m_01104	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23	
2572232748	t3m_01104	Coordinates		18613..24231(-)	
2572232748	t3m_01104	DNA_length		5619bp	
2572232748	t3m_01104	Protein_length		1872aa	
2572232748	t3m_01104	GC		0.65	
2572232748	t3m_01104	Transmembrane		Yes	
2572232749	t3m_01105	Locus_type		CDS	
2572232749	t3m_01105	Product_name		hypothetical protein	
2572232749	t3m_01105	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23	
2572232749	t3m_01105	Coordinates		24994..27759(-)	
2572232749	t3m_01105	DNA_length		2766bp	
2572232749	t3m_01105	Protein_length		921aa	
2572232749	t3m_01105	GC		0.64	
2572232749	t3m_01105	Transmembrane		Yes	
2572232750	t3m_01106	Locus_type		CDS	
2572232750	t3m_01106	Product_name		hypothetical protein	
2572232750	t3m_01106	Scaffold		t3m_contig_70_177_len_28436_read_count_2535366.23	

2572232750	t3m_01106	Coordinates		27959..28087(+)		
2572232750	t3m_01106	DNA_length		129bp		
2572232750	t3m_01106	Protein_length		42aa		
2572232750	t3m_01106	GC			0.58	
2572232751	t3m_01107	pfam02515	CoA_transf_3			1.10E-14
2572232751	t3m_01107	Locus_type		CDS		
2572232751	t3m_01107	Product_name		CoA-transferase family III		
2572232751	t3m_01107	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232751	t3m_01107	Coordinates		1..690(+)		
2572232751	t3m_01107	DNA_length		690bp		
2572232751	t3m_01107	Protein_length		229aa		
2572232751	t3m_01107	GC			0.68	
2572232752	t3m_01108	KEGG_module	M00540: Benzoate degradation, cyclohexanecarboxylic acid =>pimeloyl-CoA			
2572232752	t3m_01108	Metacyc	PWY-6670: citronellol degradation			
2572232752	t3m_01108	Metacyc	CARNMET-PWY: carnitine degradation I			
2572232752	t3m_01108	Metacyc	PWY-6948: sitosterol degradation to androstenedione			
2572232752	t3m_01108	Metacyc	PWY-6946: cholesterol degradation to androstenedione II (cholesterol dehydrogenase)			
2572232752	t3m_01108	Metacyc	PWY-6672: <i>cis</i>-genanyl-CoA degradation			
2572232752	t3m_01108	Metacyc	PWY-6945: cholesterol degradation to androstenedione I (cholesterol oxidase)			
2572232752	t3m_01108	Metacyc	PWY-6993: nicotine degradation II			
2572232752	t3m_01108	Metacyc	PWY-6944: androstenedione degradation			
2572232752	t3m_01108	Metacyc	PWY66-201: nicotine degradation IV			
2572232752	t3m_01108	COG_category	[I] Lipid transport and metabolism			
2572232752	t3m_01108	COG1960	Acyl-CoA dehydrogenases			4.00E-56
2572232752	t3m_01108	pfam02770	Acyl-CoA_dh_M			5.00E-12
2572232752	t3m_01108	pfam02771	Acyl-CoA_dh_N			8.70E-13
2572232752	t3m_01108	pfam00441	Acyl-CoA_dh_1			7.90E-34
2572232752	t3m_01108	EC:1.3.99.-	Oxidoreductases. Acting on the CH-CH group of donors. With other acceptors.			
2572232752	t3m_01108	KO:K04117	cyclohexanecarboxyl-CoA dehydrogenase [EC:1.3.99.-]			0.00E+00
2572232752	t3m_01108	Locus_type		CDS		
2572232752	t3m_01108	Product_name		Acyl-CoA dehydrogenases		
2572232752	t3m_01108	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		

2572232752	t3m_01108	Coordinates		691..1854(+)	
2572232752	t3m_01108	DNA_length		1164bp	
2572232752	t3m_01108	Protein_length		387aa	
2572232752	t3m_01108	GC		0.68	
2572232753	t3m_01109	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572232753	t3m_01109	COG1215	Glycosyltransferases, probably involved in cell wall biogenesis		1.00E-34
2572232753	t3m_01109	pfam13641	Glyco_tranf_2_3		7.90E-30
2572232753	t3m_01109	Locus_type		CDS	
2572232753	t3m_01109	Product_name		Glycosyltransferases, probably involved in cell wall biogenesis	
2572232753	t3m_01109	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24	
2572232753	t3m_01109	Coordinates		1964..4036(-)	
2572232753	t3m_01109	DNA_length		2073bp	
2572232753	t3m_01109	Protein_length		690aa	
2572232753	t3m_01109	GC		0.64	
2572232753	t3m_01109	Transmembrane		Yes	
2572232754	t3m_01110	Locus_type		CDS	
2572232754	t3m_01110	Product_name		hypothetical protein	
2572232754	t3m_01110	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24	
2572232754	t3m_01110	Coordinates		4105..5247(-)	
2572232754	t3m_01110	DNA_length		1143bp	
2572232754	t3m_01110	Protein_length		380aa	
2572232754	t3m_01110	GC		0.62	
2572232754	t3m_01110	Transmembrane		Yes	
2572232755	t3m_01111	Locus_type		CDS	
2572232755	t3m_01111	Product_name		hypothetical protein	
2572232755	t3m_01111	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24	
2572232755	t3m_01111	Coordinates		7734..11042(-)	
2572232755	t3m_01111	DNA_length		3309bp	
2572232755	t3m_01111	Protein_length		1102aa	
2572232755	t3m_01111	GC		0.62	
2572232755	t3m_01111	Transmembrane		Yes	

2572232756	t3m_01112	COG_category	[R] General function prediction only			
2572232756	t3m_01112	COG3291	FOG: PKD repeat			3.00E-06
2572232756	t3m_01112	pfam00801	PKD			5.70E-07
2572232756	t3m_01112	pfam00801	PKD			7.70E-06
2572232756	t3m_01112	pfam00801	PKD			1.70E-06
2572232756	t3m_01112	Locus_type		CDS		
2572232756	t3m_01112	Product_name		FOG: PKD repeat		
2572232756	t3m_01112	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232756	t3m_01112	Coordinates		11265..13760(+)		
2572232756	t3m_01112	DNA_length		2496bp		
2572232756	t3m_01112	Protein_length		831aa		
2572232756	t3m_01112	GC			0.64	
2572232756	t3m_01112	Transmembrane		Yes		

2572232757	t3m_01113	COG_category	[S] Function unknown			
2572232757	t3m_01113	COG1520	FOG: WD40-like repeat			6.00E-15
2572232757	t3m_01113	pfam13360	PQQ_2			1.50E-16
2572232757	t3m_01113	pfam13360	PQQ_2			1.10E-09
2572232757	t3m_01113	pfam13360	PQQ_2			1.40E-15
2572232757	t3m_01113	pfam13360	PQQ_2			3.40E-09
2572232757	t3m_01113	Locus_type		CDS		
2572232757	t3m_01113	Product_name		FOG: WD40-like repeat		
2572232757	t3m_01113	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232757	t3m_01113	Coordinates		13851..16931(+)		
2572232757	t3m_01113	DNA_length		3081bp		
2572232757	t3m_01113	Protein_length		1026aa		
2572232757	t3m_01113	GC			0.65	
2572232757	t3m_01113	Signal_peptide		Yes		

2572232758	t3m_01114	Locus_type		CDS		
2572232758	t3m_01114	Product_name		hypothetical protein		
2572232758	t3m_01114	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232758	t3m_01114	Coordinates		17133..18566(+)		

2572232758	t3m_01114	DNA_length		1434bp		
2572232758	t3m_01114	Protein_length		477aa		
2572232758	t3m_01114	GC			0.64	
2572232758	t3m_01114	Transmembrane		Yes		
2572232759	t3m_01115	Locus_type		CDS		
2572232759	t3m_01115	Product_name		hypothetical protein		
2572232759	t3m_01115	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232759	t3m_01115	Coordinates		18809..20005(+)		
2572232759	t3m_01115	DNA_length		1197bp		
2572232759	t3m_01115	Protein_length		398aa		
2572232759	t3m_01115	GC			0.66	
2572232759	t3m_01115	Transmembrane		Yes		
2572232760	t3m_01116	pfam01814	Hemerythrin			1.00E-05
2572232760	t3m_01116	Locus_type		CDS		
2572232760	t3m_01116	Product_name		Hemerythrin HHE cation binding domain		
2572232760	t3m_01116	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232760	t3m_01116	Coordinates		20393..20932(+)		
2572232760	t3m_01116	DNA_length		540bp		
2572232760	t3m_01116	Protein_length		179aa		
2572232760	t3m_01116	GC			0.66	
2572232761	t3m_01117	Locus_type		CDS		
2572232761	t3m_01117	Product_name		hypothetical protein		
2572232761	t3m_01117	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232761	t3m_01117	Coordinates		21039..21314(+)		
2572232761	t3m_01117	DNA_length		276bp		
2572232761	t3m_01117	Protein_length		91aa		
2572232761	t3m_01117	GC			0.67	
2572232762	t3m_01118	Locus_type		CDS		
2572232762	t3m_01118	Product_name		hypothetical protein		
2572232762	t3m_01118	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		

2572232762	t3m_01118	Coordinates		21446..21985(-)		
2572232762	t3m_01118	DNA_length		540bp		
2572232762	t3m_01118	Protein_length		179aa		
2572232762	t3m_01118	GC			0.64	
2572232762	t3m_01118	Transmembrane		Yes		
2572232763	t3m_01119	KEGG_module	M00153: Cytochrome d ubiquinol oxidase			
2572232763	t3m_01119	Metacyc	PWY-6498: eumelanin biosynthesis			
2572232763	t3m_01119	Metacyc	PWY-6824: justicidin B biosynthesis			
2572232763	t3m_01119	Metacyc	PWY0-1353: succinate to cytochrome <i>bd</i> oxidase electron transfer			
2572232763	t3m_01119	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572232763	t3m_01119	Metacyc	PWY-5476: cornusiin E biosynthesis			
2572232763	t3m_01119	Metacyc	PWY-5466: matairesinol biosynthesis			
2572232763	t3m_01119	Metacyc	PWY-5787: oligomeric urushiol biosynthesis			
2572232763	t3m_01119	Metacyc	PWY-5404: betaxanthin biosynthesis (via dopaxanthin)			
2572232763	t3m_01119	Metacyc	PWY-5439: betacyanin biosynthesis (via dopamine)			
2572232763	t3m_01119	COG_category	[C] Energy production and conversion			
2572232763	t3m_01119	COG1271	Cytochrome bd-type quinol oxidase, subunit 1			2.00E-88
2572232763	t3m_01119	pfam01654	Bac_Ubq_Cox			5.50E-83
2572232763	t3m_01119	EC:1.10.3.-	Oxidoreductases. Acting on diphenols and related substances as donors. With oxygen as acceptor.			
2572232763	t3m_01119	KO:K00425	cytochrome d ubiquinol oxidase subunit I [EC:1.10.3.-]			0.00E+00
2572232763	t3m_01119	ITERM:06137	cytochrome bd-I ubiquinol oxidase subunit 1 apoprotein (EC 1.10.3.10)			
2572232763	t3m_01119	Locus_type		CDS		
2572232763	t3m_01119	Product_name		cytochrome bd-I ubiquinol oxidase subunit 1 apoprotein (EC 1.10.3.10)		
2572232763	t3m_01119	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232763	t3m_01119	Coordinates		22247..23602(+)		
2572232763	t3m_01119	DNA_length		1356bp		
2572232763	t3m_01119	Protein_length		451aa		
2572232763	t3m_01119	GC			0.63	
2572232763	t3m_01119	Transmembrane		Yes		
2572232764	t3m_01120	KEGG_module	M00153: Cytochrome d ubiquinol oxidase			
2572232764	t3m_01120	Metacyc	PWY-5439: betacyanin biosynthesis (via dopamine)			
2572232764	t3m_01120	Metacyc	PWY-6824: justicidin B biosynthesis			

2572232764	t3m_01120	Metacyc	PWY-5466: matairesinol biosynthesis			
2572232764	t3m_01120	Metacyc	PWY0-1353: succinate to cytochrome <i>bd</i> oxidase electron transfer			
2572232764	t3m_01120	Metacyc	PWY-6498: eumelanin biosynthesis			
2572232764	t3m_01120	Metacyc	PWY-5787: oligomeric urushiol biosynthesis			
2572232764	t3m_01120	Metacyc	PWY-5404: betaxanthin biosynthesis (via dopaxanthin)			
2572232764	t3m_01120	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572232764	t3m_01120	Metacyc	PWY-5476: cornusiin E biosynthesis			
2572232764	t3m_01120	EC:1.10.3.-	Oxidoreductases. Acting on diphenols and related substances as donors. With oxygen as acceptor.			
2572232764	t3m_01120	KO:K00426	cytochrome d ubiquinol oxidase subunit II [EC:1.10.3.-]			0.00E+00
2572232764	t3m_01120	Locus_type		CDS		
2572232764	t3m_01120	Product_name		hypothetical protein		
2572232764	t3m_01120	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232764	t3m_01120	Coordinates		23589..24581(+)		
2572232764	t3m_01120	DNA_length		993bp		
2572232764	t3m_01120	Protein_length		330aa		
2572232764	t3m_01120	GC			0.64	
2572232764	t3m_01120	Transmembrane		Yes		
2572232765	t3m_01121	Locus_type		CDS		
2572232765	t3m_01121	Product_name		hypothetical protein		
2572232765	t3m_01121	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232765	t3m_01121	Coordinates		24670..25347(-)		
2572232765	t3m_01121	DNA_length		678bp		
2572232765	t3m_01121	Protein_length		225aa		
2572232765	t3m_01121	GC			0.66	
2572232765	t3m_01121	Transmembrane		Yes		
2572232766	t3m_01122	pfam13191	AAA_16			7.40E-12
2572232766	t3m_01122	Locus_type		CDS		
2572232766	t3m_01122	Product_name		AAA ATPase domain		
2572232766	t3m_01122	Scaffold		t3m_contig_70_180_len_28208_read_count_2610123.24		
2572232766	t3m_01122	Coordinates		25737..28157(+)		
2572232766	t3m_01122	DNA_length		2421bp		
2572232766	t3m_01122	Protein_length		806aa		

2572232766	t3m_01122	GC	0.66
2572232767	t3m_01123	Locus_type	tRNA
2572232767	t3m_01123	Product_name	tRNA_Ile_GAT
2572232767	t3m_01123	Scaffold	t3m_contig_70_180_len_28208_read_count_2610123.24
2572232767	t3m_01123	Coordinates	28148..28207(-)
2572232767	t3m_01123	DNA_length	60bp
2572232767	t3m_01123	GC	0.57
2572232768	t3m_01124	Locus_type	CDS
2572232768	t3m_01124	Product_name	hypothetical protein
2572232768	t3m_01124	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232768	t3m_01124	Coordinates	40..261(+)
2572232768	t3m_01124	DNA_length	222bp
2572232768	t3m_01124	Protein_length	73aa
2572232768	t3m_01124	GC	0.66
2572232769	t3m_01125	Locus_type	CDS
2572232769	t3m_01125	Product_name	hypothetical protein
2572232769	t3m_01125	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232769	t3m_01125	Coordinates	262..546(+)
2572232769	t3m_01125	DNA_length	285bp
2572232769	t3m_01125	Protein_length	94aa
2572232769	t3m_01125	GC	0.67
2572232770	t3m_01126	Locus_type	CDS
2572232770	t3m_01126	Product_name	hypothetical protein
2572232770	t3m_01126	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232770	t3m_01126	Coordinates	547..822(+)
2572232770	t3m_01126	DNA_length	276bp
2572232770	t3m_01126	Protein_length	91aa
2572232770	t3m_01126	GC	0.59
2572232771	t3m_01127	Locus_type	CDS

2572232771	t3m_01127	Product_name		hypothetical protein	
2572232771	t3m_01127	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232771	t3m_01127	Coordinates		823..996(+)	
2572232771	t3m_01127	DNA_length		174bp	
2572232771	t3m_01127	Protein_length		57aa	
2572232771	t3m_01127	GC		0.6	
2572232772	t3m_01128	pfam02796	HTH_7		1.20E-05
2572232772	t3m_01128	Locus_type		CDS	
2572232772	t3m_01128	Product_name		Helix-turn-helix domain of resolvase	
2572232772	t3m_01128	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232772	t3m_01128	Coordinates		1483..1881(+)	
2572232772	t3m_01128	DNA_length		399bp	
2572232772	t3m_01128	Protein_length		132aa	
2572232772	t3m_01128	GC		0.64	
2572232773	t3m_01129	COG_category	[K] Transcription		
2572232773	t3m_01129	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatio		2.00E-19
2572232773	t3m_01129	Locus_type		CDS	
2572232773	t3m_01129	Product_name		Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatior	
2572232773	t3m_01129	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232773	t3m_01129	Coordinates		1857..2786(+)	
2572232773	t3m_01129	DNA_length		930bp	
2572232773	t3m_01129	Protein_length		309aa	
2572232773	t3m_01129	GC		0.66	
2572232774	t3m_01130	Locus_type		CDS	
2572232774	t3m_01130	Product_name		hypothetical protein	
2572232774	t3m_01130	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232774	t3m_01130	Coordinates		2783..3379(+)	
2572232774	t3m_01130	DNA_length		597bp	
2572232774	t3m_01130	Protein_length		198aa	
2572232774	t3m_01130	GC		0.64	

2572232775	t3m_01131	COG_category	[L] Replication, recombination and repair			
2572232775	t3m_01131	COG4974	Site-specific recombinase XerD			3.00E-29
2572232775	t3m_01131	pfam00589	Phage_integrase			1.90E-26
2572232775	t3m_01131	KO:K04763	integrase/recombinase XerD			7.60E-26
2572232775	t3m_01131	Locus_type		CDS		
2572232775	t3m_01131	Product_name		Site-specific recombinase XerD		
2572232775	t3m_01131	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25		
2572232775	t3m_01131	Coordinates		3610..4662(-)		
2572232775	t3m_01131	DNA_length		1053bp		
2572232775	t3m_01131	Protein_length		350aa		
2572232775	t3m_01131	GC			0.65	
2572232776	t3m_01132	Locus_type		CDS		
2572232776	t3m_01132	Product_name		hypothetical protein		
2572232776	t3m_01132	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25		
2572232776	t3m_01132	Coordinates		4843..5232(-)		
2572232776	t3m_01132	DNA_length		390bp		
2572232776	t3m_01132	Protein_length		129aa		
2572232776	t3m_01132	GC			0.64	
2572232777	t3m_01133	Locus_type		CDS		
2572232777	t3m_01133	Product_name		hypothetical protein		
2572232777	t3m_01133	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25		
2572232777	t3m_01133	Coordinates		5329..6225(+)		
2572232777	t3m_01133	DNA_length		897bp		
2572232777	t3m_01133	Protein_length		298aa		
2572232777	t3m_01133	GC			0.67	
2572232778	t3m_01134	Locus_type		CDS		
2572232778	t3m_01134	Product_name		hypothetical protein		
2572232778	t3m_01134	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25		
2572232778	t3m_01134	Coordinates		6235..6828(+)		
2572232778	t3m_01134	DNA_length		594bp		
2572232778	t3m_01134	Protein_length		197aa		

2572232778	t3m_01134	GC	0.63
2572232779	t3m_01135	Locus_type	CDS
2572232779	t3m_01135	Product_name	hypothetical protein
2572232779	t3m_01135	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232779	t3m_01135	Coordinates	6829..7866(+)
2572232779	t3m_01135	DNA_length	1038bp
2572232779	t3m_01135	Protein_length	345aa
2572232779	t3m_01135	GC	0.62
2572232779	t3m_01135	Signal_peptide	Yes
2572232779	t3m_01135	Transmembrane	Yes
2572232780	t3m_01136	Locus_type	CDS
2572232780	t3m_01136	Product_name	hypothetical protein
2572232780	t3m_01136	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232780	t3m_01136	Coordinates	7869..8990(+)
2572232780	t3m_01136	DNA_length	1122bp
2572232780	t3m_01136	Protein_length	373aa
2572232780	t3m_01136	GC	0.63
2572232780	t3m_01136	Transmembrane	Yes
2572232781	t3m_01137	Locus_type	CDS
2572232781	t3m_01137	Product_name	hypothetical protein
2572232781	t3m_01137	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232781	t3m_01137	Coordinates	8999..9697(+)
2572232781	t3m_01137	DNA_length	699bp
2572232781	t3m_01137	Protein_length	232aa
2572232781	t3m_01137	GC	0.65
2572232782	t3m_01138	Locus_type	CDS
2572232782	t3m_01138	Product_name	hypothetical protein
2572232782	t3m_01138	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232782	t3m_01138	Coordinates	9701..11299(+)
2572232782	t3m_01138	DNA_length	1599bp

2572232782	t3m_01138	Protein_length	532aa	
2572232782	t3m_01138	GC		0.63
2572232783	t3m_01139	Locus_type	CDS	
2572232783	t3m_01139	Product_name	hypothetical protein	
2572232783	t3m_01139	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232783	t3m_01139	Coordinates	11374..11670(+)	
2572232783	t3m_01139	DNA_length	297bp	
2572232783	t3m_01139	Protein_length	98aa	
2572232783	t3m_01139	GC		0.62
2572232784	t3m_01140	Locus_type	CDS	
2572232784	t3m_01140	Product_name	hypothetical protein	
2572232784	t3m_01140	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232784	t3m_01140	Coordinates	11671..12312(+)	
2572232784	t3m_01140	DNA_length	642bp	
2572232784	t3m_01140	Protein_length	213aa	
2572232784	t3m_01140	GC		0.68
2572232785	t3m_01141	Locus_type	CDS	
2572232785	t3m_01141	Product_name	hypothetical protein	
2572232785	t3m_01141	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232785	t3m_01141	Coordinates	12492..12719(+)	
2572232785	t3m_01141	DNA_length	228bp	
2572232785	t3m_01141	Protein_length	75aa	
2572232785	t3m_01141	GC		0.68
2572232786	t3m_01142	Locus_type	CDS	
2572232786	t3m_01142	Product_name	hypothetical protein	
2572232786	t3m_01142	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232786	t3m_01142	Coordinates	12716..12916(+)	
2572232786	t3m_01142	DNA_length	201bp	
2572232786	t3m_01142	Protein_length	66aa	
2572232786	t3m_01142	GC		0.65

2572232787	t3m_01143	Locus_type	CDS
2572232787	t3m_01143	Product_name	hypothetical protein
2572232787	t3m_01143	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232787	t3m_01143	Coordinates	12997..13146(+)
2572232787	t3m_01143	DNA_length	150bp
2572232787	t3m_01143	Protein_length	49aa
2572232787	t3m_01143	GC	0.63
2572232788	t3m_01144	Locus_type	CDS
2572232788	t3m_01144	Product_name	hypothetical protein
2572232788	t3m_01144	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232788	t3m_01144	Coordinates	13143..13361(+)
2572232788	t3m_01144	DNA_length	219bp
2572232788	t3m_01144	Protein_length	72aa
2572232788	t3m_01144	GC	0.61
2572232788	t3m_01144	Transmembrane	Yes
2572232789	t3m_01145	Locus_type	CDS
2572232789	t3m_01145	Product_name	hypothetical protein
2572232789	t3m_01145	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232789	t3m_01145	Coordinates	13358..14008(+)
2572232789	t3m_01145	DNA_length	651bp
2572232789	t3m_01145	Protein_length	216aa
2572232789	t3m_01145	GC	0.65
2572232789	t3m_01145	Transmembrane	Yes
2572232790	t3m_01146	Locus_type	CDS
2572232790	t3m_01146	Product_name	hypothetical protein
2572232790	t3m_01146	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232790	t3m_01146	Coordinates	14030..14512(+)
2572232790	t3m_01146	DNA_length	483bp
2572232790	t3m_01146	Protein_length	160aa
2572232790	t3m_01146	GC	0.67

2572232790	t3m_01146	Transmembrane	Yes
2572232791	t3m_01147	Locus_type	CDS
2572232791	t3m_01147	Product_name	hypothetical protein
2572232791	t3m_01147	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232791	t3m_01147	Coordinates	14618..14893(+)
2572232791	t3m_01147	DNA_length	276bp
2572232791	t3m_01147	Protein_length	91aa
2572232791	t3m_01147	GC	0.68
2572232792	t3m_01148	Locus_type	CDS
2572232792	t3m_01148	Product_name	hypothetical protein
2572232792	t3m_01148	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232792	t3m_01148	Coordinates	15164..16021(+)
2572232792	t3m_01148	DNA_length	858bp
2572232792	t3m_01148	Protein_length	285aa
2572232792	t3m_01148	GC	0.64
2572232792	t3m_01148	Transmembrane	Yes
2572232793	t3m_01149	Locus_type	CDS
2572232793	t3m_01149	Product_name	hypothetical protein
2572232793	t3m_01149	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232793	t3m_01149	Coordinates	16097..16435(+)
2572232793	t3m_01149	DNA_length	339bp
2572232793	t3m_01149	Protein_length	112aa
2572232793	t3m_01149	GC	0.62
2572232793	t3m_01149	Transmembrane	Yes
2572232794	t3m_01150	Locus_type	CDS
2572232794	t3m_01150	Product_name	hypothetical protein
2572232794	t3m_01150	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232794	t3m_01150	Coordinates	16436..16687(+)
2572232794	t3m_01150	DNA_length	252bp
2572232794	t3m_01150	Protein_length	83aa

2572232794	t3m_01150	GC		0.65
2572232795	t3m_01151	Locus_type	CDS	
2572232795	t3m_01151	Product_name	hypothetical protein	
2572232795	t3m_01151	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232795	t3m_01151	Coordinates	16693..17022(+)	
2572232795	t3m_01151	DNA_length	330bp	
2572232795	t3m_01151	Protein_length	109aa	
2572232795	t3m_01151	GC		0.64
2572232796	t3m_01152	Locus_type	CDS	
2572232796	t3m_01152	Product_name	hypothetical protein	
2572232796	t3m_01152	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232796	t3m_01152	Coordinates	17042..17305(+)	
2572232796	t3m_01152	DNA_length	264bp	
2572232796	t3m_01152	Protein_length	87aa	
2572232796	t3m_01152	GC		0.67
2572232797	t3m_01153	Locus_type	CDS	
2572232797	t3m_01153	Product_name	hypothetical protein	
2572232797	t3m_01153	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232797	t3m_01153	Coordinates	17310..17528(+)	
2572232797	t3m_01153	DNA_length	219bp	
2572232797	t3m_01153	Protein_length	72aa	
2572232797	t3m_01153	GC		0.64
2572232797	t3m_01153	Transmembrane	Yes	
2572232798	t3m_01154	Locus_type	CDS	
2572232798	t3m_01154	Product_name	hypothetical protein	
2572232798	t3m_01154	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232798	t3m_01154	Coordinates	17531..17899(+)	
2572232798	t3m_01154	DNA_length	369bp	
2572232798	t3m_01154	Protein_length	122aa	
2572232798	t3m_01154	GC		0.67

2572232799	t3m_01155	Locus_type	CDS
2572232799	t3m_01155	Product_name	hypothetical protein
2572232799	t3m_01155	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232799	t3m_01155	Coordinates	17900..18385(+)
2572232799	t3m_01155	DNA_length	486bp
2572232799	t3m_01155	Protein_length	161aa
2572232799	t3m_01155	GC	0.61

2572232800	t3m_01156	Locus_type	CDS
2572232800	t3m_01156	Product_name	hypothetical protein
2572232800	t3m_01156	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232800	t3m_01156	Coordinates	18390..18599(+)
2572232800	t3m_01156	DNA_length	210bp
2572232800	t3m_01156	Protein_length	69aa
2572232800	t3m_01156	GC	0.61

2572232801	t3m_01157	Locus_type	CDS
2572232801	t3m_01157	Product_name	hypothetical protein
2572232801	t3m_01157	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232801	t3m_01157	Coordinates	18600..18842(+)
2572232801	t3m_01157	DNA_length	243bp
2572232801	t3m_01157	Protein_length	80aa
2572232801	t3m_01157	GC	0.63

2572232802	t3m_01158	Locus_type	CDS
2572232802	t3m_01158	Product_name	hypothetical protein
2572232802	t3m_01158	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232802	t3m_01158	Coordinates	18843..19214(+)
2572232802	t3m_01158	DNA_length	372bp
2572232802	t3m_01158	Protein_length	123aa
2572232802	t3m_01158	GC	0.61

2572232803	t3m_01159	Locus_type	CDS

2572232803	t3m_01159	Product_name	hypothetical protein
2572232803	t3m_01159	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232803	t3m_01159	Coordinates	19215..19388(+)
2572232803	t3m_01159	DNA_length	174bp
2572232803	t3m_01159	Protein_length	57aa
2572232803	t3m_01159	GC	0.64
2572232803	t3m_01159	Transmembrane	Yes
2572232804	t3m_01160	Locus_type	CDS
2572232804	t3m_01160	Product_name	hypothetical protein
2572232804	t3m_01160	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232804	t3m_01160	Coordinates	19385..19600(+)
2572232804	t3m_01160	DNA_length	216bp
2572232804	t3m_01160	Protein_length	71aa
2572232804	t3m_01160	GC	0.62
2572232805	t3m_01161	Locus_type	CDS
2572232805	t3m_01161	Product_name	hypothetical protein
2572232805	t3m_01161	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232805	t3m_01161	Coordinates	19601..19843(+)
2572232805	t3m_01161	DNA_length	243bp
2572232805	t3m_01161	Protein_length	80aa
2572232805	t3m_01161	GC	0.62
2572232806	t3m_01162	Locus_type	CDS
2572232806	t3m_01162	Product_name	hypothetical protein
2572232806	t3m_01162	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232806	t3m_01162	Coordinates	19882..20172(+)
2572232806	t3m_01162	DNA_length	291bp
2572232806	t3m_01162	Protein_length	96aa
2572232806	t3m_01162	GC	0.61
2572232806	t3m_01162	Transmembrane	Yes
2572232807	t3m_01163	Locus_type	CDS

2572232807	t3m_01163	Product_name	hypothetical protein
2572232807	t3m_01163	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232807	t3m_01163	Coordinates	20183..20461(+)
2572232807	t3m_01163	DNA_length	279bp
2572232807	t3m_01163	Protein_length	92aa
2572232807	t3m_01163	GC	0.59
2572232807	t3m_01163	Transmembrane	Yes
2572232808	t3m_01164	Locus_type	CDS
2572232808	t3m_01164	Product_name	hypothetical protein
2572232808	t3m_01164	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232808	t3m_01164	Coordinates	20481..20942(+)
2572232808	t3m_01164	DNA_length	462bp
2572232808	t3m_01164	Protein_length	153aa
2572232808	t3m_01164	GC	0.61
2572232808	t3m_01164	Transmembrane	Yes
2572232809	t3m_01165	Locus_type	CDS
2572232809	t3m_01165	Product_name	hypothetical protein
2572232809	t3m_01165	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232809	t3m_01165	Coordinates	20936..21394(+)
2572232809	t3m_01165	DNA_length	459bp
2572232809	t3m_01165	Protein_length	152aa
2572232809	t3m_01165	GC	0.68
2572232810	t3m_01166	Locus_type	CDS
2572232810	t3m_01166	Product_name	hypothetical protein
2572232810	t3m_01166	Scaffold	t3m_contig_70_195_len_26934_read_count_2495649.25
2572232810	t3m_01166	Coordinates	21395..21793(+)
2572232810	t3m_01166	DNA_length	399bp
2572232810	t3m_01166	Protein_length	132aa
2572232810	t3m_01166	GC	0.66
2572232811	t3m_01167	Locus_type	CDS

2572232811	t3m_01167	Product_name		hypothetical protein	
2572232811	t3m_01167	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232811	t3m_01167	Coordinates		21796..22047(+)	
2572232811	t3m_01167	DNA_length		252bp	
2572232811	t3m_01167	Protein_length		83aa	
2572232811	t3m_01167	GC		0.6	
2572232811	t3m_01167	Transmembrane		Yes	
2572232812	t3m_01168	Locus_type		CDS	
2572232812	t3m_01168	Product_name		hypothetical protein	
2572232812	t3m_01168	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232812	t3m_01168	Coordinates		22078..23802(+)	
2572232812	t3m_01168	DNA_length		1725bp	
2572232812	t3m_01168	Protein_length		574aa	
2572232812	t3m_01168	GC		0.6	
2572232812	t3m_01168	Transmembrane		Yes	
2572232813	t3m_01169	Locus_type		CDS	
2572232813	t3m_01169	Product_name		hypothetical protein	
2572232813	t3m_01169	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232813	t3m_01169	Coordinates		23819..25030(+)	
2572232813	t3m_01169	DNA_length		1212bp	
2572232813	t3m_01169	Protein_length		403aa	
2572232813	t3m_01169	GC		0.61	
2572232813	t3m_01169	Transmembrane		Yes	
2572232814	t3m_01170	pfam00801	PKD		3.40E-07
2572232814	t3m_01170	Locus_type		CDS	
2572232814	t3m_01170	Product_name		PKD domain	
2572232814	t3m_01170	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25	
2572232814	t3m_01170	Coordinates		25060..26058(+)	
2572232814	t3m_01170	DNA_length		999bp	
2572232814	t3m_01170	Protein_length		332aa	
2572232814	t3m_01170	GC		0.62	

2572232814	t3m_01170	Transmembrane		Yes		
2572232815	t3m_01171	Locus_type		CDS		
2572232815	t3m_01171	Product_name		hypothetical protein		
2572232815	t3m_01171	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25		
2572232815	t3m_01171	Coordinates		26117..26533(+)		
2572232815	t3m_01171	DNA_length		417bp		
2572232815	t3m_01171	Protein_length		138aa		
2572232815	t3m_01171	GC			0.65	
2572232816	t3m_01172	Locus_type		CDS		
2572232816	t3m_01172	Product_name		hypothetical protein		
2572232816	t3m_01172	Scaffold		t3m_contig_70_195_len_26934_read_count_2495649.25		
2572232816	t3m_01172	Coordinates		26534..26875(+)		
2572232816	t3m_01172	DNA_length		342bp		
2572232816	t3m_01172	Protein_length		113aa		
2572232816	t3m_01172	GC			0.61	
2572232817	t3m_01173	COG_category	[R] General function prediction only			
2572232817	t3m_01173	COG1938	Archaeal enzymes of ATP-grasp superfamily			2.00E-39
2572232817	t3m_01173	pfam09754	PAC2			2.50E-28
2572232817	t3m_01173	TIGR00161	TIGR00161 family protein			7.10E-44
2572232817	t3m_01173	KO:K06869	uncharacterized protein			0.00E+00
2572232817	t3m_01173	Locus_type		CDS		
2572232817	t3m_01173	Product_name		Archaeal enzymes of ATP-grasp superfamily		
2572232817	t3m_01173	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232817	t3m_01173	Coordinates		241..1056(-)		
2572232817	t3m_01173	DNA_length		816bp		
2572232817	t3m_01173	Protein_length		271aa		
2572232817	t3m_01173	GC			0.67	
2572232818	t3m_01174	Locus_type		CDS		
2572232818	t3m_01174	Product_name		hypothetical protein		
2572232818	t3m_01174	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		

2572232818	t3m_01174	Coordinates		1061..1420(-)	
2572232818	t3m_01174	DNA_length		360bp	
2572232818	t3m_01174	Protein_length		119aa	
2572232818	t3m_01174	GC		0.67	
2572232819	t3m_01175	COG_category	[K] Transcription		
2572232819	t3m_01175	COG1709	Predicted transcriptional regulator		6.00E-66
2572232819	t3m_01175	pfam13560	HTH_31		1.10E-08
2572232819	t3m_01175	KO:K07731	putative transcriptional regulator		0.00E+00
2572232819	t3m_01175	Locus_type		CDS	
2572232819	t3m_01175	Product_name		Predicted transcriptional regulator	
2572232819	t3m_01175	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232819	t3m_01175	Coordinates		1772..2461(+)	
2572232819	t3m_01175	DNA_length		690bp	
2572232819	t3m_01175	Protein_length		229aa	
2572232819	t3m_01175	GC		0.69	
2572232820	t3m_01176	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway		
2572232820	t3m_01176	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone		
2572232820	t3m_01176	Metacyc	PWY-6174: mevalonate pathway II (archaea)		
2572232820	t3m_01176	Metacyc	PWY66-367: ketogenesis		
2572232820	t3m_01176	Metacyc	PWY-922: mevalonate pathway I		
2572232820	t3m_01176	IMG_pathway	178: Mevalonate pathway for isopentenyl pyrophopsphate synthesis		
2572232820	t3m_01176	IMG_pathway	591: Archaeal mevalonate pathway for isopentenyl pyrophosphate synthesis		
2572232820	t3m_01176	COG_category	[I] Lipid transport and metabolism		
2572232820	t3m_01176	COG3425	3-hydroxy-3-methylglutaryl CoA synthase		1.00E-103
2572232820	t3m_01176	pfam01154	HMG_CoA_synt_N		1.10E-06
2572232820	t3m_01176	pfam08541	ACP_syn_III_C		2.30E-10
2572232820	t3m_01176	EC:2.3.3.10	Hydroxymethylglutaryl-CoA synthase.		
2572232820	t3m_01176	TIGR00748	hydroxymethylglutaryl-CoA synthase, putative		0.00E+00
2572232820	t3m_01176	KO:K01641	hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]		0.00E+00
2572232820	t3m_01176	ITERM:00461	hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)		
2572232820	t3m_01176	Locus_type		CDS	
2572232820	t3m_01176	Product_name		hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)	

2572232820	t3m_01176	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232820	t3m_01176	Coordinates		2480..3532(+)	
2572232820	t3m_01176	DNA_length		1053bp	
2572232820	t3m_01176	Protein_length		350aa	
2572232820	t3m_01176	GC		0.69	
2572232821	t3m_01177	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone		
2572232821	t3m_01177	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle		
2572232821	t3m_01177	KEGG_module	M00373: Ethylmalonyl pathway		
2572232821	t3m_01177	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway		
2572232821	t3m_01177	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2572232821	t3m_01177	Metacyc	PWY-922: mevalonate pathway I		
2572232821	t3m_01177	Metacyc	PWY-5741: ethylmalonyl pathway		
2572232821	t3m_01177	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate		
2572232821	t3m_01177	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2572232821	t3m_01177	Metacyc	PWY66-367: ketogenesis		
2572232821	t3m_01177	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2572232821	t3m_01177	Metacyc	PWY66-368: ketolysis		
2572232821	t3m_01177	Metacyc	PWY-6876: isopropanol biosynthesis		
2572232821	t3m_01177	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II		
2572232821	t3m_01177	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2572232821	t3m_01177	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis		
2572232821	t3m_01177	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2572232821	t3m_01177	Metacyc	PWY-6583: pyruvate fermentation to butanol I		
2572232821	t3m_01177	Metacyc	PWY-6174: mevalonate pathway II (archaea)		
2572232821	t3m_01177	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis		
2572232821	t3m_01177	Metacyc	PWY-5177: glutaryl-CoA degradation		
2572232821	t3m_01177	Metacyc	PWY-6883: pyruvate fermentation to butanol II		
2572232821	t3m_01177	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2572232821	t3m_01177	Metacyc	PWY-7003: glycerol degradation to butanol		
2572232821	t3m_01177	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)		
2572232821	t3m_01177	COG_category	[I] Lipid transport and metabolism		
2572232821	t3m_01177	COG0183	Acetyl-CoA acetyltransferase		3.00E-65
2572232821	t3m_01177	pfam00108	Thiolase_N		6.70E-06

2572232821	t3m_01177	pfam02803	Thiolase_C		7.20E-09
2572232821	t3m_01177	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.		
2572232821	t3m_01177	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]		0.00E+00
2572232821	t3m_01177	Locus_type		CDS	
2572232821	t3m_01177	Product_name		Acetyl-CoA acetyltransferase	
2572232821	t3m_01177	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232821	t3m_01177	Coordinates		3535..4704(+)	
2572232821	t3m_01177	DNA_length		1170bp	
2572232821	t3m_01177	Protein_length		389aa	
2572232821	t3m_01177	GC		0.7	
2572232822	t3m_01178	COG_category	[R] General function prediction only		
2572232822	t3m_01178	COG1545	Predicted nucleic-acid-binding protein containing a Zn-ribbon		9.00E-30
2572232822	t3m_01178	pfam12172	DUF35_N		5.40E-08
2572232822	t3m_01178	pfam01796	DUF35		4.50E-17
2572232822	t3m_01178	Locus_type		CDS	
2572232822	t3m_01178	Product_name		Predicted nucleic-acid-binding protein containing a Zn-ribbon	
2572232822	t3m_01178	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232822	t3m_01178	Coordinates		4714..5205(+)	
2572232822	t3m_01178	DNA_length		492bp	
2572232822	t3m_01178	Protein_length		163aa	
2572232822	t3m_01178	GC		0.67	
2572232823	t3m_01179	pfam05763	DUF835		9.10E-07
2572232823	t3m_01179	Locus_type		CDS	
2572232823	t3m_01179	Product_name		Protein of unknown function (DUF835)	
2572232823	t3m_01179	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232823	t3m_01179	Coordinates		5202..5990(+)	
2572232823	t3m_01179	DNA_length		789bp	
2572232823	t3m_01179	Protein_length		262aa	
2572232823	t3m_01179	GC		0.73	
2572232824	t3m_01180	COG_category	[V] Defense mechanisms		
2572232824	t3m_01180	COG1680	Beta-lactamase class C and other penicillin binding proteins		1.00E-45

2572232824	t3m_01180	pfam00144	Beta-lactamase			1.20E-63
2572232824	t3m_01180	Locus_type		CDS		
2572232824	t3m_01180	Product_name		Beta-lactamase class C and other penicillin binding proteins		
2572232824	t3m_01180	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232824	t3m_01180	Coordinates		5994..7466(-)		
2572232824	t3m_01180	DNA_length		1473bp		
2572232824	t3m_01180	Protein_length		490aa		
2572232824	t3m_01180	GC			0.69	
2572232825	t3m_01181	Locus_type		CDS		
2572232825	t3m_01181	Product_name		hypothetical protein		
2572232825	t3m_01181	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232825	t3m_01181	Coordinates		7665..8729(+)		
2572232825	t3m_01181	DNA_length		1065bp		
2572232825	t3m_01181	Protein_length		354aa		
2572232825	t3m_01181	GC			0.71	
2572232826	t3m_01182	COG_category	[S] Function unknown			
2572232826	t3m_01182	COG1628	Uncharacterized conserved protein			7.00E-30
2572232826	t3m_01182	pfam01949	DUF99			4.20E-42
2572232826	t3m_01182	KO:K09120	hypothetical protein			8.30E-24
2572232826	t3m_01182	Locus_type		CDS		
2572232826	t3m_01182	Product_name		Uncharacterized conserved protein		
2572232826	t3m_01182	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232826	t3m_01182	Coordinates		8867..9418(-)		
2572232826	t3m_01182	DNA_length		552bp		
2572232826	t3m_01182	Protein_length		183aa		
2572232826	t3m_01182	GC			0.73	
2572232827	t3m_01183	pfam13620	CarboxypepD_reg			1.00E-06
2572232827	t3m_01183	Locus_type		CDS		
2572232827	t3m_01183	Product_name		Carboxypeptidase regulatory-like domain		
2572232827	t3m_01183	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232827	t3m_01183	Coordinates		9497..10423(+)		

2572232827	t3m_01183	DNA_length		927bp		
2572232827	t3m_01183	Protein_length		308aa		
2572232827	t3m_01183	GC			0.73	
2572232827	t3m_01183	Transmembrane		Yes		
2572232828	t3m_01184	COG_category	[S] Function unknown			
2572232828	t3m_01184	COG4911	Uncharacterized conserved protein			5.00E-13
2572232828	t3m_01184	pfam09969	DUF2203			6.80E-25
2572232828	t3m_01184	Locus_type		CDS		
2572232828	t3m_01184	Product_name		Uncharacterized conserved protein		
2572232828	t3m_01184	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232828	t3m_01184	Coordinates		10420..10911(-)		
2572232828	t3m_01184	DNA_length		492bp		
2572232828	t3m_01184	Protein_length		163aa		
2572232828	t3m_01184	GC			0.72	
2572232829	t3m_01185	Metacyc	THREONINE-DEG2-PWY: threonine degradation II			
2572232829	t3m_01185	COG_category	[H] Coenzyme transport and metabolism			
2572232829	t3m_01185	COG0156	7-keto-8-aminopelargonate synthetase and related enzymes			7.00E-116
2572232829	t3m_01185	pfam00155	Aminotran_1_2			1.70E-59
2572232829	t3m_01185	EC:2.3.1.29	Glycine C-acetyltransferase.			
2572232829	t3m_01185	TIGR00858	8-amino-7-oxononanoate synthase			7.00E-119
2572232829	t3m_01185	TIGR01825	pyridoxal phosphate-dependent acyltransferase, putative			0.00E+00
2572232829	t3m_01185	KO:K00639	glycine C-acetyltransferase [EC:2.3.1.29]			0.00E+00
2572232829	t3m_01185	Locus_type		CDS		
2572232829	t3m_01185	Product_name		2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29)		
2572232829	t3m_01185	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232829	t3m_01185	Coordinates		10990..12183(-)		
2572232829	t3m_01185	DNA_length		1194bp		
2572232829	t3m_01185	Protein_length		397aa		
2572232829	t3m_01185	GC			0.69	
2572232830	t3m_01186	Metacyc	PWY-5443: aminopropanol phosphate biosynthesis			
2572232830	t3m_01186	Metacyc	THRDLCTCAT-PWY: threonine degradation III (to methylglyoxal)			

2572232830	t3m_01186	Metacyc	THREONINE-DEG2-PWY: threonine degradation II		
2572232830	t3m_01186	IMG_pathway	177: L-threonine conversion to glycine and acetyl-CoA		
2572232830	t3m_01186	COG_category	[E] Amino acid transport and metabolism		
2572232830	t3m_01186	COG_category	[R] General function prediction only		
2572232830	t3m_01186	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases		4.00E-65
2572232830	t3m_01186	pfam00107	ADH_zinc_N		1.00E-26
2572232830	t3m_01186	pfam08240	ADH_N		1.60E-30
2572232830	t3m_01186	EC:1.1.1.103	L-threonine 3-dehydrogenase.		
2572232830	t3m_01186	TIGR00692	L-threonine 3-dehydrogenase		7.70E-124
2572232830	t3m_01186	TIGR01202	2-desacetyl-2-hydroxyethyl bacteriochlorophyllide A dehydrogenase		1.30E-20
2572232830	t3m_01186	KO:K00060	threonine 3-dehydrogenase [EC:1.1.1.103]		0.00E+00
2572232830	t3m_01186	ITERM:00465	L-threonine 3-dehydrogenase (EC 1.1.1.103)		
2572232830	t3m_01186	Locus_type		CDS	
2572232830	t3m_01186	Product_name		L-threonine 3-dehydrogenase (EC 1.1.1.103)	
2572232830	t3m_01186	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232830	t3m_01186	Coordinates		12189..13250(-)	
2572232830	t3m_01186	DNA_length		1062bp	
2572232830	t3m_01186	Protein_length		353aa	
2572232830	t3m_01186	GC		0.68	

2572232831	t3m_01187	KEGG_module	M00179: Ribosome, archaea		
2572232831	t3m_01187	KEGG_module	M00178: Ribosome, bacteria		
2572232831	t3m_01187	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232831	t3m_01187	COG0087	Ribosomal protein L3		4.00E-36
2572232831	t3m_01187	pfam00297	Ribosomal_L3		1.40E-62
2572232831	t3m_01187	TIGR03626	archaeal ribosomal protein L3		1.70E-111
2572232831	t3m_01187	KO:K02906	large subunit ribosomal protein L3		0.00E+00
2572232831	t3m_01187	Locus_type		CDS	
2572232831	t3m_01187	Product_name		LSU ribosomal protein L3P	
2572232831	t3m_01187	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232831	t3m_01187	Coordinates		13554..14495(+)	
2572232831	t3m_01187	DNA_length		942bp	
2572232831	t3m_01187	Protein_length		313aa	
2572232831	t3m_01187	GC		0.68	

2572232832	t3m_01188	KEGG_module	M00177: Ribosome, eukaryotes			
2572232832	t3m_01188	KEGG_module	M00179: Ribosome, archaea			
2572232832	t3m_01188	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232832	t3m_01188	COG0088	Ribosomal protein L4			1.00E-27
2572232832	t3m_01188	pfam00573	Ribosomal_L4			3.50E-39
2572232832	t3m_01188	TIGR03672	50S ribosomal protein L4P			6.70E-87
2572232832	t3m_01188	KO:K02930	large subunit ribosomal protein L4e			0.00E+00
2572232832	t3m_01188	ITERM:00203	LSU ribosomal protein L4P			
2572232832	t3m_01188	Locus_type		CDS		
2572232832	t3m_01188	Product_name		LSU ribosomal protein L4P		
2572232832	t3m_01188	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232832	t3m_01188	Coordinates		14498..15331(+)		
2572232832	t3m_01188	DNA_length		834bp		
2572232832	t3m_01188	Protein_length		277aa		
2572232832	t3m_01188	GC			0.74	
2572232833	t3m_01189	KEGG_module	M00178: Ribosome, bacteria			
2572232833	t3m_01189	KEGG_module	M00179: Ribosome, archaea			
2572232833	t3m_01189	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232833	t3m_01189	COG0089	Ribosomal protein L23			3.00E-12
2572232833	t3m_01189	pfam00276	Ribosomal_L23			4.80E-13
2572232833	t3m_01189	KO:K02892	large subunit ribosomal protein L23			1.80E-13
2572232833	t3m_01189	Locus_type		CDS		
2572232833	t3m_01189	Product_name		Ribosomal protein L23		
2572232833	t3m_01189	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232833	t3m_01189	Coordinates		15328..15591(+)		
2572232833	t3m_01189	DNA_length		264bp		
2572232833	t3m_01189	Protein_length		87aa		
2572232833	t3m_01189	GC			0.62	
2572232834	t3m_01190	KEGG_module	M00179: Ribosome, archaea			
2572232834	t3m_01190	KEGG_module	M00178: Ribosome, bacteria			
2572232834	t3m_01190	COG_category	[J] Translation, ribosomal structure and biogenesis			

2572232834	t3m_01190	COG0090	Ribosomal protein L2			2.00E-52
2572232834	t3m_01190	pfam00181	Ribosomal_L2			2.80E-06
2572232834	t3m_01190	pfam03947	Ribosomal_L2_C			6.20E-39
2572232834	t3m_01190	KO:K02886	large subunit ribosomal protein L2			0.00E+00
2572232834	t3m_01190	Locus_type		CDS		
2572232834	t3m_01190	Product_name		Ribosomal protein L2		
2572232834	t3m_01190	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232834	t3m_01190	Coordinates		15591..16319(+)		
2572232834	t3m_01190	DNA_length		729bp		
2572232834	t3m_01190	Protein_length		242aa		
2572232834	t3m_01190	GC			0.72	
2572232835	t3m_01191	KEGG_module	M00179: Ribosome, archaea			
2572232835	t3m_01191	KEGG_module	M00178: Ribosome, bacteria			
2572232835	t3m_01191	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232835	t3m_01191	COG0185	Ribosomal protein S19			2.00E-23
2572232835	t3m_01191	pfam00203	Ribosomal_S19			2.40E-23
2572232835	t3m_01191	TIGR01025	ribosomal protein S19(archaeal)/S15(eukaryotic)			6.90E-53
2572232835	t3m_01191	KO:K02965	small subunit ribosomal protein S19			2.40E-39
2572232835	t3m_01191	ITERM:00334	SSU ribosomal protein S19P			
2572232835	t3m_01191	Locus_type		CDS		
2572232835	t3m_01191	Product_name		SSU ribosomal protein S19P		
2572232835	t3m_01191	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232835	t3m_01191	Coordinates		16325..16750(+)		
2572232835	t3m_01191	DNA_length		426bp		
2572232835	t3m_01191	Protein_length		141aa		
2572232835	t3m_01191	GC			0.68	
2572232836	t3m_01192	KEGG_module	M00179: Ribosome, archaea			
2572232836	t3m_01192	KEGG_module	M00178: Ribosome, bacteria			
2572232836	t3m_01192	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232836	t3m_01192	COG0091	Ribosomal protein L22			2.00E-21
2572232836	t3m_01192	pfam00237	Ribosomal_L22			2.70E-33
2572232836	t3m_01192	TIGR01038	ribosomal protein L22(archaeal)/L17(eukaryotic/archaeal)			1.40E-47

2572232836	t3m_01192	KO:K02890	large subunit ribosomal protein L22		6.50E-30
2572232836	t3m_01192	Locus_type		CDS	
2572232836	t3m_01192	Product_name		ribosomal protein L22(archaeal)/L17(eukaryotic/archaeal)	
2572232836	t3m_01192	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232836	t3m_01192	Coordinates		16767..17225(+)	
2572232836	t3m_01192	DNA_length		459bp	
2572232836	t3m_01192	Protein_length		152aa	
2572232836	t3m_01192	GC		0.69	
2572232837	t3m_01193	KEGG_module	M00178: Ribosome, bacteria		
2572232837	t3m_01193	KEGG_module	M00179: Ribosome, archaea		
2572232837	t3m_01193	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232837	t3m_01193	COG0092	Ribosomal protein S3		3.00E-50
2572232837	t3m_01193	pfam00189	Ribosomal_S3_C		2.50E-18
2572232837	t3m_01193	pfam07650	KH_2		9.50E-09
2572232837	t3m_01193	TIGR01009	ribosomal protein S3, bacterial type		8.60E-30
2572232837	t3m_01193	TIGR01008	ribosomal protein S3, eukaryotic/archaeal type		2.60E-76
2572232837	t3m_01193	KO:K02982	small subunit ribosomal protein S3		0.00E+00
2572232837	t3m_01193	Locus_type		CDS	
2572232837	t3m_01193	Product_name		SSU ribosomal protein S3P	
2572232837	t3m_01193	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232837	t3m_01193	Coordinates		17222..17914(+)	
2572232837	t3m_01193	DNA_length		693bp	
2572232837	t3m_01193	Protein_length		230aa	
2572232837	t3m_01193	GC		0.68	
2572232838	t3m_01194	KEGG_module	M00179: Ribosome, archaea		
2572232838	t3m_01194	KEGG_module	M00178: Ribosome, bacteria		
2572232838	t3m_01194	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232838	t3m_01194	COG0255	Ribosomal protein L29		6.00E-05
2572232838	t3m_01194	pfam00831	Ribosomal_L29		1.50E-11
2572232838	t3m_01194	TIGR00012	ribosomal protein L29		1.20E-15
2572232838	t3m_01194	KO:K02904	large subunit ribosomal protein L29		1.60E-10
2572232838	t3m_01194	ITERM:00255	LSU ribosomal protein L29P		

2572232838	t3m_01194	Locus_type		CDS		
2572232838	t3m_01194	Product_name		LSU ribosomal protein L29P		
2572232838	t3m_01194	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232838	t3m_01194	Coordinates		17911..18135(+)		
2572232838	t3m_01194	DNA_length		225bp		
2572232838	t3m_01194	Protein_length		74aa		
2572232838	t3m_01194	GC			0.72	
2572232839	t3m_01195	pfam01868	UPF0086			1.80E-05
2572232839	t3m_01195	Locus_type		CDS		
2572232839	t3m_01195	Product_name		Domain of unknown function UPF0086		
2572232839	t3m_01195	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232839	t3m_01195	Coordinates		18155..18481(+)		
2572232839	t3m_01195	DNA_length		327bp		
2572232839	t3m_01195	Protein_length		108aa		
2572232839	t3m_01195	GC			0.68	
2572232840	t3m_01196	KEGG_module	M00179: Ribosome, archaea			
2572232840	t3m_01196	KEGG_module	M00178: Ribosome, bacteria			
2572232840	t3m_01196	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232840	t3m_01196	COG0186	Ribosomal protein S17			2.00E-20
2572232840	t3m_01196	pfam00366	Ribosomal_S17			1.40E-20
2572232840	t3m_01196	TIGR03630	archaeal ribosomal protein S17P			4.30E-45
2572232840	t3m_01196	KO:K02961	small subunit ribosomal protein S17			2.40E-31
2572232840	t3m_01196	Locus_type		CDS		
2572232840	t3m_01196	Product_name		SSU ribosomal protein S17P		
2572232840	t3m_01196	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232840	t3m_01196	Coordinates		18478..18906(+)		
2572232840	t3m_01196	DNA_length		429bp		
2572232840	t3m_01196	Protein_length		142aa		
2572232840	t3m_01196	GC			0.72	
2572232841	t3m_01197	KEGG_module	M00179: Ribosome, archaea			
2572232841	t3m_01197	KEGG_module	M00178: Ribosome, bacteria			

2572232841	t3m_01197	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232841	t3m_01197	COG0093	Ribosomal protein L14			7.00E-30
2572232841	t3m_01197	pfam00238	Ribosomal_L14			8.10E-34
2572232841	t3m_01197	TIGR03673	50S ribosomal protein L14P			4.70E-63
2572232841	t3m_01197	KO:K02874	large subunit ribosomal protein L14			0.00E+00
2572232841	t3m_01197	Locus_type		CDS		
2572232841	t3m_01197	Product_name		LSU ribosomal protein L14P		
2572232841	t3m_01197	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232841	t3m_01197	Coordinates		18903..19301(+)		
2572232841	t3m_01197	DNA_length		399bp		
2572232841	t3m_01197	Protein_length		132aa		
2572232841	t3m_01197	GC			0.69	
2572232842	t3m_01198	TIGR01080	ribosomal protein L24p/L26e, archaeal/eukaryotic			8.00E-31
2572232842	t3m_01198	Locus_type		CDS		
2572232842	t3m_01198	Product_name		ribosomal protein L24p/L26e, archaeal/eukaryotic		
2572232842	t3m_01198	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232842	t3m_01198	Coordinates		19316..19909(+)		
2572232842	t3m_01198	DNA_length		594bp		
2572232842	t3m_01198	Protein_length		197aa		
2572232842	t3m_01198	GC			0.7	
2572232843	t3m_01199	KEGG_module	M00179: Ribosome, archaea			
2572232843	t3m_01199	KEGG_module	M00177: Ribosome, eukaryotes			
2572232843	t3m_01199	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232843	t3m_01199	COG1471	Ribosomal protein S4E			1.00E-61
2572232843	t3m_01199	pfam00900	Ribosomal_S4e			9.10E-23
2572232843	t3m_01199	pfam01479	S4			1.10E-05
2572232843	t3m_01199	pfam08071	RS4NT			2.10E-09
2572232843	t3m_01199	KO:K02987	small subunit ribosomal protein S4e			0.00E+00
2572232843	t3m_01199	Locus_type		CDS		
2572232843	t3m_01199	Product_name		Ribosomal protein S4E		
2572232843	t3m_01199	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232843	t3m_01199	Coordinates		19906..20622(+)		

2572232843	t3m_01199	DNA_length		717bp		
2572232843	t3m_01199	Protein_length		238aa		
2572232843	t3m_01199	GC			0.68	
2572232844	t3m_01200	KEGG_module	M00178: Ribosome, bacteria			
2572232844	t3m_01200	KEGG_module	M00179: Ribosome, archaea			
2572232844	t3m_01200	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232844	t3m_01200	COG0094	Ribosomal protein L5			3.00E-36
2572232844	t3m_01200	pfam00673	Ribosomal_L5_C			9.80E-22
2572232844	t3m_01200	pfam00281	Ribosomal_L5			9.00E-13
2572232844	t3m_01200	KO:K02931	large subunit ribosomal protein L5			6.50E-40
2572232844	t3m_01200	ITERM:00204	LSU ribosomal protein L5P			
2572232844	t3m_01200	Locus_type		CDS		
2572232844	t3m_01200	Product_name		LSU ribosomal protein L5P		
2572232844	t3m_01200	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232844	t3m_01200	Coordinates		20619..21182(+)		
2572232844	t3m_01200	DNA_length		564bp		
2572232844	t3m_01200	Protein_length		187aa		
2572232844	t3m_01200	GC			0.68	
2572232845	t3m_01201	KEGG_module	M00178: Ribosome, bacteria			
2572232845	t3m_01201	KEGG_module	M00179: Ribosome, archaea			
2572232845	t3m_01201	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232845	t3m_01201	COG0199	Ribosomal protein S14			2.00E-04
2572232845	t3m_01201	pfam00253	Ribosomal_S14			3.20E-16
2572232845	t3m_01201	KO:K02954	small subunit ribosomal protein S14			1.30E-16
2572232845	t3m_01201	Locus_type		CDS		
2572232845	t3m_01201	Product_name		SSU ribosomal protein S14P		
2572232845	t3m_01201	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232845	t3m_01201	Coordinates		21175..21324(+)		
2572232845	t3m_01201	DNA_length		150bp		
2572232845	t3m_01201	Protein_length		49aa		
2572232845	t3m_01201	GC			0.65	

2572232846	t3m_01202	KEGG_module	M00179: Ribosome, archaea			
2572232846	t3m_01202	KEGG_module	M00178: Ribosome, bacteria			
2572232846	t3m_01202	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232846	t3m_01202	COG0096	Ribosomal protein S8			4.00E-27
2572232846	t3m_01202	pfam00410	Ribosomal_S8			3.50E-20
2572232846	t3m_01202	KO:K02994	small subunit ribosomal protein S8			6.80E-33
2572232846	t3m_01202	Locus_type		CDS		
2572232846	t3m_01202	Product_name		SSU ribosomal protein S8P		
2572232846	t3m_01202	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232846	t3m_01202	Coordinates		21344..21727(+)		
2572232846	t3m_01202	DNA_length		384bp		
2572232846	t3m_01202	Protein_length		127aa		
2572232846	t3m_01202	GC			0.66	

2572232847	t3m_01203	KEGG_module	M00178: Ribosome, bacteria			
2572232847	t3m_01203	KEGG_module	M00179: Ribosome, archaea			
2572232847	t3m_01203	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232847	t3m_01203	COG0097	Ribosomal protein L6P/L9E			2.00E-34
2572232847	t3m_01203	pfam00347	Ribosomal_L6			6.30E-09
2572232847	t3m_01203	pfam00347	Ribosomal_L6			2.80E-05
2572232847	t3m_01203	KO:K02933	large subunit ribosomal protein L6			7.90E-38
2572232847	t3m_01203	Locus_type		CDS		
2572232847	t3m_01203	Product_name		Ribosomal protein L6P/L9E		
2572232847	t3m_01203	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232847	t3m_01203	Coordinates		21717..22280(+)		
2572232847	t3m_01203	DNA_length		564bp		
2572232847	t3m_01203	Protein_length		187aa		
2572232847	t3m_01203	GC			0.68	

2572232848	t3m_01204	KEGG_module	M00179: Ribosome, archaea			
2572232848	t3m_01204	KEGG_module	M00177: Ribosome, eukaryotes			
2572232848	t3m_01204	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232848	t3m_01204	COG1717	Ribosomal protein L32E			5.00E-24
2572232848	t3m_01204	pfam01655	Ribosomal_L32e			5.10E-31

2572232848	t3m_01204	KO:K02912	large subunit ribosomal protein L32e			1.10E-23
2572232848	t3m_01204	Locus_type		CDS		
2572232848	t3m_01204	Product_name		Ribosomal protein L32E		
2572232848	t3m_01204	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232848	t3m_01204	Coordinates		22280..22861(+)		
2572232848	t3m_01204	DNA_length		582bp		
2572232848	t3m_01204	Protein_length		193aa		
2572232848	t3m_01204	GC			0.72	
2572232849	t3m_01205	KEGG_module	M00177: Ribosome, eukaryotes			
2572232849	t3m_01205	KEGG_module	M00179: Ribosome, archaea			
2572232849	t3m_01205	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232849	t3m_01205	COG2147	Ribosomal protein L19E			9.00E-38
2572232849	t3m_01205	pfam01280	Ribosomal_L19e			1.80E-52
2572232849	t3m_01205	KO:K02885	large subunit ribosomal protein L19e			2.60E-39
2572232849	t3m_01205	Locus_type		CDS		
2572232849	t3m_01205	Product_name		LSU ribosomal protein L19E		
2572232849	t3m_01205	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232849	t3m_01205	Coordinates		22865..23326(+)		
2572232849	t3m_01205	DNA_length		462bp		
2572232849	t3m_01205	Protein_length		153aa		
2572232849	t3m_01205	GC			0.7	
2572232850	t3m_01206	KEGG_module	M00178: Ribosome, bacteria			
2572232850	t3m_01206	KEGG_module	M00179: Ribosome, archaea			
2572232850	t3m_01206	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232850	t3m_01206	COG0256	Ribosomal protein L18			3.00E-19
2572232850	t3m_01206	pfam00861	Ribosomal_L18p			2.00E-18
2572232850	t3m_01206	KO:K02881	large subunit ribosomal protein L18			3.40E-35
2572232850	t3m_01206	ITERM:00239	LSU ribosomal protein L18P			
2572232850	t3m_01206	Locus_type		CDS		
2572232850	t3m_01206	Product_name		LSU ribosomal protein L18P		
2572232850	t3m_01206	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232850	t3m_01206	Coordinates		23323..23850(+)		

2572232850	t3m_01206	DNA_length		528bp	
2572232850	t3m_01206	Protein_length		175aa	
2572232850	t3m_01206	GC		0.71	
2572232851	t3m_01207	KEGG_module	M00179: Ribosome, archaea		
2572232851	t3m_01207	KEGG_module	M00178: Ribosome, bacteria		
2572232851	t3m_01207	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232851	t3m_01207	COG0098	Ribosomal protein S5		9.00E-37
2572232851	t3m_01207	pfam03719	Ribosomal_S5_C		1.70E-16
2572232851	t3m_01207	pfam00333	Ribosomal_S5		4.20E-23
2572232851	t3m_01207	TIGR01020	ribosomal protein S5(archaeal type)/S2(eukaryote cytosolic type)		2.70E-84
2572232851	t3m_01207	KO:K02988	small subunit ribosomal protein S5		0.00E+00
2572232851	t3m_01207	ITERM:00284	SSU ribosomal protein S5P		
2572232851	t3m_01207	Locus_type		CDS	
2572232851	t3m_01207	Product_name		SSU ribosomal protein S5P	
2572232851	t3m_01207	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232851	t3m_01207	Coordinates		23916..24707(+)	
2572232851	t3m_01207	DNA_length		792bp	
2572232851	t3m_01207	Protein_length		263aa	
2572232851	t3m_01207	GC		0.73	
2572232852	t3m_01208	KEGG_module	M00179: Ribosome, archaea		
2572232852	t3m_01208	KEGG_module	M00178: Ribosome, bacteria		
2572232852	t3m_01208	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232852	t3m_01208	COG1841	Ribosomal protein L30/L7E		5.00E-09
2572232852	t3m_01208	pfam00327	Ribosomal_L30		7.10E-11
2572232852	t3m_01208	TIGR01309	50S ribosomal protein L30P, archaeal		1.20E-42
2572232852	t3m_01208	KO:K02907	large subunit ribosomal protein L30		7.10E-29
2572232852	t3m_01208	ITERM:00257	LSU ribosomal protein L30P		
2572232852	t3m_01208	Locus_type		CDS	
2572232852	t3m_01208	Product_name		LSU ribosomal protein L30P	
2572232852	t3m_01208	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26	
2572232852	t3m_01208	Coordinates		24710..25168(+)	
2572232852	t3m_01208	DNA_length		459bp	

2572232852	t3m_01208	Protein_length		152aa		
2572232852	t3m_01208	GC			0.69	
2572232853	t3m_01209	KEGG_module	M00179: Ribosome, archaea			
2572232853	t3m_01209	KEGG_module	M00178: Ribosome, bacteria			
2572232853	t3m_01209	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232853	t3m_01209	COG0200	Ribosomal protein L15			3.00E-08
2572232853	t3m_01209	pfam00828	Ribosomal_L18e			1.70E-17
2572232853	t3m_01209	KO:K02876	large subunit ribosomal protein L15			2.20E-22
2572232853	t3m_01209	ITERM:00234	LSU ribosomal protein L15P			
2572232853	t3m_01209	Locus_type		CDS		
2572232853	t3m_01209	Product_name		LSU ribosomal protein L15P		
2572232853	t3m_01209	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232853	t3m_01209	Coordinates		25182..25634(+)		
2572232853	t3m_01209	DNA_length		453bp		
2572232853	t3m_01209	Protein_length		150aa		
2572232853	t3m_01209	GC			0.7	
2572232854	t3m_01210	pfam10559	Plug_translocon			9.80E-10
2572232854	t3m_01210	pfam00344	SecY			3.80E-27
2572232854	t3m_01210	Locus_type		CDS		
2572232854	t3m_01210	Product_name		Plug domain of Sec61p/SecY translocase		
2572232854	t3m_01210	Scaffold		t3m_contig_70_201_len_26407_read_count_2002865.26		
2572232854	t3m_01210	Coordinates		25671..26405(+)		
2572232854	t3m_01210	DNA_length		735bp		
2572232854	t3m_01210	Protein_length		245aa		
2572232854	t3m_01210	GC			0.64	
2572232854	t3m_01210	Transmembrane		Yes		
2572232855	t3m_01211	KEGG_module	M00177: Ribosome, eukaryotes			
2572232855	t3m_01211	KEGG_module	M00179: Ribosome, archaea			
2572232855	t3m_01211	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232855	t3m_01211	COG1890	Ribosomal protein S3AE			8.00E-46
2572232855	t3m_01211	pfam01015	Ribosomal_S3Ae			1.50E-54

2572232855	t3m_01211	KO:K02984	small subunit ribosomal protein S3Ae			3.10E-42
2572232855	t3m_01211	Locus_type		CDS		
2572232855	t3m_01211	Product_name		Ribosomal protein S3AE		
2572232855	t3m_01211	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232855	t3m_01211	Coordinates		300..1022(+)		
2572232855	t3m_01211	DNA_length		723bp		
2572232855	t3m_01211	Protein_length		240aa		
2572232855	t3m_01211	GC			0.67	
2572232856	t3m_01212	Locus_type		tRNA		
2572232856	t3m_01212	Product_name		tRNA_Met_CAT		
2572232856	t3m_01212	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232856	t3m_01212	Coordinates		1057..1158(+)		
2572232856	t3m_01212	DNA_length		76bp		
2572232856	t3m_01212	GC			0.63	
2572232857	t3m_01213	COG_category	[P] Inorganic ion transport and metabolism			
2572232857	t3m_01213	COG0798	Arsenite efflux pump ACR3 and related permeases			1.00E-87
2572232857	t3m_01213	pfam01758	SBF			1.20E-47
2572232857	t3m_01213	TIGR00832	arsenical-resistance protein			1.80E-120
2572232857	t3m_01213	KO:K03325	arsenite transporter, ACR3 family			0.00E+00
2572232857	t3m_01213	Locus_type		CDS		
2572232857	t3m_01213	Product_name		arsenical-resistance protein		
2572232857	t3m_01213	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232857	t3m_01213	Coordinates		1518..2618(-)		
2572232857	t3m_01213	DNA_length		1101bp		
2572232857	t3m_01213	Protein_length		366aa		
2572232857	t3m_01213	GC			0.64	
2572232857	t3m_01213	Transmembrane		Yes		
2572232858	t3m_01214	COG_category	[T] Signal transduction mechanisms			
2572232858	t3m_01214	COG0394	Protein-tyrosine-phosphatase			3.00E-23
2572232858	t3m_01214	pfam01451	LMWPc			6.40E-23
2572232858	t3m_01214	Locus_type		CDS		

2572232858	t3m_01214	Product_name		Protein-tyrosine-phosphatase		
2572232858	t3m_01214	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232858	t3m_01214	Coordinates		2848..3309(-)		
2572232858	t3m_01214	DNA_length		462bp		
2572232858	t3m_01214	Protein_length		153aa		
2572232858	t3m_01214	GC			0.68	
2572232859	t3m_01215	pfam13847	Methyltransf_31			1.70E-33
2572232859	t3m_01215	Locus_type		CDS		
2572232859	t3m_01215	Product_name		Methyltransferase domain		
2572232859	t3m_01215	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232859	t3m_01215	Coordinates		3306..3860(-)		
2572232859	t3m_01215	DNA_length		555bp		
2572232859	t3m_01215	Protein_length		184aa		
2572232859	t3m_01215	GC			0.65	
2572232860	t3m_01216	COG_category	[K] Transcription			
2572232860	t3m_01216	COG0640	Predicted transcriptional regulators			2.00E-13
2572232860	t3m_01216	pfam01022	HTH_5			1.00E-12
2572232860	t3m_01216	Locus_type		CDS		
2572232860	t3m_01216	Product_name		Predicted transcriptional regulators		
2572232860	t3m_01216	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232860	t3m_01216	Coordinates		4127..4513(-)		
2572232860	t3m_01216	DNA_length		387bp		
2572232860	t3m_01216	Protein_length		128aa		
2572232860	t3m_01216	GC			0.65	
2572232861	t3m_01217	COG_category	[C] Energy production and conversion			
2572232861	t3m_01217	COG4658	Predicted NADH:ubiquinone oxidoreductase, subunit RnfD			9.00E-09
2572232861	t3m_01217	pfam03116	NQR2_RnfD_RnfE			6.30E-07
2572232861	t3m_01217	Locus_type		CDS		
2572232861	t3m_01217	Product_name		Predicted NADH:ubiquinone oxidoreductase, subunit RnfD		
2572232861	t3m_01217	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232861	t3m_01217	Coordinates		4629..5891(-)		

2572232861	t3m_01217	DNA_length		1263bp		
2572232861	t3m_01217	Protein_length		420aa		
2572232861	t3m_01217	GC			0.67	
2572232861	t3m_01217	Transmembrane		Yes		
2572232862	t3m_01218	COG_category	[S] Function unknown			
2572232862	t3m_01218	COG0586	Uncharacterized membrane-associated protein			5.00E-24
2572232862	t3m_01218	pfam09335	SNARE_assoc			8.40E-19
2572232862	t3m_01218	Locus_type		CDS		
2572232862	t3m_01218	Product_name		Uncharacterized membrane-associated protein		
2572232862	t3m_01218	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232862	t3m_01218	Coordinates		6144..6836(-)		
2572232862	t3m_01218	DNA_length		693bp		
2572232862	t3m_01218	Protein_length		230aa		
2572232862	t3m_01218	GC			0.64	
2572232862	t3m_01218	Transmembrane		Yes		
2572232863	t3m_01219	Locus_type		CDS		
2572232863	t3m_01219	Product_name		hypothetical protein		
2572232863	t3m_01219	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232863	t3m_01219	Coordinates		7240..7671(+)		
2572232863	t3m_01219	DNA_length		432bp		
2572232863	t3m_01219	Protein_length		143aa		
2572232863	t3m_01219	GC			0.65	
2572232864	t3m_01220	Locus_type		CDS		
2572232864	t3m_01220	Product_name		hypothetical protein		
2572232864	t3m_01220	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232864	t3m_01220	Coordinates		7784..8140(+)		
2572232864	t3m_01220	DNA_length		357bp		
2572232864	t3m_01220	Protein_length		118aa		
2572232864	t3m_01220	GC			0.64	
2572232864	t3m_01220	Transmembrane		Yes		

2572232865	t3m_01221	Locus_type		CDS		
2572232865	t3m_01221	Product_name		hypothetical protein		
2572232865	t3m_01221	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232865	t3m_01221	Coordinates		8285..8467(-)		
2572232865	t3m_01221	DNA_length		183bp		
2572232865	t3m_01221	Protein_length		60aa		
2572232865	t3m_01221	GC			0.64	

2572232866	t3m_01222	pfam07088	GvpD			8.60E-09
2572232866	t3m_01222	Locus_type		CDS		
2572232866	t3m_01222	Product_name		GvpD gas vesicle protein		
2572232866	t3m_01222	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232866	t3m_01222	Coordinates		8480..9268(-)		
2572232866	t3m_01222	DNA_length		789bp		
2572232866	t3m_01222	Protein_length		262aa		
2572232866	t3m_01222	GC			0.65	

2572232867	t3m_01223	COG_category	[S] Function unknown			
2572232867	t3m_01223	COG2210	Uncharacterized conserved protein			2.00E-27
2572232867	t3m_01223	pfam13686	DrsE_2			4.30E-50
2572232867	t3m_01223	Locus_type		CDS		
2572232867	t3m_01223	Product_name		Uncharacterized conserved protein		
2572232867	t3m_01223	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232867	t3m_01223	Coordinates		9727..10188(+)		
2572232867	t3m_01223	DNA_length		462bp		
2572232867	t3m_01223	Protein_length		153aa		
2572232867	t3m_01223	GC			0.62	
2572232867	t3m_01223	Transmembrane		Yes		

2572232868	t3m_01224	COG_category	[K] Transcription			
2572232868	t3m_01224	COG0640	Predicted transcriptional regulators			1.00E-07
2572232868	t3m_01224	pfam12840	HTH_20			6.70E-13
2572232868	t3m_01224	KO:K03892	ArsR family transcriptional regulator			4.70E-13
2572232868	t3m_01224	Locus_type		CDS		

2572232868	t3m_01224	Product_name		Predicted transcriptional regulators		
2572232868	t3m_01224	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232868	t3m_01224	Coordinates		10204..10632(+)		
2572232868	t3m_01224	DNA_length		429bp		
2572232868	t3m_01224	Protein_length		142aa		
2572232868	t3m_01224	GC			0.67	
2572232869	t3m_01225	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232869	t3m_01225	COG0425	Predicted redox protein, regulator of disulfide bond formation			3.00E-13
2572232869	t3m_01225	pfam01206	TusA			3.40E-18
2572232869	t3m_01225	Locus_type		CDS		
2572232869	t3m_01225	Product_name		Predicted redox protein, regulator of disulfide bond formation		
2572232869	t3m_01225	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232869	t3m_01225	Coordinates		10651..10905(+)		
2572232869	t3m_01225	DNA_length		255bp		
2572232869	t3m_01225	Protein_length		84aa		
2572232869	t3m_01225	GC			0.63	
2572232870	t3m_01226	COG_category	[C] Energy production and conversion			
2572232870	t3m_01226	COG1908	Coenzyme F420-reducing hydrogenase, delta subunit			5.00E-15
2572232870	t3m_01226	pfam02662	FlpD			4.80E-23
2572232870	t3m_01226	Locus_type		CDS		
2572232870	t3m_01226	Product_name		Coenzyme F420-reducing hydrogenase, delta subunit		
2572232870	t3m_01226	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232870	t3m_01226	Coordinates		10956..11339(+)		
2572232870	t3m_01226	DNA_length		384bp		
2572232870	t3m_01226	Protein_length		127aa		
2572232870	t3m_01226	GC			0.67	
2572232871	t3m_01227	COG_category	[E] Amino acid transport and metabolism			
2572232871	t3m_01227	COG_category	[R] General function prediction only			
2572232871	t3m_01227	COG0493	NADPH-dependent glutamate synthase beta chain and related oxidorec			2.00E-71
2572232871	t3m_01227	pfam07992	Pyr_redox_2			9.90E-19
2572232871	t3m_01227	pfam07992	Pyr_redox_2			1.00E-05

2572232871	t3m_01227	pfam14691	Fer4_20			8.50E-11
2572232871	t3m_01227	Locus_type		CDS		
2572232871	t3m_01227	Product_name		NADPH-dependent glutamate synthase beta chain and related oxidoredu		
2572232871	t3m_01227	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232871	t3m_01227	Coordinates		11340..14072(+)		
2572232871	t3m_01227	DNA_length		2733bp		
2572232871	t3m_01227	Protein_length		910aa		
2572232871	t3m_01227	GC			0.67	

2572232872	t3m_01228	KEGG_module	M00357: Methanogenesis, acetate => methane			
2572232872	t3m_01228	KEGG_module	M00562: Methanogenesis, dimethylamine => methane			
2572232872	t3m_01228	KEGG_module	M00356: Methanogenesis, methanol => methane			
2572232872	t3m_01228	KEGG_module	M00561: Methanogenesis, trimethylamine => methane			
2572232872	t3m_01228	KEGG_module	M00567: Methanogenesis, CO2 => methane			
2572232872	t3m_01228	KEGG_module	M00563: Methanogenesis, methylamine => methane			
2572232872	t3m_01228	KEGG_module	M00347: Methanogenesis, formate => methane			
2572232872	t3m_01228	Metacyc	PWY-5207: coenzyme B/coenzyme M regeneration			
2572232872	t3m_01228	pfam13450	NAD_binding_8			7.80E-09
2572232872	t3m_01228	EC:1.8.98.1	CoB--CoM heterodisulfide reductase.			
2572232872	t3m_01228	KO:K03388	heterodisulfide reductase subunit A [EC:1.8.98.1]			0.00E+00
2572232872	t3m_01228	Locus_type		CDS		
2572232872	t3m_01228	Product_name		NAD(P)-binding Rossmann-like domain		
2572232872	t3m_01228	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232872	t3m_01228	Coordinates		14069..15802(+)		
2572232872	t3m_01228	DNA_length		1734bp		
2572232872	t3m_01228	Protein_length		577aa		
2572232872	t3m_01228	GC			0.66	

2572232873	t3m_01229	Locus_type		CDS		
2572232873	t3m_01229	Product_name		hypothetical protein		
2572232873	t3m_01229	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232873	t3m_01229	Coordinates		15799..16050(+)		
2572232873	t3m_01229	DNA_length		252bp		
2572232873	t3m_01229	Protein_length		83aa		

2572232873	t3m_01229	GC			0.69	
2572232874	t3m_01230	pfam13183	Fer4_8			2.20E-10
2572232874	t3m_01230	Locus_type		CDS		
2572232874	t3m_01230	Product_name		4Fe-4S dicluster domain		
2572232874	t3m_01230	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232874	t3m_01230	Coordinates		16047..16355(+)		
2572232874	t3m_01230	DNA_length		309bp		
2572232874	t3m_01230	Protein_length		102aa		
2572232874	t3m_01230	GC			0.66	
2572232875	t3m_01231	COG_category	[C] Energy production and conversion			
2572232875	t3m_01231	COG0247	Fe-S oxidoreductase			1.00E-27
2572232875	t3m_01231	pfam02754	CCG			3.10E-07
2572232875	t3m_01231	Locus_type		CDS		
2572232875	t3m_01231	Product_name		Fe-S oxidoreductase		
2572232875	t3m_01231	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232875	t3m_01231	Coordinates		16369..17340(+)		
2572232875	t3m_01231	DNA_length		972bp		
2572232875	t3m_01231	Protein_length		323aa		
2572232875	t3m_01231	GC			0.67	
2572232876	t3m_01232	COG_category	[C] Energy production and conversion			
2572232876	t3m_01232	COG2086	Electron transfer flavoprotein, beta subunit			8.00E-53
2572232876	t3m_01232	pfam01012	ETF			1.90E-39
2572232876	t3m_01232	KO:K03521	electron transfer flavoprotein beta subunit			0.00E+00
2572232876	t3m_01232	ITERM:01639	electron transfer flavoprotein beta subunit			
2572232876	t3m_01232	Locus_type		CDS		
2572232876	t3m_01232	Product_name		electron transfer flavoprotein beta subunit		
2572232876	t3m_01232	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232876	t3m_01232	Coordinates		17427..18221(-)		
2572232876	t3m_01232	DNA_length		795bp		
2572232876	t3m_01232	Protein_length		264aa		
2572232876	t3m_01232	GC			0.69	

2572232877	t3m_01233	COG_category	[C] Energy production and conversion		
2572232877	t3m_01233	COG2025	Electron transfer flavoprotein, alpha subunit		3.00E-73
2572232877	t3m_01233	pfam00766	ETF_alpha		1.90E-24
2572232877	t3m_01233	pfam01012	ETF		4.30E-35
2572232877	t3m_01233	KO:K03522	electron transfer flavoprotein alpha subunit		0.00E+00
2572232877	t3m_01233	ITERM:01638	electron transfer flavoprotein alpha subunit apoprotein		
2572232877	t3m_01233	Locus_type		CDS	
2572232877	t3m_01233	Product_name		electron transfer flavoprotein alpha subunit apoprotein	
2572232877	t3m_01233	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27	
2572232877	t3m_01233	Coordinates		18224..19204(-)	
2572232877	t3m_01233	DNA_length		981bp	
2572232877	t3m_01233	Protein_length		326aa	
2572232877	t3m_01233	GC		0.71	
2572232878	t3m_01234	COG_category	[C] Energy production and conversion		
2572232878	t3m_01234	COG0247	Fe-S oxidoreductase		4.00E-51
2572232878	t3m_01234	pfam02754	CCG		8.30E-16
2572232878	t3m_01234	pfam13183	Fer4_8		8.20E-10
2572232878	t3m_01234	pfam02754	CCG		7.10E-13
2572232878	t3m_01234	Locus_type		CDS	
2572232878	t3m_01234	Product_name		Fe-S oxidoreductase	
2572232878	t3m_01234	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27	
2572232878	t3m_01234	Coordinates		19209..20333(-)	
2572232878	t3m_01234	DNA_length		1125bp	
2572232878	t3m_01234	Protein_length		374aa	
2572232878	t3m_01234	GC		0.7	
2572232879	t3m_01235	KEGG_module	M00561: Methanogenesis, trimethylamine => methane		
2572232879	t3m_01235	KEGG_module	M00563: Methanogenesis, methylamine => methane		
2572232879	t3m_01235	KEGG_module	M00347: Methanogenesis, formate => methane		
2572232879	t3m_01235	KEGG_module	M00357: Methanogenesis, acetate => methane		
2572232879	t3m_01235	KEGG_module	M00356: Methanogenesis, methanol => methane		
2572232879	t3m_01235	KEGG_module	M00567: Methanogenesis, CO2 => methane		

2572232879	t3m_01235	KEGG_module	M00562: Methanogenesis, dimethylamine => methane			
2572232879	t3m_01235	Metacyc	PWY-5207: coenzyme B/coenzyme M regeneration			
2572232879	t3m_01235	COG_category	[C] Energy production and conversion			
2572232879	t3m_01235	COG1148	Heterodisulfide reductase, subunit A and related polyferredoxins			3.00E-109
2572232879	t3m_01235	pfam00037	Fer4			7.80E-09
2572232879	t3m_01235	pfam07992	Pyr_redox_2			1.30E-10
2572232879	t3m_01235	pfam07992	Pyr_redox_2			1.40E-08
2572232879	t3m_01235	pfam02662	FlpD			4.90E-42
2572232879	t3m_01235	pfam00070	Pyr_redox			2.20E-05
2572232879	t3m_01235	EC:1.8.98.1	CoB--CoM heterodisulfide reductase.			
2572232879	t3m_01235	KO:K03388	heterodisulfide reductase subunit A [EC:1.8.98.1]			0.00E+00
2572232879	t3m_01235	Locus_type		CDS		
2572232879	t3m_01235	Product_name		Pyridine nucleotide-disulphide oxidoreductase/Methyl-viologen-reducin		
2572232879	t3m_01235	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27		
2572232879	t3m_01235	Coordinates		20344..23748(-)		
2572232879	t3m_01235	DNA_length		3405bp		
2572232879	t3m_01235	Protein_length		1134aa		
2572232879	t3m_01235	GC			0.67	
2572232879	t3m_01235	Fused_gene		Yes		

2572232880	t3m_01236	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate		
2572232880	t3m_01236	KEGG_module	M00311: 2-oxoglutarate:ferredoxin oxidoreductase		
2572232880	t3m_01236	Metacyc	REDCITCYC: TCA cycle III (helicobacter)		
2572232880	t3m_01236	Metacyc	P23-PWY: reductive TCA cycle I		
2572232880	t3m_01236	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2572232880	t3m_01236	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2572232880	t3m_01236	Metacyc	PWY-5392: reductive TCA cycle II		
2572232880	t3m_01236	COG_category	[C] Energy production and conversion		
2572232880	t3m_01236	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o		2.00E-24
2572232880	t3m_01236	pfam01558	POR		1.00E-30
2572232880	t3m_01236	EC:1.2.7.3	2-oxoglutarate synthase.		
2572232880	t3m_01236	KO:K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]		5.60E-38
2572232880	t3m_01236	Locus_type		CDS	
2572232880	t3m_01236	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin ox	

2572232880	t3m_01236	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27	
2572232880	t3m_01236	Coordinates		23745..24266(-)	
2572232880	t3m_01236	DNA_length		522bp	
2572232880	t3m_01236	Protein_length		173aa	
2572232880	t3m_01236	GC		0.67	
2572232880	t3m_01236	Transmembrane		Yes	

2572232881	t3m_01237	pfam02775	TPP_enzyme_C		3.70E-12
2572232881	t3m_01237	Locus_type		CDS	
2572232881	t3m_01237	Product_name		Thiamine pyrophosphate enzyme, C-terminal TPP binding domain	
2572232881	t3m_01237	Scaffold		t3m_contig_70_218_len_24774_read_count_2256939.27	
2572232881	t3m_01237	Coordinates		24263..24757(-)	
2572232881	t3m_01237	DNA_length		495bp	
2572232881	t3m_01237	Protein_length		164aa	
2572232881	t3m_01237	GC		0.64	

2572232882	t3m_01238	COG_category	[S] Function unknown		
2572232882	t3m_01238	COG1860	Uncharacterized protein conserved in archaea		9.00E-25
2572232882	t3m_01238	pfam03684	UPF0179		7.50E-32
2572232882	t3m_01238	KO:K09730	hypothetical protein		1.20E-17
2572232882	t3m_01238	Locus_type		CDS	
2572232882	t3m_01238	Product_name		Uncharacterized protein conserved in archaea	
2572232882	t3m_01238	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28	
2572232882	t3m_01238	Coordinates		129..557(-)	
2572232882	t3m_01238	DNA_length		429bp	
2572232882	t3m_01238	Protein_length		142aa	
2572232882	t3m_01238	GC		0.69	

2572232883	t3m_01239	Metacyc	PWY-6349: CDP-archaeol biosynthesis		
2572232883	t3m_01239	COG_category	[C] Energy production and conversion		
2572232883	t3m_01239	COG0371	Glycerol dehydrogenase and related enzymes		6.00E-89
2572232883	t3m_01239	pfam13685	Fe-ADH_2		8.40E-62
2572232883	t3m_01239	EC:1.1.1.261	sn-glycerol-1-phosphate dehydrogenase.		
2572232883	t3m_01239	KO:K00096	glycerol-1-phosphate dehydrogenase [NAD(P)] [EC:1.1.1.261]		0.00E+00

2572232883	t3m_01239	Locus_type		CDS		
2572232883	t3m_01239	Product_name		Glycerol dehydrogenase and related enzymes		
2572232883	t3m_01239	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232883	t3m_01239	Coordinates		559..1668(-)		
2572232883	t3m_01239	DNA_length		1110bp		
2572232883	t3m_01239	Protein_length		369aa		
2572232883	t3m_01239	GC			0.67	
2572232884	t3m_01240	Metacyc	PWY-6703: preQ₀ biosynthesis			
2572232884	t3m_01240	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232884	t3m_01240	COG0602	Organic radical activating enzymes			3.00E-35
2572232884	t3m_01240	pfam13394	Fer4_14			9.20E-16
2572232884	t3m_01240	pfam04055	Radical_SAM			1.40E-17
2572232884	t3m_01240	EC:4.3.99.3	7-carboxy-7-deazaguanine synthase.			
2572232884	t3m_01240	TIGR03365	7-cyano-7-deazaguanosine (preQ0) biosynthesis protein QueE			4.80E-33
2572232884	t3m_01240	KO:K10026	7-carboxy-7-deazaguanine synthase [EC:4.3.99.3]			0.00E+00
2572232884	t3m_01240	Locus_type		CDS		
2572232884	t3m_01240	Product_name		Organic radical activating enzymes		
2572232884	t3m_01240	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232884	t3m_01240	Coordinates		1736..2365(-)		
2572232884	t3m_01240	DNA_length		630bp		
2572232884	t3m_01240	Protein_length		209aa		
2572232884	t3m_01240	GC			0.68	
2572232885	t3m_01241	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232885	t3m_01241	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232885	t3m_01241	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232885	t3m_01241	IMG_pathway	495: L-leucine ligation to tRNA(Leu)			
2572232885	t3m_01241	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232885	t3m_01241	COG0495	Leucyl-tRNA synthetase			2.00E-109
2572232885	t3m_01241	pfam00133	tRNA-synt_1			3.80E-20
2572232885	t3m_01241	EC:6.1.1.4	Leucine--tRNA ligase.			
2572232885	t3m_01241	TIGR00395	leucyl-tRNA synthetase, archaeal and cytosolic family			0.00E+00
2572232885	t3m_01241	KO:K01869	leucyl-tRNA synthetase [EC:6.1.1.4]			0.00E+00

2572232885	t3m_01241	ITERM:00405	leucyl-tRNA synthetase (EC 6.1.1.4)		
2572232885	t3m_01241	Locus_type		CDS	
2572232885	t3m_01241	Product_name		leucyl-tRNA synthetase (EC 6.1.1.4)	
2572232885	t3m_01241	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28	
2572232885	t3m_01241	Coordinates		2470..5355(+)	
2572232885	t3m_01241	DNA_length		2886bp	
2572232885	t3m_01241	Protein_length		961aa	
2572232885	t3m_01241	GC		0.7	
2572232886	t3m_01242	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572232886	t3m_01242	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins		1.00E-23
2572232886	t3m_01242	pfam13302	Acetyltransf_3		8.10E-29
2572232886	t3m_01242	Locus_type		CDS	
2572232886	t3m_01242	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins	
2572232886	t3m_01242	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28	
2572232886	t3m_01242	Coordinates		5383..5973(-)	
2572232886	t3m_01242	DNA_length		591bp	
2572232886	t3m_01242	Protein_length		196aa	
2572232886	t3m_01242	GC		0.72	
2572232887	t3m_01243	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP		
2572232887	t3m_01243	Metacyc	PWY-7187: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis II		
2572232887	t3m_01243	Metacyc	PWY0-166: superpathway of pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis (E. coli		
2572232887	t3m_01243	COG_category	[F] Nucleotide transport and metabolism		
2572232887	t3m_01243	COG0717	Deoxycytidine deaminase		1.00E-27
2572232887	t3m_01243	EC:3.5.4.13	dCTP deaminase.		
2572232887	t3m_01243	TIGR02274	deoxycytidine triphosphate deaminase		1.50E-33
2572232887	t3m_01243	KO:K01494	dCTP deaminase [EC:3.5.4.13]		0.00E+00
2572232887	t3m_01243	Locus_type		CDS	
2572232887	t3m_01243	Product_name		dCTP deaminase (EC 3.5.4.13)	
2572232887	t3m_01243	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28	
2572232887	t3m_01243	Coordinates		5978..6544(-)	
2572232887	t3m_01243	DNA_length		567bp	
2572232887	t3m_01243	Protein_length		188aa	

2572232887	t3m_01243	GC			0.65	
2572232888	t3m_01244	COG_category	[R] General function prediction only			
2572232888	t3m_01244	COG1355	Predicted dioxygenase			2.00E-66
2572232888	t3m_01244	pfam01875	Memo			1.50E-63
2572232888	t3m_01244	TIGR04336	AmmeMemoRadiSam system protein B			1.10E-81
2572232888	t3m_01244	Locus_type		CDS		
2572232888	t3m_01244	Product_name		AmmeMemoRadiSam system protein B		
2572232888	t3m_01244	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232888	t3m_01244	Coordinates		6574..7410(-)		
2572232888	t3m_01244	DNA_length		837bp		
2572232888	t3m_01244	Protein_length		278aa		
2572232888	t3m_01244	GC			0.68	
2572232889	t3m_01245	COG_category	[F] Nucleotide transport and metabolism			
2572232889	t3m_01245	COG_category	[G] Carbohydrate transport and metabolism			
2572232889	t3m_01245	COG_category	[R] General function prediction only			
2572232889	t3m_01245	COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hyd			2.00E-29
2572232889	t3m_01245	pfam01230	HIT			1.20E-24
2572232889	t3m_01245	KO:K02503	Hit-like protein involved in cell-cycle regulation			3.10E-26
2572232889	t3m_01245	Locus_type		CDS		
2572232889	t3m_01245	Product_name		Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydr		
2572232889	t3m_01245	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232889	t3m_01245	Coordinates		7444..7869(-)		
2572232889	t3m_01245	DNA_length		426bp		
2572232889	t3m_01245	Protein_length		141aa		
2572232889	t3m_01245	GC			0.67	
2572232890	t3m_01246	pfam00082	Peptidase_S8			2.00E-07
2572232890	t3m_01246	pfam09286	Pro-kuma_activ			7.90E-20
2572232890	t3m_01246	Locus_type		CDS		
2572232890	t3m_01246	Product_name		Pro-kumamolisin, activation domain/Subtilase family		
2572232890	t3m_01246	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232890	t3m_01246	Coordinates		7958..10309(+)		

2572232890	t3m_01246	DNA_length		2352bp		
2572232890	t3m_01246	Protein_length		783aa		
2572232890	t3m_01246	GC			0.68	
2572232890	t3m_01246	Signal_peptide		Yes		
2572232890	t3m_01246	Transmembrane		Yes		
2572232891	t3m_01247	COG_category	[K] Transcription			
2572232891	t3m_01247	COG1386	Predicted transcriptional regulator containing the HTH domain			7.00E-19
2572232891	t3m_01247	pfam04079	DUF387			2.00E-29
2572232891	t3m_01247	TIGR00281	segregation and condensation protein B			1.00E-27
2572232891	t3m_01247	KO:K06024	segregation and condensation protein B			3.50E-29
2572232891	t3m_01247	Locus_type		CDS		
2572232891	t3m_01247	Product_name		Predicted transcriptional regulator containing the HTH domain		
2572232891	t3m_01247	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232891	t3m_01247	Coordinates		10318..10980(-)		
2572232891	t3m_01247	DNA_length		663bp		
2572232891	t3m_01247	Protein_length		220aa		
2572232891	t3m_01247	GC			0.7	
2572232892	t3m_01248	COG_category	[S] Function unknown			
2572232892	t3m_01248	COG1354	Uncharacterized conserved protein			2.00E-13
2572232892	t3m_01248	pfam02616	ScpA_ScpB			5.50E-06
2572232892	t3m_01248	ITERM:00133	condensin subunit ScpA			
2572232892	t3m_01248	Locus_type		CDS		
2572232892	t3m_01248	Product_name		condensin subunit ScpA		
2572232892	t3m_01248	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232892	t3m_01248	Coordinates		10990..11946(-)		
2572232892	t3m_01248	DNA_length		957bp		
2572232892	t3m_01248	Protein_length		318aa		
2572232892	t3m_01248	GC			0.67	
2572232893	t3m_01249	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2572232893	t3m_01249	COG1196	Chromosome segregation ATPases			0.00E+00
2572232893	t3m_01249	pfam06470	SMC_hinge			1.80E-25

2572232893	t3m_01249	pfam02463	SMC_N		4.50E-63
2572232893	t3m_01249	TIGR02169	chromosome segregation protein SMC, primarily archaeal type		0.00E+00
2572232893	t3m_01249	TIGR02168	chromosome segregation protein SMC, common bacterial type		0.00E+00
2572232893	t3m_01249	KO:K03529	chromosome segregation protein		0.00E+00
2572232893	t3m_01249	ITERM:00131	condensin subunit Smc		
2572232893	t3m_01249	Locus_type		CDS	
2572232893	t3m_01249	Product_name		condensin subunit Smc	
2572232893	t3m_01249	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28	
2572232893	t3m_01249	Coordinates		11943..15569(-)	
2572232893	t3m_01249	DNA_length		3627bp	
2572232893	t3m_01249	Protein_length		1208aa	
2572232893	t3m_01249	GC		0.67	
2572232894	t3m_01250	Locus_type		CDS	
2572232894	t3m_01250	Product_name		hypothetical protein	
2572232894	t3m_01250	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28	
2572232894	t3m_01250	Coordinates		15864..16208(+)	
2572232894	t3m_01250	DNA_length		345bp	
2572232894	t3m_01250	Protein_length		114aa	
2572232894	t3m_01250	GC		0.7	
2572232895	t3m_01251	COG_category	[G] Carbohydrate transport and metabolism		
2572232895	t3m_01251	COG2814	Arabinose efflux permease		1.00E-08
2572232895	t3m_01251	pfam07690	MFS_1		2.50E-16
2572232895	t3m_01251	Locus_type		CDS	
2572232895	t3m_01251	Product_name		Arabinose efflux permease	
2572232895	t3m_01251	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28	
2572232895	t3m_01251	Coordinates		16246..17451(-)	
2572232895	t3m_01251	DNA_length		1206bp	
2572232895	t3m_01251	Protein_length		401aa	
2572232895	t3m_01251	GC		0.65	
2572232895	t3m_01251	Transmembrane		Yes	
2572232896	t3m_01252	pfam00583	Acetyltransf_1		1.80E-06

2572232896	t3m_01252	pfam00583	Acetyltransf_1			8.80E-07
2572232896	t3m_01252	Locus_type		CDS		
2572232896	t3m_01252	Product_name		Acetyltransferase (GNAT) family		
2572232896	t3m_01252	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232896	t3m_01252	Coordinates		17655..18662(+)		
2572232896	t3m_01252	DNA_length		1008bp		
2572232896	t3m_01252	Protein_length		335aa		
2572232896	t3m_01252	GC			0.66	

2572232897	t3m_01253	COG_category	[C] Energy production and conversion			
2572232897	t3m_01253	COG0778	Nitroreductase			9.00E-20
2572232897	t3m_01253	pfam00881	Nitroreductase			6.40E-29
2572232897	t3m_01253	Locus_type		CDS		
2572232897	t3m_01253	Product_name		Nitroreductase		
2572232897	t3m_01253	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232897	t3m_01253	Coordinates		18825..19361(+)		
2572232897	t3m_01253	DNA_length		537bp		
2572232897	t3m_01253	Protein_length		178aa		
2572232897	t3m_01253	GC			0.66	

2572232898	t3m_01254	IMG_pathway	622: dITP and XTP hydrolysis			
2572232898	t3m_01254	COG_category	[F] Nucleotide transport and metabolism			
2572232898	t3m_01254	COG0127	Xanthosine triphosphate pyrophosphatase			4.00E-42
2572232898	t3m_01254	pfam01725	Ham1p_like			1.50E-42
2572232898	t3m_01254	EC:3.6.1.19	Nucleoside-triphosphate diphosphatase.			
2572232898	t3m_01254	TIGR00042	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family			4.70E-45
2572232898	t3m_01254	KO:K02428	dITP/XTP pyrophosphatase [EC:3.6.1.19]			2.10E-35
2572232898	t3m_01254	ITERM:05394	dITPase (EC 3.6.1.-)			
2572232898	t3m_01254	Locus_type		CDS		
2572232898	t3m_01254	Product_name		dITPase (EC 3.6.1.-)		
2572232898	t3m_01254	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232898	t3m_01254	Coordinates		19364..19918(+)		
2572232898	t3m_01254	DNA_length		555bp		
2572232898	t3m_01254	Protein_length		184aa		

2572232898	t3m_01254	GC			0.68	

2572232899	t3m_01255	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232899	t3m_01255	COG0459	Chaperonin GroEL (HSP60 family)			0.00E+00
2572232899	t3m_01255	pfam00118	Cpn60_TCP1			0.00E+00
2572232899	t3m_01255	TIGR02339	thermosome, various subunits, archaeal			0.00E+00
2572232899	t3m_01255	Locus_type		CDS		
2572232899	t3m_01255	Product_name		thermosome subunit		
2572232899	t3m_01255	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232899	t3m_01255	Coordinates		20030..21697(-)		
2572232899	t3m_01255	DNA_length		1668bp		
2572232899	t3m_01255	Protein_length		555aa		
2572232899	t3m_01255	GC			0.66	

2572232900	t3m_01256	COG_category	[G] Carbohydrate transport and metabolism			
2572232900	t3m_01256	COG2211	Na+/melibiose symporter and related transporters			8.00E-08
2572232900	t3m_01256	pfam05977	MFS_3			9.80E-22
2572232900	t3m_01256	Locus_type		CDS		
2572232900	t3m_01256	Product_name		Transmembrane secretion effector		
2572232900	t3m_01256	Scaffold		t3m_contig_70_225_len_24160_read_count_2040884.28		
2572232900	t3m_01256	Coordinates		21888..23174(+)		
2572232900	t3m_01256	DNA_length		1287bp		
2572232900	t3m_01256	Protein_length		428aa		
2572232900	t3m_01256	GC			0.69	
2572232900	t3m_01256	Transmembrane		Yes		

2572232901	t3m_01257	COG_category	[I] Lipid transport and metabolism			
2572232901	t3m_01257	COG0020	Undecaprenyl pyrophosphate synthase			5.00E-82
2572232901	t3m_01257	pfam01255	Prenyltransf			2.40E-81
2572232901	t3m_01257	EC:2.5.1.89	Tritrans,polycis-undecaprenyl-diphosphate synthase (geranylgeranyl- diphosphate specific).			
2572232901	t3m_01257	TIGR00055	undecaprenyl diphosphate synthase			4.30E-87
2572232901	t3m_01257	KO:K15888	tritrans,polycis-undecaprenyl-diphosphate synthase [geranylgeranyl-di			0.00E+00
2572232901	t3m_01257	Locus_type		CDS		
2572232901	t3m_01257	Product_name		Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)		

2572232901	t3m_01257	Scaffold	t3m_contig_70_225_len_24160_read_count_2040884.28
2572232901	t3m_01257	Coordinates	23107..23922(-)
2572232901	t3m_01257	DNA_length	816bp
2572232901	t3m_01257	Protein_length	271aa
2572232901	t3m_01257	GC	0.67
2572232902	t3m_01258	Locus_type	tRNA
2572232902	t3m_01258	Product_name	tRNA_Asp_GTC
2572232902	t3m_01258	Scaffold	t3m_contig_70_225_len_24160_read_count_2040884.28
2572232902	t3m_01258	Coordinates	24027..24114(-)
2572232902	t3m_01258	DNA_length	88bp
2572232902	t3m_01258	GC	0.64
2572232903	t3m_01259	Locus_type	CDS
2572232903	t3m_01259	Product_name	hypothetical protein
2572232903	t3m_01259	Scaffold	t3m_contig_70_235_len_23691_read_count_2097101.29
2572232903	t3m_01259	Coordinates	2..310(-)
2572232903	t3m_01259	DNA_length	309bp
2572232903	t3m_01259	Protein_length	103aa
2572232903	t3m_01259	GC	0.62
2572232904	t3m_01260	Locus_type	CDS
2572232904	t3m_01260	Product_name	hypothetical protein
2572232904	t3m_01260	Scaffold	t3m_contig_70_235_len_23691_read_count_2097101.29
2572232904	t3m_01260	Coordinates	611..1840(+)
2572232904	t3m_01260	DNA_length	1230bp
2572232904	t3m_01260	Protein_length	409aa
2572232904	t3m_01260	GC	0.62
2572232904	t3m_01260	Transmembrane	Yes
2572232905	t3m_01261	Locus_type	CDS
2572232905	t3m_01261	Product_name	hypothetical protein
2572232905	t3m_01261	Scaffold	t3m_contig_70_235_len_23691_read_count_2097101.29
2572232905	t3m_01261	Coordinates	1914..2132(-)

2572232905	t3m_01261	DNA_length		219bp		
2572232905	t3m_01261	Protein_length		72aa		
2572232905	t3m_01261	GC			0.68	
2572232906	t3m_01262	COG_category	[K] Transcription			
2572232906	t3m_01262	COG2101	TATA-box binding protein (TBP), component of TFIID and TFIIIB			9.00E-67
2572232906	t3m_01262	pfam00352	TBP			5.70E-30
2572232906	t3m_01262	pfam00352	TBP			8.10E-30
2572232906	t3m_01262	KO:K03120	transcription initiation factor TFIID TATA-box-binding protein			0.00E+00
2572232906	t3m_01262	ITERM:01960	TATA binding protein of transcription factor TFIID			
2572232906	t3m_01262	Locus_type		CDS		
2572232906	t3m_01262	Product_name		TATA binding protein of transcription factor TFIID		
2572232906	t3m_01262	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232906	t3m_01262	Coordinates		2171..2851(-)		
2572232906	t3m_01262	DNA_length		681bp		
2572232906	t3m_01262	Protein_length		226aa		
2572232906	t3m_01262	GC			0.64	
2572232907	t3m_01263	COG_category	[S] Function unknown			
2572232907	t3m_01263	COG2318	Uncharacterized protein conserved in bacteria			6.00E-15
2572232907	t3m_01263	pfam05163	DinB			2.50E-20
2572232907	t3m_01263	Locus_type		CDS		
2572232907	t3m_01263	Product_name		Uncharacterized protein conserved in bacteria		
2572232907	t3m_01263	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232907	t3m_01263	Coordinates		3088..3567(-)		
2572232907	t3m_01263	DNA_length		480bp		
2572232907	t3m_01263	Protein_length		159aa		
2572232907	t3m_01263	GC			0.64	
2572232908	t3m_01264	KEGG_module	M00254: ABC-2 type transport system			
2572232908	t3m_01264	COG_category	[V] Defense mechanisms			
2572232908	t3m_01264	COG0842	ABC-type multidrug transport system, permease component			3.00E-06
2572232908	t3m_01264	pfam01061	ABC2_membrane			1.10E-20
2572232908	t3m_01264	KO:K01992	ABC-2 type transport system permease protein			1.90E-24

2572232908	t3m_01264	Locus_type		CDS	
2572232908	t3m_01264	Product_name		ABC-type multidrug transport system, permease component	
2572232908	t3m_01264	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29	
2572232908	t3m_01264	Coordinates		3630..4448(-)	
2572232908	t3m_01264	DNA_length		819bp	
2572232908	t3m_01264	Protein_length		272aa	
2572232908	t3m_01264	GC		0.65	
2572232908	t3m_01264	Transmembrane		Yes	
2572232909	t3m_01265	KEGG_module	M00248: Putative antibiotic transport system		
2572232909	t3m_01265	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572232909	t3m_01265	COG_category	[G] Carbohydrate transport and metabolism		
2572232909	t3m_01265	COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease c		3.00E-07
2572232909	t3m_01265	pfam01061	ABC2_membrane		3.20E-10
2572232909	t3m_01265	KO:K09686	antibiotic transport system permease protein		1.90E-23
2572232909	t3m_01265	Locus_type		CDS	
2572232909	t3m_01265	Product_name		ABC-type polysaccharide/polyol phosphate export systems, permease c	
2572232909	t3m_01265	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29	
2572232909	t3m_01265	Coordinates		4467..5273(-)	
2572232909	t3m_01265	DNA_length		807bp	
2572232909	t3m_01265	Protein_length		268aa	
2572232909	t3m_01265	GC		0.66	
2572232909	t3m_01265	Transmembrane		Yes	
2572232910	t3m_01266	KEGG_module	M00248: Putative antibiotic transport system		
2572232910	t3m_01266	COG_category	[V] Defense mechanisms		
2572232910	t3m_01266	COG1131	ABC-type multidrug transport system, ATPase component		2.00E-66
2572232910	t3m_01266	pfam00005	ABC_tran		1.40E-28
2572232910	t3m_01266	KO:K09687	antibiotic transport system ATP-binding protein		0.00E+00
2572232910	t3m_01266	Locus_type		CDS	
2572232910	t3m_01266	Product_name		ABC-type multidrug transport system, ATPase component	
2572232910	t3m_01266	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29	
2572232910	t3m_01266	Coordinates		5274..6260(-)	
2572232910	t3m_01266	DNA_length		987bp	

2572232910	t3m_01266	Protein_length		328aa		
2572232910	t3m_01266	GC			0.66	
2572232911	t3m_01267	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232911	t3m_01267	COG1180	Pyruvate-formate lyase-activating enzyme			4.00E-38
2572232911	t3m_01267	pfam04055	Radical_SAM			6.60E-17
2572232911	t3m_01267	EC:1.97.1.4	[Formate-C-acetyltransferase]-activating enzyme.			
2572232911	t3m_01267	TIGR02494	glycyl-radical enzyme activating protein family			1.60E-62
2572232911	t3m_01267	KO:K04069	pyruvate formate lyase activating enzyme [EC:1.97.1.4]			0.00E+00
2572232911	t3m_01267	Locus_type		CDS		
2572232911	t3m_01267	Product_name		glycyl-radical enzyme activating protein family		
2572232911	t3m_01267	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232911	t3m_01267	Coordinates		6874..7461(+)		
2572232911	t3m_01267	DNA_length		588bp		
2572232911	t3m_01267	Protein_length		195aa		
2572232911	t3m_01267	GC			0.63	
2572232912	t3m_01268	Metacyc	FERMENTATION-PWY: mixed acid fermentation			
2572232912	t3m_01268	Metacyc	PWY-5480: pyruvate fermentation to ethanol I			
2572232912	t3m_01268	Metacyc	PWY-5493: reductive monocarboxylic acid cycle			
2572232912	t3m_01268	Metacyc	PWY-5485: pyruvate fermentation to acetate IV			
2572232912	t3m_01268	Metacyc	ANARESP1-PWY: respiration (anaerobic)			
2572232912	t3m_01268	Metacyc	PWY4LZ-257: superpathway of fermentation (<i>Chlamydomonas reinhardtii</i>)			
2572232912	t3m_01268	COG_category	[C] Energy production and conversion			
2572232912	t3m_01268	COG1882	Pyruvate-formate lyase			8.00E-123
2572232912	t3m_01268	pfam02901	PFL			0.00E+00
2572232912	t3m_01268	pfam01228	Gly_radical			7.80E-28
2572232912	t3m_01268	EC:2.3.1.54	Formate C-acetyltransferase.			
2572232912	t3m_01268	TIGR01774	glycyl radical enzyme, PFL2/glycerol dehydratase family			0.00E+00
2572232912	t3m_01268	KO:K00656	formate C-acetyltransferase [EC:2.3.1.54]			0.00E+00
2572232912	t3m_01268	Locus_type		CDS		
2572232912	t3m_01268	Product_name		glycyl radical enzyme, PFL2/glycerol dehydratase family		
2572232912	t3m_01268	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232912	t3m_01268	Coordinates		7463..9850(+)		

2572232912	t3m_01268	DNA_length		2388bp		
2572232912	t3m_01268	Protein_length		795aa		
2572232912	t3m_01268	GC			0.64	
2572232913	t3m_01269	COG_category	[E] Amino acid transport and metabolism			
2572232913	t3m_01269	COG0531	Amino acid transporters			1.00E-21
2572232913	t3m_01269	pfam13520	AA_permease_2			1.20E-27
2572232913	t3m_01269	Locus_type		CDS		
2572232913	t3m_01269	Product_name		Amino acid transporters		
2572232913	t3m_01269	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232913	t3m_01269	Coordinates		9890..11326(+)		
2572232913	t3m_01269	DNA_length		1437bp		
2572232913	t3m_01269	Protein_length		478aa		
2572232913	t3m_01269	GC			0.71	
2572232913	t3m_01269	Transmembrane		Yes		
2572232914	t3m_01270	pfam07690	MFS_1			7.90E-51
2572232914	t3m_01270	TIGR00711	drug resistance transporter, EmrB/QacA subfamily			3.90E-68
2572232914	t3m_01270	Locus_type		CDS		
2572232914	t3m_01270	Product_name		Major Facilitator Superfamily		
2572232914	t3m_01270	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232914	t3m_01270	Coordinates		11452..12915(+)		
2572232914	t3m_01270	DNA_length		1464bp		
2572232914	t3m_01270	Protein_length		487aa		
2572232914	t3m_01270	GC			0.66	
2572232914	t3m_01270	Transmembrane		Yes		
2572232915	t3m_01271	COG_category	[F] Nucleotide transport and metabolism			
2572232915	t3m_01271	COG0563	Adenylate kinase and related kinases			2.00E-06
2572232915	t3m_01271	pfam13671	AAA_33			3.50E-11
2572232915	t3m_01271	Locus_type		CDS		
2572232915	t3m_01271	Product_name		Adenylate kinase and related kinases		
2572232915	t3m_01271	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232915	t3m_01271	Coordinates		13018..13509(-)		

2572232915	t3m_01271	DNA_length		492bp		
2572232915	t3m_01271	Protein_length		163aa		
2572232915	t3m_01271	GC			0.61	
2572232916	t3m_01272	Locus_type		CDS		
2572232916	t3m_01272	Product_name		hypothetical protein		
2572232916	t3m_01272	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232916	t3m_01272	Coordinates		13848..14651(+)		
2572232916	t3m_01272	DNA_length		804bp		
2572232916	t3m_01272	Protein_length		267aa		
2572232916	t3m_01272	GC			0.65	
2572232916	t3m_01272	Transmembrane		Yes		
2572232917	t3m_01273	COG_category	[H] Coenzyme transport and metabolism			
2572232917	t3m_01273	COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis			2.00E-14
2572232917	t3m_01273	pfam08241	Methyltransf_11			4.70E-15
2572232917	t3m_01273	Locus_type		CDS		
2572232917	t3m_01273	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis		
2572232917	t3m_01273	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232917	t3m_01273	Coordinates		14697..15431(-)		
2572232917	t3m_01273	DNA_length		735bp		
2572232917	t3m_01273	Protein_length		244aa		
2572232917	t3m_01273	GC			0.66	
2572232918	t3m_01274	Metacyc	PWY-5386: methylglyoxal degradation I			
2572232918	t3m_01274	COG_category	[E] Amino acid transport and metabolism			
2572232918	t3m_01274	COG0346	Lactoylglutathione lyase and related lyases			5.00E-09
2572232918	t3m_01274	pfam12681	Glyoxalase_2			2.30E-12
2572232918	t3m_01274	EC:4.4.1.5	Lactoylglutathione lyase.			
2572232918	t3m_01274	KO:K01759	lactoylglutathione lyase [EC:4.4.1.5]			5.50E-09
2572232918	t3m_01274	Locus_type		CDS		
2572232918	t3m_01274	Product_name		Lactoylglutathione lyase and related lyases		
2572232918	t3m_01274	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232918	t3m_01274	Coordinates		15441..15878(-)		

2572232918	t3m_01274	DNA_length		438bp		
2572232918	t3m_01274	Protein_length		145aa		
2572232918	t3m_01274	GC			0.69	
2572232919	t3m_01275	Locus_type		CDS		
2572232919	t3m_01275	Product_name		hypothetical protein		
2572232919	t3m_01275	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232919	t3m_01275	Coordinates		15984..16430(-)		
2572232919	t3m_01275	DNA_length		447bp		
2572232919	t3m_01275	Protein_length		148aa		
2572232919	t3m_01275	GC			0.64	
2572232919	t3m_01275	Transmembrane		Yes		
2572232920	t3m_01276	pfam08241	Methyltransf_11			1.70E-17
2572232920	t3m_01276	Locus_type		CDS		
2572232920	t3m_01276	Product_name		Methyltransferase domain		
2572232920	t3m_01276	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232920	t3m_01276	Coordinates		16623..17411(+)		
2572232920	t3m_01276	DNA_length		789bp		
2572232920	t3m_01276	Protein_length		262aa		
2572232920	t3m_01276	GC			0.7	
2572232921	t3m_01277	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2572232921	t3m_01277	KEGG_module	M00433: Lysine biosynthesis, 2-oxoglutarate => 2-oxoadipate			
2572232921	t3m_01277	KEGG_module	M00030: Lysine biosynthesis, AAA pathway, 2-oxoglutarate => 2-aminoadipate => lysine			
2572232921	t3m_01277	KEGG_module	M00012: Glyoxylate cycle			
2572232921	t3m_01277	KEGG_module	M00010: Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate			
2572232921	t3m_01277	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)			
2572232921	t3m_01277	Metacyc	PWY-6679: jadomycin biosynthesis			
2572232921	t3m_01277	Metacyc	PWY1A0-6325: actinorhodin biosynthesis			
2572232921	t3m_01277	Metacyc	PWY-5367: petroselinate biosynthesis			
2572232921	t3m_01277	Metacyc	PWY-7053: docosahexanoate biosynthesis I			
2572232921	t3m_01277	Metacyc	PWY-6863: pyruvate fermentation to hexanol			
2572232921	t3m_01277	Metacyc	PWY-721: 3-methylquinoline degradation			

2572232921	t3m_01277	Metacyc	PWY-7130: L-glucose degradation
2572232921	t3m_01277	Metacyc	PWY-7104: dTDP-L-megosamine biosynthesis
2572232921	t3m_01277	Metacyc	PWY-6951: docosahexanoate biosynthesis II
2572232921	t3m_01277	Metacyc	PWY-6583: pyruvate fermentation to butanol I
2572232921	t3m_01277	Metacyc	3-HYDROXYPHENYLACETATE-DEGRADATION-PWY: 4-hydroxyphenylacetate degradation
2572232921	t3m_01277	Metacyc	PWY-6948: sitosterol degradation to androstenedione
2572232921	t3m_01277	Metacyc	PWY-7189: C-glycosylflavone biosynthesis III
2572232921	t3m_01277	Metacyc	PWY-6627: salinosporamide A biosynthesis
2572232921	t3m_01277	Metacyc	PWY-5353: arachidonate biosynthesis
2572232921	t3m_01277	Metacyc	PWY-6883: pyruvate fermentation to butanol II
2572232921	t3m_01277	Metacyc	PWY-6946: cholesterol degradation to androstenedione II (cholesterol dehydrogenase)
2572232921	t3m_01277	Metacyc	PWY-6945: cholesterol degradation to androstenedione I (cholesterol oxidase)
2572232921	t3m_01277	Metacyc	PWY-6974: dTDP-L-olivose biosynthesis
2572232921	t3m_01277	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate
2572232921	t3m_01277	Metacyc	CARNMET-PWY: carnitine degradation I
2572232921	t3m_01277	Metacyc	PWY-6976: dTDP-L-mycarose biosynthesis
2572232921	t3m_01277	Metacyc	PWY-2463: medicarpin biosynthesis
2572232921	t3m_01277	Metacyc	PWY-5972: stearate biosynthesis I (animals)
2572232921	t3m_01277	Metacyc	PWY-6672: <i>cis</i>-genanyl-CoA degradation
2572232921	t3m_01277	Metacyc	P3-PWY: gallate degradation III (anaerobic)
2572232921	t3m_01277	Metacyc	PWY-5177: glutaryl-CoA degradation
2572232921	t3m_01277	Metacyc	PWY-6944: androstenedione degradation
2572232921	t3m_01277	Metacyc	PWY-6973: dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycarose biosynthesis
2572232921	t3m_01277	Metacyc	PWY-5061: 6,7,4'-trihydroxyisoflavone biosynthesis
2572232921	t3m_01277	Metacyc	PWY-7188: C-glycosylflavone biosynthesis II
2572232921	t3m_01277	Metacyc	PWY-2761: glyceollin biosynthesis I
2572232921	t3m_01277	Metacyc	PWY-2464: maackiain biosynthesis
2572232921	t3m_01277	Metacyc	PWYG-321: mycolate biosynthesis
2572232921	t3m_01277	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle
2572232921	t3m_01277	Metacyc	PWY-6749: CMP-legionaminate biosynthesis I
2572232921	t3m_01277	Metacyc	PWY-6808: dTDP-D-forosamine biosynthesis
2572232921	t3m_01277	Metacyc	PWY-6721: sangivamycin biosynthesis
2572232921	t3m_01277	Metacyc	PWY-6602: C-glycosylflavone biosynthesis I
2572232921	t3m_01277	Metacyc	P162-PWY: glutamate degradation V (via hydroxyglutarate)

2572232921	t3m_01277	Metacyc	P345-PWY: aldoxime degradation			
2572232921	t3m_01277	COG_category	[C] Energy production and conversion			
2572232921	t3m_01277	COG1048	Aconitase A			0.00E+00
2572232921	t3m_01277	pfam00330	Aconitase			0.00E+00
2572232921	t3m_01277	pfam00694	Aconitase_C			4.20E-39
2572232921	t3m_01277	EC:4.2.1.-	Lyases. Carbon-oxygen lyases. Hydro-lyases.			
2572232921	t3m_01277	EC:4.2.1.3	Aconitate hydratase.			
2572232921	t3m_01277	TIGR01341	aconitate hydratase 1			0.00E+00
2572232921	t3m_01277	KO:K01681	aconitate hydratase 1 / homoaconitase [EC:4.2.1.3 4.2.1.-]			0.00E+00
2572232921	t3m_01277	Locus_type		CDS		
2572232921	t3m_01277	Product_name		aconitate hydratase 1		
2572232921	t3m_01277	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232921	t3m_01277	Coordinates		17432..20113(-)		
2572232921	t3m_01277	DNA_length		2682bp		
2572232921	t3m_01277	Protein_length		893aa		
2572232921	t3m_01277	GC			0.69	
2572232922	t3m_01278	KEGG_module	M00190: Iron(III) transport system			
2572232922	t3m_01278	COG_category	[G] Carbohydrate transport and metabolism			
2572232922	t3m_01278	COG3839	ABC-type sugar transport systems, ATPase components			1.00E-73
2572232922	t3m_01278	pfam00005	ABC_tran			1.50E-34
2572232922	t3m_01278	pfam08402	TOBE_2			1.30E-04
2572232922	t3m_01278	EC:3.6.3.30	Fe(3+)-transporting ATPase.			
2572232922	t3m_01278	KO:K02010	iron(III) transport system ATP-binding protein [EC:3.6.3.30]			0.00E+00
2572232922	t3m_01278	Locus_type		CDS		
2572232922	t3m_01278	Product_name		ABC-type sugar transport systems, ATPase components		
2572232922	t3m_01278	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29		
2572232922	t3m_01278	Coordinates		20160..21125(-)		
2572232922	t3m_01278	DNA_length		966bp		
2572232922	t3m_01278	Protein_length		321aa		
2572232922	t3m_01278	GC			0.7	
2572232923	t3m_01279	KEGG_module	M00191: Thiamine transport system			
2572232923	t3m_01279	COG_category	[P] Inorganic ion transport and metabolism			

2572232923	t3m_01279	COG1178	ABC-type Fe3+ transport system, permease component		1.00E-41
2572232923	t3m_01279	pfam00528	BPD_transp_1		5.60E-10
2572232923	t3m_01279	KO:K02063	thiamine transport system permease protein		0.00E+00
2572232923	t3m_01279	Locus_type		CDS	
2572232923	t3m_01279	Product_name		ABC-type Fe3+ transport system, permease component	
2572232923	t3m_01279	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29	
2572232923	t3m_01279	Coordinates		21112..22740(-)	
2572232923	t3m_01279	DNA_length		1629bp	
2572232923	t3m_01279	Protein_length		542aa	
2572232923	t3m_01279	GC		0.7	
2572232923	t3m_01279	Transmembrane		Yes	
2572232923	t3m_01279	Fused_gene		Yes	
2572232924	t3m_01280	KEGG_module	M00191: Thiamine transport system		
2572232924	t3m_01280	COG_category	[H] Coenzyme transport and metabolism		
2572232924	t3m_01280	COG4143	ABC-type thiamine transport system, periplasmic component		4.00E-28
2572232924	t3m_01280	TIGR01254	ABC transporter periplasmic binding protein, thiB subfamily		1.50E-29
2572232924	t3m_01280	KO:K02064	thiamine transport system substrate-binding protein		2.30E-37
2572232924	t3m_01280	Locus_type		CDS	
2572232924	t3m_01280	Product_name		ABC-type thiamine transport system, periplasmic component	
2572232924	t3m_01280	Scaffold		t3m_contig_70_235_len_23691_read_count_2097101.29	
2572232924	t3m_01280	Coordinates		22737..23690(-)	
2572232924	t3m_01280	DNA_length		954bp	
2572232924	t3m_01280	Protein_length		317aa	
2572232924	t3m_01280	GC		0.68	
2572232925	t3m_01281	pfam01061	ABC2_membrane		2.40E-15
2572232925	t3m_01281	Locus_type		CDS	
2572232925	t3m_01281	Product_name		ABC-2 type transporter	
2572232925	t3m_01281	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30	
2572232925	t3m_01281	Coordinates		3..314(+)	
2572232925	t3m_01281	DNA_length		312bp	
2572232925	t3m_01281	Protein_length		103aa	
2572232925	t3m_01281	GC		0.6	

2572232925	t3m_01281	Transmembrane		Yes		
2572232926	t3m_01282	COG_category	[R] General function prediction only			
2572232926	t3m_01282	COG1853	Conserved protein/domain typically associated with flavoprotein oxyge			6.00E-27
2572232926	t3m_01282	pfam01613	Flavin_Reduct			4.40E-34
2572232926	t3m_01282	Locus_type		CDS		
2572232926	t3m_01282	Product_name		Conserved protein/domain typically associated with flavoprotein oxyger		
2572232926	t3m_01282	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232926	t3m_01282	Coordinates		311..850(+)		
2572232926	t3m_01282	DNA_length		540bp		
2572232926	t3m_01282	Protein_length		179aa		
2572232926	t3m_01282	GC			0.7	
2572232927	t3m_01283	Metacyc	THIOREDOX-PWY: thioredoxin pathway			
2572232927	t3m_01283	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232927	t3m_01283	COG0492	Thioredoxin reductase			1.00E-91
2572232927	t3m_01283	pfam00070	Pyr_redox			2.00E-14
2572232927	t3m_01283	pfam07992	Pyr_redox_2			1.70E-30
2572232927	t3m_01283	EC:1.8.1.9	Thioredoxin-disulfide reductase.			
2572232927	t3m_01283	TIGR01292	thioredoxin-disulfide reductase			1.30E-126
2572232927	t3m_01283	KO:K00384	thioredoxin reductase (NADPH) [EC:1.8.1.9]			0.00E+00
2572232927	t3m_01283	Locus_type		CDS		
2572232927	t3m_01283	Product_name		thioredoxin-disulfide reductase		
2572232927	t3m_01283	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232927	t3m_01283	Coordinates		889..1857(+)		
2572232927	t3m_01283	DNA_length		969bp		
2572232927	t3m_01283	Protein_length		322aa		
2572232927	t3m_01283	GC			0.7	
2572232928	t3m_01284	pfam12838	Fer4_7			3.30E-10
2572232928	t3m_01284	Locus_type		CDS		
2572232928	t3m_01284	Product_name		4Fe-4S dicluster domain		
2572232928	t3m_01284	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232928	t3m_01284	Coordinates		1926..2117(+)		

2572232928	t3m_01284	DNA_length		192bp		
2572232928	t3m_01284	Protein_length		63aa		
2572232928	t3m_01284	GC			0.62	
2572232929	t3m_01285	COG_category	[C] Energy production and conversion			
2572232929	t3m_01285	COG0644	Dehydrogenases (flavoproteins)			7.00E-63
2572232929	t3m_01285	pfam01494	FAD_binding_3			9.40E-17
2572232929	t3m_01285	TIGR02032	geranylgeranyl reductase family			2.50E-69
2572232929	t3m_01285	ITERM:05620	2,3-di-O-geranylgeranylglyceryl phosphate reductase (NADH) (EC 1.3.1.-)			
2572232929	t3m_01285	Locus_type		CDS		
2572232929	t3m_01285	Product_name		2,3-di-O-geranylgeranylglyceryl phosphate reductase (NADH) (EC 1.3.1.-		
2572232929	t3m_01285	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232929	t3m_01285	Coordinates		2140..3327(+)		
2572232929	t3m_01285	DNA_length		1188bp		
2572232929	t3m_01285	Protein_length		395aa		
2572232929	t3m_01285	GC			0.65	
2572232930	t3m_01286	Locus_type		CDS		
2572232930	t3m_01286	Product_name		hypothetical protein		
2572232930	t3m_01286	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232930	t3m_01286	Coordinates		3346..3969(+)		
2572232930	t3m_01286	DNA_length		624bp		
2572232930	t3m_01286	Protein_length		207aa		
2572232930	t3m_01286	GC			0.73	
2572232931	t3m_01287	Locus_type		CDS		
2572232931	t3m_01287	Product_name		hypothetical protein		
2572232931	t3m_01287	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232931	t3m_01287	Coordinates		3976..4326(+)		
2572232931	t3m_01287	DNA_length		351bp		
2572232931	t3m_01287	Protein_length		116aa		
2572232931	t3m_01287	GC			0.74	
2572232932	t3m_01288	COG_category	[S] Function unknown			

2572232932	t3m_01288	COG3342	Uncharacterized conserved protein			2.00E-75
2572232932	t3m_01288	pfam08823	PG_binding_2			1.10E-13
2572232932	t3m_01288	pfam06267	DUF1028			7.90E-70
2572232932	t3m_01288	Locus_type		CDS		
2572232932	t3m_01288	Product_name		Uncharacterized conserved protein		
2572232932	t3m_01288	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232932	t3m_01288	Coordinates		4353..5354(+)		
2572232932	t3m_01288	DNA_length		1002bp		
2572232932	t3m_01288	Protein_length		333aa		
2572232932	t3m_01288	GC			0.69	
2572232933	t3m_01289	Locus_type		CDS		
2572232933	t3m_01289	Product_name		hypothetical protein		
2572232933	t3m_01289	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232933	t3m_01289	Coordinates		5405..5590(+)		
2572232933	t3m_01289	DNA_length		186bp		
2572232933	t3m_01289	Protein_length		61aa		
2572232933	t3m_01289	GC			0.72	
2572232934	t3m_01290	pfam02517	Abi			1.50E-13
2572232934	t3m_01290	Locus_type		CDS		
2572232934	t3m_01290	Product_name		CAAX protease self-immunity		
2572232934	t3m_01290	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232934	t3m_01290	Coordinates		5623..6474(+)		
2572232934	t3m_01290	DNA_length		852bp		
2572232934	t3m_01290	Protein_length		283aa		
2572232934	t3m_01290	GC			0.68	
2572232934	t3m_01290	Transmembrane		Yes		
2572232935	t3m_01291	COG_category	[R] General function prediction only			
2572232935	t3m_01291	COG1832	Predicted CoA-binding protein			1.00E-43
2572232935	t3m_01291	pfam13380	CoA_binding_2			2.40E-40
2572232935	t3m_01291	Locus_type		CDS		
2572232935	t3m_01291	Product_name		Predicted CoA-binding protein		

2572232935	t3m_01291	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232935	t3m_01291	Coordinates		6538..6972(+)		
2572232935	t3m_01291	DNA_length		435bp		
2572232935	t3m_01291	Protein_length		144aa		
2572232935	t3m_01291	GC			0.68	

2572232936	t3m_01292	Locus_type		CDS		
2572232936	t3m_01292	Product_name		hypothetical protein		
2572232936	t3m_01292	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232936	t3m_01292	Coordinates		6982..7791(+)		
2572232936	t3m_01292	DNA_length		810bp		
2572232936	t3m_01292	Protein_length		269aa		
2572232936	t3m_01292	GC			0.71	

2572232937	t3m_01293	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232937	t3m_01293	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232937	t3m_01293	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232937	t3m_01293	IMG_pathway	494: L-isoleucine ligation to tRNA(Ile)			
2572232937	t3m_01293	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232937	t3m_01293	COG0060	Isoleucyl-tRNA synthetase			0.00E+00
2572232937	t3m_01293	pfam00133	tRNA-synt_1			0.00E+00
2572232937	t3m_01293	pfam08264	Anticodon_1			3.10E-27
2572232937	t3m_01293	EC:6.1.1.5	Isoleucine--tRNA ligase.			
2572232937	t3m_01293	TIGR00392	isoleucyl-tRNA synthetase			0.00E+00
2572232937	t3m_01293	KO:K01870	isoleucyl-tRNA synthetase [EC:6.1.1.5]			0.00E+00
2572232937	t3m_01293	ITERM:00399	Isoleucyl-tRNA synthetase (EC 6.1.1.5)			
2572232937	t3m_01293	Locus_type		CDS		
2572232937	t3m_01293	Product_name		Isoleucyl-tRNA synthetase (EC 6.1.1.5)		
2572232937	t3m_01293	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232937	t3m_01293	Coordinates		7843..10806(+)		
2572232937	t3m_01293	DNA_length		2964bp		
2572232937	t3m_01293	Protein_length		987aa		
2572232937	t3m_01293	GC			0.71	

2572232938	t3m_01294	COG_category	[S] Function unknown			
2572232938	t3m_01294	COG2078	Uncharacterized conserved protein			4.00E-51
2572232938	t3m_01294	pfam01871	AMMECR1			1.40E-49
2572232938	t3m_01294	TIGR00296	uncharacterized protein, PH0010 family			9.40E-60
2572232938	t3m_01294	TIGR04335	AmmeMemoRadiSam system protein A			1.20E-50
2572232938	t3m_01294	KO:K09141	hypothetical protein			4.20E-45
2572232938	t3m_01294	Locus_type		CDS		
2572232938	t3m_01294	Product_name		uncharacterized protein, PH0010 family/AmmeMemoRadiSam system p		
2572232938	t3m_01294	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232938	t3m_01294	Coordinates		10772..11428(-)		
2572232938	t3m_01294	DNA_length		657bp		
2572232938	t3m_01294	Protein_length		218aa		
2572232938	t3m_01294	GC			0.73	
2572232939	t3m_01295	KEGG_module	M00177: Ribosome, eukaryotes			
2572232939	t3m_01295	KEGG_module	M00179: Ribosome, archaea			
2572232939	t3m_01295	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232939	t3m_01295	COG1552	Ribosomal protein L40E			2.00E-07
2572232939	t3m_01295	pfam01020	Ribosomal_L40e			2.60E-05
2572232939	t3m_01295	KO:K02927	large subunit ribosomal protein L40e			2.40E-13
2572232939	t3m_01295	ITERM:00273	LSU ribosomal protein L40E			
2572232939	t3m_01295	Locus_type		CDS		
2572232939	t3m_01295	Product_name		LSU ribosomal protein L40E		
2572232939	t3m_01295	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232939	t3m_01295	Coordinates		11517..11669(+)		
2572232939	t3m_01295	DNA_length		153bp		
2572232939	t3m_01295	Protein_length		50aa		
2572232939	t3m_01295	GC			0.65	
2572232940	t3m_01296	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572232940	t3m_01296	COG0463	Glycosyltransferases involved in cell wall biogenesis			2.00E-14
2572232940	t3m_01296	pfam00535	Glycos_transf_2			3.80E-19
2572232940	t3m_01296	Locus_type		CDS		
2572232940	t3m_01296	Product_name		Glycosyltransferases involved in cell wall biogenesis		

2572232940	t3m_01296	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30	
2572232940	t3m_01296	Coordinates		11742..12533(-)	
2572232940	t3m_01296	DNA_length		792bp	
2572232940	t3m_01296	Protein_length		263aa	
2572232940	t3m_01296	GC		0.69	
2572232941	t3m_01297	COG_category	[S] Function unknown		
2572232941	t3m_01297	COG1371	Uncharacterized conserved protein		8.00E-15
2572232941	t3m_01297	pfam01951	Archease		1.50E-19
2572232941	t3m_01297	Locus_type		CDS	
2572232941	t3m_01297	Product_name		Uncharacterized conserved protein	
2572232941	t3m_01297	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30	
2572232941	t3m_01297	Coordinates		12731..13039(+)	
2572232941	t3m_01297	DNA_length		309bp	
2572232941	t3m_01297	Protein_length		102aa	
2572232941	t3m_01297	GC		0.7	
2572232942	t3m_01298	Metacyc	PWY-6749: CMP-legionaminate biosynthesis I		
2572232942	t3m_01298	Metacyc	PWY-6627: salinosporamide A biosynthesis		
2572232942	t3m_01298	Metacyc	PWY-6942: dTDP-D-desosamine biosynthesis		
2572232942	t3m_01298	Metacyc	PWY-1186: homomethionine biosynthesis		
2572232942	t3m_01298	Metacyc	PWY-7014: paromamine biosynthesis I		
2572232942	t3m_01298	Metacyc	PWY-5710: capsaicin biosynthesis		
2572232942	t3m_01298	Metacyc	PWYQT-4474: glucosinolate biosynthesis from pentahomomethionine		
2572232942	t3m_01298	Metacyc	CYSTEINE-DEG-PWY: L-cysteine degradation I		
2572232942	t3m_01298	Metacyc	PWY-6328: lysine degradation X		
2572232942	t3m_01298	Metacyc	PWY-6682: dehydrophos biosynthesis		
2572232942	t3m_01298	Metacyc	PWY-7000: kanamycin biosynthesis		
2572232942	t3m_01298	Metacyc	PWY-5748: γ-coniciene and coniine biosynthesis		
2572232942	t3m_01298	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		
2572232942	t3m_01298	Metacyc	LYSDEGII-PWY: lysine degradation III		
2572232942	t3m_01298	Metacyc	PWY-3: putrescine degradation V		
2572232942	t3m_01298	Metacyc	PWY-6511: 3-methylarginine biosynthesis		
2572232942	t3m_01298	Metacyc	PWY-6322: phosphinothricin tripeptide biosynthesis		

2572232942	t3m_01298	Metacyc	PWY-7022: paromamine biosynthesis II			
2572232942	t3m_01298	Metacyc	PWY-6456: serinol biosynthesis			
2572232942	t3m_01298	Metacyc	PWY-5826: hypoglycin biosynthesis			
2572232942	t3m_01298	Metacyc	PWY-7018: paromomycin biosynthesis			
2572232942	t3m_01298	Metacyc	PWYQT-4471: glucosinolate biosynthesis from dihomomethionine			
2572232942	t3m_01298	Metacyc	PWYQT-4473: glucosinolate biosynthesis from tetrahomomethionine			
2572232942	t3m_01298	Metacyc	PWYQT-4472: glucosinolate biosynthesis from trihomomethionine			
2572232942	t3m_01298	Metacyc	PWY-7104: dTDP-L-megosamine biosynthesis			
2572232942	t3m_01298	Metacyc	PWYQT-4475: glucosinolate biosynthesis from hexahomomethionine			
2572232942	t3m_01298	Metacyc	PWY-6321: homotaurine degradation			
2572232942	t3m_01298	Metacyc	P621-PWY: nylon-6 oligomer degradation			
2572232942	t3m_01298	COG_category	[E] Amino acid transport and metabolism			
2572232942	t3m_01298	COG0075	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferas			1.00E-96
2572232942	t3m_01298	pfam00266	Aminotran_5			2.30E-37
2572232942	t3m_01298	EC:2.6.1.-	Transferases. Transferring nitrogenous groups. Transaminases (aminotransferases).			
2572232942	t3m_01298	KO:K00839	aminotransferase [EC:2.6.1.-]			0.00E+00
2572232942	t3m_01298	Locus_type		CDS		
2572232942	t3m_01298	Product_name		Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase		
2572232942	t3m_01298	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232942	t3m_01298	Coordinates		13065..14201(-)		
2572232942	t3m_01298	DNA_length		1137bp		
2572232942	t3m_01298	Protein_length		378aa		
2572232942	t3m_01298	GC			0.7	
2572232943	t3m_01299	KEGG_module	M00020: Serine biosynthesis, glycerate-3P => serine			
2572232943	t3m_01299	Metacyc	SERSYN-PWY: serine biosynthesis			
2572232943	t3m_01299	COG_category	[H] Coenzyme transport and metabolism			
2572232943	t3m_01299	COG_category	[E] Amino acid transport and metabolism			
2572232943	t3m_01299	COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases			2.00E-72
2572232943	t3m_01299	pfam00389	2-Hacid_dh			9.30E-31
2572232943	t3m_01299	pfam02826	2-Hacid_dh_C			3.80E-55
2572232943	t3m_01299	EC:1.1.1.95	Phosphoglycerate dehydrogenase.			
2572232943	t3m_01299	TIGR01327	D-3-phosphoglycerate dehydrogenase			4.90E-96
2572232943	t3m_01299	KO:K00058	D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]			0.00E+00

2572232943	t3m_01299	Locus_type		CDS	
2572232943	t3m_01299	Product_name		Phosphoglycerate dehydrogenase and related dehydrogenases	
2572232943	t3m_01299	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30	
2572232943	t3m_01299	Coordinates		14198..15148(-)	
2572232943	t3m_01299	DNA_length		951bp	
2572232943	t3m_01299	Protein_length		316aa	
2572232943	t3m_01299	GC		0.7	
2572232944	t3m_01300	Metacyc	PWYG-321: mycolate biosynthesis		
2572232944	t3m_01300	Metacyc	PWY-6972: oleandomycin activation/inactivation		
2572232944	t3m_01300	COG_category	[R] General function prediction only		
2572232944	t3m_01300	COG0714	MoxR-like ATPases		6.00E-67
2572232944	t3m_01300	pfam07726	AAA_3		1.20E-60
2572232944	t3m_01300	EC:3.6.3.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; catalyzing transmembrane move		
2572232944	t3m_01300	KO:K03924	MoxR-like ATPase [EC:3.6.3.-]		0.00E+00
2572232944	t3m_01300	Locus_type		CDS	
2572232944	t3m_01300	Product_name		MoxR-like ATPases	
2572232944	t3m_01300	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30	
2572232944	t3m_01300	Coordinates		15198..16148(-)	
2572232944	t3m_01300	DNA_length		951bp	
2572232944	t3m_01300	Protein_length		316aa	
2572232944	t3m_01300	GC		0.7	
2572232945	t3m_01301	Locus_type		CDS	
2572232945	t3m_01301	Product_name		hypothetical protein	
2572232945	t3m_01301	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30	
2572232945	t3m_01301	Coordinates		16441..16959(-)	
2572232945	t3m_01301	DNA_length		519bp	
2572232945	t3m_01301	Protein_length		172aa	
2572232945	t3m_01301	GC		0.73	
2572232945	t3m_01301	Transmembrane		Yes	
2572232946	t3m_01302	COG_category	[R] General function prediction only		
2572232946	t3m_01302	COG1721	Uncharacterized conserved protein (some members contain a von Wille		6.00E-22

2572232946	t3m_01302	pfam01882	DUF58			1.90E-14
2572232946	t3m_01302	Locus_type		CDS		
2572232946	t3m_01302	Product_name		Uncharacterized conserved protein (some members contain a von Wille		
2572232946	t3m_01302	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232946	t3m_01302	Coordinates		16959..18242(-)		
2572232946	t3m_01302	DNA_length		1284bp		
2572232946	t3m_01302	Protein_length		427aa		
2572232946	t3m_01302	GC			0.71	
2572232946	t3m_01302	Transmembrane		Yes		
2572232947	t3m_01303	Locus_type		CDS		
2572232947	t3m_01303	Product_name		hypothetical protein		
2572232947	t3m_01303	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232947	t3m_01303	Coordinates		18239..18643(-)		
2572232947	t3m_01303	DNA_length		405bp		
2572232947	t3m_01303	Protein_length		134aa		
2572232947	t3m_01303	GC			0.7	
2572232947	t3m_01303	Signal_peptide		Yes		
2572232947	t3m_01303	Transmembrane		Yes		
2572232948	t3m_01304	pfam13559	DUF4129			2.20E-07
2572232948	t3m_01304	Locus_type		CDS		
2572232948	t3m_01304	Product_name		Domain of unknown function (DUF4129)		
2572232948	t3m_01304	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232948	t3m_01304	Coordinates		18640..19557(-)		
2572232948	t3m_01304	DNA_length		918bp		
2572232948	t3m_01304	Protein_length		305aa		
2572232948	t3m_01304	GC			0.69	
2572232948	t3m_01304	Transmembrane		Yes		
2572232949	t3m_01305	COG_category	[S] Function unknown			
2572232949	t3m_01305	COG3375	Uncharacterized conserved protein			1.00E-42
2572232949	t3m_01305	Locus_type		CDS		
2572232949	t3m_01305	Product_name		Uncharacterized conserved protein		

2572232949	t3m_01305	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232949	t3m_01305	Coordinates		19600..20499(-)		
2572232949	t3m_01305	DNA_length		900bp		
2572232949	t3m_01305	Protein_length		299aa		
2572232949	t3m_01305	GC			0.68	
2572232950	t3m_01306	Locus_type		CDS		
2572232950	t3m_01306	Product_name		hypothetical protein		
2572232950	t3m_01306	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232950	t3m_01306	Coordinates		20567..20989(-)		
2572232950	t3m_01306	DNA_length		423bp		
2572232950	t3m_01306	Protein_length		140aa		
2572232950	t3m_01306	GC			0.64	
2572232950	t3m_01306	Transmembrane		Yes		
2572232951	t3m_01307	Locus_type		CDS		
2572232951	t3m_01307	Product_name		hypothetical protein		
2572232951	t3m_01307	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30		
2572232951	t3m_01307	Coordinates		21063..21851(-)		
2572232951	t3m_01307	DNA_length		789bp		
2572232951	t3m_01307	Protein_length		262aa		
2572232951	t3m_01307	GC			0.7	
2572232951	t3m_01307	Transmembrane		Yes		
2572232952	t3m_01308	Metacyc	PWY-6829: tRNA methylation (yeast)			
2572232952	t3m_01308	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232952	t3m_01308	COG2519	tRNA(1-methyladenosine) methyltransferase and related methyltransfe			6.00E-61
2572232952	t3m_01308	pfam08704	GCD14			1.50E-26
2572232952	t3m_01308	EC:2.1.1.220	tRNA (adenine(58)-N(1))-methyltransferase.			
2572232952	t3m_01308	EC:2.1.1.219	tRNA (adenine(57)-N(1)/adenine(58)-N(1))-methyltransferase.			
2572232952	t3m_01308	KO:K07442	tRNA (adenine57-N1/adenine58-N1)-methyltransferase [EC:2.1.1.219 2			4.20E-45
2572232952	t3m_01308	ITERM:00706	tRNA (adenine-57, 58-N(1)-) methyltransferase (EC 2.1.1.-)			
2572232952	t3m_01308	Locus_type		CDS		
2572232952	t3m_01308	Product_name		tRNA (adenine-57, 58-N(1)-) methyltransferase (EC 2.1.1.-)		

2572232952	t3m_01308	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30	
2572232952	t3m_01308	Coordinates		21854..22642(-)	
2572232952	t3m_01308	DNA_length		789bp	
2572232952	t3m_01308	Protein_length		262aa	
2572232952	t3m_01308	GC		0.73	
2572232953	t3m_01309	Locus_type		CDS	
2572232953	t3m_01309	Product_name		hypothetical protein	
2572232953	t3m_01309	Scaffold		t3m_contig_70_244_len_23258_read_count_1799640.30	
2572232953	t3m_01309	Coordinates		22739..23185(+)	
2572232953	t3m_01309	DNA_length		447bp	
2572232953	t3m_01309	Protein_length		148aa	
2572232953	t3m_01309	GC		0.64	
2572232954	t3m_01310	Locus_type		CDS	
2572232954	t3m_01310	Product_name		hypothetical protein	
2572232954	t3m_01310	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31	
2572232954	t3m_01310	Coordinates		183..422(-)	
2572232954	t3m_01310	DNA_length		240bp	
2572232954	t3m_01310	Protein_length		79aa	
2572232954	t3m_01310	GC		0.68	
2572232955	t3m_01311	KEGG_module	M00248: Putative antibiotic transport system		
2572232955	t3m_01311	COG_category	[V] Defense mechanisms		
2572232955	t3m_01311	COG0842	ABC-type multidrug transport system, permease component		9.00E-08
2572232955	t3m_01311	pfam01061	ABC2_membrane		1.80E-15
2572232955	t3m_01311	KO:K09686	antibiotic transport system permease protein		0.00E+00
2572232955	t3m_01311	Locus_type		CDS	
2572232955	t3m_01311	Product_name		ABC-type multidrug transport system, permease component	
2572232955	t3m_01311	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31	
2572232955	t3m_01311	Coordinates		507..1256(-)	
2572232955	t3m_01311	DNA_length		750bp	
2572232955	t3m_01311	Protein_length		249aa	
2572232955	t3m_01311	GC		0.67	

2572232955	t3m_01311	Transmembrane		Yes	
2572232956	t3m_01312	KEGG_module	M00254: ABC-2 type transport system		
2572232956	t3m_01312	COG_category	[V] Defense mechanisms		
2572232956	t3m_01312	COG1131	ABC-type multidrug transport system, ATPase component		4.00E-63
2572232956	t3m_01312	pfam00005	ABC_tran		1.10E-25
2572232956	t3m_01312	KO:K01990	ABC-2 type transport system ATP-binding protein		0.00E+00
2572232956	t3m_01312	Locus_type		CDS	
2572232956	t3m_01312	Product_name		ABC-type multidrug transport system, ATPase component	
2572232956	t3m_01312	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31	
2572232956	t3m_01312	Coordinates		1253..2215(-)	
2572232956	t3m_01312	DNA_length		963bp	
2572232956	t3m_01312	Protein_length		320aa	
2572232956	t3m_01312	GC		0.67	
2572232957	t3m_01313	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572232957	t3m_01313	Metacyc	PWY-6720: toyocamycin biosynthesis		
2572232957	t3m_01313	COG_category	[R] General function prediction only		
2572232957	t3m_01313	COG1759	ATP-utilizing enzymes of ATP-grasp superfamily (probably carboligases)		2.00E-100
2572232957	t3m_01313	pfam06849	DUF1246		7.40E-37
2572232957	t3m_01313	pfam06973	DUF1297		2.40E-59
2572232957	t3m_01313	EC:6.3.4.-	Ligases. Forming carbon-nitrogen bonds. Other carbon--nitrogen ligases.		
2572232957	t3m_01313	KO:K06863	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuranosyl 5'-mon		0.00E+00
2572232957	t3m_01313	Locus_type		CDS	
2572232957	t3m_01313	Product_name		ATP-utilizing enzymes of ATP-grasp superfamily (probably carboligases)	
2572232957	t3m_01313	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31	
2572232957	t3m_01313	Coordinates		2270..3337(-)	
2572232957	t3m_01313	DNA_length		1068bp	
2572232957	t3m_01313	Protein_length		355aa	
2572232957	t3m_01313	GC		0.68	
2572232958	t3m_01314	COG_category	[L] Replication, recombination and repair		
2572232958	t3m_01314	COG2887	RecB family exonuclease		2.00E-07
2572232958	t3m_01314	pfam12705	PDDEXK_1		3.90E-40

2572232958	t3m_01314	Locus_type		CDS		
2572232958	t3m_01314	Product_name		RecB family exonuclease		
2572232958	t3m_01314	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232958	t3m_01314	Coordinates		3388..4608(-)		
2572232958	t3m_01314	DNA_length		1221bp		
2572232958	t3m_01314	Protein_length		406aa		
2572232958	t3m_01314	GC			0.71	

2572232959	t3m_01315	COG_category	[K] Transcription			
2572232959	t3m_01315	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatio			1.00E-69
2572232959	t3m_01315	pfam08271	TF_Zn_Ribbon			3.80E-12
2572232959	t3m_01315	pfam00382	TFIIB			3.90E-11
2572232959	t3m_01315	pfam00382	TFIIB			1.40E-16
2572232959	t3m_01315	KO:K03124	transcription initiation factor TFIIB			0.00E+00
2572232959	t3m_01315	Locus_type		CDS		
2572232959	t3m_01315	Product_name		Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiatio		
2572232959	t3m_01315	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232959	t3m_01315	Coordinates		4656..5711(-)		
2572232959	t3m_01315	DNA_length		1056bp		
2572232959	t3m_01315	Protein_length		351aa		
2572232959	t3m_01315	GC			0.69	

2572232960	t3m_01316	COG_category	[K] Transcription			
2572232960	t3m_01316	COG1378	Predicted transcriptional regulators			2.00E-17
2572232960	t3m_01316	pfam11495	Regulator_TrmB			3.10E-05
2572232960	t3m_01316	pfam01978	TrmB			1.20E-08
2572232960	t3m_01316	Locus_type		CDS		
2572232960	t3m_01316	Product_name		Predicted transcriptional regulators		
2572232960	t3m_01316	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232960	t3m_01316	Coordinates		5870..7144(-)		
2572232960	t3m_01316	DNA_length		1275bp		
2572232960	t3m_01316	Protein_length		424aa		
2572232960	t3m_01316	GC			0.7	

2572232961	t3m_01317	KEGG_module	M00179: Ribosome, archaea			
2572232961	t3m_01317	KEGG_module	M00178: Ribosome, bacteria			
2572232961	t3m_01317	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232961	t3m_01317	COG0052	Ribosomal protein S2			9.00E-44
2572232961	t3m_01317	pfam00318	Ribosomal_S2			2.40E-17
2572232961	t3m_01317	pfam00318	Ribosomal_S2			6.30E-18
2572232961	t3m_01317	TIGR01012	ribosomal protein Sa(cytosolic)/S2(archaeal)			6.80E-81
2572232961	t3m_01317	KO:K02967	small subunit ribosomal protein S2			0.00E+00
2572232961	t3m_01317	Locus_type		CDS		
2572232961	t3m_01317	Product_name		ribosomal protein Sa(cytosolic)/S2(archaeal)		
2572232961	t3m_01317	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232961	t3m_01317	Coordinates		7219..7917(-)		
2572232961	t3m_01317	DNA_length		699bp		
2572232961	t3m_01317	Protein_length		232aa		
2572232961	t3m_01317	GC			0.67	

2572232962	t3m_01318	KEGG_module	M00346: Formaldehyde assimilation, serine pathway
2572232962	t3m_01318	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds
2572232962	t3m_01318	KEGG_module	M00003: Gluconeogenesis, oxaloacetate => fructose-6P
2572232962	t3m_01318	KEGG_module	M00394: RNA degradosome
2572232962	t3m_01318	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate
2572232962	t3m_01318	Metacyc	ANARESP1-PWY: respiration (anaerobic)
2572232962	t3m_01318	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)
2572232962	t3m_01318	Metacyc	GLUCONEO-PWY: gluconeogenesis I
2572232962	t3m_01318	Metacyc	PWY-5723: Rubisco shunt
2572232962	t3m_01318	Metacyc	PWY-7124: ethylene biosynthesis V
2572232962	t3m_01318	Metacyc	PWY-1042: glycolysis IV (plant cytosol)
2572232962	t3m_01318	Metacyc	GLYCOLYSIS: glycolysis I
2572232962	t3m_01318	Metacyc	P124-PWY: Bifidobacterium shunt
2572232962	t3m_01318	Metacyc	PWY-2221: Entner-Doudoroff pathway III (semi-phosphorylative)
2572232962	t3m_01318	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)
2572232962	t3m_01318	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis
2572232962	t3m_01318	Metacyc	P122-PWY: heterolactic fermentation
2572232962	t3m_01318	Metacyc	PWY-6901: xylose degradation IV

2572232962	t3m_01318	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)			
2572232962	t3m_01318	Metacyc	PWY-7003: glycerol degradation to butanol			
2572232962	t3m_01318	Metacyc	P341-PWY: glycolysis V (Pyrococcus)			
2572232962	t3m_01318	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2572232962	t3m_01318	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2572232962	t3m_01318	COG_category	[G] Carbohydrate transport and metabolism			
2572232962	t3m_01318	COG0148	Enolase			3.00E-103
2572232962	t3m_01318	pfam00113	Enolase_C			9.70E-53
2572232962	t3m_01318	pfam03952	Enolase_N			3.60E-32
2572232962	t3m_01318	EC:4.2.1.11	Phosphopyruvate hydratase.			
2572232962	t3m_01318	TIGR01060	phosphopyruvate hydratase			8.50E-106
2572232962	t3m_01318	KO:K01689	enolase [EC:4.2.1.11]			0.00E+00
2572232962	t3m_01318	Locus_type		CDS		
2572232962	t3m_01318	Product_name		Enolase		
2572232962	t3m_01318	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232962	t3m_01318	Coordinates		7880..9094(-)		
2572232962	t3m_01318	DNA_length		1215bp		
2572232962	t3m_01318	Protein_length		404aa		
2572232962	t3m_01318	GC			0.69	

2572232963	t3m_01319	KEGG_module	M00376: 3-Hydroxypropionate bicycle	
2572232963	t3m_01319	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle	
2572232963	t3m_01319	KEGG_module	M00373: Ethylmalonyl pathway	
2572232963	t3m_01319	Metacyc	PWY-5743: 3-hydroxypropionate cycle	
2572232963	t3m_01319	Metacyc	P108-PWY: pyruvate fermentation to propionate I	
2572232963	t3m_01319	Metacyc	PROPIONMET-PWY: methylmalonyl pathway	
2572232963	t3m_01319	Metacyc	PWY-6728: methylaspartate cycle	
2572232963	t3m_01319	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle	
2572232963	t3m_01319	IMG_pathway	370: Oxaloacetate conversion to propionate via methylmalonyl-CoA	
2572232963	t3m_01319	IMG_pathway	525: Hydroxypropionate cycle	
2572232963	t3m_01319	IMG_pathway	596: 3-hydroxypropionate/4-hydroxybutyrate cycle	
2572232963	t3m_01319	IMG_pathway	837: Propionyl-CoA conversion to succinyl-CoA via methylmalonyl pathway	
2572232963	t3m_01319	IMG_pathway	962: Glyoxylate from acetyl-CoA via ethylmalonyl-CoA pathway	
2572232963	t3m_01319	pfam13669	Glyoxalase_4	2.40E-20

2572232963	t3m_01319	EC:5.1.99.1	Methylmalonyl-CoA epimerase.			
2572232963	t3m_01319	TIGR03081	methylmalonyl-CoA epimerase			1.10E-38
2572232963	t3m_01319	KO:K05606	methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1]			5.00E-30
2572232963	t3m_01319	ITERM:01586	methylmalonyl-CoA epimerase (EC 5.1.99.1)			
2572232963	t3m_01319	Locus_type		CDS		
2572232963	t3m_01319	Product_name		methylmalonyl-CoA epimerase (EC 5.1.99.1)		
2572232963	t3m_01319	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232963	t3m_01319	Coordinates		9091..9489(-)		
2572232963	t3m_01319	DNA_length		399bp		
2572232963	t3m_01319	Protein_length		132aa		
2572232963	t3m_01319	GC			0.7	
2572232964	t3m_01320	KEGG_module	M00376: 3-Hydroxypropionate bicycle			
2572232964	t3m_01320	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle			
2572232964	t3m_01320	Metacyc	PWY0-43: conversion of succinate to propionate			
2572232964	t3m_01320	Metacyc	P108-PWY: pyruvate fermentation to propionate I			
2572232964	t3m_01320	Metacyc	PROPIONMET-PWY: methylmalonyl pathway			
2572232964	t3m_01320	Metacyc	PWY-6728: methylaspartate cycle			
2572232964	t3m_01320	Metacyc	PWY-5743: 3-hydroxypropionate cycle			
2572232964	t3m_01320	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			
2572232964	t3m_01320	COG_category	[I] Lipid transport and metabolism			
2572232964	t3m_01320	COG1884	Methylmalonyl-CoA mutase, N-terminal domain/subunit			0.00E+00
2572232964	t3m_01320	pfam01642	MM_CoA_mutase			0.00E+00
2572232964	t3m_01320	EC:5.4.99.2	Methylmalonyl-CoA mutase.			
2572232964	t3m_01320	TIGR00641	methylmalonyl-CoA mutase N-terminal domain			0.00E+00
2572232964	t3m_01320	KO:K01848	methylmalonyl-CoA mutase, N-terminal domain [EC:5.4.99.2]			0.00E+00
2572232964	t3m_01320	Locus_type		CDS		
2572232964	t3m_01320	Product_name		methylmalonyl-CoA mutase (EC 5.4.99.2)		
2572232964	t3m_01320	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232964	t3m_01320	Coordinates		9498..11177(-)		
2572232964	t3m_01320	DNA_length		1680bp		
2572232964	t3m_01320	Protein_length		559aa		
2572232964	t3m_01320	GC			0.69	

2572232965	t3m_01321	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232965	t3m_01321	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232965	t3m_01321	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232965	t3m_01321	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232965	t3m_01321	COG0072	Phenylalanyl-tRNA synthetase beta subunit			9.00E-58
2572232965	t3m_01321	pfam03484	B5			7.30E-06
2572232965	t3m_01321	EC:6.1.1.20	Phenylalanine--tRNA ligase.			
2572232965	t3m_01321	KO:K01890	phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]			0.00E+00
2572232965	t3m_01321	ITERM:00403	phenylalanyl-tRNA synthetase beta subunit (EC 6.1.1.20)			
2572232965	t3m_01321	Locus_type		CDS		
2572232965	t3m_01321	Product_name		phenylalanyl-tRNA synthetase beta subunit (EC 6.1.1.20)		
2572232965	t3m_01321	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232965	t3m_01321	Coordinates		11201..12895(-)		
2572232965	t3m_01321	DNA_length		1695bp		
2572232965	t3m_01321	Protein_length		564aa		
2572232965	t3m_01321	GC			0.71	
2572232966	t3m_01322	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572232966	t3m_01322	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572232966	t3m_01322	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572232966	t3m_01322	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232966	t3m_01322	COG0016	Phenylalanyl-tRNA synthetase alpha subunit			6.00E-72
2572232966	t3m_01322	pfam01409	tRNA-synt_2d			2.40E-73
2572232966	t3m_01322	EC:6.1.1.20	Phenylalanine--tRNA ligase.			
2572232966	t3m_01322	TIGR00468	phenylalanyl-tRNA synthetase, alpha subunit			1.30E-84
2572232966	t3m_01322	KO:K01889	phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]			0.00E+00
2572232966	t3m_01322	ITERM:01968	phenylalanyl-tRNA synthetase, alpha subunit (EC 6.1.1.20)			
2572232966	t3m_01322	Locus_type		CDS		
2572232966	t3m_01322	Product_name		phenylalanyl-tRNA synthetase, alpha subunit (EC 6.1.1.20)		
2572232966	t3m_01322	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232966	t3m_01322	Coordinates		12898..14427(-)		
2572232966	t3m_01322	DNA_length		1530bp		
2572232966	t3m_01322	Protein_length		509aa		
2572232966	t3m_01322	GC			0.7	

2572232967	t3m_01323	pfam09286	Pro-kuma_activ			1.50E-06
2572232967	t3m_01323	Locus_type		CDS		
2572232967	t3m_01323	Product_name		Pro-kumamolisin, activation domain		
2572232967	t3m_01323	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232967	t3m_01323	Coordinates		14279..16909(-)		
2572232967	t3m_01323	DNA_length		2631bp		
2572232967	t3m_01323	Protein_length		876aa		
2572232967	t3m_01323	GC			0.71	
2572232967	t3m_01323	Transmembrane		Yes		
2572232968	t3m_01324	Metacyc	GLUTSYN-PWY: glutamate biosynthesis I			
2572232968	t3m_01324	Metacyc	PWY-6963: ammonia assimilation cycle I			
2572232968	t3m_01324	Metacyc	GLUGLNSYN-PWY: glutamate biosynthesis IV			
2572232968	t3m_01324	Metacyc	GLUTAMINEFUM-PWY: glutamine degradation II			
2572232968	t3m_01324	COG_category	[E] Amino acid transport and metabolism			
2572232968	t3m_01324	COG_category	[R] General function prediction only			
2572232968	t3m_01324	COG0493	NADPH-dependent glutamate synthase beta chain and related oxidorec			1.00E-76
2572232968	t3m_01324	pfam07992	Pyr_redox_2			1.70E-09
2572232968	t3m_01324	pfam14691	Fer4_20			1.40E-25
2572232968	t3m_01324	EC:1.4.1.13	Glutamate synthase (NADPH).			
2572232968	t3m_01324	EC:1.4.1.14	Glutamate synthase (NADH).			
2572232968	t3m_01324	KO:K00266	glutamate synthase (NADPH/NADH) small chain [EC:1.4.1.13 1.4.1.14]			0.00E+00
2572232968	t3m_01324	Locus_type		CDS		
2572232968	t3m_01324	Product_name		NADPH-dependent glutamate synthase beta chain and related oxidored		
2572232968	t3m_01324	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232968	t3m_01324	Coordinates		16977..18440(-)		
2572232968	t3m_01324	DNA_length		1464bp		
2572232968	t3m_01324	Protein_length		487aa		
2572232968	t3m_01324	GC			0.69	
2572232969	t3m_01325	KEGG_module	M00335: Sec (secretion) system			
2572232969	t3m_01325	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2572232969	t3m_01325	COG0541	Signal recognition particle GTPase			0.00E+00

2572232969	t3m_01325	pfam02881	SRP54_N			5.00E-14
2572232969	t3m_01325	pfam02978	SRP_SPB			6.40E-28
2572232969	t3m_01325	pfam00448	SRP54			6.70E-66
2572232969	t3m_01325	KO:K03106	signal recognition particle subunit SRP54			0.00E+00
2572232969	t3m_01325	ITERM:01969	signal recognition particle subunit FFH/SRP54 (srp54)			
2572232969	t3m_01325	Locus_type		CDS		
2572232969	t3m_01325	Product_name		signal recognition particle subunit FFH/SRP54 (srp54)		
2572232969	t3m_01325	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232969	t3m_01325	Coordinates		18592..19932(+)		
2572232969	t3m_01325	DNA_length		1341bp		
2572232969	t3m_01325	Protein_length		446aa		
2572232969	t3m_01325	GC			0.69	

2572232970	t3m_01326	pfam07760	DUF1616			2.00E-11
2572232970	t3m_01326	Locus_type		CDS		
2572232970	t3m_01326	Product_name		Protein of unknown function (DUF1616)		
2572232970	t3m_01326	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232970	t3m_01326	Coordinates		19949..20491(+)		
2572232970	t3m_01326	DNA_length		543bp		
2572232970	t3m_01326	Protein_length		180aa		
2572232970	t3m_01326	GC			0.69	
2572232970	t3m_01326	Transmembrane		Yes		

2572232971	t3m_01327	Metacyc	PWY490-4: asparagine biosynthesis III (tRNA-dependent)			
2572232971	t3m_01327	COG_category	[S] Function unknown			
2572232971	t3m_01327	COG1990	Uncharacterized conserved protein			6.00E-24
2572232971	t3m_01327	pfam01981	PTH2			5.40E-36
2572232971	t3m_01327	EC:3.1.1.29	Aminoacyl-tRNA hydrolase.			
2572232971	t3m_01327	TIGR00283	peptidyl-tRNA hydrolase			3.20E-35
2572232971	t3m_01327	KO:K04794	peptidyl-tRNA hydrolase, PTH2 family [EC:3.1.1.29]			6.70E-24
2572232971	t3m_01327	Locus_type		CDS		
2572232971	t3m_01327	Product_name		peptidyl-tRNA hydrolase (EC 3.1.1.29)		
2572232971	t3m_01327	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232971	t3m_01327	Coordinates		20520..20861(+)		

2572232971	t3m_01327	DNA_length		342bp		
2572232971	t3m_01327	Protein_length		113aa		
2572232971	t3m_01327	GC			0.72	
2572232972	t3m_01328	KEGG_module	M00239: Peptides/nickel transport system			
2572232972	t3m_01328	COG_category	[E] Amino acid transport and metabolism			
2572232972	t3m_01328	COG_category	[P] Inorganic ion transport and metabolism			
2572232972	t3m_01328	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c			1.00E-59
2572232972	t3m_01328	pfam00528	BPD_transp_1			4.40E-32
2572232972	t3m_01328	KO:K02033	peptide/nickel transport system permease protein			0.00E+00
2572232972	t3m_01328	Locus_type		CDS		
2572232972	t3m_01328	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease co		
2572232972	t3m_01328	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232972	t3m_01328	Coordinates		20969..22177(+)		
2572232972	t3m_01328	DNA_length		1209bp		
2572232972	t3m_01328	Protein_length		402aa		
2572232972	t3m_01328	GC			0.59	
2572232972	t3m_01328	Transmembrane		Yes		
2572232973	t3m_01329	pfam12911	OppC_N			2.50E-08
2572232973	t3m_01329	Locus_type		CDS		
2572232973	t3m_01329	Product_name		N-terminal TM domain of oligopeptide transport permease C		
2572232973	t3m_01329	Scaffold		t3m_contig_70_255_len_22838_read_count_1766313.31		
2572232973	t3m_01329	Coordinates		22199..22837(+)		
2572232973	t3m_01329	DNA_length		639bp		
2572232973	t3m_01329	Protein_length		213aa		
2572232973	t3m_01329	GC			0.65	
2572232973	t3m_01329	Transmembrane		Yes		
2572232974	t3m_01330	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572232974	t3m_01330	COG5256	Translation elongation factor EF-1alpha (GTPase)			0.00E+00
2572232974	t3m_01330	pfam00009	GTP_EFTU			1.10E-58
2572232974	t3m_01330	pfam03144	GTP_EFTU_D2			1.20E-20
2572232974	t3m_01330	pfam03143	GTP_EFTU_D3			3.60E-31

2572232974	t3m_01330	TIGR00231	small GTP-binding protein domain			4.00E-18
2572232974	t3m_01330	TIGR00483	translation elongation factor EF-1 alpha			0.00E+00
2572232974	t3m_01330	TIGR00485	translation elongation factor TU			3.80E-70
2572232974	t3m_01330	KO:K03231	elongation factor 1-alpha			0.00E+00
2572232974	t3m_01330	Locus_type		CDS		
2572232974	t3m_01330	Product_name		translation elongation factor 1A (EF-1A/EF-Tu)		
2572232974	t3m_01330	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232974	t3m_01330	Coordinates		33..1310(-)		
2572232974	t3m_01330	DNA_length		1278bp		
2572232974	t3m_01330	Protein_length		425aa		
2572232974	t3m_01330	GC			0.64	

2572232975	t3m_01331	COG_category	[E] Amino acid transport and metabolism			
2572232975	t3m_01331	COG0346	Lactoylglutathione lyase and related lyases			3.00E-07
2572232975	t3m_01331	pfam12681	Glyoxalase_2			1.10E-14
2572232975	t3m_01331	Locus_type		CDS		
2572232975	t3m_01331	Product_name		Lactoylglutathione lyase and related lyases		
2572232975	t3m_01331	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232975	t3m_01331	Coordinates		1480..1911(-)		
2572232975	t3m_01331	DNA_length		432bp		
2572232975	t3m_01331	Protein_length		143aa		
2572232975	t3m_01331	GC			0.66	

2572232976	t3m_01332	COG_category	[K] Transcription			
2572232976	t3m_01332	COG1695	Predicted transcriptional regulators			1.00E-08
2572232976	t3m_01332	pfam03551	PadR			3.90E-12
2572232976	t3m_01332	Locus_type		CDS		
2572232976	t3m_01332	Product_name		Predicted transcriptional regulators		
2572232976	t3m_01332	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232976	t3m_01332	Coordinates		2094..2489(+)		
2572232976	t3m_01332	DNA_length		396bp		
2572232976	t3m_01332	Protein_length		131aa		
2572232976	t3m_01332	GC			0.68	

2572232977	t3m_01333	Locus_type		CDS	
2572232977	t3m_01333	Product_name		hypothetical protein	
2572232977	t3m_01333	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232977	t3m_01333	Coordinates		2533..2817(+)	
2572232977	t3m_01333	DNA_length		285bp	
2572232977	t3m_01333	Protein_length		94aa	
2572232977	t3m_01333	GC		0.64	
2572232977	t3m_01333	Transmembrane		Yes	
2572232978	t3m_01334	COG_category	[H] Coenzyme transport and metabolism		
2572232978	t3m_01334	COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis		3.00E-19
2572232978	t3m_01334	pfam08241	Methyltransf_11		8.10E-17
2572232978	t3m_01334	Locus_type		CDS	
2572232978	t3m_01334	Product_name		Methylase involved in ubiquinone/menaquinone biosynthesis	
2572232978	t3m_01334	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232978	t3m_01334	Coordinates		2869..3429(+)	
2572232978	t3m_01334	DNA_length		561bp	
2572232978	t3m_01334	Protein_length		186aa	
2572232978	t3m_01334	GC		0.71	
2572232979	t3m_01335	COG_category	[I] Lipid transport and metabolism		
2572232979	t3m_01335	COG1607	Acyl-CoA hydrolase		1.00E-35
2572232979	t3m_01335	pfam03061	4HBT		7.70E-18
2572232979	t3m_01335	Locus_type		CDS	
2572232979	t3m_01335	Product_name		Acyl-CoA hydrolase	
2572232979	t3m_01335	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232979	t3m_01335	Coordinates		3560..3988(+)	
2572232979	t3m_01335	DNA_length		429bp	
2572232979	t3m_01335	Protein_length		142aa	
2572232979	t3m_01335	GC		0.7	
2572232980	t3m_01336	COG_category	[K] Transcription		
2572232980	t3m_01336	COG1813	Predicted transcription factor, homolog of eukaryotic MBF1		2.00E-19
2572232980	t3m_01336	pfam01381	HTH_3		2.30E-06

2572232980	t3m_01336	TIGR00270	TIGR00270 family protein			2.60E-22
2572232980	t3m_01336	KO:K03627	putative transcription factor			4.20E-18
2572232980	t3m_01336	ITERM:01905	transcriptional regulator, XRE family			
2572232980	t3m_01336	Locus_type		CDS		
2572232980	t3m_01336	Product_name		transcriptional regulator, XRE family		
2572232980	t3m_01336	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232980	t3m_01336	Coordinates		4010..4456(+)		
2572232980	t3m_01336	DNA_length		447bp		
2572232980	t3m_01336	Protein_length		148aa		
2572232980	t3m_01336	GC			0.69	
2572232981	t3m_01337	Locus_type		CDS		
2572232981	t3m_01337	Product_name		hypothetical protein		
2572232981	t3m_01337	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232981	t3m_01337	Coordinates		4462..4848(-)		
2572232981	t3m_01337	DNA_length		387bp		
2572232981	t3m_01337	Protein_length		128aa		
2572232981	t3m_01337	GC			0.74	
2572232981	t3m_01337	Transmembrane		Yes		
2572232982	t3m_01338	KEGG_module	M00029: Urea cycle			
2572232982	t3m_01338	Metacyc	ARGSYNBSUB-PWY: arginine biosynthesis II (acetyl cycle)			
2572232982	t3m_01338	Metacyc	PWY-4984: urea cycle			
2572232982	t3m_01338	Metacyc	ARGSYN-PWY: arginine biosynthesis I			
2572232982	t3m_01338	Metacyc	ARGININE-SYN4-PWY: arginine biosynthesis IV			
2572232982	t3m_01338	Metacyc	CITRULLINE-DEG-PWY: citrulline degradation			
2572232982	t3m_01338	Metacyc	CITRULBIO-PWY: citrulline biosynthesis			
2572232982	t3m_01338	Metacyc	PWY-4981: proline biosynthesis II (from arginine)			
2572232982	t3m_01338	IMG_pathway	168: L-arginine synthesis from L-ornithine			
2572232982	t3m_01338	IMG_pathway	184: L-arginine degradation by Arg deiminase pathway			
2572232982	t3m_01338	COG_category	[E] Amino acid transport and metabolism			
2572232982	t3m_01338	COG0078	Ornithine carbamoyltransferase			8.00E-116
2572232982	t3m_01338	pfam00185	OTCace			6.30E-50
2572232982	t3m_01338	pfam02729	OTCace_N			9.60E-47

2572232982	t3m_01338	EC:2.1.3.3	Ornithine carbamoyltransferase.		
2572232982	t3m_01338	TIGR00658	ornithine carbamoyltransferase		1.30E-125
2572232982	t3m_01338	KO:K00611	ornithine carbamoyltransferase [EC:2.1.3.3]		0.00E+00
2572232982	t3m_01338	ITERM:00433	ornithine carbamoyltransferase (EC 2.1.3.3)		
2572232982	t3m_01338	Locus_type		CDS	
2572232982	t3m_01338	Product_name		ornithine carbamoyltransferase (EC 2.1.3.3)	
2572232982	t3m_01338	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232982	t3m_01338	Coordinates		4876..5838(-)	
2572232982	t3m_01338	DNA_length		963bp	
2572232982	t3m_01338	Protein_length		320aa	
2572232982	t3m_01338	GC		0.7	
2572232983	t3m_01339	KEGG_module	M00373: Ethylmalonyl pathway		
2572232983	t3m_01339	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway		
2572232983	t3m_01339	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone		
2572232983	t3m_01339	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2572232983	t3m_01339	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle		
2572232983	t3m_01339	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II		
2572232983	t3m_01339	Metacyc	PWY66-368: ketolysis		
2572232983	t3m_01339	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2572232983	t3m_01339	Metacyc	PWY-6174: mevalonate pathway II (archaea)		
2572232983	t3m_01339	Metacyc	PWY-7003: glycerol degradation to butanol		
2572232983	t3m_01339	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2572232983	t3m_01339	Metacyc	PWY-6883: pyruvate fermentation to butanol II		
2572232983	t3m_01339	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2572232983	t3m_01339	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2572232983	t3m_01339	Metacyc	PWY-6876: isopropanol biosynthesis		
2572232983	t3m_01339	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate		
2572232983	t3m_01339	Metacyc	PWY-6583: pyruvate fermentation to butanol I		
2572232983	t3m_01339	Metacyc	PWY-5177: glutaryl-CoA degradation		
2572232983	t3m_01339	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)		
2572232983	t3m_01339	Metacyc	PWY-922: mevalonate pathway I		
2572232983	t3m_01339	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis		
2572232983	t3m_01339	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis		

2572232983	t3m_01339	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			
2572232983	t3m_01339	Metacyc	PWY-5741: ethylmalonyl pathway			
2572232983	t3m_01339	Metacyc	PWY66-367: ketogenesis			
2572232983	t3m_01339	COG_category	[I] Lipid transport and metabolism			
2572232983	t3m_01339	COG0183	Acetyl-CoA acetyltransferase			5.00E-60
2572232983	t3m_01339	pfam02803	Thiolase_C			2.00E-07
2572232983	t3m_01339	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.			
2572232983	t3m_01339	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]			0.00E+00
2572232983	t3m_01339	Locus_type		CDS		
2572232983	t3m_01339	Product_name		Acetyl-CoA acetyltransferase		
2572232983	t3m_01339	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232983	t3m_01339	Coordinates		5949..7382(+)		
2572232983	t3m_01339	DNA_length		1434bp		
2572232983	t3m_01339	Protein_length		477aa		
2572232983	t3m_01339	GC			0.68	
2572232984	t3m_01340	COG_category	[R] General function prediction only			
2572232984	t3m_01340	COG1545	Predicted nucleic-acid-binding protein containing a Zn-ribbon			6.00E-26
2572232984	t3m_01340	pfam01796	DUF35			2.50E-13
2572232984	t3m_01340	Locus_type		CDS		
2572232984	t3m_01340	Product_name		Predicted nucleic-acid-binding protein containing a Zn-ribbon		
2572232984	t3m_01340	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232984	t3m_01340	Coordinates		7379..7906(+)		
2572232984	t3m_01340	DNA_length		528bp		
2572232984	t3m_01340	Protein_length		175aa		
2572232984	t3m_01340	GC			0.66	
2572232985	t3m_01341	Locus_type		tRNA		
2572232985	t3m_01341	Product_name		tRNA_Phe_GAA		
2572232985	t3m_01341	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232985	t3m_01341	Coordinates		8028..8101(-)		
2572232985	t3m_01341	DNA_length		74bp		
2572232985	t3m_01341	GC			0.62	

2572232986	t3m_01342	COG_category	[L] Replication, recombination and repair			
2572232986	t3m_01342	COG0550	Topoisomerase IA			0.00E+00
2572232986	t3m_01342	pfam01396	zf-C4_Topoisom			4.40E-12
2572232986	t3m_01342	pfam01751	Toprim			4.60E-14
2572232986	t3m_01342	pfam01131	Topoisom_bac			1.50E-105
2572232986	t3m_01342	EC:5.99.1.2	DNA topoisomerase.			
2572232986	t3m_01342	TIGR01057	DNA topoisomerase I, archaeal			1.30E-128
2572232986	t3m_01342	KO:K03168	DNA topoisomerase I [EC:5.99.1.2]			0.00E+00
2572232986	t3m_01342	Locus_type		CDS		
2572232986	t3m_01342	Product_name		Topoisomerase IA		
2572232986	t3m_01342	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232986	t3m_01342	Coordinates		8288..10870(+)		
2572232986	t3m_01342	DNA_length		2583bp		
2572232986	t3m_01342	Protein_length		860aa		
2572232986	t3m_01342	GC			0.68	
2572232987	t3m_01343	pfam13418	Kelch_4			4.20E-05
2572232987	t3m_01343	pfam13418	Kelch_4			2.80E-04
2572232987	t3m_01343	Locus_type		CDS		
2572232987	t3m_01343	Product_name		Galactose oxidase, central domain		
2572232987	t3m_01343	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232987	t3m_01343	Coordinates		11161..12216(+)		
2572232987	t3m_01343	DNA_length		1056bp		
2572232987	t3m_01343	Protein_length		351aa		
2572232987	t3m_01343	GC			0.66	
2572232987	t3m_01343	Transmembrane		Yes		
2572232988	t3m_01344	Metacyc	CRNFORCAT-PWY: creatinine degradation I			
2572232988	t3m_01344	COG_category	[R] General function prediction only			
2572232988	t3m_01344	COG1402	Uncharacterized protein, putative amidase			1.00E-33
2572232988	t3m_01344	pfam02633	Creatininase			2.20E-56
2572232988	t3m_01344	EC:3.5.2.10	Creatininase.			
2572232988	t3m_01344	KO:K01470	creatinine amidohydrolase [EC:3.5.2.10]			1.30E-40
2572232988	t3m_01344	Locus_type		CDS		

2572232988	t3m_01344	Product_name		Uncharacterized protein, putative amidase	
2572232988	t3m_01344	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232988	t3m_01344	Coordinates		12430..13152(+)	
2572232988	t3m_01344	DNA_length		723bp	
2572232988	t3m_01344	Protein_length		240aa	
2572232988	t3m_01344	GC		0.71	
2572232989	t3m_01345	COG_category	[L] Replication, recombination and repair		
2572232989	t3m_01345	COG0178	Excinuclease ATPase subunit		0.00E+00
2572232989	t3m_01345	TIGR00630	excinuclease ABC, A subunit		0.00E+00
2572232989	t3m_01345	KO:K03701	excinuclease ABC subunit A		0.00E+00
2572232989	t3m_01345	ITERM:00496	Excinuclease ABC subunit A		
2572232989	t3m_01345	Locus_type		CDS	
2572232989	t3m_01345	Product_name		Excinuclease ABC subunit A	
2572232989	t3m_01345	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232989	t3m_01345	Coordinates		13162..16005(+)	
2572232989	t3m_01345	DNA_length		2844bp	
2572232989	t3m_01345	Protein_length		947aa	
2572232989	t3m_01345	GC		0.68	
2572232990	t3m_01346	IMG_pathway	194: DNA incision (NER)		
2572232990	t3m_01346	COG_category	[L] Replication, recombination and repair		
2572232990	t3m_01346	COG0322	Nuclease subunit of the excinuclease complex		1.00E-118
2572232990	t3m_01346	pfam08459	UvrC_HhH_N		9.40E-50
2572232990	t3m_01346	pfam01541	GIY-YIG		3.70E-08
2572232990	t3m_01346	TIGR00194	excinuclease ABC, C subunit		8.10E-124
2572232990	t3m_01346	KO:K03703	excinuclease ABC subunit C		0.00E+00
2572232990	t3m_01346	ITERM:00498	Excinuclease ABC subunit C		
2572232990	t3m_01346	Locus_type		CDS	
2572232990	t3m_01346	Product_name		Excinuclease ABC subunit C	
2572232990	t3m_01346	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232990	t3m_01346	Coordinates		16002..17720(+)	
2572232990	t3m_01346	DNA_length		1719bp	
2572232990	t3m_01346	Protein_length		572aa	

2572232990	t3m_01346	GC			0.71	
2572232991	t3m_01347	COG_category	[S] Function unknown			
2572232991	t3m_01347	COG2318	Uncharacterized protein conserved in bacteria			1.00E-07
2572232991	t3m_01347	pfam12867	DinB_2			4.10E-12
2572232991	t3m_01347	Locus_type		CDS		
2572232991	t3m_01347	Product_name		Uncharacterized protein conserved in bacteria		
2572232991	t3m_01347	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232991	t3m_01347	Coordinates		17726..18289(-)		
2572232991	t3m_01347	DNA_length		564bp		
2572232991	t3m_01347	Protein_length		187aa		
2572232991	t3m_01347	GC			0.69	
2572232992	t3m_01348	KEGG_module	M00343: Archaeal proteasome			
2572232992	t3m_01348	KEGG_module	M00342: Bacterial proteasome			
2572232992	t3m_01348	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572232992	t3m_01348	COG0638	20S proteasome, alpha and beta subunits			5.00E-49
2572232992	t3m_01348	pfam00227	Proteasome			6.90E-45
2572232992	t3m_01348	pfam10584	Proteasome_A_N			8.00E-14
2572232992	t3m_01348	EC:3.4.25.1	Proteasome endopeptidase complex.			
2572232992	t3m_01348	KO:K03432	proteasome alpha subunit [EC:3.4.25.1]			0.00E+00
2572232992	t3m_01348	Locus_type		CDS		
2572232992	t3m_01348	Product_name		20S proteasome, alpha and beta subunits		
2572232992	t3m_01348	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32		
2572232992	t3m_01348	Coordinates		18320..19057(-)		
2572232992	t3m_01348	DNA_length		738bp		
2572232992	t3m_01348	Protein_length		245aa		
2572232992	t3m_01348	GC			0.69	
2572232993	t3m_01349	COG_category	[R] General function prediction only			
2572232993	t3m_01349	COG2108	Uncharacterized conserved protein related to pyruvate formate-lyase a			4.00E-76
2572232993	t3m_01349	pfam04055	Radical_SAM			1.10E-09
2572232993	t3m_01349	Locus_type		CDS		
2572232993	t3m_01349	Product_name		Uncharacterized conserved protein related to pyruvate formate-lyase ac		

2572232993	t3m_01349	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232993	t3m_01349	Coordinates		19272..20411(+)	
2572232993	t3m_01349	DNA_length		1140bp	
2572232993	t3m_01349	Protein_length		379aa	
2572232993	t3m_01349	GC		0.7	
2572232994	t3m_01350	KEGG_module	M00377: Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)		
2572232994	t3m_01350	KEGG_module	M00140: C1-unit interconversion, prokaryotes		
2572232994	t3m_01350	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2572232994	t3m_01350	Metacyc	PWY-3841: folate transformations II		
2572232994	t3m_01350	Metacyc	1CMET2-PWY: formylTHF biosynthesis I		
2572232994	t3m_01350	Metacyc	PWY-5030: histidine degradation III		
2572232994	t3m_01350	Metacyc	PWY-1722: formaldehyde oxidation V (tetrahydrofolate pathway)		
2572232994	t3m_01350	Metacyc	PWY-6613: tetrahydrofolate salvage from 5,10-methenyltetrahydrofolate		
2572232994	t3m_01350	Metacyc	P164-PWY: purine nucleobases degradation I (anaerobic)		
2572232994	t3m_01350	Metacyc	CODH-PWY: reductive acetyl coenzyme A pathway		
2572232994	t3m_01350	Metacyc	PWY-2201: folate transformations I		
2572232994	t3m_01350	COG_category	[H] Coenzyme transport and metabolism		
2572232994	t3m_01350	COG0190	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydro		1.00E-58
2572232994	t3m_01350	pfam02882	THF_DHG_CYH_C		8.50E-45
2572232994	t3m_01350	pfam00763	THF_DHG_CYH		2.40E-19
2572232994	t3m_01350	EC:3.5.4.9	Methenyltetrahydrofolate cyclohydrolase.		
2572232994	t3m_01350	EC:1.5.1.5	Methylenetetrahydrofolate dehydrogenase (NADP(+)).		
2572232994	t3m_01350	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahy		0.00E+00
2572232994	t3m_01350	Locus_type		CDS	
2572232994	t3m_01350	Product_name		5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrof	
2572232994	t3m_01350	Scaffold		t3m_contig_70_270_len_21778_read_count_1746931.32	
2572232994	t3m_01350	Coordinates		20578..21468(-)	
2572232994	t3m_01350	DNA_length		891bp	
2572232994	t3m_01350	Protein_length		296aa	
2572232994	t3m_01350	GC		0.7	
2572232995	t3m_01351	COG_category	[T] Signal transduction mechanisms		
2572232995	t3m_01351	COG1956	GAF domain-containing protein		4.00E-33

2572232995	t3m_01351	pfam13492	GAF_3			2.30E-12
2572232995	t3m_01351	KO:K07170	GAF domain-containing protein			3.70E-38
2572232995	t3m_01351	Locus_type		CDS		
2572232995	t3m_01351	Product_name		GAF domain-containing protein		
2572232995	t3m_01351	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572232995	t3m_01351	Coordinates		110..601(+)		
2572232995	t3m_01351	DNA_length		492bp		
2572232995	t3m_01351	Protein_length		163aa		
2572232995	t3m_01351	GC			0.69	

2572232996	t3m_01352	Metacyc	PWY-6654: phosphopantothenate biosynthesis III			
2572232996	t3m_01352	IMG_pathway	116: Coenzyme A biosynthesis			
2572232996	t3m_01352	COG_category	[S] Function unknown			
2572232996	t3m_01352	COG1701	Uncharacterized protein conserved in archaea			1.00E-67
2572232996	t3m_01352	pfam02006	DUF137			7.90E-60
2572232996	t3m_01352	EC:6.3.2.36	4-phosphopantoate--beta-alanine ligase.			
2572232996	t3m_01352	KO:K09722	4-phosphopantoate---beta-alanine ligase [EC:6.3.2.36]			0.00E+00
2572232996	t3m_01352	ITERM:03320	pantothenate synthetase (EC 6.3.2.1)			
2572232996	t3m_01352	Locus_type		CDS		
2572232996	t3m_01352	Product_name		pantothenate synthetase (EC 6.3.2.1)		
2572232996	t3m_01352	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572232996	t3m_01352	Coordinates		501..1325(-)		
2572232996	t3m_01352	DNA_length		825bp		
2572232996	t3m_01352	Protein_length		274aa		
2572232996	t3m_01352	GC			0.74	

2572232997	t3m_01353	Locus_type		CDS		
2572232997	t3m_01353	Product_name		hypothetical protein		
2572232997	t3m_01353	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572232997	t3m_01353	Coordinates		1338..2063(-)		
2572232997	t3m_01353	DNA_length		726bp		
2572232997	t3m_01353	Protein_length		241aa		
2572232997	t3m_01353	GC			0.68	

2572232998	t3m_01354	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA			
2572232998	t3m_01354	Metacyc	LEU-DEG2-PWY: leucine degradation I			
2572232998	t3m_01354	COG_category	[I] Lipid transport and metabolism			
2572232998	t3m_01354	COG1960	Acyl-CoA dehydrogenases			3.00E-86
2572232998	t3m_01354	pfam02771	Acyl-CoA_dh_N			6.10E-28
2572232998	t3m_01354	pfam00441	Acyl-CoA_dh_1			7.30E-44
2572232998	t3m_01354	pfam02770	Acyl-CoA_dh_M			9.80E-22
2572232998	t3m_01354	EC:1.3.8.4	Isovaleryl-CoA dehydrogenase.			
2572232998	t3m_01354	KO:K00253	isovaleryl-CoA dehydrogenase [EC:1.3.8.4]			0.00E+00
2572232998	t3m_01354	Locus_type		CDS		
2572232998	t3m_01354	Product_name		Acyl-CoA dehydrogenases		
2572232998	t3m_01354	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572232998	t3m_01354	Coordinates		2186..3340(-)		
2572232998	t3m_01354	DNA_length		1155bp		
2572232998	t3m_01354	Protein_length		384aa		
2572232998	t3m_01354	GC			0.68	
2572232999	t3m_01355	KEGG_module	M00115: NAD biosynthesis, aspartate => NAD			
2572232999	t3m_01355	Metacyc	PWY-5316: nicotine biosynthesis			
2572232999	t3m_01355	Metacyc	PYRIDNUCSYN-PWY: NAD biosynthesis I (from aspartate)			
2572232999	t3m_01355	IMG_pathway	210: Quinolinate biosynthesis via aspartate			
2572232999	t3m_01355	COG_category	[H] Coenzyme transport and metabolism			
2572232999	t3m_01355	COG0029	Aspartate oxidase			0.00E+00
2572232999	t3m_01355	pfam00890	FAD_binding_2			5.20E-85
2572232999	t3m_01355	pfam02910	Succ_DH_flav_C			5.10E-14
2572232999	t3m_01355	EC:1.4.3.16	L-aspartate oxidase.			
2572232999	t3m_01355	TIGR00551	L-aspartate oxidase			0.00E+00
2572232999	t3m_01355	KO:K00278	L-aspartate oxidase [EC:1.4.3.16]			0.00E+00
2572232999	t3m_01355	ITERM:00561	L-aspartate oxidase (EC 1.4.3.16)			
2572232999	t3m_01355	Locus_type		CDS		
2572232999	t3m_01355	Product_name		L-aspartate oxidase (EC 1.4.3.16)		
2572232999	t3m_01355	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572232999	t3m_01355	Coordinates		3383..4951(-)		
2572232999	t3m_01355	DNA_length		1569bp		

2572232999	t3m_01355	Protein_length		522aa		
2572232999	t3m_01355	GC			0.72	

2572233000	t3m_01356	Locus_type		CDS		
2572233000	t3m_01356	Product_name		hypothetical protein		
2572233000	t3m_01356	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233000	t3m_01356	Coordinates		5039..6430(+)		
2572233000	t3m_01356	DNA_length		1392bp		
2572233000	t3m_01356	Protein_length		463aa		
2572233000	t3m_01356	GC			0.71	

2572233001	t3m_01357	pfam00583	Acetyltransf_1			6.20E-13
2572233001	t3m_01357	Locus_type		CDS		
2572233001	t3m_01357	Product_name		Acetyltransferase (GNAT) family		
2572233001	t3m_01357	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233001	t3m_01357	Coordinates		6379..7344(-)		
2572233001	t3m_01357	DNA_length		966bp		
2572233001	t3m_01357	Protein_length		321aa		
2572233001	t3m_01357	GC			0.7	

2572233002	t3m_01358	KEGG_module	M00005: PRPP biosynthesis, ribose 5P => PRPP			
2572233002	t3m_01358	Metacyc	PWY0-662: PRPP biosynthesis I			
2572233002	t3m_01358	COG_category	[E] Amino acid transport and metabolism			
2572233002	t3m_01358	COG_category	[F] Nucleotide transport and metabolism			
2572233002	t3m_01358	COG0462	Phosphoribosylpyrophosphate synthetase			8.00E-71
2572233002	t3m_01358	pfam00156	Pribosyltran			1.60E-13
2572233002	t3m_01358	pfam13793	Pribosyltran_N			3.80E-25
2572233002	t3m_01358	EC:2.7.6.1	Ribose-phosphate diphosphokinase.			
2572233002	t3m_01358	TIGR01251	ribose-phosphate pyrophosphokinase			3.00E-79
2572233002	t3m_01358	KO:K00948	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]			0.00E+00
2572233002	t3m_01358	Locus_type		CDS		
2572233002	t3m_01358	Product_name		ribose-phosphate pyrophosphokinase		
2572233002	t3m_01358	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233002	t3m_01358	Coordinates		7359..8234(-)		

2572233002	t3m_01358	DNA_length		876bp	
2572233002	t3m_01358	Protein_length		291aa	
2572233002	t3m_01358	GC		0.67	
2572233003	t3m_01359	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport		
2572233003	t3m_01359	COG0681	Signal peptidase I		6.00E-11
2572233003	t3m_01359	Locus_type		CDS	
2572233003	t3m_01359	Product_name		hypothetical protein	
2572233003	t3m_01359	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33	
2572233003	t3m_01359	Coordinates		8358..9719(-)	
2572233003	t3m_01359	DNA_length		1362bp	
2572233003	t3m_01359	Protein_length		453aa	
2572233003	t3m_01359	GC		0.67	
2572233003	t3m_01359	Transmembrane		Yes	
2572233004	t3m_01360	KEGG_module	M00038: Tryptophan metabolism, tryptophan => kynurenine => 2-aminomuconate		
2572233004	t3m_01360	Metacyc	TRPCAT-PWY: tryptophan degradation I (via anthranilate)		
2572233004	t3m_01360	Metacyc	PWY-5651: tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde		
2572233004	t3m_01360	Metacyc	PWY-6309: tryptophan degradation XI (mammalian, via kynurenine)		
2572233004	t3m_01360	IMG_pathway	211: Quinolinate biosynthesis via tryptophan		
2572233004	t3m_01360	IMG_pathway	881: L-tryptophan degradation to anthranilate		
2572233004	t3m_01360	COG_category	[R] General function prediction only		
2572233004	t3m_01360	COG1878	Predicted metal-dependent hydrolase		3.00E-41
2572233004	t3m_01360	pfam04199	Cyclase		1.90E-26
2572233004	t3m_01360	EC:3.5.1.9	Arylformamidase.		
2572233004	t3m_01360	KO:K07130	arylformamidase [EC:3.5.1.9]		5.30E-42
2572233004	t3m_01360	ITERM:00589	Kynurenine formamidase (EC 3.5.1.9)		
2572233004	t3m_01360	Locus_type		CDS	
2572233004	t3m_01360	Product_name		Kynurenine formamidase (EC 3.5.1.9)	
2572233004	t3m_01360	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33	
2572233004	t3m_01360	Coordinates		9874..10503(+)	
2572233004	t3m_01360	DNA_length		630bp	
2572233004	t3m_01360	Protein_length		209aa	
2572233004	t3m_01360	GC		0.7	

2572233005	t3m_01361	Locus_type		CDS		
2572233005	t3m_01361	Product_name		hypothetical protein		
2572233005	t3m_01361	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233005	t3m_01361	Coordinates		10517..10945(+)		
2572233005	t3m_01361	DNA_length		429bp		
2572233005	t3m_01361	Protein_length		142aa		
2572233005	t3m_01361	GC			0.66	
2572233005	t3m_01361	Transmembrane		Yes		
2572233006	t3m_01362	COG_category	[S] Function unknown			
2572233006	t3m_01362	COG2835	Uncharacterized conserved protein			4.00E-07
2572233006	t3m_01362	pfam03966	Trm112p			8.30E-11
2572233006	t3m_01362	Locus_type		CDS		
2572233006	t3m_01362	Product_name		Uncharacterized conserved protein		
2572233006	t3m_01362	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233006	t3m_01362	Coordinates		10961..11143(-)		
2572233006	t3m_01362	DNA_length		183bp		
2572233006	t3m_01362	Protein_length		60aa		
2572233006	t3m_01362	GC			0.64	
2572233007	t3m_01363	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233007	t3m_01363	COG5257	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)			0.00E+00
2572233007	t3m_01363	pfam09173	eIF2_C			2.90E-22
2572233007	t3m_01363	pfam00009	GTP_EFTU			1.10E-39
2572233007	t3m_01363	TIGR03680	translation initiation factor 2 subunit gamma			0.00E+00
2572233007	t3m_01363	TIGR00231	small GTP-binding protein domain			1.80E-16
2572233007	t3m_01363	KO:K03242	translation initiation factor 2 subunit 3			0.00E+00
2572233007	t3m_01363	Locus_type		CDS		
2572233007	t3m_01363	Product_name		translation initiation factor 2 subunit gamma (aeIF-2g)		
2572233007	t3m_01363	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233007	t3m_01363	Coordinates		11140..12375(-)		
2572233007	t3m_01363	DNA_length		1236bp		
2572233007	t3m_01363	Protein_length		411aa		

2572233007	t3m_01363	GC			0.68	
2572233008	t3m_01364	KEGG_module	M00177: Ribosome, eukaryotes			
2572233008	t3m_01364	KEGG_module	M00179: Ribosome, archaea			
2572233008	t3m_01364	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233008	t3m_01364	COG2125	Ribosomal protein S6E (S10)			5.00E-26
2572233008	t3m_01364	pfam01092	Ribosomal_S6e			4.40E-25
2572233008	t3m_01364	KO:K02991	small subunit ribosomal protein S6e			1.30E-28
2572233008	t3m_01364	ITERM:00285	SSU ribosomal protein S6E			
2572233008	t3m_01364	Locus_type		CDS		
2572233008	t3m_01364	Product_name		SSU ribosomal protein S6E		
2572233008	t3m_01364	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233008	t3m_01364	Coordinates		12372..12749(-)		
2572233008	t3m_01364	DNA_length		378bp		
2572233008	t3m_01364	Protein_length		125aa		
2572233008	t3m_01364	GC			0.67	
2572233009	t3m_01365	pfam06847	Arc_PepC_II			2.10E-08
2572233009	t3m_01365	Locus_type		CDS		
2572233009	t3m_01365	Product_name		Archaeal Peptidase A24 C-terminus Type II		
2572233009	t3m_01365	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233009	t3m_01365	Coordinates		12962..13882(+)		
2572233009	t3m_01365	DNA_length		921bp		
2572233009	t3m_01365	Protein_length		306aa		
2572233009	t3m_01365	GC			0.69	
2572233009	t3m_01365	Transmembrane		Yes		
2572233010	t3m_01366	KEGG_module	M00376: 3-Hydroxypropionate bicycle			
2572233010	t3m_01366	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle			
2572233010	t3m_01366	Metacyc	PWY-5743: 3-hydroxypropionate cycle			
2572233010	t3m_01366	Metacyc	PWY0-43: conversion of succinate to propionate			
2572233010	t3m_01366	Metacyc	PROPIONMET-PWY: methylmalonyl pathway			
2572233010	t3m_01366	Metacyc	P108-PWY: pyruvate fermentation to propionate I			
2572233010	t3m_01366	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			

2572233010	t3m_01366	Metacyc	PWY-6728: methylaspartate cycle		
2572233010	t3m_01366	COG_category	[I] Lipid transport and metabolism		
2572233010	t3m_01366	COG2185	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-bir		8.00E-36
2572233010	t3m_01366	pfam02310	B12-binding		1.70E-22
2572233010	t3m_01366	EC:5.4.99.2	Methylmalonyl-CoA mutase.		
2572233010	t3m_01366	TIGR00640	methylmalonyl-CoA mutase C-terminal domain		7.40E-55
2572233010	t3m_01366	KO:K01849	methylmalonyl-CoA mutase, C-terminal domain [EC:5.4.99.2]		1.10E-44
2572233010	t3m_01366	Locus_type		CDS	
2572233010	t3m_01366	Product_name		methylmalonyl-CoA mutase C-terminal domain	
2572233010	t3m_01366	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33	
2572233010	t3m_01366	Coordinates		13935..14357(+)	
2572233010	t3m_01366	DNA_length		423bp	
2572233010	t3m_01366	Protein_length		140aa	
2572233010	t3m_01366	GC		0.68	
2572233011	t3m_01367	COG_category	[E] Amino acid transport and metabolism		
2572233011	t3m_01367	COG1703	Putative periplasmic protein kinase ArgK and related GTPases of G3E fa		2.00E-76
2572233011	t3m_01367	pfam03308	ArgK		5.50E-90
2572233011	t3m_01367	EC:2.7.-	Transferases. Transferring phosphorous-containing groups.		
2572233011	t3m_01367	TIGR00750	LAO/AO transport system ATPase		7.30E-99
2572233011	t3m_01367	KO:K07588	LAO/AO transport system kinase [EC:2.7.-.-]		0.00E+00
2572233011	t3m_01367	Locus_type		CDS	
2572233011	t3m_01367	Product_name		LAO/AO transport system ATPase	
2572233011	t3m_01367	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33	
2572233011	t3m_01367	Coordinates		14354..15322(+)	
2572233011	t3m_01367	DNA_length		969bp	
2572233011	t3m_01367	Protein_length		322aa	
2572233011	t3m_01367	GC		0.72	
2572233012	t3m_01368	Locus_type		CDS	
2572233012	t3m_01368	Product_name		hypothetical protein	
2572233012	t3m_01368	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33	
2572233012	t3m_01368	Coordinates		15319..15906(+)	
2572233012	t3m_01368	DNA_length		588bp	

2572233012	t3m_01368	Protein_length		195aa		
2572233012	t3m_01368	GC			0.69	
2572233012	t3m_01368	Transmembrane		Yes		

2572233013	t3m_01369	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233013	t3m_01369	COG1047	FKBP-type peptidyl-prolyl cis-trans isomerases 2			3.00E-20
2572233013	t3m_01369	EC:5.2.1.8	Peptidylprolyl isomerase.			
2572233013	t3m_01369	KO:K03775	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [EC:5.2.1.8]			7.30E-38
2572233013	t3m_01369	Locus_type		CDS		
2572233013	t3m_01369	Product_name		FKBP-type peptidyl-prolyl cis-trans isomerases 2		
2572233013	t3m_01369	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233013	t3m_01369	Coordinates		16011..16892(-)		
2572233013	t3m_01369	DNA_length		882bp		
2572233013	t3m_01369	Protein_length		293aa		
2572233013	t3m_01369	GC			0.68	

2572233014	t3m_01370	pfam13641	Glyco_tranf_2_3			1.10E-07
2572233014	t3m_01370	Locus_type		CDS		
2572233014	t3m_01370	Product_name		Glycosyltransferase like family 2		
2572233014	t3m_01370	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233014	t3m_01370	Coordinates		16955..17833(-)		
2572233014	t3m_01370	DNA_length		879bp		
2572233014	t3m_01370	Protein_length		292aa		
2572233014	t3m_01370	GC			0.71	

2572233015	t3m_01371	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572233015	t3m_01371	COG0438	Glycosyltransferase			2.00E-24
2572233015	t3m_01371	pfam13692	Glyco_trans_1_4			2.00E-16
2572233015	t3m_01371	pfam13579	Glyco_trans_4_4			1.10E-14
2572233015	t3m_01371	Locus_type		CDS		
2572233015	t3m_01371	Product_name		Glycosyltransferase		
2572233015	t3m_01371	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233015	t3m_01371	Coordinates		17923..18960(+)		
2572233015	t3m_01371	DNA_length		1038bp		

2572233015	t3m_01371	Protein_length		345aa		
2572233015	t3m_01371	GC			0.69	
2572233016	t3m_01372	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes			
2572233016	t3m_01372	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes			
2572233016	t3m_01372	Metacyc	PWY-3821: galactose degradation III			
2572233016	t3m_01372	Metacyc	PWY-6397: mycolyl-arabinogalactan-peptidoglycan complex biosynthesis			
2572233016	t3m_01372	Metacyc	PWY-6527: stachyose degradation			
2572233016	t3m_01372	Metacyc	PWY-6317: galactose degradation I (Leloir pathway)			
2572233016	t3m_01372	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis			
2572233016	t3m_01372	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572233016	t3m_01372	COG_category	[G] Carbohydrate transport and metabolism			
2572233016	t3m_01372	COG0451	Nucleoside-diphosphate-sugar epimerases			6.00E-44
2572233016	t3m_01372	pfam01370	Epimerase			1.20E-38
2572233016	t3m_01372	EC:5.1.3.2	UDP-glucose 4-epimerase.			
2572233016	t3m_01372	KO:K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]			0.00E+00
2572233016	t3m_01372	Locus_type		CDS		
2572233016	t3m_01372	Product_name		Nucleoside-diphosphate-sugar epimerases		
2572233016	t3m_01372	Scaffold		t3m_contig_70_309_len_20133_read_count_1504061.33		
2572233016	t3m_01372	Coordinates		18957..19943(-)		
2572233016	t3m_01372	DNA_length		987bp		
2572233016	t3m_01372	Protein_length		328aa		
2572233016	t3m_01372	GC			0.7	
2572233017	t3m_01373	pfam00709	Adenylsucc_synt			9.00E-19
2572233017	t3m_01373	TIGR00184	adenylosuccinate synthase			3.20E-21
2572233017	t3m_01373	Locus_type		CDS		
2572233017	t3m_01373	Product_name		Adenylosuccinate synthetase		
2572233017	t3m_01373	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233017	t3m_01373	Coordinates		1..360(+)		
2572233017	t3m_01373	DNA_length		360bp		
2572233017	t3m_01373	Protein_length		119aa		
2572233017	t3m_01373	GC			0.69	

2572233018	t3m_01374	COG_category	[S] Function unknown			
2572233018	t3m_01374	COG2431	Predicted membrane protein			3.00E-19
2572233018	t3m_01374	pfam03956	DUF340			2.40E-32
2572233018	t3m_01374	Locus_type		CDS		
2572233018	t3m_01374	Product_name		Predicted membrane protein		
2572233018	t3m_01374	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233018	t3m_01374	Coordinates		370..1239(+)		
2572233018	t3m_01374	DNA_length		870bp		
2572233018	t3m_01374	Protein_length		289aa		
2572233018	t3m_01374	GC			0.71	
2572233018	t3m_01374	Transmembrane		Yes		
2572233019	t3m_01375	Locus_type		tRNA		
2572233019	t3m_01375	Product_name		tRNA_Val_CAC		
2572233019	t3m_01375	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233019	t3m_01375	Coordinates		1277..1349(+)		
2572233019	t3m_01375	DNA_length		73bp		
2572233019	t3m_01375	GC			0.67	
2572233020	t3m_01376	COG_category	[S] Function unknown			
2572233020	t3m_01376	COG1814	Uncharacterized membrane protein			5.00E-18
2572233020	t3m_01376	pfam01988	VIT1			7.60E-53
2572233020	t3m_01376	TIGR00267	TIGR00267 family protein			3.00E-12
2572233020	t3m_01376	Locus_type		CDS		
2572233020	t3m_01376	Product_name		Uncharacterized membrane protein		
2572233020	t3m_01376	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233020	t3m_01376	Coordinates		1390..2514(-)		
2572233020	t3m_01376	DNA_length		1125bp		
2572233020	t3m_01376	Protein_length		374aa		
2572233020	t3m_01376	GC			0.7	
2572233020	t3m_01376	Transmembrane		Yes		
2572233021	t3m_01377	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233021	t3m_01377	COG0425	Predicted redox protein, regulator of disulfide bond formation			1.00E-12

2572233021	t3m_01377	pfam01206	TusA			2.80E-18
2572233021	t3m_01377	Locus_type		CDS		
2572233021	t3m_01377	Product_name		Predicted redox protein, regulator of disulfide bond formation		
2572233021	t3m_01377	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233021	t3m_01377	Coordinates		2663..2917(-)		
2572233021	t3m_01377	DNA_length		255bp		
2572233021	t3m_01377	Protein_length		84aa		
2572233021	t3m_01377	GC			0.64	
2572233022	t3m_01378	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme			
2572233022	t3m_01378	Metacyc	PWY-5189: tetrapyrrole biosynthesis II (from glycine)			
2572233022	t3m_01378	Metacyc	PWY-5188: tetrapyrrole biosynthesis I (from glutamate)			
2572233022	t3m_01378	COG_category	[H] Coenzyme transport and metabolism			
2572233022	t3m_01378	COG0113	Delta-aminolevulinic acid dehydratase			4.00E-125
2572233022	t3m_01378	pfam00490	ALAD			0.00E+00
2572233022	t3m_01378	EC:4.2.1.24	Porphobilinogen synthase.			
2572233022	t3m_01378	KO:K01698	porphobilinogen synthase [EC:4.2.1.24]			0.00E+00
2572233022	t3m_01378	Locus_type		CDS		
2572233022	t3m_01378	Product_name		porphobilinogen synthase (EC 4.2.1.24)		
2572233022	t3m_01378	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233022	t3m_01378	Coordinates		3044..4063(-)		
2572233022	t3m_01378	DNA_length		1020bp		
2572233022	t3m_01378	Protein_length		339aa		
2572233022	t3m_01378	GC			0.7	
2572233023	t3m_01379	COG_category	[H] Coenzyme transport and metabolism			
2572233023	t3m_01379	COG1587	Uroporphyrinogen-III synthase			3.00E-18
2572233023	t3m_01379	pfam02602	HEM4			4.30E-32
2572233023	t3m_01379	Locus_type		CDS		
2572233023	t3m_01379	Product_name		Uroporphyrinogen-III synthase		
2572233023	t3m_01379	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233023	t3m_01379	Coordinates		4050..4814(-)		
2572233023	t3m_01379	DNA_length		765bp		
2572233023	t3m_01379	Protein_length		254aa		

2572233023	t3m_01379	GC			0.7	
2572233024	t3m_01380	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme			
2572233024	t3m_01380	Metacyc	PWY-5189: tetrapyrrole biosynthesis II (from glycine)			
2572233024	t3m_01380	Metacyc	PWY-5188: tetrapyrrole biosynthesis I (from glutamate)			
2572233024	t3m_01380	IMG_pathway	80: Uroporphyrinogen biosynthesis			
2572233024	t3m_01380	COG_category	[H] Coenzyme transport and metabolism			
2572233024	t3m_01380	COG0181	Porphobilinogen deaminase			4.00E-79
2572233024	t3m_01380	pfam01379	Porphobil_deam			2.30E-56
2572233024	t3m_01380	pfam03900	Porphobil_deamC			3.20E-15
2572233024	t3m_01380	EC:2.5.1.61	Hydroxymethylbilane synthase.			
2572233024	t3m_01380	TIGR00212	porphobilinogen deaminase			7.20E-87
2572233024	t3m_01380	KO:K01749	hydroxymethylbilane synthase [EC:2.5.1.61]			0.00E+00
2572233024	t3m_01380	ITERM:00116	hydroxymethylbilane synthase (EC 2.5.1.61)			
2572233024	t3m_01380	Locus_type		CDS		
2572233024	t3m_01380	Product_name		hydroxymethylbilane synthase (EC 2.5.1.61)		
2572233024	t3m_01380	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233024	t3m_01380	Coordinates		4822..5730(-)		
2572233024	t3m_01380	DNA_length		909bp		
2572233024	t3m_01380	Protein_length		302aa		
2572233024	t3m_01380	GC			0.71	
2572233025	t3m_01381	Metacyc	P381-PWY: adenosylcobalamin biosynthesis II (late cobalt incorporation)			
2572233025	t3m_01381	Metacyc	PWY-5507: adenosylcobalamin biosynthesis I (early cobalt insertion)			
2572233025	t3m_01381	COG_category	[H] Coenzyme transport and metabolism			
2572233025	t3m_01381	COG1797	Cobyrinic acid a,c-diamide synthase			1.00E-116
2572233025	t3m_01381	pfam01656	CbiA			1.60E-15
2572233025	t3m_01381	pfam07685	GATase_3			1.20E-29
2572233025	t3m_01381	EC:6.3.5.11	Cobyrinate a,c-diamide synthase (glutamine-hydrolyzing).			
2572233025	t3m_01381	EC:6.3.5.9	Hydrogenobyrinic acid a,c-diamide synthase (glutamine-hydrolyzing).			
2572233025	t3m_01381	TIGR00379	cobyrinic acid a,c-diamide synthase			1.00E-118
2572233025	t3m_01381	KO:K02224	cobyrinic acid a,c-diamide synthase [EC:6.3.5.9 6.3.5.11]			0.00E+00
2572233025	t3m_01381	Locus_type		CDS		
2572233025	t3m_01381	Product_name		hydrogenobyrinic acid a,c-diamide synthase (glutamine-hydrolysing) (EC		

2572233025	t3m_01381	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233025	t3m_01381	Coordinates		5752..7146(-)		
2572233025	t3m_01381	DNA_length		1395bp		
2572233025	t3m_01381	Protein_length		464aa		
2572233025	t3m_01381	GC			0.67	

2572233026	t3m_01382	COG_category	[H] Coenzyme transport and metabolism			
2572233026	t3m_01382	COG0007	Uroporphyrinogen-III methylase			1.00E-72
2572233026	t3m_01382	pfam00590	TP_methylase			1.10E-47
2572233026	t3m_01382	TIGR01469	uroporphyrin-III C-methyltransferase			2.30E-86
2572233026	t3m_01382	Locus_type		CDS		
2572233026	t3m_01382	Product_name		uroporphyrin-III C-methyltransferase		
2572233026	t3m_01382	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233026	t3m_01382	Coordinates		7143..7997(-)		
2572233026	t3m_01382	DNA_length		855bp		
2572233026	t3m_01382	Protein_length		284aa		
2572233026	t3m_01382	GC			0.66	

2572233027	t3m_01383	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme			
2572233027	t3m_01383	Metacyc	PWY-5194: siroheme biosynthesis			
2572233027	t3m_01383	COG_category	[H] Coenzyme transport and metabolism			
2572233027	t3m_01383	COG1648	Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain)			6.00E-26
2572233027	t3m_01383	pfam13241	NAD_binding_7			4.80E-09
2572233027	t3m_01383	EC:1.3.1.76	Precorrin-2 dehydrogenase.			
2572233027	t3m_01383	EC:4.99.1.4	Sirohydrochlorin ferrochelatase.			
2572233027	t3m_01383	TIGR01470	siroheme synthase, N-terminal domain			9.00E-26
2572233027	t3m_01383	KO:K02304	precorrin-2 dehydrogenase / sirohydrochlorin ferrochelatase [EC:1.3.1.			2.10E-17
2572233027	t3m_01383	Locus_type		CDS		
2572233027	t3m_01383	Product_name		siroheme synthase, N-terminal domain		
2572233027	t3m_01383	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233027	t3m_01383	Coordinates		8000..8659(-)		
2572233027	t3m_01383	DNA_length		660bp		
2572233027	t3m_01383	Protein_length		219aa		
2572233027	t3m_01383	GC			0.7	

2572233028	t3m_01384	COG_category	[P] Inorganic ion transport and metabolism		
2572233028	t3m_01384	COG2920	Dissimilatory sulfite reductase (desulfoviridin), gamma subunit		1.00E-34
2572233028	t3m_01384	pfam04358	DsrC		4.90E-34
2572233028	t3m_01384	EC:2.8.1.-	Transferases. Transferring sulfur-containing groups. Sulfurtransferases.		
2572233028	t3m_01384	TIGR03342	sulfur relay protein, TusE/DsrC/DsvC family		6.10E-35
2572233028	t3m_01384	KO:K11179	tRNA 2-thiouridine synthesizing protein E [EC:2.8.1.-]		2.80E-45
2572233028	t3m_01384	Locus_type		CDS	
2572233028	t3m_01384	Product_name		sulfur relay protein, TusE/DsrC/DsvC family	
2572233028	t3m_01384	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34	
2572233028	t3m_01384	Coordinates		8821..9156(+)	
2572233028	t3m_01384	DNA_length		336bp	
2572233028	t3m_01384	Protein_length		111aa	
2572233028	t3m_01384	GC		0.64	
2572233029	t3m_01385	COG_category	[R] General function prediction only		
2572233029	t3m_01385	COG2044	Predicted peroxiredoxins		9.00E-18
2572233029	t3m_01385	pfam02635	DrsE		2.60E-10
2572233029	t3m_01385	Locus_type		CDS	
2572233029	t3m_01385	Product_name		Predicted peroxiredoxins	
2572233029	t3m_01385	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34	
2572233029	t3m_01385	Coordinates		9259..9600(-)	
2572233029	t3m_01385	DNA_length		342bp	
2572233029	t3m_01385	Protein_length		113aa	
2572233029	t3m_01385	GC		0.64	
2572233030	t3m_01386	COG_category	[C] Energy production and conversion		
2572233030	t3m_01386	COG0247	Fe-S oxidoreductase		5.00E-37
2572233030	t3m_01386	pfam13183	Fer4_8		7.00E-12
2572233030	t3m_01386	pfam02754	CCG		1.30E-09
2572233030	t3m_01386	Locus_type		CDS	
2572233030	t3m_01386	Product_name		Fe-S oxidoreductase	
2572233030	t3m_01386	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34	
2572233030	t3m_01386	Coordinates		9701..11116(-)	

2572233030	t3m_01386	DNA_length		1416bp		
2572233030	t3m_01386	Protein_length		471aa		
2572233030	t3m_01386	GC			0.67	
2572233031	t3m_01387	KEGG_module	M00530: Dissimilatory nitrate reduction, nitrate => ammonia			
2572233031	t3m_01387	KEGG_module	M00529: Denitrification, nitrate => nitrogen			
2572233031	t3m_01387	Metacyc	PWY-6748: nitrate reduction VII (denitrification)			
2572233031	t3m_01387	Metacyc	DENITRIFICATION-PWY: nitrate reduction I (denitrification)			
2572233031	t3m_01387	COG_category	[C] Energy production and conversion			
2572233031	t3m_01387	COG2181	Nitrate reductase gamma subunit			3.00E-23
2572233031	t3m_01387	pfam02665	Nitrate_red_gam			5.10E-32
2572233031	t3m_01387	EC:1.7.99.4	Nitrate reductase.			
2572233031	t3m_01387	KO:K00374	nitrate reductase 1, gamma subunit [EC:1.7.99.4]			0.00E+00
2572233031	t3m_01387	Locus_type		CDS		
2572233031	t3m_01387	Product_name		Nitrate reductase gamma subunit		
2572233031	t3m_01387	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233031	t3m_01387	Coordinates		11123..11902(-)		
2572233031	t3m_01387	DNA_length		780bp		
2572233031	t3m_01387	Protein_length		259aa		
2572233031	t3m_01387	GC			0.63	
2572233031	t3m_01387	Transmembrane		Yes		
2572233032	t3m_01388	Metacyc	P224-PWY: sulfate reduction V (dissimilatory)			
2572233032	t3m_01388	COG_category	[C] Energy production and conversion			
2572233032	t3m_01388	COG2221	Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits			5.00E-64
2572233032	t3m_01388	pfam01077	NIR_SIR			3.00E-25
2572233032	t3m_01388	pfam03460	NIR_SIR_ferr			1.50E-06
2572233032	t3m_01388	EC:1.8.99.3	Hydrogensulfite reductase.			
2572233032	t3m_01388	TIGR02066	sulfite reductase, dissimilatory-type beta subunit			3.60E-99
2572233032	t3m_01388	KO:K11181	sulfite reductase, dissimilatory-type beta subunit [EC:1.8.99.3]			0.00E+00
2572233032	t3m_01388	ITERM:06636	dissimilatory sulfite reductase beta subunit (EC 1.8.99.1)			
2572233032	t3m_01388	Locus_type		CDS		
2572233032	t3m_01388	Product_name		dissimilatory sulfite reductase beta subunit (EC 1.8.99.1)		
2572233032	t3m_01388	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		

2572233032	t3m_01388	Coordinates		11907..13013(-)		
2572233032	t3m_01388	DNA_length		1107bp		
2572233032	t3m_01388	Protein_length		368aa		
2572233032	t3m_01388	GC			0.65	

2572233033	t3m_01389	Metacyc	P224-PWY: sulfate reduction V (dissimilatory)			
2572233033	t3m_01389	COG_category	[C] Energy production and conversion			
2572233033	t3m_01389	COG2221	Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits			2.00E-53
2572233033	t3m_01389	pfam01077	NIR_SIR			2.90E-16
2572233033	t3m_01389	EC:1.8.99.3	Hydrogensulfite reductase.			
2572233033	t3m_01389	TIGR02064	sulfite reductase, dissimilatory-type alpha subunit			7.50E-96
2572233033	t3m_01389	KO:K11180	sulfite reductase, dissimilatory-type alpha subunit [EC:1.8.99.3]			0.00E+00
2572233033	t3m_01389	ITERM:06635	dissimilatory sulfite reductase alpha subunit (EC 1.8.99.1)			
2572233033	t3m_01389	Locus_type		CDS		
2572233033	t3m_01389	Product_name		dissimilatory sulfite reductase alpha subunit (EC 1.8.99.1)		
2572233033	t3m_01389	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233033	t3m_01389	Coordinates		13040..14212(-)		
2572233033	t3m_01389	DNA_length		1173bp		
2572233033	t3m_01389	Protein_length		390aa		
2572233033	t3m_01389	GC			0.65	

2572233034	t3m_01390	Locus_type		CDS		
2572233034	t3m_01390	Product_name		hypothetical protein		
2572233034	t3m_01390	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233034	t3m_01390	Coordinates		14529..15206(+)		
2572233034	t3m_01390	DNA_length		678bp		
2572233034	t3m_01390	Protein_length		225aa		
2572233034	t3m_01390	GC			0.64	
2572233034	t3m_01390	Transmembrane		Yes		

2572233035	t3m_01391	KEGG_module	M00018: Threonine biosynthesis, aspartate => homoserine => threonine			
2572233035	t3m_01391	Metacyc	HOMOSER-THRESYN-PWY: threonine biosynthesis from homoserine			
2572233035	t3m_01391	COG_category	[E] Amino acid transport and metabolism			
2572233035	t3m_01391	COG0498	Threonine synthase			3.00E-72

2572233035	t3m_01391	pfam00291	PALP			6.90E-70
2572233035	t3m_01391	EC:4.2.3.1	Threonine synthase.			
2572233035	t3m_01391	TIGR00260	threonine synthase			1.10E-51
2572233035	t3m_01391	KO:K01733	threonine synthase [EC:4.2.3.1]			0.00E+00
2572233035	t3m_01391	Locus_type		CDS		
2572233035	t3m_01391	Product_name		L-threonine synthase (EC 4.2.3.1)		
2572233035	t3m_01391	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233035	t3m_01391	Coordinates		15283..16473(+)		
2572233035	t3m_01391	DNA_length		1191bp		
2572233035	t3m_01391	Protein_length		396aa		
2572233035	t3m_01391	GC			0.7	

2572233036	t3m_01392	COG_category	[R] General function prediction only			
2572233036	t3m_01392	COG2085	Predicted dinucleotide-binding enzymes			5.00E-29
2572233036	t3m_01392	pfam03807	F420_oxidored			5.70E-12
2572233036	t3m_01392	Locus_type		CDS		
2572233036	t3m_01392	Product_name		Predicted dinucleotide-binding enzymes		
2572233036	t3m_01392	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233036	t3m_01392	Coordinates		16504..17151(-)		
2572233036	t3m_01392	DNA_length		648bp		
2572233036	t3m_01392	Protein_length		215aa		
2572233036	t3m_01392	GC			0.66	

2572233037	t3m_01393	COG_category	[V] Defense mechanisms			
2572233037	t3m_01393	COG1403	Restriction endonuclease			2.00E-07
2572233037	t3m_01393	pfam01844	HNH			1.40E-11
2572233037	t3m_01393	Locus_type		CDS		
2572233037	t3m_01393	Product_name		Restriction endonuclease		
2572233037	t3m_01393	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233037	t3m_01393	Coordinates		17175..17651(-)		
2572233037	t3m_01393	DNA_length		477bp		
2572233037	t3m_01393	Protein_length		158aa		
2572233037	t3m_01393	GC			0.67	

2572233038	t3m_01394	COG_category	[E] Amino acid transport and metabolism			
2572233038	t3m_01394	COG0436	Aspartate/tyrosine/aromatic aminotransferase			1.00E-14
2572233038	t3m_01394	pfam00155	Aminotran_1_2			1.30E-05
2572233038	t3m_01394	Locus_type		CDS		
2572233038	t3m_01394	Product_name		Aspartate/tyrosine/aromatic aminotransferase		
2572233038	t3m_01394	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233038	t3m_01394	Coordinates		17796..18779(+)		
2572233038	t3m_01394	DNA_length		984bp		
2572233038	t3m_01394	Protein_length		327aa		
2572233038	t3m_01394	GC			0.7	
2572233039	t3m_01395	Locus_type		CDS		
2572233039	t3m_01395	Product_name		hypothetical protein		
2572233039	t3m_01395	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233039	t3m_01395	Coordinates		18792..19076(-)		
2572233039	t3m_01395	DNA_length		285bp		
2572233039	t3m_01395	Protein_length		94aa		
2572233039	t3m_01395	GC			0.68	
2572233040	t3m_01396	pfam00202	Aminotran_3			1.60E-39
2572233040	t3m_01396	Locus_type		CDS		
2572233040	t3m_01396	Product_name		Aminotransferase class-III		
2572233040	t3m_01396	Scaffold		t3m_contig_70_317_len_19889_read_count_1752268.34		
2572233040	t3m_01396	Coordinates		19194..19886(+)		
2572233040	t3m_01396	DNA_length		693bp		
2572233040	t3m_01396	Protein_length		231aa		
2572233040	t3m_01396	GC			0.66	
2572233041	t3m_01397	Locus_type		CDS		
2572233041	t3m_01397	Product_name		hypothetical protein		
2572233041	t3m_01397	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233041	t3m_01397	Coordinates		3..137(-)		
2572233041	t3m_01397	DNA_length		135bp		
2572233041	t3m_01397	Protein_length		45aa		

2572233041	t3m_01397	GC			0.68	

2572233042	t3m_01398	KEGG_module	M00184: RNA polymerase, archaea			
2572233042	t3m_01398	COG_category	[K] Transcription			
2572233042	t3m_01398	COG1761	DNA-directed RNA polymerase, subunit L			1.00E-11
2572233042	t3m_01398	pfam13656	RNA_pol_L_2			2.80E-14
2572233042	t3m_01398	EC:2.7.7.6	DNA-directed RNA polymerase.			
2572233042	t3m_01398	KO:K03056	DNA-directed RNA polymerase subunit L [EC:2.7.7.6]			1.80E-17
2572233042	t3m_01398	ITERM:01879	DNA-directed RNA polymerase, subunit L (EC 2.7.7.6)			
2572233042	t3m_01398	Locus_type		CDS		
2572233042	t3m_01398	Product_name		DNA-directed RNA polymerase, subunit L (EC 2.7.7.6)		
2572233042	t3m_01398	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233042	t3m_01398	Coordinates		152..439(-)		
2572233042	t3m_01398	DNA_length		288bp		
2572233042	t3m_01398	Protein_length		95aa		
2572233042	t3m_01398	GC			0.62	

2572233043	t3m_01399	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP			
2572233043	t3m_01399	Metacyc	PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I			
2572233043	t3m_01399	Metacyc	PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II			
2572233043	t3m_01399	Metacyc	PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis			
2572233043	t3m_01399	IMG_pathway	297: 5-amino-1-(5-phospho-D-ribosyl)imidazole synthesis			
2572233043	t3m_01399	COG_category	[F] Nucleotide transport and metabolism			
2572233043	t3m_01399	COG0151	Phosphoribosylamine-glycine ligase			2.00E-102
2572233043	t3m_01399	pfam02844	GARS_N			1.70E-25
2572233043	t3m_01399	pfam01071	GARS_A			4.70E-49
2572233043	t3m_01399	pfam02843	GARS_C			2.90E-10
2572233043	t3m_01399	EC:6.3.4.13	Phosphoribosylamine--glycine ligase.			
2572233043	t3m_01399	TIGR00877	phosphoribosylamine--glycine ligase			9.00E-113
2572233043	t3m_01399	KO:K01945	phosphoribosylamine--glycine ligase [EC:6.3.4.13]			0.00E+00
2572233043	t3m_01399	ITERM:01300	phosphoribosylamine--glycine ligase (EC 6.3.4.13)			
2572233043	t3m_01399	Locus_type		CDS		
2572233043	t3m_01399	Product_name		phosphoribosylamine--glycine ligase (EC 6.3.4.13)		
2572233043	t3m_01399	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		

2572233043	t3m_01399	Coordinates		572..1978(+)		
2572233043	t3m_01399	DNA_length		1407bp		
2572233043	t3m_01399	Protein_length		468aa		
2572233043	t3m_01399	GC			0.71	
2572233044	t3m_01400	COG_category	[K] Transcription			
2572233044	t3m_01400	COG1594	DNA-directed RNA polymerase, subunit M/Transcription elongation fac			4.00E-15
2572233044	t3m_01400	pfam01096	TFIIS_C			4.10E-18
2572233044	t3m_01400	TIGR01384	transcription factor S, archaeal			6.20E-24
2572233044	t3m_01400	KO:K03057	transcription elongation factor			3.50E-18
2572233044	t3m_01400	Locus_type		CDS		
2572233044	t3m_01400	Product_name		transcription factor S, archaeal		
2572233044	t3m_01400	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233044	t3m_01400	Coordinates		2061..2345(+)		
2572233044	t3m_01400	DNA_length		285bp		
2572233044	t3m_01400	Protein_length		94aa		
2572233044	t3m_01400	GC			0.71	
2572233045	t3m_01401	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572233045	t3m_01401	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572233045	t3m_01401	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572233045	t3m_01401	IMG_pathway	499: L-asparagine ligation to tRNA(Asn)			
2572233045	t3m_01401	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233045	t3m_01401	COG0017	Aspartyl/asparaginyl-tRNA synthetases			2.00E-123
2572233045	t3m_01401	pfam01336	tRNA_anti-codon			6.30E-12
2572233045	t3m_01401	pfam00152	tRNA-synt_2			7.50E-72
2572233045	t3m_01401	EC:6.1.1.22	Asparagine--tRNA ligase.			
2572233045	t3m_01401	TIGR00457	asparaginyl-tRNA synthetase			4.50E-116
2572233045	t3m_01401	KO:K01893	asparaginyl-tRNA synthetase [EC:6.1.1.22]			0.00E+00
2572233045	t3m_01401	ITERM:00392	asparaginyl-tRNA synthetase (EC 6.1.1.22)			
2572233045	t3m_01401	Locus_type		CDS		
2572233045	t3m_01401	Product_name		asparaginyl-tRNA synthetase (EC 6.1.1.22)		
2572233045	t3m_01401	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233045	t3m_01401	Coordinates		2342..3646(+)		

2572233045	t3m_01401	DNA_length		1305bp		
2572233045	t3m_01401	Protein_length		434aa		
2572233045	t3m_01401	GC			0.68	
2572233046	t3m_01402	pfam13673	Acetyltransf_10			4.10E-15
2572233046	t3m_01402	Locus_type		CDS		
2572233046	t3m_01402	Product_name		Acetyltransferase (GNAT) domain		
2572233046	t3m_01402	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233046	t3m_01402	Coordinates		3749..4282(+)		
2572233046	t3m_01402	DNA_length		534bp		
2572233046	t3m_01402	Protein_length		177aa		
2572233046	t3m_01402	GC			0.69	
2572233047	t3m_01403	Locus_type		CDS		
2572233047	t3m_01403	Product_name		hypothetical protein		
2572233047	t3m_01403	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233047	t3m_01403	Coordinates		4279..5310(-)		
2572233047	t3m_01403	DNA_length		1032bp		
2572233047	t3m_01403	Protein_length		343aa		
2572233047	t3m_01403	GC			0.71	
2572233048	t3m_01404	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP			
2572233048	t3m_01404	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds			
2572233048	t3m_01404	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP			
2572233048	t3m_01404	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2572233048	t3m_01404	Metacyc	PWY-5723: Rubisco shunt			
2572233048	t3m_01404	Metacyc	ANARESP1-PWY: respiration (anaerobic)			
2572233048	t3m_01404	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)			
2572233048	t3m_01404	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)			
2572233048	t3m_01404	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2572233048	t3m_01404	Metacyc	PWY-7003: glycerol degradation to butanol			
2572233048	t3m_01404	Metacyc	PWY-2221: Entner-Doudoroff pathway III (semi-phosphorylative)			
2572233048	t3m_01404	Metacyc	GLYCOLYSIS: glycolysis I			
2572233048	t3m_01404	Metacyc	P122-PWY: heterolactic fermentation			

2572233048	t3m_01404	Metacyc	P341-PWY: glycolysis V (Pyrococcus)			
2572233048	t3m_01404	Metacyc	P124-PWY: Bifidobacterium shunt			
2572233048	t3m_01404	Metacyc	FERMENTATION-PWY: mixed acid fermentation			
2572233048	t3m_01404	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis			
2572233048	t3m_01404	Metacyc	PWY-6901: xylose degradation IV			
2572233048	t3m_01404	Metacyc	PWY-1042: glycolysis IV (plant cytosol)			
2572233048	t3m_01404	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2572233048	t3m_01404	pfam00224	PK			4.50E-09
2572233048	t3m_01404	pfam00224	PK			1.80E-37
2572233048	t3m_01404	EC:2.7.1.40	Pyruvate kinase.			
2572233048	t3m_01404	KO:K00873	pyruvate kinase [EC:2.7.1.40]			0.00E+00
2572233048	t3m_01404	Locus_type		CDS		
2572233048	t3m_01404	Product_name		Pyruvate kinase, barrel domain		
2572233048	t3m_01404	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233048	t3m_01404	Coordinates		5464..7350(-)		
2572233048	t3m_01404	DNA_length		1887bp		
2572233048	t3m_01404	Protein_length		628aa		
2572233048	t3m_01404	GC			0.7	
2572233049	t3m_01405	Locus_type		CDS		
2572233049	t3m_01405	Product_name		hypothetical protein		
2572233049	t3m_01405	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233049	t3m_01405	Coordinates		7420..7875(-)		
2572233049	t3m_01405	DNA_length		456bp		
2572233049	t3m_01405	Protein_length		151aa		
2572233049	t3m_01405	GC			0.66	
2572233050	t3m_01406	Locus_type		tRNA		
2572233050	t3m_01406	Product_name		tRNA_Leu_GAG		
2572233050	t3m_01406	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233050	t3m_01406	Coordinates		8069..8153(-)		
2572233050	t3m_01406	DNA_length		85bp		
2572233050	t3m_01406	GC			0.59	

2572233051	t3m_01407	IMG_pathway	433: Archaeal nucleoid proteins			
2572233051	t3m_01407	COG_category	[K] Transcription			
2572233051	t3m_01407	COG1581	Archaeal DNA-binding protein			3.00E-21
2572233051	t3m_01407	pfam01918	Alba			3.90E-15
2572233051	t3m_01407	TIGR00285	DNA-binding protein Alba			1.80E-33
2572233051	t3m_01407	KO:K03622	archaea-specific DNA-binding protein			3.40E-18
2572233051	t3m_01407	ITERM:00143	nucleoid protein Alba			
2572233051	t3m_01407	Locus_type		CDS		
2572233051	t3m_01407	Product_name		nucleoid protein Alba		
2572233051	t3m_01407	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233051	t3m_01407	Coordinates		8274..8630(+)		
2572233051	t3m_01407	DNA_length		357bp		
2572233051	t3m_01407	Protein_length		118aa		
2572233051	t3m_01407	GC			0.69	

2572233052	t3m_01408	pfam07758	DUF1614			1.90E-14
2572233052	t3m_01408	pfam06271	RDD			1.90E-14
2572233052	t3m_01408	Locus_type		CDS		
2572233052	t3m_01408	Product_name		Protein of unknown function (DUF1614)/RDD family		
2572233052	t3m_01408	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233052	t3m_01408	Coordinates		8551..10437(-)		
2572233052	t3m_01408	DNA_length		1887bp		
2572233052	t3m_01408	Protein_length		628aa		
2572233052	t3m_01408	GC			0.71	
2572233052	t3m_01408	Transmembrane		Yes		

2572233053	t3m_01409	Metacyc	GLUTDEG-PWY: glutamate degradation II			
2572233053	t3m_01409	COG_category	[E] Amino acid transport and metabolism			
2572233053	t3m_01409	COG1027	Aspartate ammonia-lyase			0.00E+00
2572233053	t3m_01409	pfam00206	Lyase_1			5.30E-79
2572233053	t3m_01409	pfam10415	FumaraseC_C			1.10E-09
2572233053	t3m_01409	EC:4.3.1.1	Aspartate ammonia-lyase.			
2572233053	t3m_01409	KO:K01744	aspartate ammonia-lyase [EC:4.3.1.1]			0.00E+00
2572233053	t3m_01409	Locus_type		CDS		

2572233053	t3m_01409	Product_name		Aspartate ammonia-lyase		
2572233053	t3m_01409	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233053	t3m_01409	Coordinates		10524..11924(+)		
2572233053	t3m_01409	DNA_length		1401bp		
2572233053	t3m_01409	Protein_length		466aa		
2572233053	t3m_01409	GC			0.68	
2572233054	t3m_01410	COG_category	[K] Transcription			
2572233054	t3m_01410	COG1378	Predicted transcriptional regulators			2.00E-25
2572233054	t3m_01410	pfam01978	TrmB			8.50E-19
2572233054	t3m_01410	Locus_type		CDS		
2572233054	t3m_01410	Product_name		Predicted transcriptional regulators		
2572233054	t3m_01410	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233054	t3m_01410	Coordinates		11982..12737(+)		
2572233054	t3m_01410	DNA_length		756bp		
2572233054	t3m_01410	Protein_length		251aa		
2572233054	t3m_01410	GC			0.7	
2572233055	t3m_01411	Metacyc	PWY-702: methionine biosynthesis II			
2572233055	t3m_01411	Metacyc	PWY-6151: <i>S</i>-adenosyl-L-methionine cycle I			
2572233055	t3m_01411	Metacyc	PWY-7076: 3,5-dimethoxytoluene biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-6955: lincomycin biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-5135: xanthohumol biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-7157: eupatolitin 3-<i>O</i>-glucoside biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-7079: geodin biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-7138: noscapine biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-5876: magnoflorine biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-5467: gramine biosynthesis			
2572233055	t3m_01411	Metacyc	PWYG-321: mycolate biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-6154: autoinducer AI-2 biosynthesis II (<i>Vibrio</i>)			
2572233055	t3m_01411	Metacyc	PWY-1422: vitamin E biosynthesis			
2572233055	t3m_01411	Metacyc	PWY-6978: plastoquinol-9 biosynthesis II			
2572233055	t3m_01411	Metacyc	METHIONINE-DEG1-PWY: methionine degradation I (to homocysteine)			
2572233055	t3m_01411	Metacyc	PWY-6575: juvenile hormone III biosynthesis I			

2572233055	t3m_01411	Metacyc	PWY-5041: <i>S</i>-adenosyl-L-methionine cycle II
2572233055	t3m_01411	Metacyc	PWY-6835: 6-gingerol biosynthesis
2572233055	t3m_01411	Metacyc	PWY-5479: podophyllotoxin and 6-methoxypodophyllotoxin biosynthesis
2572233055	t3m_01411	Metacyc	PWY-6442: spermidine hydroxycinnamic acid conjugates biosynthesis
2572233055	t3m_01411	Metacyc	PWY-5290: secologanin and strictosidine biosynthesis
2572233055	t3m_01411	Metacyc	PWY-3542: choline biosynthesis II
2572233055	t3m_01411	Metacyc	PWY-6933: seleno-amino acid detoxification and volatilization III
2572233055	t3m_01411	Metacyc	PWY-7097: vanillin and vanillate degradation I
2572233055	t3m_01411	Metacyc	PWY-6052: dimethylsulfoniopropionate degradation III (demethylation)
2572233055	t3m_01411	Metacyc	PWY-6045: methylthiopropionate degradation II (demethylation)
2572233055	t3m_01411	Metacyc	PWY-6736: sulfur volatiles biosynthesis
2572233055	t3m_01411	Metacyc	PWY-6666: pyocyanin biosynthesis
2572233055	t3m_01411	Metacyc	PWY-7025: gentamicin biosynthesis
2572233055	t3m_01411	Metacyc	PWY-5882: epoxypseudoisoeugenol-2-methylbutyrate biosynthesis
2572233055	t3m_01411	Metacyc	PWY-7151: polymethylated quercetin glucoside biosynthesis II - quercetagetin series (Chrysosplen
2572233055	t3m_01411	Metacyc	PWY-6631: <i>O</i> -methylation of tricetin
2572233055	t3m_01411	Metacyc	PWY-7055: daphnetin modification
2572233055	t3m_01411	Metacyc	PWY-5867: <i>t</i>-anethole biosynthesis
2572233055	t3m_01411	Metacyc	PWY-5748: γ-coniciene and coniine biosynthesis
2572233055	t3m_01411	Metacyc	PWY-6477: gibberellin inactivation II (methylation)
2572233055	t3m_01411	Metacyc	PWY-6682: dehydrophos biosynthesis
2572233055	t3m_01411	Metacyc	PWY-5665: vanilla biosynthesis
2572233055	t3m_01411	Metacyc	PWY-5391: syringetin biosynthesis
2572233055	t3m_01411	Metacyc	PWY-5305: bixin biosynthesis
2572233055	t3m_01411	Metacyc	PWY-4942: cyclopropane and cyclopropene fatty acid biosynthesis
2572233055	t3m_01411	Metacyc	PWY-1581: plastoquinol-9 biosynthesis I
2572233055	t3m_01411	Metacyc	PWY-7104: dTDP-L-megosamine biosynthesis
2572233055	t3m_01411	Metacyc	PWY-5765: 1,3,5-trimethoxybenzene biosynthesis
2572233055	t3m_01411	Metacyc	PWY-7161: polymethylated quercetin biosynthesis
2572233055	t3m_01411	Metacyc	PWY-6286: spheroidene and spheroidenone biosynthesis
2572233055	t3m_01411	Metacyc	PWY-6153: autoinducer AI-2 biosynthesis I
2572233055	t3m_01411	Metacyc	METH-ACETATE-PWY: methanogenesis from acetate
2572233055	t3m_01411	Metacyc	PWY-1061: homogalacturonan biosynthesis
2572233055	t3m_01411	Metacyc	PWY-6973: dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycarose biosynthesis

2572233055	t3m_01411	Metacyc	PWY-6976: dTDP-L-mycarose biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-6739: pinitol biosynthesis II		
2572233055	t3m_01411	Metacyc	PWY-4021: β-alanine betaine biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-6650: juvenile hormone III biosynthesis II		
2572233055	t3m_01411	Metacyc	PWY-5729: vestitol and sativan biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-5987: sorgoleone biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-5846: colchicine biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-5209: methyl-coenzyme M oxidation to CO₂		
2572233055	t3m_01411	Metacyc	PWY-6303: methyl indole-3-acetate interconversion		
2572233055	t3m_01411	Metacyc	PWY-5975: furaneol biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-7149: superpathway polymethylated quercetin/quercetagetin glucoside biosynthesis (Chrysc		
2572233055	t3m_01411	Metacyc	PWY-7150: polymethylated quercetin glucoside biosynthesis I - quercetin series (Chrysosplenium)		
2572233055	t3m_01411	Metacyc	PWY-6427: rot-2'-enonate biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-7058: esculetin modification		
2572233055	t3m_01411	Metacyc	PWY-5287: sanguinarine and macarpine biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-6581: spirilloxanthin and 2,2'-diketo-spirilloxanthin biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-5507: adenosylcobalamin biosynthesis I (early cobalt insertion)		
2572233055	t3m_01411	Metacyc	PWY-7045: mithramycin biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-7163: polymethylated kaempferol biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-7160: polymethylated myricetin biosynthesis (tomato)		
2572233055	t3m_01411	Metacyc	PWY-7186: superpathway of scopolin and esculin biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-7135: emetine biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-5773: gossypol biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-6424: sitosterol biosynthesis		
2572233055	t3m_01411	Metacyc	PWY-6339: syringate degradation		
2572233055	t3m_01411	COG_category	[R] General function prediction only		
2572233055	t3m_01411	COG2520	Predicted methyltransferase		3.00E-54
2572233055	t3m_01411	pfam02475	Met_10		2.20E-46
2572233055	t3m_01411	EC:2.1.1.-	Transferases. Transferring one-carbon groups. Methyltransferases.		
2572233055	t3m_01411	KO:K07055	tRNA wybutosine-synthesizing protein 2 [EC:2.1.1.-]		2.70E-40
2572233055	t3m_01411	Locus_type		CDS	
2572233055	t3m_01411	Product_name		Predicted methyltransferase	
2572233055	t3m_01411	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35	
2572233055	t3m_01411	Coordinates		12734..13615(+)	

2572233055	t3m_01411	DNA_length		882bp		
2572233055	t3m_01411	Protein_length		293aa		
2572233055	t3m_01411	GC			0.72	
2572233056	t3m_01412	COG_category	[E] Amino acid transport and metabolism			
2572233056	t3m_01412	COG0436	Aspartate/tyrosine/aromatic aminotransferase			7.00E-48
2572233056	t3m_01412	pfam00155	Aminotran_1_2			1.70E-36
2572233056	t3m_01412	Locus_type		CDS		
2572233056	t3m_01412	Product_name		Aspartate/tyrosine/aromatic aminotransferase		
2572233056	t3m_01412	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233056	t3m_01412	Coordinates		13612..14739(-)		
2572233056	t3m_01412	DNA_length		1128bp		
2572233056	t3m_01412	Protein_length		375aa		
2572233056	t3m_01412	GC			0.69	
2572233057	t3m_01413	KEGG_module	M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone			
2572233057	t3m_01413	KEGG_module	M00116: Menaquinone biosynthesis, chorismate => menaquinone			
2572233057	t3m_01413	Metacyc	PWY-5872: ubiquinol-10 biosynthesis (eukaryotic)			
2572233057	t3m_01413	Metacyc	PWY-5856: ubiquinol-9 biosynthesis (prokaryotic)			
2572233057	t3m_01413	Metacyc	PWY-5844: menaquinol-9 biosynthesis			
2572233057	t3m_01413	Metacyc	PWY-5873: ubiquinol-7 biosynthesis (eukaryotic)			
2572233057	t3m_01413	Metacyc	PWY-5871: ubiquinol-9 biosynthesis (eukaryotic)			
2572233057	t3m_01413	Metacyc	MENAQUINONESYN-PWY: menaquinol-8 biosynthesis			
2572233057	t3m_01413	Metacyc	PWY-5857: ubiquinol-10 biosynthesis (prokaryotic)			
2572233057	t3m_01413	Metacyc	PWY-5855: ubiquinol-7 biosynthesis (prokaryotic)			
2572233057	t3m_01413	Metacyc	PWY-5839: menaquinol-7 biosynthesis			
2572233057	t3m_01413	Metacyc	PWY-6708: ubiquinol-8 biosynthesis (prokaryotic)			
2572233057	t3m_01413	Metacyc	PWY-5870: ubiquinol-8 biosynthesis (eukaryotic)			
2572233057	t3m_01413	Metacyc	PWY-5892: menaquinol-12 biosynthesis			
2572233057	t3m_01413	Metacyc	PWY-5849: menaquinol-6 biosynthesis			
2572233057	t3m_01413	Metacyc	PWY-5891: menaquinol-11 biosynthesis			
2572233057	t3m_01413	Metacyc	PWY3O-19: ubiquinol-6 biosynthesis (eukaryotic)			
2572233057	t3m_01413	Metacyc	PWY-5890: menaquinol-10 biosynthesis			
2572233057	t3m_01413	Metacyc	PWY-5895: menaquinol-13 biosynthesis			

2572233057	t3m_01413	COG_category	[H] Coenzyme transport and metabolism			
2572233057	t3m_01413	COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis			9.00E-45
2572233057	t3m_01413	pfam01209	Ubie_methyltran			1.20E-39
2572233057	t3m_01413	EC:2.1.1.163	Demethylmenaquinone methyltransferase.			
2572233057	t3m_01413	EC:2.1.1.201	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase.			
2572233057	t3m_01413	TIGR01934	ubiquinone/menaquinone biosynthesis methyltransferases			1.70E-53
2572233057	t3m_01413	KO:K03183	ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.16			4.10E-37
2572233057	t3m_01413	Locus_type		CDS		
2572233057	t3m_01413	Product_name		ubiquinone/menaquinone biosynthesis methyltransferases		
2572233057	t3m_01413	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233057	t3m_01413	Coordinates		14764..15594(-)		
2572233057	t3m_01413	DNA_length		831bp		
2572233057	t3m_01413	Protein_length		276aa		
2572233057	t3m_01413	GC			0.71	
2572233058	t3m_01414	pfam13424	TPR_12			2.30E-09
2572233058	t3m_01414	pfam13191	AAA_16			9.10E-18
2572233058	t3m_01414	Locus_type		CDS		
2572233058	t3m_01414	Product_name		Tetratricopeptide repeat/AAA ATPase domain		
2572233058	t3m_01414	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233058	t3m_01414	Coordinates		15606..18005(-)		
2572233058	t3m_01414	DNA_length		2400bp		
2572233058	t3m_01414	Protein_length		799aa		
2572233058	t3m_01414	GC			0.69	
2572233059	t3m_01415	Locus_type		CDS		
2572233059	t3m_01415	Product_name		hypothetical protein		
2572233059	t3m_01415	Scaffold		t3m_contig_70_337_len_19247_read_count_1552515.35		
2572233059	t3m_01415	Coordinates		18029..19246(-)		
2572233059	t3m_01415	DNA_length		1218bp		
2572233059	t3m_01415	Protein_length		405aa		
2572233059	t3m_01415	GC			0.68	
2572233060	t3m_01416	COG_category	[E] Amino acid transport and metabolism			

2572233060	t3m_01416	COG0747	ABC-type dipeptide transport system, periplasmic component		4.00E-25
2572233060	t3m_01416	pfam00496	SBP_bac_5		4.20E-31
2572233060	t3m_01416	Locus_type		CDS	
2572233060	t3m_01416	Product_name		Bacterial extracellular solute-binding proteins, family 5 Middle	
2572233060	t3m_01416	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36	
2572233060	t3m_01416	Coordinates		3..1364(+)	
2572233060	t3m_01416	DNA_length		1362bp	
2572233060	t3m_01416	Protein_length		453aa	
2572233060	t3m_01416	GC		0.63	
2572233061	t3m_01417	pfam00005	ABC_tran		7.30E-11
2572233061	t3m_01417	pfam08352	oligo_HPY		2.10E-18
2572233061	t3m_01417	pfam00005	ABC_tran		7.00E-17
2572233061	t3m_01417	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termina		7.40E-28
2572233061	t3m_01417	Locus_type		CDS	
2572233061	t3m_01417	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termina	
2572233061	t3m_01417	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36	
2572233061	t3m_01417	Coordinates		1367..2959(-)	
2572233061	t3m_01417	DNA_length		1593bp	
2572233061	t3m_01417	Protein_length		530aa	
2572233061	t3m_01417	GC		0.71	
2572233062	t3m_01418	COG_category	[P] Inorganic ion transport and metabolism		
2572233062	t3m_01418	COG_category	[E] Amino acid transport and metabolism		
2572233062	t3m_01418	COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase comp		2.00E-109
2572233062	t3m_01418	pfam00005	ABC_tran		2.50E-26
2572233062	t3m_01418	pfam08352	oligo_HPY		3.10E-21
2572233062	t3m_01418	TIGR01727	oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termina		1.10E-29
2572233062	t3m_01418	Locus_type		CDS	
2572233062	t3m_01418	Product_name		oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-termina	
2572233062	t3m_01418	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36	
2572233062	t3m_01418	Coordinates		2956..4104(-)	
2572233062	t3m_01418	DNA_length		1149bp	
2572233062	t3m_01418	Protein_length		382aa	

2572233062	t3m_01418	GC			0.69	
2572233063	t3m_01419	KEGG_module	M00239: Peptides/nickel transport system			
2572233063	t3m_01419	COG_category	[E] Amino acid transport and metabolism			
2572233063	t3m_01419	COG_category	[P] Inorganic ion transport and metabolism			
2572233063	t3m_01419	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c			5.00E-61
2572233063	t3m_01419	pfam00528	BPD_transp_1			1.50E-25
2572233063	t3m_01419	KO:K02034	peptide/nickel transport system permease protein			0.00E+00
2572233063	t3m_01419	Locus_type		CDS		
2572233063	t3m_01419	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease co		
2572233063	t3m_01419	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233063	t3m_01419	Coordinates		4101..5174(-)		
2572233063	t3m_01419	DNA_length		1074bp		
2572233063	t3m_01419	Protein_length		357aa		
2572233063	t3m_01419	GC			0.67	
2572233063	t3m_01419	Transmembrane		Yes		
2572233064	t3m_01420	KEGG_module	M00239: Peptides/nickel transport system			
2572233064	t3m_01420	COG_category	[P] Inorganic ion transport and metabolism			
2572233064	t3m_01420	COG_category	[E] Amino acid transport and metabolism			
2572233064	t3m_01420	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c			4.00E-63
2572233064	t3m_01420	pfam00528	BPD_transp_1			1.50E-35
2572233064	t3m_01420	KO:K02033	peptide/nickel transport system permease protein			0.00E+00
2572233064	t3m_01420	Locus_type		CDS		
2572233064	t3m_01420	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease co		
2572233064	t3m_01420	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233064	t3m_01420	Coordinates		5181..6200(-)		
2572233064	t3m_01420	DNA_length		1020bp		
2572233064	t3m_01420	Protein_length		339aa		
2572233064	t3m_01420	GC			0.65	
2572233064	t3m_01420	Transmembrane		Yes		
2572233065	t3m_01421	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme			
2572233065	t3m_01421	Metacyc	PWY-5188: tetrapyrrole biosynthesis I (from glutamate)			

2572233065	t3m_01421	COG_category	[H] Coenzyme transport and metabolism			
2572233065	t3m_01421	COG0001	Glutamate-1-semialdehyde aminotransferase			6.00E-130
2572233065	t3m_01421	pfam00202	Aminotran_3			1.30E-59
2572233065	t3m_01421	EC:5.4.3.8	Glutamate-1-semialdehyde 2,1-aminomutase.			
2572233065	t3m_01421	TIGR00713	glutamate-1-semialdehyde-2,1-aminomutase			9.50E-128
2572233065	t3m_01421	KO:K01845	glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]			0.00E+00
2572233065	t3m_01421	Locus_type		CDS		
2572233065	t3m_01421	Product_name		Glutamate-1-semialdehyde aminotransferase		
2572233065	t3m_01421	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233065	t3m_01421	Coordinates		6338..8002(-)		
2572233065	t3m_01421	DNA_length		1665bp		
2572233065	t3m_01421	Protein_length		554aa		
2572233065	t3m_01421	GC			0.65	
2572233066	t3m_01422	COG_category	[E] Amino acid transport and metabolism			
2572233066	t3m_01422	COG1748	Saccharopine dehydrogenase and related proteins			2.00E-46
2572233066	t3m_01422	pfam03435	Saccharop_dh			2.00E-39
2572233066	t3m_01422	Locus_type		CDS		
2572233066	t3m_01422	Product_name		Saccharopine dehydrogenase and related proteins		
2572233066	t3m_01422	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233066	t3m_01422	Coordinates		8199..9341(-)		
2572233066	t3m_01422	DNA_length		1143bp		
2572233066	t3m_01422	Protein_length		380aa		
2572233066	t3m_01422	GC			0.68	
2572233067	t3m_01423	Locus_type		CDS		
2572233067	t3m_01423	Product_name		hypothetical protein		
2572233067	t3m_01423	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233067	t3m_01423	Coordinates		9450..10094(-)		
2572233067	t3m_01423	DNA_length		645bp		
2572233067	t3m_01423	Protein_length		214aa		
2572233067	t3m_01423	GC			0.69	
2572233068	t3m_01424	COG_category	[R] General function prediction only			

2572233068	t3m_01424	COG1574	Predicted metal-dependent hydrolase with the TIM-barrel fold			2.00E-87
2572233068	t3m_01424	pfam07969	Amidohydro_3			1.10E-60
2572233068	t3m_01424	Locus_type		CDS		
2572233068	t3m_01424	Product_name		Predicted metal-dependent hydrolase with the TIM-barrel fold		
2572233068	t3m_01424	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233068	t3m_01424	Coordinates		10118..11695(-)		
2572233068	t3m_01424	DNA_length		1578bp		
2572233068	t3m_01424	Protein_length		525aa		
2572233068	t3m_01424	GC			0.72	

2572233069	t3m_01425	Metacyc	PWY-381: nitrate reduction II (assimilatory)			
2572233069	t3m_01425	Metacyc	PWY-6549: glutamine biosynthesis III			
2572233069	t3m_01425	Metacyc	GLNSYN-PWY: glutamine biosynthesis I			
2572233069	t3m_01425	Metacyc	PWY-5675: nitrate reduction V (assimilatory)			
2572233069	t3m_01425	Metacyc	PWY490-3: nitrate reduction VI (assimilatory)			
2572233069	t3m_01425	Metacyc	PWY-6964: ammonia assimilation cycle II			
2572233069	t3m_01425	Metacyc	PWY-6963: ammonia assimilation cycle I			
2572233069	t3m_01425	COG_category	[E] Amino acid transport and metabolism			
2572233069	t3m_01425	COG0174	Glutamine synthetase			1.00E-117
2572233069	t3m_01425	pfam00120	Gln-synt_C			3.00E-80
2572233069	t3m_01425	pfam03951	Gln-synt_N			2.80E-21
2572233069	t3m_01425	EC:6.3.1.2	Glutamate--ammonia ligase.			
2572233069	t3m_01425	TIGR00653	glutamine synthetase, type I			0.00E+00
2572233069	t3m_01425	KO:K01915	glutamine synthetase [EC:6.3.1.2]			0.00E+00
2572233069	t3m_01425	Locus_type		CDS		
2572233069	t3m_01425	Product_name		L-glutamine synthetase (EC 6.3.1.2)		
2572233069	t3m_01425	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233069	t3m_01425	Coordinates		11766..13193(-)		
2572233069	t3m_01425	DNA_length		1428bp		
2572233069	t3m_01425	Protein_length		475aa		
2572233069	t3m_01425	GC			0.66	

2572233070	t3m_01426	COG_category	[K] Transcription			
2572233070	t3m_01426	COG1522	Transcriptional regulators			9.00E-22

2572233070	t3m_01426	pfam01037	AsnC_trans_reg			1.10E-10
2572233070	t3m_01426	pfam13404	HTH_AsnC-type			9.50E-15
2572233070	t3m_01426	Locus_type		CDS		
2572233070	t3m_01426	Product_name		Transcriptional regulators		
2572233070	t3m_01426	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233070	t3m_01426	Coordinates		13348..13839(+)		
2572233070	t3m_01426	DNA_length		492bp		
2572233070	t3m_01426	Protein_length		163aa		
2572233070	t3m_01426	GC			0.67	
2572233071	t3m_01427	Metacyc	3-HYDROXYPHENYLACETATE-DEGRADATION-PWY: 4-hydroxyphenylacetate degradation			
2572233071	t3m_01427	Metacyc	PWY-7046: 4-coumarate degradation (anaerobic)			
2572233071	t3m_01427	Metacyc	PWY-7085: triethylamine degradation			
2572233071	t3m_01427	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)			
2572233071	t3m_01427	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle			
2572233071	t3m_01427	Metacyc	PWY-7153: grixazone biosynthesis			
2572233071	t3m_01427	Metacyc	PWY0-1517: sedoheptulose bisphosphate bypass			
2572233071	t3m_01427	Metacyc	PWY-6713: L-rhamnose degradation II			
2572233071	t3m_01427	COG_category	[G] Carbohydrate transport and metabolism			
2572233071	t3m_01427	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes			1.00E-56
2572233071	t3m_01427	pfam01791	DeoC			1.80E-18
2572233071	t3m_01427	EC:4.1.2.-	Lyases. Carbon-carbon lyases. Aldehyde-lyases.			
2572233071	t3m_01427	KO:K08321	putative autoinducer-2 (AI-2) aldolase [EC:4.1.2.-]			0.00E+00
2572233071	t3m_01427	Locus_type		CDS		
2572233071	t3m_01427	Product_name		DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes		
2572233071	t3m_01427	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233071	t3m_01427	Coordinates		13930..14742(+)		
2572233071	t3m_01427	DNA_length		813bp		
2572233071	t3m_01427	Protein_length		270aa		
2572233071	t3m_01427	GC			0.69	
2572233072	t3m_01428	Locus_type		tRNA		
2572233072	t3m_01428	Product_name		tRNA_Leu_CAG		
2572233072	t3m_01428	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		

2572233072	t3m_01428	Coordinates		14804..14888(+)		
2572233072	t3m_01428	DNA_length		85bp		
2572233072	t3m_01428	GC			0.62	
2572233073	t3m_01429	Locus_type		CDS		
2572233073	t3m_01429	Product_name		hypothetical protein		
2572233073	t3m_01429	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233073	t3m_01429	Coordinates		15013..15309(+)		
2572233073	t3m_01429	DNA_length		297bp		
2572233073	t3m_01429	Protein_length		98aa		
2572233073	t3m_01429	GC			0.71	
2572233074	t3m_01430	COG_category	[C] Energy production and conversion			
2572233074	t3m_01430	COG1454	Alcohol dehydrogenase, class IV			1.00E-63
2572233074	t3m_01430	pfam00465	Fe-ADH			1.20E-68
2572233074	t3m_01430	Locus_type		CDS		
2572233074	t3m_01430	Product_name		Alcohol dehydrogenase, class IV		
2572233074	t3m_01430	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233074	t3m_01430	Coordinates		15338..16492(+)		
2572233074	t3m_01430	DNA_length		1155bp		
2572233074	t3m_01430	Protein_length		384aa		
2572233074	t3m_01430	GC			0.72	
2572233075	t3m_01431	COG_category	[P] Inorganic ion transport and metabolism			
2572233075	t3m_01431	COG1392	Phosphate transport regulator (distant homolog of PhoU)			3.00E-28
2572233075	t3m_01431	pfam00083	Sugar_tr			1.10E-51
2572233075	t3m_01431	pfam01865	PhoU_div			1.20E-20
2572233075	t3m_01431	TIGR00153	TIGR00153 family protein			3.30E-16
2572233075	t3m_01431	Locus_type		CDS		
2572233075	t3m_01431	Product_name		Phosphate transport regulator (distant homolog of PhoU)		
2572233075	t3m_01431	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233075	t3m_01431	Coordinates		16569..18647(+)		
2572233075	t3m_01431	DNA_length		2079bp		
2572233075	t3m_01431	Protein_length		692aa		

2572233075	t3m_01431	GC			0.67	
2572233075	t3m_01431	Transmembrane		Yes		
2572233075	t3m_01431	Fused_gene		Yes		
2572233076	t3m_01432	Locus_type		CDS		
2572233076	t3m_01432	Product_name		hypothetical protein		
2572233076	t3m_01432	Scaffold		t3m_contig_70_355_len_18762_read_count_1744420.36		
2572233076	t3m_01432	Coordinates		18629..18760(-)		
2572233076	t3m_01432	DNA_length		132bp		
2572233076	t3m_01432	Protein_length		43aa		
2572233076	t3m_01432	GC			0.77	
2572233077	t3m_01433	Locus_type		tRNA		
2572233077	t3m_01433	Product_name		tRNA_Cys_GCA		
2572233077	t3m_01433	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37		
2572233077	t3m_01433	Coordinates		3..75(+)		
2572233077	t3m_01433	DNA_length		73bp		
2572233077	t3m_01433	GC			0.58	
2572233078	t3m_01434	pfam01828	Peptidase_A4			1.70E-14
2572233078	t3m_01434	Locus_type		CDS		
2572233078	t3m_01434	Product_name		Peptidase A4 family		
2572233078	t3m_01434	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37		
2572233078	t3m_01434	Coordinates		188..1144(-)		
2572233078	t3m_01434	DNA_length		957bp		
2572233078	t3m_01434	Protein_length		318aa		
2572233078	t3m_01434	GC			0.63	
2572233078	t3m_01434	Transmembrane		Yes		
2572233079	t3m_01435	pfam13418	Kelch_4			1.40E-05
2572233079	t3m_01435	Locus_type		CDS		
2572233079	t3m_01435	Product_name		Galactose oxidase, central domain		
2572233079	t3m_01435	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37		
2572233079	t3m_01435	Coordinates		1473..2432(-)		

2572233079	t3m_01435	DNA_length		960bp	
2572233079	t3m_01435	Protein_length		319aa	
2572233079	t3m_01435	GC		0.68	
2572233079	t3m_01435	Transmembrane		Yes	

2572233080	t3m_01436	COG_category	[R] General function prediction only		
2572233080	t3m_01436	COG0312	Predicted Zn-dependent proteases and their inactivated homologs		7.00E-43
2572233080	t3m_01436	pfam01523	PmbA_TldD		3.00E-32
2572233080	t3m_01436	Locus_type		CDS	
2572233080	t3m_01436	Product_name		Predicted Zn-dependent proteases and their inactivated homologs	
2572233080	t3m_01436	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233080	t3m_01436	Coordinates		2609..4039(-)	
2572233080	t3m_01436	DNA_length		1431bp	
2572233080	t3m_01436	Protein_length		476aa	
2572233080	t3m_01436	GC		0.7	

2572233081	t3m_01437	COG_category	[R] General function prediction only		
2572233081	t3m_01437	COG0312	Predicted Zn-dependent proteases and their inactivated homologs		5.00E-70
2572233081	t3m_01437	pfam01523	PmbA_TldD		7.10E-49
2572233081	t3m_01437	KO:K03568	TldD protein		0.00E+00
2572233081	t3m_01437	Locus_type		CDS	
2572233081	t3m_01437	Product_name		Predicted Zn-dependent proteases and their inactivated homologs	
2572233081	t3m_01437	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233081	t3m_01437	Coordinates		4036..5664(-)	
2572233081	t3m_01437	DNA_length		1629bp	
2572233081	t3m_01437	Protein_length		542aa	
2572233081	t3m_01437	GC		0.67	

2572233082	t3m_01438	pfam08445	FR47		6.50E-15
2572233082	t3m_01438	Locus_type		CDS	
2572233082	t3m_01438	Product_name		FR47-like protein	
2572233082	t3m_01438	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233082	t3m_01438	Coordinates		5639..6427(+)	
2572233082	t3m_01438	DNA_length		789bp	

2572233082	t3m_01438	Protein_length		262aa		
2572233082	t3m_01438	GC			0.66	
2572233083	t3m_01439	COG_category	[R] General function prediction only			
2572233083	t3m_01439	COG0384	Predicted epimerase, PhzC/PhzF homolog			9.00E-61
2572233083	t3m_01439	pfam02567	PhzC-PhzF			5.50E-53
2572233083	t3m_01439	TIGR00654	phenazine biosynthesis protein PhzF family			8.10E-58
2572233083	t3m_01439	Locus_type		CDS		
2572233083	t3m_01439	Product_name		phenazine biosynthesis protein PhzF family		
2572233083	t3m_01439	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37		
2572233083	t3m_01439	Coordinates		6536..7417(+)		
2572233083	t3m_01439	DNA_length		882bp		
2572233083	t3m_01439	Protein_length		293aa		
2572233083	t3m_01439	GC			0.67	
2572233084	t3m_01440	Locus_type		CDS		
2572233084	t3m_01440	Product_name		hypothetical protein		
2572233084	t3m_01440	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37		
2572233084	t3m_01440	Coordinates		7414..7635(-)		
2572233084	t3m_01440	DNA_length		222bp		
2572233084	t3m_01440	Protein_length		73aa		
2572233084	t3m_01440	GC			0.62	
2572233085	t3m_01441	pfam13485	Peptidase_MA_2			7.50E-05
2572233085	t3m_01441	Locus_type		CDS		
2572233085	t3m_01441	Product_name		Peptidase MA superfamily		
2572233085	t3m_01441	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37		
2572233085	t3m_01441	Coordinates		7714..8412(-)		
2572233085	t3m_01441	DNA_length		699bp		
2572233085	t3m_01441	Protein_length		232aa		
2572233085	t3m_01441	GC			0.68	
2572233085	t3m_01441	Transmembrane		Yes		
2572233086	t3m_01442	Locus_type		CDS		

2572233086	t3m_01442	Product_name		hypothetical protein	
2572233086	t3m_01442	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233086	t3m_01442	Coordinates		8938..9186(+)	
2572233086	t3m_01442	DNA_length		249bp	
2572233086	t3m_01442	Protein_length		82aa	
2572233086	t3m_01442	GC		0.7	
2572233087	t3m_01443	Locus_type		CDS	
2572233087	t3m_01443	Product_name		hypothetical protein	
2572233087	t3m_01443	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233087	t3m_01443	Coordinates		9402..9686(+)	
2572233087	t3m_01443	DNA_length		285bp	
2572233087	t3m_01443	Protein_length		94aa	
2572233087	t3m_01443	GC		0.69	
2572233088	t3m_01444	COG_category	[R] General function prediction only		
2572233088	t3m_01444	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfa		3.00E-12
2572233088	t3m_01444	pfam12697	Abhydrolase_6		1.30E-22
2572233088	t3m_01444	Locus_type		CDS	
2572233088	t3m_01444	Product_name		Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfan	
2572233088	t3m_01444	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233088	t3m_01444	Coordinates		9683..10483(+)	
2572233088	t3m_01444	DNA_length		801bp	
2572233088	t3m_01444	Protein_length		266aa	
2572233088	t3m_01444	GC		0.69	
2572233089	t3m_01445	Locus_type		CDS	
2572233089	t3m_01445	Product_name		hypothetical protein	
2572233089	t3m_01445	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233089	t3m_01445	Coordinates		10599..11231(-)	
2572233089	t3m_01445	DNA_length		633bp	
2572233089	t3m_01445	Protein_length		210aa	
2572233089	t3m_01445	GC		0.65	
2572233089	t3m_01445	Transmembrane		Yes	

2572233090	t3m_01446	Metacyc	TRYPDEG-PWY: tryptophan degradation II (via pyruvate)		
2572233090	t3m_01446	COG_category	[E] Amino acid transport and metabolism		
2572233090	t3m_01446	COG3033	Tryptophanase		0.00E+00
2572233090	t3m_01446	pfam01212	Beta_elim_lyase		8.30E-79
2572233090	t3m_01446	EC:4.1.99.1	Tryptophanase.		
2572233090	t3m_01446	KO:K01667	tryptophanase [EC:4.1.99.1]		0.00E+00
2572233090	t3m_01446	Locus_type		CDS	
2572233090	t3m_01446	Product_name		Tryptophanase	
2572233090	t3m_01446	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233090	t3m_01446	Coordinates		11410..12810(+)	
2572233090	t3m_01446	DNA_length		1401bp	
2572233090	t3m_01446	Protein_length		466aa	
2572233090	t3m_01446	GC		0.67	

2572233091	t3m_01447	pfam08327	AHSA1		1.80E-18
2572233091	t3m_01447	Locus_type		CDS	
2572233091	t3m_01447	Product_name		Activator of Hsp90 ATPase homolog 1-like protein	
2572233091	t3m_01447	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233091	t3m_01447	Coordinates		12912..13304(+)	
2572233091	t3m_01447	DNA_length		393bp	
2572233091	t3m_01447	Protein_length		130aa	
2572233091	t3m_01447	GC		0.66	

2572233092	t3m_01448	Locus_type		CDS	
2572233092	t3m_01448	Product_name		hypothetical protein	
2572233092	t3m_01448	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233092	t3m_01448	Coordinates		13403..13921(+)	
2572233092	t3m_01448	DNA_length		519bp	
2572233092	t3m_01448	Protein_length		172aa	
2572233092	t3m_01448	GC		0.74	

2572233093	t3m_01449	COG_category	[S] Function unknown		
2572233093	t3m_01449	COG3342	Uncharacterized conserved protein		2.00E-58

2572233093	t3m_01449	pfam06267	DUF1028		8.20E-69
2572233093	t3m_01449	Locus_type		CDS	
2572233093	t3m_01449	Product_name		Uncharacterized conserved protein	
2572233093	t3m_01449	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233093	t3m_01449	Coordinates		13976..14680(+)	
2572233093	t3m_01449	DNA_length		705bp	
2572233093	t3m_01449	Protein_length		234aa	
2572233093	t3m_01449	GC		0.69	
2572233094	t3m_01450	COG_category	[T] Signal transduction mechanisms		
2572233094	t3m_01450	COG0589	Universal stress protein UspA and related nucleotide-binding proteins		1.00E-14
2572233094	t3m_01450	pfam00582	Usp		9.00E-30
2572233094	t3m_01450	Locus_type		CDS	
2572233094	t3m_01450	Product_name		Universal stress protein UspA and related nucleotide-binding proteins	
2572233094	t3m_01450	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233094	t3m_01450	Coordinates		14730..15185(-)	
2572233094	t3m_01450	DNA_length		456bp	
2572233094	t3m_01450	Protein_length		151aa	
2572233094	t3m_01450	GC		0.68	
2572233095	t3m_01451	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes		
2572233095	t3m_01451	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes		
2572233095	t3m_01451	KEGG_module	M00114: Ascorbate biosynthesis, plants, glucose-6P => ascorbate		
2572233095	t3m_01451	Metacyc	PWY-6073: alginate biosynthesis I		
2572233095	t3m_01451	Metacyc	PWY-5659: GDP-mannose biosynthesis		
2572233095	t3m_01451	Metacyc	PWY-882: L-ascorbate biosynthesis I (L-galactose pathway)		
2572233095	t3m_01451	Metacyc	PWY-6082: alginate biosynthesis II		
2572233095	t3m_01451	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233095	t3m_01451	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572233095	t3m_01451	COG1208	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolys		9.00E-64
2572233095	t3m_01451	pfam00483	NTP_transferase		3.30E-30
2572233095	t3m_01451	EC:2.7.7.13	Mannose-1-phosphate guanylyltransferase.		
2572233095	t3m_01451	KO:K00966	mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]		0.00E+00
2572233095	t3m_01451	Locus_type		CDS	

2572233095	t3m_01451	Product_name		Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysa	
2572233095	t3m_01451	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233095	t3m_01451	Coordinates		15355..16329(+)	
2572233095	t3m_01451	DNA_length		975bp	
2572233095	t3m_01451	Protein_length		324aa	
2572233095	t3m_01451	GC		0.69	
2572233096	t3m_01452	Metacyc	PWY-4101: sorbitol degradation I		
2572233096	t3m_01452	Metacyc	PWY-6693: galactose degradation IV		
2572233096	t3m_01452	COG_category	[E] Amino acid transport and metabolism		
2572233096	t3m_01452	COG_category	[R] General function prediction only		
2572233096	t3m_01452	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases		8.00E-54
2572233096	t3m_01452	pfam00107	ADH_zinc_N		3.30E-17
2572233096	t3m_01452	pfam08240	ADH_N		6.30E-26
2572233096	t3m_01452	EC:1.1.1.14	L-iditol 2-dehydrogenase.		
2572233096	t3m_01452	TIGR01202	2-desacetyl-2-hydroxyethyl bacteriochlorophyllide A dehydrogenase		2.20E-22
2572233096	t3m_01452	KO:K00008	L-iditol 2-dehydrogenase [EC:1.1.1.14]		0.00E+00
2572233096	t3m_01452	Locus_type		CDS	
2572233096	t3m_01452	Product_name		Threonine dehydrogenase and related Zn-dependent dehydrogenases	
2572233096	t3m_01452	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233096	t3m_01452	Coordinates		16342..17385(-)	
2572233096	t3m_01452	DNA_length		1044bp	
2572233096	t3m_01452	Protein_length		347aa	
2572233096	t3m_01452	GC		0.72	
2572233097	t3m_01453	KEGG_module	M00027: GABA (gamma-Aminobutyrate) shunt		
2572233097	t3m_01453	Metacyc	PWY-4321: glutamate degradation IV		
2572233097	t3m_01453	Metacyc	PWY-6536: 4-aminobutyrate degradation III		
2572233097	t3m_01453	Metacyc	PWY-6537: 4-aminobutyrate degradation II		
2572233097	t3m_01453	Metacyc	PWY-5022: 4-aminobutyrate degradation V		
2572233097	t3m_01453	Metacyc	GLUDEG-I-PWY: glutamate degradation III (via 4-aminobutyrate)		
2572233097	t3m_01453	Metacyc	PWY-6535: 4-aminobutyrate degradation I		
2572233097	t3m_01453	Metacyc	BETA-ALA-DEGRADATION-I-PWY: β-alanine degradation I		
2572233097	t3m_01453	Metacyc	P181-PWY: nicotine degradation I		

2572233097	t3m_01453	pfam00202	Aminotran_3		7.10E-58
2572233097	t3m_01453	EC:2.6.1.19	4-aminobutyrate--2-oxoglutarate transaminase.		
2572233097	t3m_01453	KO:K00823	4-aminobutyrate aminotransferase [EC:2.6.1.19]		0.00E+00
2572233097	t3m_01453	Locus_type		CDS	
2572233097	t3m_01453	Product_name		Aminotransferase class-III	
2572233097	t3m_01453	Scaffold		t3m_contig_70_375_len_18148_read_count_1598522.37	
2572233097	t3m_01453	Coordinates		17382..18146(-)	
2572233097	t3m_01453	DNA_length		765bp	
2572233097	t3m_01453	Protein_length		254aa	
2572233097	t3m_01453	GC		0.67	
2572233098	t3m_01454	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2572233098	t3m_01454	KEGG_module	M00310: Pyruvate:ferredoxin oxidoreductase		
2572233098	t3m_01454	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA		
2572233098	t3m_01454	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2572233098	t3m_01454	Metacyc	P142-PWY: pyruvate fermentation to acetate I		
2572233098	t3m_01454	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2572233098	t3m_01454	Metacyc	PWY-6587: pyruvate fermentation to ethanol III		
2572233098	t3m_01454	Metacyc	PWY-5493: reductive monocarboxylic acid cycle		
2572233098	t3m_01454	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2572233098	t3m_01454	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)		
2572233098	t3m_01454	Metacyc	PWY-5538: pyruvate fermentation to acetate VI		
2572233098	t3m_01454	Metacyc	PWY-6876: isopropanol biosynthesis		
2572233098	t3m_01454	Metacyc	P23-PWY: reductive TCA cycle I		
2572233098	t3m_01454	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2572233098	t3m_01454	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2572233098	t3m_01454	Metacyc	PWY-6583: pyruvate fermentation to butanol I		
2572233098	t3m_01454	Metacyc	PWY-5600: pyruvate fermentation to acetate VII		
2572233098	t3m_01454	Metacyc	PWY-7003: glycerol degradation to butanol		
2572233098	t3m_01454	Metacyc	PWY-5483: pyruvate fermentation to acetate III		
2572233098	t3m_01454	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2572233098	t3m_01454	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)		
2572233098	t3m_01454	Metacyc	PWY-5392: reductive TCA cycle II		
2572233098	t3m_01454	Metacyc	P42-PWY: incomplete reductive TCA cycle		

2572233098	t3m_01454	COG_category	[C] Energy production and conversion		
2572233098	t3m_01454	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o		5.00E-31
2572233098	t3m_01454	pfam01558	POR		2.10E-31
2572233098	t3m_01454	EC:1.2.7.1	Pyruvate synthase.		
2572233098	t3m_01454	TIGR02175	2-oxoacid:acceptor oxidoreductase, gamma subunit, pyruvate/2-ketois		3.30E-62
2572233098	t3m_01454	KO:K00172	pyruvate ferredoxin oxidoreductase, gamma subunit [EC:1.2.7.1]		0.00E+00
2572233098	t3m_01454	ITERM:00696	ketoisovalerate ferredoxin oxidoreductase, gamma subunit (EC 1.2.7.7)		
2572233098	t3m_01454	Locus_type		CDS	
2572233098	t3m_01454	Product_name		ketoisovalerate ferredoxin oxidoreductase, gamma subunit (EC 1.2.7.7)	
2572233098	t3m_01454	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38	
2572233098	t3m_01454	Coordinates		3..755(-)	
2572233098	t3m_01454	DNA_length		753bp	
2572233098	t3m_01454	Protein_length		251aa	
2572233098	t3m_01454	GC		0.69	
2572233099	t3m_01455	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA		
2572233099	t3m_01455	KEGG_module	M00570: Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine		
2572233099	t3m_01455	KEGG_module	M00019: Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine		
2572233099	t3m_01455	KEGG_module	M00119: Pantothenate biosynthesis, valine/L-aspartate => pantothenate		
2572233099	t3m_01455	Metacyc	ILEUSYN-PWY: isoleucine biosynthesis I (from threonine)		
2572233099	t3m_01455	Metacyc	PWY-5108: isoleucine biosynthesis V		
2572233099	t3m_01455	Metacyc	VALDEG-PWY: valine degradation I		
2572233099	t3m_01455	Metacyc	PWY-5078: isoleucine degradation II		
2572233099	t3m_01455	Metacyc	PWY-5076: leucine degradation III		
2572233099	t3m_01455	Metacyc	ALANINE-VALINESYN-PWY: alanine biosynthesis I		
2572233099	t3m_01455	Metacyc	PWY-5101: isoleucine biosynthesis II		
2572233099	t3m_01455	Metacyc	LEUSYN-PWY: leucine biosynthesis		
2572233099	t3m_01455	Metacyc	VALSYN-PWY: valine biosynthesis		
2572233099	t3m_01455	Metacyc	PWY-5104: isoleucine biosynthesis IV		
2572233099	t3m_01455	Metacyc	PWY-5057: valine degradation II		
2572233099	t3m_01455	Metacyc	PWY-5103: isoleucine biosynthesis III		
2572233099	t3m_01455	Metacyc	LEU-DEG2-PWY: leucine degradation I		
2572233099	t3m_01455	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2572233099	t3m_01455	COG_category	[E] Amino acid transport and metabolism		

2572233099	t3m_01455	COG_category	[H] Coenzyme transport and metabolism			
2572233099	t3m_01455	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorism			3.00E-65
2572233099	t3m_01455	pfam01063	Aminotran_4			5.50E-41
2572233099	t3m_01455	EC:2.6.1.42	Branched-chain-amino-acid transaminase.			
2572233099	t3m_01455	TIGR01122	branched-chain amino acid aminotransferase, group I			2.90E-117
2572233099	t3m_01455	KO:K00826	branched-chain amino acid aminotransferase [EC:2.6.1.42]			0.00E+00
2572233099	t3m_01455	Locus_type		CDS		
2572233099	t3m_01455	Product_name		branched-chain amino acid aminotransferase, group I		
2572233099	t3m_01455	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38		
2572233099	t3m_01455	Coordinates		855..1775(+)		
2572233099	t3m_01455	DNA_length		921bp		
2572233099	t3m_01455	Protein_length		306aa		
2572233099	t3m_01455	GC			0.65	
2572233100	t3m_01456	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233100	t3m_01456	COG0309	Hydrogenase maturation factor			1.00E-86
2572233100	t3m_01456	pfam02769	AIRS_C			3.10E-17
2572233100	t3m_01456	pfam00586	AIRS			3.60E-15
2572233100	t3m_01456	TIGR02124	hydrogenase expression/formation protein HypE			6.20E-130
2572233100	t3m_01456	KO:K04655	hydrogenase expression/formation protein HypE			0.00E+00
2572233100	t3m_01456	Locus_type		CDS		
2572233100	t3m_01456	Product_name		Hydrogenase maturation protein, carbamoyl dehydratase HypE		
2572233100	t3m_01456	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38		
2572233100	t3m_01456	Coordinates		1831..2871(-)		
2572233100	t3m_01456	DNA_length		1041bp		
2572233100	t3m_01456	Protein_length		346aa		
2572233100	t3m_01456	GC			0.68	
2572233101	t3m_01457	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233101	t3m_01457	COG0409	Hydrogenase maturation factor			0.00E+00
2572233101	t3m_01457	pfam01924	HypD			0.00E+00
2572233101	t3m_01457	TIGR00075	hydrogenase expression/formation protein HypD			0.00E+00
2572233101	t3m_01457	KO:K04654	hydrogenase expression/formation protein HypD			0.00E+00
2572233101	t3m_01457	Locus_type		CDS		

2572233101	t3m_01457	Product_name		hydrogenase expression/formation protein HypD		
2572233101	t3m_01457	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38		
2572233101	t3m_01457	Coordinates		2868..4001(-)		
2572233101	t3m_01457	DNA_length		1134bp		
2572233101	t3m_01457	Protein_length		377aa		
2572233101	t3m_01457	GC			0.67	

2572233102	t3m_01458	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233102	t3m_01458	COG0298	Hydrogenase maturation factor			3.00E-16
2572233102	t3m_01458	pfam01455	HupF_HypC			1.80E-25
2572233102	t3m_01458	TIGR00074	hydrogenase assembly chaperone HypC/HupF			3.30E-25
2572233102	t3m_01458	KO:K04653	hydrogenase expression/formation protein HypC			5.20E-21
2572233102	t3m_01458	Locus_type		CDS		
2572233102	t3m_01458	Product_name		hydrogenase assembly chaperone HypC/HupF		
2572233102	t3m_01458	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38		
2572233102	t3m_01458	Coordinates		3998..4273(-)		
2572233102	t3m_01458	DNA_length		276bp		
2572233102	t3m_01458	Protein_length		91aa		
2572233102	t3m_01458	GC			0.68	

2572233103	t3m_01459	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233103	t3m_01459	COG0068	Hydrogenase maturation factor			0.00E+00
2572233103	t3m_01459	pfam07503	zf-HYPF			6.20E-17
2572233103	t3m_01459	pfam01300	Sua5_yciO_yrdC			4.20E-51
2572233103	t3m_01459	pfam07503	zf-HYPF			1.10E-11
2572233103	t3m_01459	TIGR00143	[NiFe] hydrogenase maturation protein HypF			0.00E+00
2572233103	t3m_01459	KO:K04656	hydrogenase maturation protein HypF			0.00E+00
2572233103	t3m_01459	Locus_type		CDS		
2572233103	t3m_01459	Product_name		[NiFe] hydrogenase maturation protein HypF		
2572233103	t3m_01459	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38		
2572233103	t3m_01459	Coordinates		4287..6248(-)		
2572233103	t3m_01459	DNA_length		1962bp		
2572233103	t3m_01459	Protein_length		653aa		
2572233103	t3m_01459	GC			0.66	

2572233104	t3m_01460	Locus_type		CDS	
2572233104	t3m_01460	Product_name		hypothetical protein	
2572233104	t3m_01460	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38	
2572233104	t3m_01460	Coordinates		6471..6686(+)	
2572233104	t3m_01460	DNA_length		216bp	
2572233104	t3m_01460	Protein_length		71aa	
2572233104	t3m_01460	GC		0.63	
2572233105	t3m_01461	Locus_type		CDS	
2572233105	t3m_01461	Product_name		hypothetical protein	
2572233105	t3m_01461	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38	
2572233105	t3m_01461	Coordinates		6875..8932(+)	
2572233105	t3m_01461	DNA_length		2058bp	
2572233105	t3m_01461	Protein_length		685aa	
2572233105	t3m_01461	GC		0.63	
2572233105	t3m_01461	Transmembrane		Yes	
2572233106	t3m_01462	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572233106	t3m_01462	COG0438	Glycosyltransferase		3.00E-20
2572233106	t3m_01462	pfam13692	Glyco_trans_1_4		1.20E-13
2572233106	t3m_01462	pfam13579	Glyco_trans_4_4		1.50E-09
2572233106	t3m_01462	Locus_type		CDS	
2572233106	t3m_01462	Product_name		Glycosyltransferase	
2572233106	t3m_01462	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38	
2572233106	t3m_01462	Coordinates		9430..10515(+)	
2572233106	t3m_01462	DNA_length		1086bp	
2572233106	t3m_01462	Protein_length		361aa	
2572233106	t3m_01462	GC		0.61	
2572233107	t3m_01463	pfam09852	DUF2079		2.70E-40
2572233107	t3m_01463	Locus_type		CDS	
2572233107	t3m_01463	Product_name		Predicted membrane protein (DUF2079)	
2572233107	t3m_01463	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38	

2572233107	t3m_01463	Coordinates		10749..12968(+)		
2572233107	t3m_01463	DNA_length		2220bp		
2572233107	t3m_01463	Protein_length		739aa		
2572233107	t3m_01463	GC			0.6	
2572233107	t3m_01463	Transmembrane		Yes		
2572233108	t3m_01464	pfam00535	Glycos_transf_2			1.10E-13
2572233108	t3m_01464	Locus_type		CDS		
2572233108	t3m_01464	Product_name		Glycosyl transferase family 2		
2572233108	t3m_01464	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38		
2572233108	t3m_01464	Coordinates		13060..14085(-)		
2572233108	t3m_01464	DNA_length		1026bp		
2572233108	t3m_01464	Protein_length		341aa		
2572233108	t3m_01464	GC			0.59	
2572233109	t3m_01465	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572233109	t3m_01465	COG0438	Glycosyltransferase			1.00E-22
2572233109	t3m_01465	pfam13692	Glyco_trans_1_4			1.90E-18
2572233109	t3m_01465	Locus_type		CDS		
2572233109	t3m_01465	Product_name		Glycosyltransferase		
2572233109	t3m_01465	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38		
2572233109	t3m_01465	Coordinates		14119..15267(-)		
2572233109	t3m_01465	DNA_length		1149bp		
2572233109	t3m_01465	Protein_length		382aa		
2572233109	t3m_01465	GC			0.58	
2572233110	t3m_01466	pfam03214	RGP			1.10E-16
2572233110	t3m_01466	Locus_type		CDS		
2572233110	t3m_01466	Product_name		Reversibly glycosylated polypeptide		
2572233110	t3m_01466	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38		
2572233110	t3m_01466	Coordinates		15435..16583(-)		
2572233110	t3m_01466	DNA_length		1149bp		
2572233110	t3m_01466	Protein_length		382aa		
2572233110	t3m_01466	GC			0.58	

2572233111	t3m_01467	pfam00756	Esterase		2.20E-24
2572233111	t3m_01467	KO:K07214	enterochelin esterase and related enzymes		4.10E-41
2572233111	t3m_01467	Locus_type		CDS	
2572233111	t3m_01467	Product_name		Putative esterase	
2572233111	t3m_01467	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38	
2572233111	t3m_01467	Coordinates		16855..17436(-)	
2572233111	t3m_01467	DNA_length		582bp	
2572233111	t3m_01467	Protein_length		193aa	
2572233111	t3m_01467	GC		0.66	
2572233112	t3m_01468	Locus_type		CDS	
2572233112	t3m_01468	Product_name		hypothetical protein	
2572233112	t3m_01468	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38	
2572233112	t3m_01468	Coordinates		17443..17664(-)	
2572233112	t3m_01468	DNA_length		222bp	
2572233112	t3m_01468	Protein_length		73aa	
2572233112	t3m_01468	GC		0.64	
2572233113	t3m_01469	Locus_type		tRNA	
2572233113	t3m_01469	Product_name		tRNA_Thr_GGT	
2572233113	t3m_01469	Scaffold		t3m_contig_70_379_len_18070_read_count_1700211.38	
2572233113	t3m_01469	Coordinates		18006..18069(-)	
2572233113	t3m_01469	DNA_length		64bp	
2572233113	t3m_01469	GC		0.64	
2572233114	t3m_01470	KEGG_module	M00179: Ribosome, archaea		
2572233114	t3m_01470	KEGG_module	M00178: Ribosome, bacteria		
2572233114	t3m_01470	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233114	t3m_01470	COG0051	Ribosomal protein S10		3.00E-29
2572233114	t3m_01470	pfam00338	Ribosomal_S10		3.30E-28
2572233114	t3m_01470	TIGR01046	ribosomal protein S10(archaeal)/S20(eukaryotic)		2.00E-49
2572233114	t3m_01470	KO:K02946	small subunit ribosomal protein S10		2.20E-37
2572233114	t3m_01470	Locus_type		CDS	

2572233114	t3m_01470	Product_name		SSU ribosomal protein S10P	
2572233114	t3m_01470	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39	
2572233114	t3m_01470	Coordinates		79..390(+)	
2572233114	t3m_01470	DNA_length		312bp	
2572233114	t3m_01470	Protein_length		103aa	
2572233114	t3m_01470	GC		0.64	
2572233115	t3m_01471	COG_category	[I] Lipid transport and metabolism		
2572233115	t3m_01471	COG0688	Phosphatidylserine decarboxylase		3.00E-23
2572233115	t3m_01471	pfam02666	PS_Dcarbxylase		1.20E-17
2572233115	t3m_01471	pfam01405	PsbT		1.90E-04
2572233115	t3m_01471	TIGR00164	phosphatidylserine decarboxylase precursor-related protein		1.60E-41
2572233115	t3m_01471	Locus_type		CDS	
2572233115	t3m_01471	Product_name		Phosphatidylserine decarboxylase	
2572233115	t3m_01471	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39	
2572233115	t3m_01471	Coordinates		395..1024(+)	
2572233115	t3m_01471	DNA_length		630bp	
2572233115	t3m_01471	Protein_length		209aa	
2572233115	t3m_01471	GC		0.73	
2572233115	t3m_01471	Transmembrane		Yes	
2572233116	t3m_01472	COG_category	[I] Lipid transport and metabolism		
2572233116	t3m_01472	COG1183	Phosphatidylserine synthase		5.00E-18
2572233116	t3m_01472	pfam01066	CDP-OH_P_transf		6.10E-09
2572233116	t3m_01472	Locus_type		CDS	
2572233116	t3m_01472	Product_name		Phosphatidylserine synthase	
2572233116	t3m_01472	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39	
2572233116	t3m_01472	Coordinates		1021..1779(+)	
2572233116	t3m_01472	DNA_length		759bp	
2572233116	t3m_01472	Protein_length		252aa	
2572233116	t3m_01472	GC		0.7	
2572233116	t3m_01472	Transmembrane		Yes	
2572233117	t3m_01473	COG_category	[S] Function unknown		

2572233117	t3m_01473	COG2098	Uncharacterized protein conserved in archaea			1.00E-23
2572233117	t3m_01473	pfam04038	DUF381			4.80E-07
2572233117	t3m_01473	pfam04036	DUF372			3.70E-16
2572233117	t3m_01473	KO:K09739	hypothetical protein			3.10E-16
2572233117	t3m_01473	Locus_type		CDS		
2572233117	t3m_01473	Product_name		Uncharacterized protein conserved in archaea		
2572233117	t3m_01473	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233117	t3m_01473	Coordinates		1776..2237(+)		
2572233117	t3m_01473	DNA_length		462bp		
2572233117	t3m_01473	Protein_length		153aa		
2572233117	t3m_01473	GC			0.72	
2572233118	t3m_01474	pfam07690	MFS_1			1.60E-18
2572233118	t3m_01474	Locus_type		CDS		
2572233118	t3m_01474	Product_name		Major Facilitator Superfamily		
2572233118	t3m_01474	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233118	t3m_01474	Coordinates		2194..3600(-)		
2572233118	t3m_01474	DNA_length		1407bp		
2572233118	t3m_01474	Protein_length		468aa		
2572233118	t3m_01474	GC			0.67	
2572233118	t3m_01474	Transmembrane		Yes		
2572233119	t3m_01475	pfam01037	AsnC_trans_reg			3.40E-15
2572233119	t3m_01475	Locus_type		CDS		
2572233119	t3m_01475	Product_name		AsnC family		
2572233119	t3m_01475	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233119	t3m_01475	Coordinates		3758..3991(+)		
2572233119	t3m_01475	DNA_length		234bp		
2572233119	t3m_01475	Protein_length		77aa		
2572233119	t3m_01475	GC			0.59	
2572233120	t3m_01476	Locus_type		CDS		
2572233120	t3m_01476	Product_name		hypothetical protein		
2572233120	t3m_01476	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		

2572233120	t3m_01476	Coordinates		4002..4337(+)		
2572233120	t3m_01476	DNA_length		336bp		
2572233120	t3m_01476	Protein_length		111aa		
2572233120	t3m_01476	GC			0.62	
2572233120	t3m_01476	Transmembrane		Yes		

2572233121	t3m_01477	COG_category	[S] Function unknown			
2572233121	t3m_01477	COG1912	Uncharacterized conserved protein			9.00E-52
2572233121	t3m_01477	pfam01887	SAM_adeno_trans			1.20E-60
2572233121	t3m_01477	KO:K09134	hypothetical protein			7.40E-37
2572233121	t3m_01477	Locus_type		CDS		
2572233121	t3m_01477	Product_name		Uncharacterized conserved protein		
2572233121	t3m_01477	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233121	t3m_01477	Coordinates		4420..5235(+)		
2572233121	t3m_01477	DNA_length		816bp		
2572233121	t3m_01477	Protein_length		271aa		
2572233121	t3m_01477	GC			0.72	

2572233122	t3m_01478	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233122	t3m_01478	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain			2.00E-104
2572233122	t3m_01478	pfam00684	DnaJ_CXXCXGXG			9.30E-13
2572233122	t3m_01478	pfam01556	CTDII			7.40E-21
2572233122	t3m_01478	pfam00226	DnaJ			3.50E-26
2572233122	t3m_01478	TIGR02349	chaperone protein DnaJ			3.50E-118
2572233122	t3m_01478	KO:K03686	molecular chaperone DnaJ			0.00E+00
2572233122	t3m_01478	Locus_type		CDS		
2572233122	t3m_01478	Product_name		chaperone protein DnaJ		
2572233122	t3m_01478	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233122	t3m_01478	Coordinates		5263..6411(+)		
2572233122	t3m_01478	DNA_length		1149bp		
2572233122	t3m_01478	Protein_length		382aa		
2572233122	t3m_01478	GC			0.69	

2572233123	t3m_01479	pfam05175	MTS			4.20E-40

2572233123	t3m_01479	ITERM:05207	16S rRNA m(2)G 1207 methyltransferase (EC 2.1.1.52)			
2572233123	t3m_01479	Locus_type		CDS		
2572233123	t3m_01479	Product_name		16S rRNA m(2)G 1207 methyltransferase (EC 2.1.1.52)		
2572233123	t3m_01479	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233123	t3m_01479	Coordinates		6414..7055(+)		
2572233123	t3m_01479	DNA_length		642bp		
2572233123	t3m_01479	Protein_length		213aa		
2572233123	t3m_01479	GC			0.7	

2572233124	t3m_01480	KEGG_module	M00178: Ribosome, bacteria			
2572233124	t3m_01480	KEGG_module	M00179: Ribosome, archaea			
2572233124	t3m_01480	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233124	t3m_01480	COG0099	Ribosomal protein S13			8.00E-25
2572233124	t3m_01480	pfam00416	Ribosomal_S13			5.40E-25
2572233124	t3m_01480	KO:K02952	small subunit ribosomal protein S13			0.00E+00
2572233124	t3m_01480	Locus_type		CDS		
2572233124	t3m_01480	Product_name		Ribosomal protein S13		
2572233124	t3m_01480	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233124	t3m_01480	Coordinates		7211..7951(+)		
2572233124	t3m_01480	DNA_length		741bp		
2572233124	t3m_01480	Protein_length		246aa		
2572233124	t3m_01480	GC			0.7	

2572233125	t3m_01481	KEGG_module	M00178: Ribosome, bacteria			
2572233125	t3m_01481	KEGG_module	M00179: Ribosome, archaea			
2572233125	t3m_01481	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233125	t3m_01481	COG0522	Ribosomal protein S4 and related proteins			5.00E-26
2572233125	t3m_01481	pfam01479	S4			5.70E-08
2572233125	t3m_01481	TIGR01018	ribosomal protein S4(archaeal type)/S9(eukaryote cytosolic type)			1.20E-57
2572233125	t3m_01481	KO:K02986	small subunit ribosomal protein S4			0.00E+00
2572233125	t3m_01481	ITERM:00283	SSU ribosomal protein S4P			
2572233125	t3m_01481	Locus_type		CDS		
2572233125	t3m_01481	Product_name		SSU ribosomal protein S4P		
2572233125	t3m_01481	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		

2572233125	t3m_01481	Coordinates		7962..8561(+)	
2572233125	t3m_01481	DNA_length		600bp	
2572233125	t3m_01481	Protein_length		199aa	
2572233125	t3m_01481	GC		0.7	
2572233126	t3m_01482	KEGG_module	M00179: Ribosome, archaea		
2572233126	t3m_01482	KEGG_module	M00178: Ribosome, bacteria		
2572233126	t3m_01482	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233126	t3m_01482	COG0100	Ribosomal protein S11		5.00E-31
2572233126	t3m_01482	pfam00411	Ribosomal_S11		9.50E-40
2572233126	t3m_01482	TIGR03628	archaeal ribosomal protein S11P		7.40E-62
2572233126	t3m_01482	KO:K02948	small subunit ribosomal protein S11		0.00E+00
2572233126	t3m_01482	Locus_type		CDS	
2572233126	t3m_01482	Product_name		SSU ribosomal protein S11P	
2572233126	t3m_01482	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39	
2572233126	t3m_01482	Coordinates		8565..8948(+)	
2572233126	t3m_01482	DNA_length		384bp	
2572233126	t3m_01482	Protein_length		127aa	
2572233126	t3m_01482	GC		0.71	
2572233127	t3m_01483	KEGG_module	M00184: RNA polymerase, archaea		
2572233127	t3m_01483	COG_category	[K] Transcription		
2572233127	t3m_01483	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit		1.00E-23
2572233127	t3m_01483	pfam01193	RNA_pol_L		5.10E-14
2572233127	t3m_01483	pfam01000	RNA_pol_A_bac		5.10E-15
2572233127	t3m_01483	pfam00037	Fer4		1.10E-04
2572233127	t3m_01483	EC:2.7.7.6	DNA-directed RNA polymerase.		
2572233127	t3m_01483	KO:K03047	DNA-directed RNA polymerase subunit D [EC:2.7.7.6]		0.00E+00
2572233127	t3m_01483	Locus_type		CDS	
2572233127	t3m_01483	Product_name		DNA-directed RNA polymerase, alpha subunit/40 kD subunit	
2572233127	t3m_01483	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39	
2572233127	t3m_01483	Coordinates		8952..9797(+)	
2572233127	t3m_01483	DNA_length		846bp	
2572233127	t3m_01483	Protein_length		281aa	

2572233127	t3m_01483	GC			0.68	
2572233128	t3m_01484	COG_category	[R] General function prediction only			
2572233128	t3m_01484	COG1537	Predicted RNA-binding proteins			3.00E-55
2572233128	t3m_01484	pfam03463	eRF1_1			1.60E-19
2572233128	t3m_01484	pfam03465	eRF1_3			2.30E-08
2572233128	t3m_01484	pfam03464	eRF1_2			7.70E-12
2572233128	t3m_01484	TIGR00111	mRNA surveillance protein pelota			1.50E-54
2572233128	t3m_01484	KO:K06965	protein pelota			0.00E+00
2572233128	t3m_01484	Locus_type		CDS		
2572233128	t3m_01484	Product_name		Predicted RNA-binding proteins		
2572233128	t3m_01484	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233128	t3m_01484	Coordinates		9748..11019(-)		
2572233128	t3m_01484	DNA_length		1272bp		
2572233128	t3m_01484	Protein_length		423aa		
2572233128	t3m_01484	GC			0.72	
2572233129	t3m_01485	pfam05977	MFS_3			2.40E-15
2572233129	t3m_01485	Locus_type		CDS		
2572233129	t3m_01485	Product_name		Transmembrane secretion effector		
2572233129	t3m_01485	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233129	t3m_01485	Coordinates		10937..12295(+)		
2572233129	t3m_01485	DNA_length		1359bp		
2572233129	t3m_01485	Protein_length		452aa		
2572233129	t3m_01485	GC			0.69	
2572233129	t3m_01485	Transmembrane		Yes		
2572233130	t3m_01486	Metacyc	PWY1G-0: mycothiol biosynthesis			
2572233130	t3m_01486	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233130	t3m_01486	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins			6.00E-06
2572233130	t3m_01486	pfam00583	Acetyltransf_1			2.10E-13
2572233130	t3m_01486	EC:2.3.1.189	Mycothiol synthase.			
2572233130	t3m_01486	KO:K15520	mycothiol synthase [EC:2.3.1.189]			5.50E-14
2572233130	t3m_01486	Locus_type		CDS		

2572233130	t3m_01486	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins		
2572233130	t3m_01486	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233130	t3m_01486	Coordinates		12292..13233(-)		
2572233130	t3m_01486	DNA_length		942bp		
2572233130	t3m_01486	Protein_length		313aa		
2572233130	t3m_01486	GC			0.71	

2572233131	t3m_01487	KEGG_module	M00377: Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)			
2572233131	t3m_01487	KEGG_module	M00140: C1-unit interconversion, prokaryotes			
2572233131	t3m_01487	Metacyc	PWY-1722: formaldehyde oxidation V (tetrahydrofolate pathway)			
2572233131	t3m_01487	Metacyc	PWY-3841: folate transformations II			
2572233131	t3m_01487	Metacyc	PWY-2201: folate transformations I			
2572233131	t3m_01487	Metacyc	1CMET2-PWY: formylTHF biosynthesis I			
2572233131	t3m_01487	Metacyc	P164-PWY: purine nucleobases degradation I (anaerobic)			
2572233131	t3m_01487	Metacyc	CODH-PWY: reductive acetyl coenzyme A pathway			
2572233131	t3m_01487	Metacyc	PWY-2161: folate polyglutamylation			
2572233131	t3m_01487	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)			
2572233131	t3m_01487	IMG_pathway	1030: 10-formyltetrahydrofolate polyglutamination			
2572233131	t3m_01487	IMG_pathway	482: Generation of ATP from formimino-THF			
2572233131	t3m_01487	IMG_pathway	942: Wood-Ljungdahl pathway			
2572233131	t3m_01487	IMG_pathway	958: Conversion of formate to methylenetetrahydrofolate			
2572233131	t3m_01487	COG_category	[F] Nucleotide transport and metabolism			
2572233131	t3m_01487	COG2759	Formyltetrahydrofolate synthetase			0.00E+00
2572233131	t3m_01487	pfam01268	FTHFS			0.00E+00
2572233131	t3m_01487	EC:6.3.4.3	Formate--tetrahydrofolate ligase.			
2572233131	t3m_01487	KO:K01938	formate--tetrahydrofolate ligase [EC:6.3.4.3]			0.00E+00
2572233131	t3m_01487	ITERM:01840	Formate-tetrahydrofolate ligase (EC 6.3.4.3)			
2572233131	t3m_01487	Locus_type		CDS		
2572233131	t3m_01487	Product_name		Formate-tetrahydrofolate ligase (EC 6.3.4.3)		
2572233131	t3m_01487	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233131	t3m_01487	Coordinates		13290..14978(+)		
2572233131	t3m_01487	DNA_length		1689bp		
2572233131	t3m_01487	Protein_length		562aa		
2572233131	t3m_01487	GC			0.68	

2572233132	t3m_01488	Locus_type		CDS		
2572233132	t3m_01488	Product_name		hypothetical protein		
2572233132	t3m_01488	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233132	t3m_01488	Coordinates		15068..15358(+)		
2572233132	t3m_01488	DNA_length		291bp		
2572233132	t3m_01488	Protein_length		96aa		
2572233132	t3m_01488	GC			0.71	

2572233133	t3m_01489	pfam01402	RHH_1			1.80E-04
2572233133	t3m_01489	Locus_type		CDS		
2572233133	t3m_01489	Product_name		Ribbon-helix-helix protein, copG family		
2572233133	t3m_01489	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233133	t3m_01489	Coordinates		15521..15886(+)		
2572233133	t3m_01489	DNA_length		366bp		
2572233133	t3m_01489	Protein_length		121aa		
2572233133	t3m_01489	GC			0.66	

2572233134	t3m_01490	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2572233134	t3m_01490	COG0206	Cell division GTPase			6.00E-44
2572233134	t3m_01490	pfam12327	FtsZ_C			5.80E-11
2572233134	t3m_01490	pfam00091	Tubulin			4.40E-19
2572233134	t3m_01490	KO:K03531	cell division protein FtsZ			0.00E+00
2572233134	t3m_01490	Locus_type		CDS		
2572233134	t3m_01490	Product_name		Cell division GTPase		
2572233134	t3m_01490	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39		
2572233134	t3m_01490	Coordinates		15902..16936(+)		
2572233134	t3m_01490	DNA_length		1035bp		
2572233134	t3m_01490	Protein_length		344aa		
2572233134	t3m_01490	GC			0.69	

2572233135	t3m_01491	COG_category	[S] Function unknown			
2572233135	t3m_01491	COG1901	Uncharacterized conserved protein			2.00E-33
2572233135	t3m_01491	pfam04013	Methyltrn_RNA_2			2.00E-36

2572233135	t3m_01491	EC:2.1.1.257	tRNA (pseudouridine(54)-N(1))-methyltransferase.		
2572233135	t3m_01491	KO:K16317	tRNA (pseudouridine54-N1)-methyltransferase [EC:2.1.1.257]		5.60E-32
2572233135	t3m_01491	Locus_type		CDS	
2572233135	t3m_01491	Product_name		Uncharacterized conserved protein	
2572233135	t3m_01491	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39	
2572233135	t3m_01491	Coordinates		16937..17566(-)	
2572233135	t3m_01491	DNA_length		630bp	
2572233135	t3m_01491	Protein_length		209aa	
2572233135	t3m_01491	GC		0.71	
2572233136	t3m_01492	Locus_type		CDS	
2572233136	t3m_01492	Product_name		hypothetical protein	
2572233136	t3m_01492	Scaffold		t3m_contig_70_382_len_18025_read_count_1393314.39	
2572233136	t3m_01492	Coordinates		17624..18022(-)	
2572233136	t3m_01492	DNA_length		399bp	
2572233136	t3m_01492	Protein_length		132aa	
2572233136	t3m_01492	GC		0.67	
2572233137	t3m_01493	Locus_type		CDS	
2572233137	t3m_01493	Product_name		hypothetical protein	
2572233137	t3m_01493	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233137	t3m_01493	Coordinates		195..404(+)	
2572233137	t3m_01493	DNA_length		210bp	
2572233137	t3m_01493	Protein_length		69aa	
2572233137	t3m_01493	GC		0.65	
2572233137	t3m_01493	Transmembrane		Yes	
2572233138	t3m_01494	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes		
2572233138	t3m_01494	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes		
2572233138	t3m_01494	Metacyc	TRNA-CHARGING-PWY: tRNA charging		
2572233138	t3m_01494	IMG_pathway	500: L-proline ligation to tRNA(Pro)		
2572233138	t3m_01494	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233138	t3m_01494	COG0442	Prolyl-tRNA synthetase		1.00E-98
2572233138	t3m_01494	pfam03129	HGTP_anticodon		6.20E-13

2572233138	t3m_01494	pfam00587	tRNA-synt_2b			1.20E-14
2572233138	t3m_01494	EC:6.1.1.15	Proline--tRNA ligase.			
2572233138	t3m_01494	TIGR00408	prolyl-tRNA synthetase, family I			0.00E+00
2572233138	t3m_01494	KO:K01881	prolyl-tRNA synthetase [EC:6.1.1.15]			0.00E+00
2572233138	t3m_01494	ITERM:01944	prolyl-tRNA synthetase (EC 6.1.1.15)			
2572233138	t3m_01494	Locus_type		CDS		
2572233138	t3m_01494	Product_name		prolyl-tRNA synthetase (EC 6.1.1.15)		
2572233138	t3m_01494	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233138	t3m_01494	Coordinates		419..1846(-)		
2572233138	t3m_01494	DNA_length		1428bp		
2572233138	t3m_01494	Protein_length		475aa		
2572233138	t3m_01494	GC			0.69	
2572233139	t3m_01495	COG_category	[S] Function unknown			
2572233139	t3m_01495	COG2237	Predicted membrane protein			1.00E-55
2572233139	t3m_01495	pfam04123	DUF373			1.60E-84
2572233139	t3m_01495	KO:K08975	putative membrane protein			0.00E+00
2572233139	t3m_01495	Locus_type		CDS		
2572233139	t3m_01495	Product_name		Predicted membrane protein		
2572233139	t3m_01495	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233139	t3m_01495	Coordinates		2031..3116(+)		
2572233139	t3m_01495	DNA_length		1086bp		
2572233139	t3m_01495	Protein_length		361aa		
2572233139	t3m_01495	GC			0.67	
2572233139	t3m_01495	Transmembrane		Yes		
2572233140	t3m_01496	COG_category	[R] General function prediction only			
2572233140	t3m_01496	COG2236	Predicted phosphoribosyltransferases			1.00E-36
2572233140	t3m_01496	pfam00156	Pribosyltran			4.60E-15
2572233140	t3m_01496	Locus_type		CDS		
2572233140	t3m_01496	Product_name		Predicted phosphoribosyltransferases		
2572233140	t3m_01496	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233140	t3m_01496	Coordinates		3141..3755(-)		
2572233140	t3m_01496	DNA_length		615bp		

2572233140	t3m_01496	Protein_length		204aa		
2572233140	t3m_01496	GC			0.7	
2572233141	t3m_01497	Metacyc	GLUTAMATE-SYN2-PWY: glutamate biosynthesis II			
2572233141	t3m_01497	Metacyc	ARGININE-SYN4-PWY: arginine biosynthesis IV			
2572233141	t3m_01497	Metacyc	PWY-5766: glutamate degradation X			
2572233141	t3m_01497	COG_category	[E] Amino acid transport and metabolism			
2572233141	t3m_01497	COG0334	Glutamate dehydrogenase/leucine dehydrogenase			0.00E+00
2572233141	t3m_01497	pfam02812	ELFV_dehydrog_N			2.90E-53
2572233141	t3m_01497	pfam00208	ELFV_dehydrog			5.30E-68
2572233141	t3m_01497	EC:1.4.1.3	Glutamate dehydrogenase (NAD(P)(+)).			
2572233141	t3m_01497	KO:K00261	glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]			0.00E+00
2572233141	t3m_01497	Locus_type		CDS		
2572233141	t3m_01497	Product_name		Glutamate dehydrogenase/leucine dehydrogenase		
2572233141	t3m_01497	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233141	t3m_01497	Coordinates		3801..4973(-)		
2572233141	t3m_01497	DNA_length		1173bp		
2572233141	t3m_01497	Protein_length		390aa		
2572233141	t3m_01497	GC			0.66	
2572233142	t3m_01498	KEGG_module	M00127: Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P			
2572233142	t3m_01498	Metacyc	PWY-6896: thiamin salvage I			
2572233142	t3m_01498	Metacyc	PWY-6893: thiamin diphosphate biosynthesis II (Bacillus)			
2572233142	t3m_01498	Metacyc	PWY-6894: thiamin diphosphate biosynthesis I (E. coli)			
2572233142	t3m_01498	Metacyc	PWY-6897: thiamin salvage II			
2572233142	t3m_01498	COG_category	[H] Coenzyme transport and metabolism			
2572233142	t3m_01498	COG0611	Thiamine monophosphate kinase			2.00E-55
2572233142	t3m_01498	pfam02769	AIRS_C			5.00E-09
2572233142	t3m_01498	pfam00586	AIRS			6.80E-22
2572233142	t3m_01498	EC:2.7.4.16	Thiamine-phosphate kinase.			
2572233142	t3m_01498	TIGR01379	thiamine-monophosphate kinase			4.20E-75
2572233142	t3m_01498	KO:K00946	thiamine-monophosphate kinase [EC:2.7.4.16]			1.60E-40
2572233142	t3m_01498	Locus_type		CDS		
2572233142	t3m_01498	Product_name		thiamine-monophosphate kinase		

2572233142	t3m_01498	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233142	t3m_01498	Coordinates		5188..6192(-)	
2572233142	t3m_01498	DNA_length		1005bp	
2572233142	t3m_01498	Protein_length		334aa	
2572233142	t3m_01498	GC		0.73	
2572233143	t3m_01499	KEGG_module	M00087: beta-Oxidation		
2572233143	t3m_01499	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA		
2572233143	t3m_01499	KEGG_module	M00013: Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA		
2572233143	t3m_01499	Metacyc	PWY-7094: fatty acid salvage		
2572233143	t3m_01499	COG_category	[I] Lipid transport and metabolism		
2572233143	t3m_01499	COG1960	Acyl-CoA dehydrogenases		2.00E-62
2572233143	t3m_01499	pfam00441	Acyl-CoA_dh_1		1.90E-31
2572233143	t3m_01499	pfam02771	Acyl-CoA_dh_N		1.00E-25
2572233143	t3m_01499	pfam02770	Acyl-CoA_dh_M		6.80E-14
2572233143	t3m_01499	EC:1.3.8.7	Medium-chain acyl-CoA dehydrogenase.		
2572233143	t3m_01499	KO:K00249	acyl-CoA dehydrogenase [EC:1.3.8.7]		0.00E+00
2572233143	t3m_01499	Locus_type		CDS	
2572233143	t3m_01499	Product_name		Acyl-CoA dehydrogenases	
2572233143	t3m_01499	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233143	t3m_01499	Coordinates		6200..7390(-)	
2572233143	t3m_01499	DNA_length		1191bp	
2572233143	t3m_01499	Protein_length		396aa	
2572233143	t3m_01499	GC		0.66	
2572233144	t3m_01500	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate		
2572233144	t3m_01500	KEGG_module	M00166: Reductive pentose phosphate cycle, RuBP + CO2 => glyceraldehyde-3P		
2572233144	t3m_01500	KEGG_module	M00165: Reductive pentose phosphate cycle (Calvin cycle)		
2572233144	t3m_01500	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds		
2572233144	t3m_01500	IMG_pathway	336: Standard Embden-Meyerhof pathway		
2572233144	t3m_01500	IMG_pathway	359: Conversion of glyceraldehyde-3-phosphate to pyruvate		
2572233144	t3m_01500	IMG_pathway	527: Calvin cycle		
2572233144	t3m_01500	COG_category	[G] Carbohydrate transport and metabolism		
2572233144	t3m_01500	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate de		7.00E-54

2572233144	t3m_01500	pfam02800	Gp_dh_C		5.90E-13
2572233144	t3m_01500	pfam00044	Gp_dh_N		1.20E-18
2572233144	t3m_01500	EC:1.2.1.59	Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)(+)) (phosphorylating).		
2572233144	t3m_01500	TIGR01546	glyceraldehyde-3-phosphate dehydrogenase, type II		7.40E-123
2572233144	t3m_01500	KO:K00150	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]		0.00E+00
2572233144	t3m_01500	ITERM:07087	glyceraldehyde 3-phosphate dehydrogenase (NAD(P)+) (EC 1.2.1.59)		
2572233144	t3m_01500	Locus_type		CDS	
2572233144	t3m_01500	Product_name		glyceraldehyde 3-phosphate dehydrogenase (NAD(P)+) (EC 1.2.1.59)	
2572233144	t3m_01500	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233144	t3m_01500	Coordinates		7500..8522(+)	
2572233144	t3m_01500	DNA_length		1023bp	
2572233144	t3m_01500	Protein_length		340aa	
2572233144	t3m_01500	GC		0.67	

2572233145	t3m_01501	pfam08241	Methyltransf_11		3.90E-12
2572233145	t3m_01501	Locus_type		CDS	
2572233145	t3m_01501	Product_name		Methyltransferase domain	
2572233145	t3m_01501	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233145	t3m_01501	Coordinates		8615..9514(+)	
2572233145	t3m_01501	DNA_length		900bp	
2572233145	t3m_01501	Protein_length		299aa	
2572233145	t3m_01501	GC		0.7	

2572233146	t3m_01502	KEGG_module	M00184: RNA polymerase, archaea		
2572233146	t3m_01502	COG_category	[K] Transcription		
2572233146	t3m_01502	COG1095	DNA-directed RNA polymerase, subunit E'		3.00E-57
2572233146	t3m_01502	pfam00575	S1		5.70E-11
2572233146	t3m_01502	pfam03876	SHS2_Rpb7-N		9.40E-14
2572233146	t3m_01502	EC:2.7.7.6	DNA-directed RNA polymerase.		
2572233146	t3m_01502	TIGR00448	DNA-directed RNA polymerase (rpoE), archaeal and eukaryotic form		2.30E-66
2572233146	t3m_01502	KO:K03049	DNA-directed RNA polymerase subunit E' [EC:2.7.7.6]		0.00E+00
2572233146	t3m_01502	Locus_type		CDS	
2572233146	t3m_01502	Product_name		DNA-directed RNA polymerase, subunit E' (EC 2.7.7.6)	
2572233146	t3m_01502	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	

2572233146	t3m_01502	Coordinates		9555..10214(+)		
2572233146	t3m_01502	DNA_length		660bp		
2572233146	t3m_01502	Protein_length		219aa		
2572233146	t3m_01502	GC			0.68	
2572233147	t3m_01503	KEGG_module	M00184: RNA polymerase, archaea			
2572233147	t3m_01503	COG_category	[K] Transcription			
2572233147	t3m_01503	COG2093	DNA-directed RNA polymerase, subunit E''			3.00E-14
2572233147	t3m_01503	pfam06093	Spt4			3.10E-12
2572233147	t3m_01503	EC:2.7.7.6	DNA-directed RNA polymerase.			
2572233147	t3m_01503	KO:K03050	DNA-directed RNA polymerase subunit E" [EC:2.7.7.6]			8.40E-13
2572233147	t3m_01503	Locus_type		CDS		
2572233147	t3m_01503	Product_name		DNA-directed RNA polymerase, subunit E'' (EC 2.7.7.6)		
2572233147	t3m_01503	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233147	t3m_01503	Coordinates		10223..10408(+)		
2572233147	t3m_01503	DNA_length		186bp		
2572233147	t3m_01503	Protein_length		61aa		
2572233147	t3m_01503	GC			0.65	
2572233148	t3m_01504	COG_category	[S] Function unknown			
2572233148	t3m_01504	COG1909	Uncharacterized protein conserved in archaea			6.00E-26
2572233148	t3m_01504	pfam04019	DUF359			1.30E-26
2572233148	t3m_01504	KO:K09735	hypothetical protein			9.40E-16
2572233148	t3m_01504	Locus_type		CDS		
2572233148	t3m_01504	Product_name		Uncharacterized protein conserved in archaea		
2572233148	t3m_01504	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233148	t3m_01504	Coordinates		10455..10931(+)		
2572233148	t3m_01504	DNA_length		477bp		
2572233148	t3m_01504	Protein_length		158aa		
2572233148	t3m_01504	GC			0.67	
2572233149	t3m_01505	KEGG_module	M00177: Ribosome, eukaryotes			
2572233149	t3m_01505	KEGG_module	M00179: Ribosome, archaea			
2572233149	t3m_01505	COG_category	[J] Translation, ribosomal structure and biogenesis			

2572233149	t3m_01505	COG2004	Ribosomal protein S24E			2.00E-17
2572233149	t3m_01505	pfam01282	Ribosomal_S24e			3.70E-20
2572233149	t3m_01505	KO:K02974	small subunit ribosomal protein S24e			1.10E-17
2572233149	t3m_01505	Locus_type		CDS		
2572233149	t3m_01505	Product_name		Ribosomal protein S24E		
2572233149	t3m_01505	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233149	t3m_01505	Coordinates		10921..11310(+)		
2572233149	t3m_01505	DNA_length		390bp		
2572233149	t3m_01505	Protein_length		129aa		
2572233149	t3m_01505	GC			0.73	
2572233150	t3m_01506	KEGG_module	M00177: Ribosome, eukaryotes			
2572233150	t3m_01506	KEGG_module	M00179: Ribosome, archaea			
2572233150	t3m_01506	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233150	t3m_01506	COG1998	Ribosomal protein S27AE			4.00E-12
2572233150	t3m_01506	pfam01599	Ribosomal_S27			2.60E-17
2572233150	t3m_01506	KO:K02977	small subunit ribosomal protein S27Ae			1.90E-12
2572233150	t3m_01506	Locus_type		CDS		
2572233150	t3m_01506	Product_name		Ribosomal protein S27AE		
2572233150	t3m_01506	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233150	t3m_01506	Coordinates		11317..11508(+)		
2572233150	t3m_01506	DNA_length		192bp		
2572233150	t3m_01506	Protein_length		63aa		
2572233150	t3m_01506	GC			0.66	
2572233151	t3m_01507	pfam00535	Glycos_transf_2			2.30E-06
2572233151	t3m_01507	Locus_type		CDS		
2572233151	t3m_01507	Product_name		Glycosyl transferase family 2		
2572233151	t3m_01507	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233151	t3m_01507	Coordinates		11590..12183(-)		
2572233151	t3m_01507	DNA_length		594bp		
2572233151	t3m_01507	Protein_length		197aa		
2572233151	t3m_01507	GC			0.64	

2572233152	t3m_01508	Locus_type		tRNA	
2572233152	t3m_01508	Product_name		tRNA_Arg_CCG	
2572233152	t3m_01508	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233152	t3m_01508	Coordinates		12443..12516(+)	
2572233152	t3m_01508	DNA_length		74bp	
2572233152	t3m_01508	GC		0.66	
2572233153	t3m_01509	COG_category	[S] Function unknown		
2572233153	t3m_01509	COG3388	Uncharacterized protein conserved in archaea		6.00E-14
2572233153	t3m_01509	Locus_type		CDS	
2572233153	t3m_01509	Product_name		Uncharacterized protein conserved in archaea	
2572233153	t3m_01509	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233153	t3m_01509	Coordinates		12602..13000(+)	
2572233153	t3m_01509	DNA_length		399bp	
2572233153	t3m_01509	Protein_length		132aa	
2572233153	t3m_01509	GC		0.64	
2572233154	t3m_01510	Locus_type		tRNA	
2572233154	t3m_01510	Product_name		tRNA_Pseudo_GTT	
2572233154	t3m_01510	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233154	t3m_01510	Coordinates		13027..13096(+)	
2572233154	t3m_01510	DNA_length		70bp	
2572233154	t3m_01510	GC		0.64	
2572233155	t3m_01511	Locus_type		tRNA	
2572233155	t3m_01511	Product_name		tRNA_Met_CAT	
2572233155	t3m_01511	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40	
2572233155	t3m_01511	Coordinates		13150..13225(+)	
2572233155	t3m_01511	DNA_length		76bp	
2572233155	t3m_01511	GC		0.66	
2572233156	t3m_01512	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233156	t3m_01512	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins		3.00E-05
2572233156	t3m_01512	pfam00583	Acetyltransf_1		4.30E-09

2572233156	t3m_01512	Locus_type		CDS		
2572233156	t3m_01512	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins		
2572233156	t3m_01512	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233156	t3m_01512	Coordinates		13259..13828(+)		
2572233156	t3m_01512	DNA_length		570bp		
2572233156	t3m_01512	Protein_length		189aa		
2572233156	t3m_01512	GC			0.66	

2572233157	t3m_01513	pfam01521	Fe-S_biosyn			1.30E-05
2572233157	t3m_01513	Locus_type		CDS		
2572233157	t3m_01513	Product_name		Iron-sulphur cluster biosynthesis		
2572233157	t3m_01513	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233157	t3m_01513	Coordinates		13825..14061(-)		
2572233157	t3m_01513	DNA_length		237bp		
2572233157	t3m_01513	Protein_length		78aa		
2572233157	t3m_01513	GC			0.68	

2572233158	t3m_01514	COG_category	[S] Function unknown			
2572233158	t3m_01514	COG0316	Uncharacterized conserved protein			2.00E-31
2572233158	t3m_01514	pfam01521	Fe-S_biosyn			1.70E-17
2572233158	t3m_01514	TIGR00049	Iron-sulfur cluster assembly accessory protein			1.00E-37
2572233158	t3m_01514	KO:K13628	iron-sulfur cluster assembly protein			6.50E-24
2572233158	t3m_01514	Locus_type		CDS		
2572233158	t3m_01514	Product_name		Iron-sulfur cluster assembly accessory protein		
2572233158	t3m_01514	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40		
2572233158	t3m_01514	Coordinates		14357..14686(-)		
2572233158	t3m_01514	DNA_length		330bp		
2572233158	t3m_01514	Protein_length		109aa		
2572233158	t3m_01514	GC			0.67	

2572233159	t3m_01515	COG_category	[R] General function prediction only			
2572233159	t3m_01515	COG0121	Predicted glutamine amidotransferase			7.00E-10
2572233159	t3m_01515	pfam13230	GATase_4			2.00E-09
2572233159	t3m_01515	Locus_type		CDS		

2572233159	t3m_01515	Product_name		Predicted glutamine amidotransferase
2572233159	t3m_01515	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40
2572233159	t3m_01515	Coordinates		14821..15666(+)
2572233159	t3m_01515	DNA_length		846bp
2572233159	t3m_01515	Protein_length		281aa
2572233159	t3m_01515	GC		0.66
2572233160	t3m_01516	Locus_type		CDS
2572233160	t3m_01516	Product_name		hypothetical protein
2572233160	t3m_01516	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40
2572233160	t3m_01516	Coordinates		15708..16619(+)
2572233160	t3m_01516	DNA_length		912bp
2572233160	t3m_01516	Protein_length		303aa
2572233160	t3m_01516	GC		0.72
2572233161	t3m_01517	Locus_type		CDS
2572233161	t3m_01517	Product_name		hypothetical protein
2572233161	t3m_01517	Scaffold		t3m_contig_70_392_len_17666_read_count_1526455.40
2572233161	t3m_01517	Coordinates		16689..17495(+)
2572233161	t3m_01517	DNA_length		807bp
2572233161	t3m_01517	Protein_length		268aa
2572233161	t3m_01517	GC		0.7
2572233162	t3m_01518	Locus_type		CDS
2572233162	t3m_01518	Product_name		hypothetical protein
2572233162	t3m_01518	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41
2572233162	t3m_01518	Coordinates		2..739(-)
2572233162	t3m_01518	DNA_length		738bp
2572233162	t3m_01518	Protein_length		246aa
2572233162	t3m_01518	GC		0.7
2572233163	t3m_01519	KEGG_module	M00135: GABA biosynthesis, eukaryotes, putrescine => GABA	
2572233163	t3m_01519	Metacyc	PWY-6054: dimethylsulfoniopropionate biosynthesis I (Wollastonia)	
2572233163	t3m_01519	Metacyc	PWY-2501: fatty acid α-oxidation I	

2572233163	t3m_01519	Metacyc	PWY-6313: serotonin degradation			
2572233163	t3m_01519	Metacyc	PWY6666-2: dopamine degradation			
2572233163	t3m_01519	Metacyc	P221-PWY: octane oxidation			
2572233163	t3m_01519	Metacyc	PWY-6055: dimethylsulfoniopropionate biosynthesis II (Spartina)			
2572233163	t3m_01519	Metacyc	PWY-2221: Entner-Doudoroff pathway III (semi-phosphorylative)			
2572233163	t3m_01519	Metacyc	PWY-6575: juvenile hormone III biosynthesis I			
2572233163	t3m_01519	Metacyc	PWY-6650: juvenile hormone III biosynthesis II			
2572233163	t3m_01519	Metacyc	PWY66-387: fatty acid α-oxidation II			
2572233163	t3m_01519	Metacyc	PWY-6307: tryptophan degradation X (mammalian, via tryptamine)			
2572233163	t3m_01519	Metacyc	PWY-6181: histamine degradation			
2572233163	t3m_01519	Metacyc	PWY66-388: fatty acid α-oxidation III			
2572233163	t3m_01519	Metacyc	PWY66-161: oxidative ethanol degradation III			
2572233163	t3m_01519	Metacyc	PWY-2724: alkane oxidation			
2572233163	t3m_01519	Metacyc	PWY66-21: ethanol degradation II			
2572233163	t3m_01519	Metacyc	PWY66-162: ethanol degradation IV			
2572233163	t3m_01519	Metacyc	PWY-0: putrescine degradation III			
2572233163	t3m_01519	Metacyc	PWY66-389: phytol degradation			
2572233163	t3m_01519	Metacyc	PWY-6342: noradrenaline and adrenaline degradation			
2572233163	t3m_01519	COG_category	[C] Energy production and conversion			
2572233163	t3m_01519	COG1012	NAD-dependent aldehyde dehydrogenases			0.00E+00
2572233163	t3m_01519	pfam00171	Aldedh			0.00E+00
2572233163	t3m_01519	EC:1.2.1.3	Aldehyde dehydrogenase (NAD(+)).			
2572233163	t3m_01519	KO:K00128	aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]			0.00E+00
2572233163	t3m_01519	Locus_type		CDS		
2572233163	t3m_01519	Product_name		NAD-dependent aldehyde dehydrogenases		
2572233163	t3m_01519	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233163	t3m_01519	Coordinates		878..2374(+)		
2572233163	t3m_01519	DNA_length		1497bp		
2572233163	t3m_01519	Protein_length		498aa		
2572233163	t3m_01519	GC			0.67	

2572233164	t3m_01520	Locus_type		CDS		
2572233164	t3m_01520	Product_name		hypothetical protein		
2572233164	t3m_01520	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		

2572233164	t3m_01520	Coordinates		2371..2592(+)		
2572233164	t3m_01520	DNA_length		222bp		
2572233164	t3m_01520	Protein_length		73aa		
2572233164	t3m_01520	GC			0.72	

2572233165	t3m_01521	IMG_pathway	436: Archaeal replication initiation			
2572233165	t3m_01521	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233165	t3m_01521	COG_category	[L] Replication, recombination and repair			
2572233165	t3m_01521	COG1474	Cdc6-related protein, AAA superfamily ATPase			7.00E-81
2572233165	t3m_01521	pfam13191	AAA_16			1.30E-12
2572233165	t3m_01521	pfam09079	Cdc6_C			1.70E-20
2572233165	t3m_01521	TIGR02928	orc1/cdc6 family replication initiation protein			4.30E-122
2572233165	t3m_01521	KO:K10725	archaeal cell division control protein 6			0.00E+00
2572233165	t3m_01521	ITERM:00091	ORC complex protein Cdc6/Orc1			
2572233165	t3m_01521	Locus_type		CDS		
2572233165	t3m_01521	Product_name		ORC complex protein Cdc6/Orc1		
2572233165	t3m_01521	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233165	t3m_01521	Coordinates		2664..3974(-)		
2572233165	t3m_01521	DNA_length		1311bp		
2572233165	t3m_01521	Protein_length		436aa		
2572233165	t3m_01521	GC			0.67	

2572233166	t3m_01522	Locus_type		CDS		
2572233166	t3m_01522	Product_name		hypothetical protein		
2572233166	t3m_01522	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233166	t3m_01522	Coordinates		3928..4422(+)		
2572233166	t3m_01522	DNA_length		495bp		
2572233166	t3m_01522	Protein_length		164aa		
2572233166	t3m_01522	GC			0.69	

2572233167	t3m_01523	Metacyc	PWY-6174: mevalonate pathway II (archaea)			
2572233167	t3m_01523	COG_category	[R] General function prediction only			
2572233167	t3m_01523	COG1608	Predicted archaeal kinase			9.00E-42
2572233167	t3m_01523	pfam00696	AA_kinase			1.00E-27

2572233167	t3m_01523	EC:2.7.4.26	Isopentenyl phosphate kinase.		
2572233167	t3m_01523	KO:K06981	isopentenyl phosphate kinase [EC:2.7.4.26]		3.80E-31
2572233167	t3m_01523	Locus_type		CDS	
2572233167	t3m_01523	Product_name		Predicted archaeal kinase	
2572233167	t3m_01523	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41	
2572233167	t3m_01523	Coordinates		4391..5257(+)	
2572233167	t3m_01523	DNA_length		867bp	
2572233167	t3m_01523	Protein_length		288aa	
2572233167	t3m_01523	GC		0.71	

2572233168	t3m_01524	KEGG_module	M00364: C10-C20 isoprenoid biosynthesis, bacteria		
2572233168	t3m_01524	KEGG_module	M00096: C5 isoprenoid biosynthesis, non-mevalonate pathway		
2572233168	t3m_01524	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway		
2572233168	t3m_01524	KEGG_module	M00365: C10-C20 isoprenoid biosynthesis, archaea		
2572233168	t3m_01524	KEGG_module	M00367: C10-C20 isoprenoid biosynthesis, non-plant eukaryotes		
2572233168	t3m_01524	KEGG_module	M00366: C10-C20 isoprenoid biosynthesis, plants		
2572233168	t3m_01524	Metacyc	PWY-6174: mevalonate pathway II (archaea)		
2572233168	t3m_01524	Metacyc	PWY-7102: bisabolene biosynthesis		
2572233168	t3m_01524	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis		
2572233168	t3m_01524	Metacyc	NONMEVIPP-PWY: methylerythritol phosphate pathway		
2572233168	t3m_01524	Metacyc	PWY-5123: <i>trans, trans</i>-farnesyl diphosphate biosynthesis		
2572233168	t3m_01524	Metacyc	PWY-922: mevalonate pathway I		
2572233168	t3m_01524	Metacyc	PWY-6859: <i>all-trans</i>-farnesol biosynthesis		
2572233168	t3m_01524	IMG_pathway	365: dimetyhylallyl pyrophosphate biosynthesis via isomerization of isopentenyl diphosphate		
2572233168	t3m_01524	COG_category	[C] Energy production and conversion		
2572233168	t3m_01524	COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy a		2.00E-65
2572233168	t3m_01524	pfam01070	FMN_dh		6.30E-09
2572233168	t3m_01524	pfam01070	FMN_dh		9.90E-18
2572233168	t3m_01524	EC:5.3.3.2	Isopentenyl-diphosphate Delta-isomerase.		
2572233168	t3m_01524	TIGR02151	isopentenyl-diphosphate delta-isomerase, type 2		4.70E-114
2572233168	t3m_01524	KO:K01823	isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]		0.00E+00
2572233168	t3m_01524	ITERM:00469	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)		
2572233168	t3m_01524	Locus_type		CDS	
2572233168	t3m_01524	Product_name		isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)	

2572233168	t3m_01524	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233168	t3m_01524	Coordinates		5241..6332(+)		
2572233168	t3m_01524	DNA_length		1092bp		
2572233168	t3m_01524	Protein_length		363aa		
2572233168	t3m_01524	GC			0.69	

2572233169	t3m_01525	COG_category	[K] Transcription			
2572233169	t3m_01525	COG_category	[B] Chromatin structure and dynamics			
2572233169	t3m_01525	COG1243	Histone acetyltransferase			0.00E+00
2572233169	t3m_01525	pfam00583	Acetyltransf_1			7.30E-09
2572233169	t3m_01525	pfam04055	Radical_SAM			1.00E-14
2572233169	t3m_01525	EC:2.3.1.48	Histone acetyltransferase.			
2572233169	t3m_01525	TIGR01211	histone acetyltransferase, ELP3 family			0.00E+00
2572233169	t3m_01525	KO:K07739	elongator complex protein 3 [EC:2.3.1.48]			0.00E+00
2572233169	t3m_01525	Locus_type		CDS		
2572233169	t3m_01525	Product_name		histone acetyltransferase, ELP3 family		
2572233169	t3m_01525	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233169	t3m_01525	Coordinates		6317..7864(+)		
2572233169	t3m_01525	DNA_length		1548bp		
2572233169	t3m_01525	Protein_length		515aa		
2572233169	t3m_01525	GC			0.69	

2572233170	t3m_01526	KEGG_module	M00034: Methionine salvage pathway			
2572233170	t3m_01526	KEGG_module	M00368: Ethylene biosynthesis, methionine => ethylene			
2572233170	t3m_01526	KEGG_module	M00035: Methionine degradation			
2572233170	t3m_01526	Metacyc	PWY-5912: 2'-deoxymugineic acid phytosiderophore biosynthesis			
2572233170	t3m_01526	Metacyc	PWY-5041: <i>S</i>-adenosyl-L-methionine cycle II			
2572233170	t3m_01526	Metacyc	METHIONINE-DEG1-PWY: methionine degradation I (to homocysteine)			
2572233170	t3m_01526	Metacyc	ETHYL-PWY: ethylene biosynthesis I (plants)			
2572233170	t3m_01526	Metacyc	SAM-PWY: S-adenosyl-L-methionine biosynthesis			
2572233170	t3m_01526	COG_category	[E] Amino acid transport and metabolism			
2572233170	t3m_01526	COG1812	Archaeal S-adenosylmethionine synthetase			0.00E+00
2572233170	t3m_01526	pfam01941	AdoMet_Synthase			0.00E+00
2572233170	t3m_01526	EC:2.5.1.6	Methionine adenosyltransferase.			

2572233170	t3m_01526	KO:K00789	S-adenosylmethionine synthetase [EC:2.5.1.6]		0.00E+00
2572233170	t3m_01526	Locus_type		CDS	
2572233170	t3m_01526	Product_name		methionine adenosyltransferase (EC 2.5.1.6)	
2572233170	t3m_01526	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41	
2572233170	t3m_01526	Coordinates		7948..9144(+)	
2572233170	t3m_01526	DNA_length		1197bp	
2572233170	t3m_01526	Protein_length		398aa	
2572233170	t3m_01526	GC		0.65	
2572233171	t3m_01527	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233171	t3m_01527	COG0621	2-methylthioadenine synthetase		9.00E-91
2572233171	t3m_01527	pfam04055	Radical_SAM		3.20E-22
2572233171	t3m_01527	pfam00919	UPF0004		1.30E-11
2572233171	t3m_01527	TIGR00089	radical SAM methylthiotransferase, MiaB/RimO family		5.70E-91
2572233171	t3m_01527	TIGR01578	MiaB-like tRNA modifying enzyme, archaeal-type		3.00E-104
2572233171	t3m_01527	Locus_type		CDS	
2572233171	t3m_01527	Product_name		MiaB-like tRNA modifying enzyme, archaeal-type	
2572233171	t3m_01527	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41	
2572233171	t3m_01527	Coordinates		9170..10438(+)	
2572233171	t3m_01527	DNA_length		1269bp	
2572233171	t3m_01527	Protein_length		422aa	
2572233171	t3m_01527	GC		0.7	
2572233172	t3m_01528	pfam12773	DZR		2.20E-06
2572233172	t3m_01528	Locus_type		CDS	
2572233172	t3m_01528	Product_name		Double zinc ribbon	
2572233172	t3m_01528	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41	
2572233172	t3m_01528	Coordinates		10518..11465(+)	
2572233172	t3m_01528	DNA_length		948bp	
2572233172	t3m_01528	Protein_length		315aa	
2572233172	t3m_01528	GC		0.72	
2572233172	t3m_01528	Transmembrane		Yes	
2572233173	t3m_01529	COG_category	[S] Function unknown		

2572233173	t3m_01529	COG1602	Uncharacterized conserved protein			1.00E-106
2572233173	t3m_01529	pfam04894	DUF650			4.80E-86
2572233173	t3m_01529	pfam04895	DUF651			1.10E-32
2572233173	t3m_01529	Locus_type		CDS		
2572233173	t3m_01529	Product_name		Uncharacterized conserved protein		
2572233173	t3m_01529	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233173	t3m_01529	Coordinates		11478..12806(-)		
2572233173	t3m_01529	DNA_length		1329bp		
2572233173	t3m_01529	Protein_length		442aa		
2572233173	t3m_01529	GC			0.67	
2572233174	t3m_01530	Locus_type		tRNA		
2572233174	t3m_01530	Product_name		tRNA_Pro_CGG		
2572233174	t3m_01530	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233174	t3m_01530	Coordinates		12933..13007(+)		
2572233174	t3m_01530	DNA_length		75bp		
2572233174	t3m_01530	GC			0.63	
2572233175	t3m_01531	COG_category	[R] General function prediction only			
2572233175	t3m_01531	COG0491	Zn-dependent hydrolases, including glyoxylases			1.00E-15
2572233175	t3m_01531	pfam00753	Lactamase_B			1.70E-26
2572233175	t3m_01531	Locus_type		CDS		
2572233175	t3m_01531	Product_name		Zn-dependent hydrolases, including glyoxylases		
2572233175	t3m_01531	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233175	t3m_01531	Coordinates		13058..13726(-)		
2572233175	t3m_01531	DNA_length		669bp		
2572233175	t3m_01531	Protein_length		222aa		
2572233175	t3m_01531	GC			0.65	
2572233176	t3m_01532	COG_category	[C] Energy production and conversion			
2572233176	t3m_01532	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopte			4.00E-30
2572233176	t3m_01532	pfam00296	Bac_luciferase			7.00E-54
2572233176	t3m_01532	Locus_type		CDS		
2572233176	t3m_01532	Product_name		Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopteri		

2572233176	t3m_01532	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41	
2572233176	t3m_01532	Coordinates		13759..14766(-)	
2572233176	t3m_01532	DNA_length		1008bp	
2572233176	t3m_01532	Protein_length		335aa	
2572233176	t3m_01532	GC		0.69	
2572233177	t3m_01533	COG_category	[F] Nucleotide transport and metabolism		
2572233177	t3m_01533	COG1051	ADP-ribose pyrophosphatase		5.00E-04
2572233177	t3m_01533	pfam00293	NUDIX		6.40E-13
2572233177	t3m_01533	Locus_type		CDS	
2572233177	t3m_01533	Product_name		ADP-ribose pyrophosphatase	
2572233177	t3m_01533	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41	
2572233177	t3m_01533	Coordinates		14798..15574(+)	
2572233177	t3m_01533	DNA_length		777bp	
2572233177	t3m_01533	Protein_length		258aa	
2572233177	t3m_01533	GC		0.68	
2572233178	t3m_01534	Locus_type		tRNA	
2572233178	t3m_01534	Product_name		tRNA_Ala_TGC	
2572233178	t3m_01534	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41	
2572233178	t3m_01534	Coordinates		15604..15677(+)	
2572233178	t3m_01534	DNA_length		74bp	
2572233178	t3m_01534	GC		0.59	
2572233179	t3m_01535	KEGG_module	M00239: Peptides/nickel transport system		
2572233179	t3m_01535	COG_category	[P] Inorganic ion transport and metabolism		
2572233179	t3m_01535	COG_category	[E] Amino acid transport and metabolism		
2572233179	t3m_01535	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease c		4.00E-26
2572233179	t3m_01535	pfam00528	BPD_transp_1		1.00E-15
2572233179	t3m_01535	KO:K02034	peptide/nickel transport system permease protein		8.20E-23
2572233179	t3m_01535	Locus_type		CDS	
2572233179	t3m_01535	Product_name		ABC-type dipeptide/oligopeptide/nickel transport systems, permease co	
2572233179	t3m_01535	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41	
2572233179	t3m_01535	Coordinates		15765..16691(-)	

2572233179	t3m_01535	DNA_length		927bp		
2572233179	t3m_01535	Protein_length		308aa		
2572233179	t3m_01535	GC			0.67	
2572233179	t3m_01535	Signal_peptide		Yes		
2572233179	t3m_01535	Transmembrane		Yes		
2572233180	t3m_01536	pfam00528	BPD_transp_1			7.90E-12
2572233180	t3m_01536	Locus_type		CDS		
2572233180	t3m_01536	Product_name		Binding-protein-dependent transport system inner membrane compone		
2572233180	t3m_01536	Scaffold		t3m_contig_70_406_len_17358_read_count_1362750.41		
2572233180	t3m_01536	Coordinates		16805..17356(-)		
2572233180	t3m_01536	DNA_length		552bp		
2572233180	t3m_01536	Protein_length		183aa		
2572233180	t3m_01536	GC			0.65	
2572233180	t3m_01536	Transmembrane		Yes		
2572233181	t3m_01537	pfam00118	Cpn60_TCP1			8.70E-70
2572233181	t3m_01537	Locus_type		CDS		
2572233181	t3m_01537	Product_name		TCP-1/cpn60 chaperonin family		
2572233181	t3m_01537	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233181	t3m_01537	Coordinates		3..788(-)		
2572233181	t3m_01537	DNA_length		786bp		
2572233181	t3m_01537	Protein_length		262aa		
2572233181	t3m_01537	GC			0.64	
2572233182	t3m_01538	COG_category	[R] General function prediction only			
2572233182	t3m_01538	COG5006	Predicted permease, DMT superfamily			8.00E-10
2572233182	t3m_01538	pfam00892	EamA			3.70E-13
2572233182	t3m_01538	Locus_type		CDS		
2572233182	t3m_01538	Product_name		Predicted permease, DMT superfamily		
2572233182	t3m_01538	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233182	t3m_01538	Coordinates		970..1890(+)		
2572233182	t3m_01538	DNA_length		921bp		
2572233182	t3m_01538	Protein_length		306aa		

2572233182	t3m_01538	GC			0.69	
2572233182	t3m_01538	Transmembrane		Yes		
2572233183	t3m_01539	pfam00583	Acetyltransf_1			1.40E-14
2572233183	t3m_01539	Locus_type		CDS		
2572233183	t3m_01539	Product_name		Acetyltransferase (GNAT) family		
2572233183	t3m_01539	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233183	t3m_01539	Coordinates		1957..2919(+)		
2572233183	t3m_01539	DNA_length		963bp		
2572233183	t3m_01539	Protein_length		320aa		
2572233183	t3m_01539	GC			0.69	
2572233184	t3m_01540	Locus_type		CDS		
2572233184	t3m_01540	Product_name		hypothetical protein		
2572233184	t3m_01540	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233184	t3m_01540	Coordinates		2966..3496(-)		
2572233184	t3m_01540	DNA_length		531bp		
2572233184	t3m_01540	Protein_length		176aa		
2572233184	t3m_01540	GC			0.67	
2572233185	t3m_01541	COG_category	[R] General function prediction only			
2572233185	t3m_01541	COG4122	Predicted O-methyltransferase			5.00E-42
2572233185	t3m_01541	pfam01596	Methyltransf_3			1.40E-46
2572233185	t3m_01541	Locus_type		CDS		
2572233185	t3m_01541	Product_name		Predicted O-methyltransferase		
2572233185	t3m_01541	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233185	t3m_01541	Coordinates		3497..4177(-)		
2572233185	t3m_01541	DNA_length		681bp		
2572233185	t3m_01541	Protein_length		226aa		
2572233185	t3m_01541	GC			0.69	
2572233186	t3m_01542	pfam13249	Prenyltrans_2			2.50E-09
2572233186	t3m_01542	Locus_type		CDS		
2572233186	t3m_01542	Product_name		Prenyltransferase-like		

2572233186	t3m_01542	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42	
2572233186	t3m_01542	Coordinates		4174..5199(-)	
2572233186	t3m_01542	DNA_length		1026bp	
2572233186	t3m_01542	Protein_length		341aa	
2572233186	t3m_01542	GC		0.68	
2572233187	t3m_01543	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233187	t3m_01543	COG0030	Dimethyladenosine transferase (rRNA methylation)		2.00E-55
2572233187	t3m_01543	pfam00398	RrnaAD		1.40E-43
2572233187	t3m_01543	EC:2.1.1.182	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase.		
2572233187	t3m_01543	TIGR00755	dimethyladenosine transferase		1.80E-64
2572233187	t3m_01543	KO:K02528	16S rRNA (adenine1518-N6/adenine1519-N6)-dimethyltransferase [EC:		2.80E-39
2572233187	t3m_01543	ITERM:02532	dimethyladenosine transferase (EC 2.1.1.-)		
2572233187	t3m_01543	Locus_type		CDS	
2572233187	t3m_01543	Product_name		dimethyladenosine transferase (EC 2.1.1.-)	
2572233187	t3m_01543	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42	
2572233187	t3m_01543	Coordinates		5310..6149(-)	
2572233187	t3m_01543	DNA_length		840bp	
2572233187	t3m_01543	Protein_length		279aa	
2572233187	t3m_01543	GC		0.71	
2572233188	t3m_01544	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233188	t3m_01544	COG1491	Predicted RNA-binding protein		4.00E-47
2572233188	t3m_01544	pfam04919	DUF655		9.60E-55
2572233188	t3m_01544	KO:K07572	putative nucleotide binding protein		4.20E-45
2572233188	t3m_01544	Locus_type		CDS	
2572233188	t3m_01544	Product_name		Predicted RNA-binding protein	
2572233188	t3m_01544	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42	
2572233188	t3m_01544	Coordinates		6178..6723(-)	
2572233188	t3m_01544	DNA_length		546bp	
2572233188	t3m_01544	Protein_length		181aa	
2572233188	t3m_01544	GC		0.68	
2572233189	t3m_01545	KEGG_module	M00184: RNA polymerase, archaea		

2572233189	t3m_01545	COG_category	[S] Function unknown			
2572233189	t3m_01545	COG1460	Uncharacterized protein conserved in archaea			3.00E-13
2572233189	t3m_01545	pfam03874	RNA_pol_Rpb4			7.60E-07
2572233189	t3m_01545	EC:2.7.7.6	DNA-directed RNA polymerase.			
2572233189	t3m_01545	KO:K03051	DNA-directed RNA polymerase subunit F [EC:2.7.7.6]			1.50E-17
2572233189	t3m_01545	ITERM:01967	DNA-directed RNA polymerase, subunit F (EC 2.7.7.6)			
2572233189	t3m_01545	Locus_type		CDS		
2572233189	t3m_01545	Product_name		DNA-directed RNA polymerase, subunit F (EC 2.7.7.6)		
2572233189	t3m_01545	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233189	t3m_01545	Coordinates		6740..7054(-)		
2572233189	t3m_01545	DNA_length		315bp		
2572233189	t3m_01545	Protein_length		104aa		
2572233189	t3m_01545	GC			0.69	

2572233190	t3m_01546	KEGG_module	M00179: Ribosome, archaea			
2572233190	t3m_01546	KEGG_module	M00177: Ribosome, eukaryotes			
2572233190	t3m_01546	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233190	t3m_01546	COG2139	Ribosomal protein L21E			2.00E-24
2572233190	t3m_01546	pfam01157	Ribosomal_L21e			1.10E-21
2572233190	t3m_01546	KO:K02889	large subunit ribosomal protein L21e			3.10E-20
2572233190	t3m_01546	Locus_type		CDS		
2572233190	t3m_01546	Product_name		Ribosomal protein L21E		
2572233190	t3m_01546	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233190	t3m_01546	Coordinates		7047..7358(-)		
2572233190	t3m_01546	DNA_length		312bp		
2572233190	t3m_01546	Protein_length		103aa		
2572233190	t3m_01546	GC			0.7	

2572233191	t3m_01547	Metacyc	RIBOKIN-PWY: ribose degradation			
2572233191	t3m_01547	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233191	t3m_01547	COG1258	Predicted pseudouridylate synthase			1.00E-93
2572233191	t3m_01547	EC:5.4.99.-	Isomerases. Intramolecular transferases (mutases). Transferring other groups.			
2572233191	t3m_01547	TIGR01213	tRNA pseudouridine(54/55) synthase			1.90E-113
2572233191	t3m_01547	KO:K07583	tRNA pseudouridine synthase 10 [EC:5.4.99.-]			0.00E+00

2572233191	t3m_01547	Locus_type		CDS		
2572233191	t3m_01547	Product_name		tRNA pseudouridine(54/55) synthase		
2572233191	t3m_01547	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233191	t3m_01547	Coordinates		7363..8598(-)		
2572233191	t3m_01547	DNA_length		1236bp		
2572233191	t3m_01547	Protein_length		411aa		
2572233191	t3m_01547	GC			0.69	

2572233192	t3m_01548	Locus_type		CDS		
2572233192	t3m_01548	Product_name		hypothetical protein		
2572233192	t3m_01548	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233192	t3m_01548	Coordinates		8697..9098(+)		
2572233192	t3m_01548	DNA_length		402bp		
2572233192	t3m_01548	Protein_length		133aa		
2572233192	t3m_01548	GC			0.7	

2572233193	t3m_01549	pfam13367	PrsW-protease			1.00E-25
2572233193	t3m_01549	Locus_type		CDS		
2572233193	t3m_01549	Product_name		Protease prsW family		
2572233193	t3m_01549	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233193	t3m_01549	Coordinates		9111..9956(-)		
2572233193	t3m_01549	DNA_length		846bp		
2572233193	t3m_01549	Protein_length		281aa		
2572233193	t3m_01549	GC			0.69	
2572233193	t3m_01549	Transmembrane		Yes		

2572233194	t3m_01550	COG_category	[I] Lipid transport and metabolism			
2572233194	t3m_01550	COG1250	3-hydroxyacyl-CoA dehydrogenase			5.00E-86
2572233194	t3m_01550	pfam00725	3HCDH			3.30E-31
2572233194	t3m_01550	pfam02737	3HCDH_N			1.10E-57
2572233194	t3m_01550	EC:1.1.1.157	3-hydroxybutyryl-CoA dehydrogenase.			
2572233194	t3m_01550	KO:K00074	3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]			0.00E+00
2572233194	t3m_01550	Locus_type		CDS		
2572233194	t3m_01550	Product_name		3-hydroxyacyl-CoA dehydrogenase		

2572233194	t3m_01550	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233194	t3m_01550	Coordinates		9953..10870(-)		
2572233194	t3m_01550	DNA_length		918bp		
2572233194	t3m_01550	Protein_length		305aa		
2572233194	t3m_01550	GC			0.69	

2572233195	t3m_01551	COG_category	[D] Cell cycle control, cell division, chromosome partitioning			
2572233195	t3m_01551	COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle cor			8.00E-44
2572233195	t3m_01551	pfam01171	ATP_bind_3			1.30E-10
2572233195	t3m_01551	TIGR00269	TIGR00269 family protein			8.00E-28
2572233195	t3m_01551	Locus_type		CDS		
2572233195	t3m_01551	Product_name		TIGR00269 family protein		
2572233195	t3m_01551	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233195	t3m_01551	Coordinates		10867..11805(-)		
2572233195	t3m_01551	DNA_length		939bp		
2572233195	t3m_01551	Protein_length		312aa		
2572233195	t3m_01551	GC			0.71	

2572233196	t3m_01552	COG_category	[L] Replication, recombination and repair			
2572233196	t3m_01552	COG4974	Site-specific recombinase XerD			2.00E-48
2572233196	t3m_01552	pfam00589	Phage_integrase			9.90E-41
2572233196	t3m_01552	pfam13495	Phage_int_SAM_4			1.00E-09
2572233196	t3m_01552	KO:K04763	integrase/recombinase XerD			0.00E+00
2572233196	t3m_01552	Locus_type		CDS		
2572233196	t3m_01552	Product_name		Site-specific recombinase XerD		
2572233196	t3m_01552	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233196	t3m_01552	Coordinates		11906..12817(+)		
2572233196	t3m_01552	DNA_length		912bp		
2572233196	t3m_01552	Protein_length		303aa		
2572233196	t3m_01552	GC			0.67	

2572233197	t3m_01553	Metacyc	CRNFORCAT-PWY: creatinine degradation I			
2572233197	t3m_01553	Metacyc	PWY-3661: glycine betaine degradation			
2572233197	t3m_01553	Metacyc	PWY-4722: creatinine degradation II			

2572233197	t3m_01553	COG_category	[E] Amino acid transport and metabolism			
2572233197	t3m_01553	COG0665	Glycine/D-amino acid oxidases (deaminating)			3.00E-39
2572233197	t3m_01553	pfam01266	DAO			3.90E-69
2572233197	t3m_01553	EC:1.5.3.1	Sarcosine oxidase.			
2572233197	t3m_01553	KO:K00303	sarcosine oxidase, subunit beta [EC:1.5.3.1]			0.00E+00
2572233197	t3m_01553	Locus_type		CDS		
2572233197	t3m_01553	Product_name		Glycine/D-amino acid oxidases (deaminating)		
2572233197	t3m_01553	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233197	t3m_01553	Coordinates		12841..14040(+)		
2572233197	t3m_01553	DNA_length		1200bp		
2572233197	t3m_01553	Protein_length		399aa		
2572233197	t3m_01553	GC			0.72	
2572233198	t3m_01554	Metacyc	PWY-1622: formaldehyde assimilation I (serine pathway)			
2572233198	t3m_01554	IMG_pathway	358: Conversion of glyceraldehyde to pyruvate			
2572233198	t3m_01554	IMG_pathway	569: 5-dehydro-4-deoxy-D-glucarate conversion to pyruvate and 2-phosphoglycerate			
2572233198	t3m_01554	IMG_pathway	959: Serine cycle			
2572233198	t3m_01554	COG_category	[G] Carbohydrate transport and metabolism			
2572233198	t3m_01554	COG2379	Putative glycerate kinase			9.00E-81
2572233198	t3m_01554	pfam13660	DUF4147			7.30E-72
2572233198	t3m_01554	pfam05161	MOFRL			8.40E-26
2572233198	t3m_01554	EC:1.1.1.81	Hydroxypyruvate reductase.			
2572233198	t3m_01554	KO:K00050	hydroxypyruvate reductase [EC:1.1.1.81]			0.00E+00
2572233198	t3m_01554	ITERM:01510	glycerate 2-kinase (EC 2.7.1.165)			
2572233198	t3m_01554	Locus_type		CDS		
2572233198	t3m_01554	Product_name		glycerate 2-kinase (EC 2.7.1.165)		
2572233198	t3m_01554	Scaffold		t3m_contig_70_492_len_15272_read_count_1289910.42		
2572233198	t3m_01554	Coordinates		14024..15271(+)		
2572233198	t3m_01554	DNA_length		1248bp		
2572233198	t3m_01554	Protein_length		416aa		
2572233198	t3m_01554	GC			0.72	
2572233199	t3m_01555	Locus_type		tRNA		
2572233199	t3m_01555	Product_name		tRNA_Gln_TTG		

2572233199	t3m_01555	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233199	t3m_01555	Coordinates		1..62(-)	
2572233199	t3m_01555	DNA_length		62bp	
2572233199	t3m_01555	GC		0.65	
2572233200	t3m_01556	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP		
2572233200	t3m_01556	KEGG_module	M00002: Glycolysis, core module involving three-carbon compounds		
2572233200	t3m_01556	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate		
2572233200	t3m_01556	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP		
2572233200	t3m_01556	Metacyc	GLYCOLYSIS: glycolysis I		
2572233200	t3m_01556	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)		
2572233200	t3m_01556	Metacyc	PWY-1042: glycolysis IV (plant cytosol)		
2572233200	t3m_01556	Metacyc	PWY-6901: xylose degradation IV		
2572233200	t3m_01556	Metacyc	PWY-2221: Entner-Doudoroff pathway III (semi-phosphorylative)		
2572233200	t3m_01556	Metacyc	P122-PWY: heterolactic fermentation		
2572233200	t3m_01556	Metacyc	FERMENTATION-PWY: mixed acid fermentation		
2572233200	t3m_01556	Metacyc	PWY-6886: 1-butanol autotrophic biosynthesis		
2572233200	t3m_01556	Metacyc	PWY-5723: Rubisco shunt		
2572233200	t3m_01556	Metacyc	P341-PWY: glycolysis V (Pyrococcus)		
2572233200	t3m_01556	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2572233200	t3m_01556	Metacyc	PWY-5484: glycolysis II (from fructose-6P)		
2572233200	t3m_01556	Metacyc	PWY-7003: glycerol degradation to butanol		
2572233200	t3m_01556	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)		
2572233200	t3m_01556	Metacyc	ANARESP1-PWY: respiration (anaerobic)		
2572233200	t3m_01556	Metacyc	P124-PWY: Bifidobacterium shunt		
2572233200	t3m_01556	COG_category	[G] Carbohydrate transport and metabolism		
2572233200	t3m_01556	COG0469	Pyruvate kinase		7.00E-125
2572233200	t3m_01556	pfam02887	PK_C		2.10E-20
2572233200	t3m_01556	pfam00224	PK		4.20E-99
2572233200	t3m_01556	EC:2.7.1.40	Pyruvate kinase.		
2572233200	t3m_01556	TIGR01064	pyruvate kinase		0.00E+00
2572233200	t3m_01556	KO:K00873	pyruvate kinase [EC:2.7.1.40]		0.00E+00
2572233200	t3m_01556	Locus_type		CDS	
2572233200	t3m_01556	Product_name		pyruvate kinase	

2572233200	t3m_01556	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233200	t3m_01556	Coordinates		160..1617(+)	
2572233200	t3m_01556	DNA_length		1458bp	
2572233200	t3m_01556	Protein_length		485aa	
2572233200	t3m_01556	GC		0.7	
2572233201	t3m_01557	COG_category	[P] Inorganic ion transport and metabolism		
2572233201	t3m_01557	COG2223	Nitrate/nitrite transporter		9.00E-15
2572233201	t3m_01557	pfam07690	MFS_1		1.00E-34
2572233201	t3m_01557	Locus_type		CDS	
2572233201	t3m_01557	Product_name		Nitrate/nitrite transporter	
2572233201	t3m_01557	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233201	t3m_01557	Coordinates		1582..2805(-)	
2572233201	t3m_01557	DNA_length		1224bp	
2572233201	t3m_01557	Protein_length		407aa	
2572233201	t3m_01557	GC		0.68	
2572233201	t3m_01557	Transmembrane		Yes	
2572233202	t3m_01558	COG_category	[R] General function prediction only		
2572233202	t3m_01558	COG0491	Zn-dependent hydrolases, including glyoxylases		3.00E-16
2572233202	t3m_01558	pfam00753	Lactamase_B		1.30E-22
2572233202	t3m_01558	Locus_type		CDS	
2572233202	t3m_01558	Product_name		Zn-dependent hydrolases, including glyoxylases	
2572233202	t3m_01558	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233202	t3m_01558	Coordinates		2802..3743(-)	
2572233202	t3m_01558	DNA_length		942bp	
2572233202	t3m_01558	Protein_length		313aa	
2572233202	t3m_01558	GC		0.7	
2572233203	t3m_01559	COG_category	[R] General function prediction only		
2572233203	t3m_01559	COG1994	Zn-dependent proteases		8.00E-10
2572233203	t3m_01559	pfam02163	Peptidase_M50		1.00E-14
2572233203	t3m_01559	Locus_type		CDS	
2572233203	t3m_01559	Product_name		Zn-dependent proteases	

2572233203	t3m_01559	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43		
2572233203	t3m_01559	Coordinates		3754..4467(-)		
2572233203	t3m_01559	DNA_length		714bp		
2572233203	t3m_01559	Protein_length		237aa		
2572233203	t3m_01559	GC			0.67	
2572233203	t3m_01559	Transmembrane		Yes		
2572233204	t3m_01560	KEGG_module	M00240: Iron complex transport system			
2572233204	t3m_01560	COG_category	[P] Inorganic ion transport and metabolism			
2572233204	t3m_01560	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component			2.00E-12
2572233204	t3m_01560	pfam01497	Peripla_BP_2			7.90E-19
2572233204	t3m_01560	KO:K02016	iron complex transport system substrate-binding protein			0.00E+00
2572233204	t3m_01560	Locus_type		CDS		
2572233204	t3m_01560	Product_name		ABC-type Fe3+-hydroxamate transport system, periplasmic component		
2572233204	t3m_01560	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43		
2572233204	t3m_01560	Coordinates		4464..5369(-)		
2572233204	t3m_01560	DNA_length		906bp		
2572233204	t3m_01560	Protein_length		301aa		
2572233204	t3m_01560	GC			0.7	
2572233205	t3m_01561	Locus_type		CDS		
2572233205	t3m_01561	Product_name		hypothetical protein		
2572233205	t3m_01561	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43		
2572233205	t3m_01561	Coordinates		5403..6530(-)		
2572233205	t3m_01561	DNA_length		1128bp		
2572233205	t3m_01561	Protein_length		375aa		
2572233205	t3m_01561	GC			0.7	
2572233206	t3m_01562	KEGG_module	M00365: C10-C20 isoprenoid biosynthesis, archaea			
2572233206	t3m_01562	KEGG_module	M00364: C10-C20 isoprenoid biosynthesis, bacteria			
2572233206	t3m_01562	Metacyc	PWY-7182: linalool biosynthesis I			
2572233206	t3m_01562	Metacyc	PWY2OL-4: superpathway of linalool biosynthesis			
2572233206	t3m_01562	Metacyc	PWY-6859: <i>all-trans</i>-farnesol biosynthesis			
2572233206	t3m_01562	Metacyc	PWY-7102: bisabolene biosynthesis			

2572233206	t3m_01562	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis		
2572233206	t3m_01562	Metacyc	PWY-6691: plaunotol biosynthesis		
2572233206	t3m_01562	Metacyc	PWY-7141: linalool biosynthesis II		
2572233206	t3m_01562	Metacyc	PWY-5122: geranyl diphosphate biosynthesis		
2572233206	t3m_01562	Metacyc	PWY-6659: fusicoccins biosynthesis		
2572233206	t3m_01562	Metacyc	PWY-5120: geranylgeranyldiphosphate biosynthesis		
2572233206	t3m_01562	Metacyc	PWY-5123: <i>trans, trans</i>-farnesyl diphosphate biosynthesis		
2572233206	t3m_01562	COG_category	[H] Coenzyme transport and metabolism		
2572233206	t3m_01562	COG0142	Geranylgeranyl pyrophosphate synthase		8.00E-40
2572233206	t3m_01562	pfam00348	polyprenyl_synt		1.40E-17
2572233206	t3m_01562	pfam00348	polyprenyl_synt		1.30E-12
2572233206	t3m_01562	EC:2.5.1.29	Geranylgeranyl diphosphate synthase.		
2572233206	t3m_01562	EC:2.5.1.1	Dimethylallyltranstransferase.		
2572233206	t3m_01562	EC:2.5.1.10	(2E,6E)-farnesyl diphosphate synthase.		
2572233206	t3m_01562	KO:K13787	geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10 2.5.1.2		0.00E+00
2572233206	t3m_01562	Locus_type		CDS	
2572233206	t3m_01562	Product_name		Geranylgeranyl pyrophosphate synthase	
2572233206	t3m_01562	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233206	t3m_01562	Coordinates		6586..7647(+)	
2572233206	t3m_01562	DNA_length		1062bp	
2572233206	t3m_01562	Protein_length		353aa	
2572233206	t3m_01562	GC		0.68	

2572233207	t3m_01563	COG_category	[O] Posttranslational modification, protein turnover, chaperones		
2572233207	t3m_01563	COG1382	Prefoldin, chaperonin cofactor		1.00E-13
2572233207	t3m_01563	pfam01920	Prefoldin_2		1.30E-21
2572233207	t3m_01563	TIGR02338	prefoldin, beta subunit, archaeal		1.10E-33
2572233207	t3m_01563	KO:K04798	prefoldin beta subunit		9.90E-19
2572233207	t3m_01563	Locus_type		CDS	
2572233207	t3m_01563	Product_name		prefoldin, beta subunit, archaeal	
2572233207	t3m_01563	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233207	t3m_01563	Coordinates		7670..8068(-)	
2572233207	t3m_01563	DNA_length		399bp	
2572233207	t3m_01563	Protein_length		132aa	

2572233207	t3m_01563	GC		0.65	
2572233208	t3m_01564	pfam09341	Pcc1		9.60E-09
2572233208	t3m_01564	KO:K09741	hypothetical protein		6.50E-06
2572233208	t3m_01564	Locus_type		CDS	
2572233208	t3m_01564	Product_name		Transcription factor Pcc1	
2572233208	t3m_01564	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233208	t3m_01564	Coordinates		8128..8397(-)	
2572233208	t3m_01564	DNA_length		270bp	
2572233208	t3m_01564	Protein_length		89aa	
2572233208	t3m_01564	GC		0.7	
2572233209	t3m_01565	KEGG_module	M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP		
2572233209	t3m_01565	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP		
2572233209	t3m_01565	Metacyc	PWY-6124: inosine-5'-phosphate biosynthesis II		
2572233209	t3m_01565	Metacyc	PWY-6123: inosine-5'-phosphate biosynthesis I		
2572233209	t3m_01565	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II		
2572233209	t3m_01565	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis		
2572233209	t3m_01565	COG_category	[F] Nucleotide transport and metabolism		
2572233209	t3m_01565	COG0015	Adenylosuccinate lyase		6.00E-117
2572233209	t3m_01565	pfam10397	ADSL_C		1.90E-14
2572233209	t3m_01565	pfam00206	Lyase_1		1.30E-48
2572233209	t3m_01565	EC:4.3.2.2	Adenylosuccinate lyase.		
2572233209	t3m_01565	TIGR00928	adenylosuccinate lyase		0.00E+00
2572233209	t3m_01565	KO:K01756	adenylosuccinate lyase [EC:4.3.2.2]		0.00E+00
2572233209	t3m_01565	Locus_type		CDS	
2572233209	t3m_01565	Product_name		adenylosuccinate lyase	
2572233209	t3m_01565	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233209	t3m_01565	Coordinates		8394..9761(-)	
2572233209	t3m_01565	DNA_length		1368bp	
2572233209	t3m_01565	Protein_length		455aa	
2572233209	t3m_01565	GC		0.7	
2572233210	t3m_01566	Metacyc	CITRULLINE-DEG-PWY: citrulline degradation		

2572233210	t3m_01566	Metacyc	PWY0-41: allantoin degradation IV (anaerobic)			
2572233210	t3m_01566	IMG_pathway	184: L-arginine degradation by Arg deiminase pathway			
2572233210	t3m_01566	COG_category	[E] Amino acid transport and metabolism			
2572233210	t3m_01566	COG0549	Carbamate kinase			9.00E-92
2572233210	t3m_01566	pfam00696	AA_kinase			7.30E-21
2572233210	t3m_01566	EC:2.7.2.2	Carbamate kinase.			
2572233210	t3m_01566	TIGR00746	carbamate kinase			4.00E-101
2572233210	t3m_01566	KO:K00926	carbamate kinase [EC:2.7.2.2]			0.00E+00
2572233210	t3m_01566	ITERM:00506	carbamate kinase (EC 2.7.2.2)			
2572233210	t3m_01566	Locus_type		CDS		
2572233210	t3m_01566	Product_name		carbamate kinase (EC 2.7.2.2)		
2572233210	t3m_01566	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43		
2572233210	t3m_01566	Coordinates		9881..10834(+)		
2572233210	t3m_01566	DNA_length		954bp		
2572233210	t3m_01566	Protein_length		317aa		
2572233210	t3m_01566	GC			0.71	

2572233211	t3m_01567	Metacyc	ASPARAGINE-BIOSYNTHESIS: asparagine biosynthesis I			
2572233211	t3m_01567	pfam00733	Asn_synthase			2.30E-21
2572233211	t3m_01567	EC:6.3.5.4	Asparagine synthase (glutamine-hydrolyzing).			
2572233211	t3m_01567	KO:K01953	asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]			9.80E-23
2572233211	t3m_01567	Locus_type		CDS		
2572233211	t3m_01567	Product_name		Asparagine synthase		
2572233211	t3m_01567	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43		
2572233211	t3m_01567	Coordinates		10831..11595(-)		
2572233211	t3m_01567	DNA_length		765bp		
2572233211	t3m_01567	Protein_length		254aa		
2572233211	t3m_01567	GC			0.69	

2572233212	t3m_01568	KEGG_module	M00064: ADP-L-glycero-D-manno-heptose biosynthesis			
2572233212	t3m_01568	Metacyc	PWY0-1241: ADP-L-<i>glycero</i>-β-D-<i>manno</i>-heptose biosynthesis			
2572233212	t3m_01568	Metacyc	PWY-6478: GDP-D-<i>glycero</i>-α-D-<i>manno</i>-heptose biosynthesis			
2572233212	t3m_01568	COG_category	[E] Amino acid transport and metabolism			
2572233212	t3m_01568	COG0241	Histidinol phosphatase and related phosphatases			8.00E-37

2572233212	t3m_01568	pfam13242	Hydrolase_like		2.10E-07
2572233212	t3m_01568	EC:3.1.3.82	D-glycero-beta-D-manno-heptose 1,7-bisphosphate 7-phosphatase.		
2572233212	t3m_01568	EC:3.1.3.83	D-glycero-alpha-D-manno-heptose-1,7-bisphosphate 7-phosphatase.		
2572233212	t3m_01568	TIGR01662	HAD-superfamily hydrolase, subfamily IIIA		1.40E-33
2572233212	t3m_01568	TIGR01656	histidinol-phosphate phosphatase family domain		1.20E-36
2572233212	t3m_01568	TIGR00213	D,D-heptose 1,7-bisphosphate phosphatase		1.00E-38
2572233212	t3m_01568	KO:K03273	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.8		6.70E-37
2572233212	t3m_01568	Locus_type		CDS	
2572233212	t3m_01568	Product_name		histidinol-phosphate phosphatase family domain/HAD-superfamily hydr	
2572233212	t3m_01568	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233212	t3m_01568	Coordinates		11620..12243(+)	
2572233212	t3m_01568	DNA_length		624bp	
2572233212	t3m_01568	Protein_length		207aa	
2572233212	t3m_01568	GC		0.68	
2572233213	t3m_01569	COG_category	[S] Function unknown		
2572233213	t3m_01569	COG1836	Predicted membrane protein		2.00E-27
2572233213	t3m_01569	pfam01940	DUF92		6.70E-44
2572233213	t3m_01569	TIGR00297	TIGR00297 family protein		2.00E-41
2572233213	t3m_01569	Locus_type		CDS	
2572233213	t3m_01569	Product_name		Predicted membrane protein	
2572233213	t3m_01569	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43	
2572233213	t3m_01569	Coordinates		12318..13076(+)	
2572233213	t3m_01569	DNA_length		759bp	
2572233213	t3m_01569	Protein_length		252aa	
2572233213	t3m_01569	GC		0.69	
2572233213	t3m_01569	Transmembrane		Yes	
2572233214	t3m_01570	COG_category	[R] General function prediction only		
2572233214	t3m_01570	COG0603	Predicted PP-loop superfamily ATPase		1.00E-66
2572233214	t3m_01570	pfam06508	QueC		2.10E-69
2572233214	t3m_01570	TIGR00364	queuosine biosynthesis protein QueC		9.50E-63
2572233214	t3m_01570	KO:K06920	queuosine biosynthesis protein QueC		0.00E+00
2572233214	t3m_01570	ITERM:05501	preQ(0) biosynthesis protein QueC		

2572233214	t3m_01570	Locus_type		CDS		
2572233214	t3m_01570	Product_name		preQ(0) biosynthesis protein QueC		
2572233214	t3m_01570	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43		
2572233214	t3m_01570	Coordinates		13073..13765(+)		
2572233214	t3m_01570	DNA_length		693bp		
2572233214	t3m_01570	Protein_length		230aa		
2572233214	t3m_01570	GC			0.72	

2572233215	t3m_01571	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572233215	t3m_01571	COG1970	Large-conductance mechanosensitive channel			2.00E-14
2572233215	t3m_01571	pfam01741	MscL			1.30E-18
2572233215	t3m_01571	TIGR00220	large conductance mechanosensitive channel protein			6.90E-19
2572233215	t3m_01571	KO:K03282	large conductance mechanosensitive channel			1.10E-25
2572233215	t3m_01571	Locus_type		CDS		
2572233215	t3m_01571	Product_name		Large-conductance mechanosensitive channel		
2572233215	t3m_01571	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43		
2572233215	t3m_01571	Coordinates		13762..14196(-)		
2572233215	t3m_01571	DNA_length		435bp		
2572233215	t3m_01571	Protein_length		144aa		
2572233215	t3m_01571	GC			0.63	
2572233215	t3m_01571	Transmembrane		Yes		

2572233216	t3m_01572	pfam05746	DALR_1			1.70E-30
2572233216	t3m_01572	Locus_type		CDS		
2572233216	t3m_01572	Product_name		DALR anticodon binding domain		
2572233216	t3m_01572	Scaffold		t3m_contig_70_523_len_14761_read_count_1147216.43		
2572233216	t3m_01572	Coordinates		14326..14760(-)		
2572233216	t3m_01572	DNA_length		435bp		
2572233216	t3m_01572	Protein_length		144aa		
2572233216	t3m_01572	GC			0.7	

2572233217	t3m_01573	Locus_type		CDS		
2572233217	t3m_01573	Product_name		hypothetical protein		
2572233217	t3m_01573	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		

2572233217	t3m_01573	Coordinates		3..236(-)	
2572233217	t3m_01573	DNA_length		234bp	
2572233217	t3m_01573	Protein_length		78aa	
2572233217	t3m_01573	GC		0.68	

2572233218	t3m_01575	Metacyc	PWY-6935: seleno-amino acid detoxification and volatilization II		
2572233218	t3m_01575	Metacyc	PWY1A0-6325: actinorhodin biosynthesis		
2572233218	t3m_01575	COG_category	[H] Coenzyme transport and metabolism		
2572233218	t3m_01575	COG0214	Pyridoxine biosynthesis enzyme		1.00E-121
2572233218	t3m_01575	pfam01680	SOR_SNZ		4.50E-102
2572233218	t3m_01575	EC:4.-	Lyases.		
2572233218	t3m_01575	TIGR00343	pyridoxal 5'-phosphate synthase, synthase subunit Pdx1		0.00E+00
2572233218	t3m_01575	KO:K06215	pyridoxine biosynthesis protein [EC:4.-.-.-]		0.00E+00
2572233218	t3m_01575	Locus_type		CDS	
2572233218	t3m_01575	Product_name		pyridoxal phosphate synthase yaaD subunit	
2572233218	t3m_01575	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44	
2572233218	t3m_01575	Coordinates		537..1481(+)	
2572233218	t3m_01575	DNA_length		945bp	
2572233218	t3m_01575	Protein_length		314aa	
2572233218	t3m_01575	GC		0.68	

2572233219	t3m_01576	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572233219	t3m_01576	COG0438	Glycosyltransferase		7.00E-44
2572233219	t3m_01576	pfam00534	Glycos_transf_1		1.00E-37
2572233219	t3m_01576	pfam13579	Glyco_trans_4_4		9.30E-18
2572233219	t3m_01576	EC:2.4.1.87	N-acetyllactosaminide 3-alpha-galactosyltransferase.		
2572233219	t3m_01576	KO:K00743	N-acetyllactosaminide 3-alpha-galactosyltransferase [EC:2.4.1.87]		0.00E+00
2572233219	t3m_01576	Locus_type		CDS	
2572233219	t3m_01576	Product_name		Glycosyltransferase	
2572233219	t3m_01576	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44	
2572233219	t3m_01576	Coordinates		1541..2674(+)	
2572233219	t3m_01576	DNA_length		1134bp	
2572233219	t3m_01576	Protein_length		377aa	
2572233219	t3m_01576	GC		0.7	

2572233220	t3m_01577	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP			
2572233220	t3m_01577	Metacyc	PWY-5686: UMP biosynthesis			
2572233220	t3m_01577	IMG_pathway	321: Uridine 5'-monophosphate biosynthesis			
2572233220	t3m_01577	COG_category	[F] Nucleotide transport and metabolism			
2572233220	t3m_01577	COG0284	Orotidine-5'-phosphate decarboxylase			4.00E-19
2572233220	t3m_01577	pfam00215	OMPdecase			5.20E-21
2572233220	t3m_01577	EC:4.1.1.23	Orotidine-5'-phosphate decarboxylase.			
2572233220	t3m_01577	TIGR02127	orotidine 5'-phosphate decarboxylase, subfamily 2			1.10E-55
2572233220	t3m_01577	KO:K01591	orotidine-5'-phosphate decarboxylase [EC:4.1.1.23]			2.80E-45
2572233220	t3m_01577	ITERM:01394	orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)			
2572233220	t3m_01577	Locus_type		CDS		
2572233220	t3m_01577	Product_name		orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)		
2572233220	t3m_01577	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		
2572233220	t3m_01577	Coordinates		2640..3482(-)		
2572233220	t3m_01577	DNA_length		843bp		
2572233220	t3m_01577	Protein_length		280aa		
2572233220	t3m_01577	GC			0.68	
2572233221	t3m_01578	KEGG_module	M00288: RPA complex			
2572233221	t3m_01578	COG_category	[L] Replication, recombination and repair			
2572233221	t3m_01578	COG1599	Single-stranded DNA-binding replication protein A (RPA), large (70 kD) s			2.00E-22
2572233221	t3m_01578	KO:K07466	replication factor A1			0.00E+00
2572233221	t3m_01578	Locus_type		CDS		
2572233221	t3m_01578	Product_name		Single-stranded DNA-binding replication protein A (RPA), large (70 kD) su		
2572233221	t3m_01578	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		
2572233221	t3m_01578	Coordinates		3624..4814(+)		
2572233221	t3m_01578	DNA_length		1191bp		
2572233221	t3m_01578	Protein_length		396aa		
2572233221	t3m_01578	GC			0.71	
2572233222	t3m_01579	COG_category	[S] Function unknown			
2572233222	t3m_01579	COG3390	Uncharacterized protein conserved in archaea			1.00E-21
2572233222	t3m_01579	KO:K09746	hypothetical protein			7.60E-22

2572233222	t3m_01579	Locus_type		CDS	
2572233222	t3m_01579	Product_name		Uncharacterized protein conserved in archaea	
2572233222	t3m_01579	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44	
2572233222	t3m_01579	Coordinates		4814..5734(+)	
2572233222	t3m_01579	DNA_length		921bp	
2572233222	t3m_01579	Protein_length		306aa	
2572233222	t3m_01579	GC		0.73	
2572233223	t3m_01580	pfam00254	FKBP_C		1.10E-05
2572233223	t3m_01580	Locus_type		CDS	
2572233223	t3m_01580	Product_name		FKBP-type peptidyl-prolyl cis-trans isomerase	
2572233223	t3m_01580	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44	
2572233223	t3m_01580	Coordinates		5862..6785(+)	
2572233223	t3m_01580	DNA_length		924bp	
2572233223	t3m_01580	Protein_length		307aa	
2572233223	t3m_01580	GC		0.66	
2572233223	t3m_01580	Transmembrane		Yes	
2572233224	t3m_01581	Locus_type		CDS	
2572233224	t3m_01581	Product_name		hypothetical protein	
2572233224	t3m_01581	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44	
2572233224	t3m_01581	Coordinates		6793..7695(-)	
2572233224	t3m_01581	DNA_length		903bp	
2572233224	t3m_01581	Protein_length		300aa	
2572233224	t3m_01581	GC		0.7	
2572233225	t3m_01582	COG_category	[R] General function prediction only		
2572233225	t3m_01582	COG1691	NCAIR mutase (PurE)-related proteins		5.00E-53
2572233225	t3m_01582	pfam00731	AIRC		2.40E-22
2572233225	t3m_01582	Locus_type		CDS	
2572233225	t3m_01582	Product_name		NCAIR mutase (PurE)-related proteins	
2572233225	t3m_01582	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44	
2572233225	t3m_01582	Coordinates		7777..8556(-)	
2572233225	t3m_01582	DNA_length		780bp	

2572233225	t3m_01582	Protein_length		259aa		
2572233225	t3m_01582	GC			0.72	

2572233226	t3m_01583	KEGG_module	M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA			
2572233226	t3m_01583	KEGG_module	M00013: Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA			
2572233226	t3m_01583	KEGG_module	M00087: beta-Oxidation			
2572233226	t3m_01583	Metacyc	PWY-7094: fatty acid salvage			
2572233226	t3m_01583	COG_category	[I] Lipid transport and metabolism			
2572233226	t3m_01583	COG1960	Acyl-CoA dehydrogenases			4.00E-98
2572233226	t3m_01583	pfam00441	Acyl-CoA_dh_1			3.10E-51
2572233226	t3m_01583	pfam02771	Acyl-CoA_dh_N			4.50E-31
2572233226	t3m_01583	pfam02770	Acyl-CoA_dh_M			2.50E-22
2572233226	t3m_01583	EC:1.3.8.7	Medium-chain acyl-CoA dehydrogenase.			
2572233226	t3m_01583	KO:K00249	acyl-CoA dehydrogenase [EC:1.3.8.7]			0.00E+00
2572233226	t3m_01583	Locus_type		CDS		
2572233226	t3m_01583	Product_name		Acyl-CoA dehydrogenases		
2572233226	t3m_01583	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		
2572233226	t3m_01583	Coordinates		8605..9753(+)		
2572233226	t3m_01583	DNA_length		1149bp		
2572233226	t3m_01583	Protein_length		382aa		
2572233226	t3m_01583	GC			0.67	

2572233227	t3m_01584	COG_category	[C] Energy production and conversion			
2572233227	t3m_01584	COG2086	Electron transfer flavoprotein, beta subunit			7.00E-41
2572233227	t3m_01584	pfam01012	ETF			4.20E-27
2572233227	t3m_01584	KO:K03521	electron transfer flavoprotein beta subunit			7.30E-41
2572233227	t3m_01584	ITERM:01639	electron transfer flavoprotein beta subunit			
2572233227	t3m_01584	Locus_type		CDS		
2572233227	t3m_01584	Product_name		electron transfer flavoprotein beta subunit		
2572233227	t3m_01584	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		
2572233227	t3m_01584	Coordinates		9768..10550(+)		
2572233227	t3m_01584	DNA_length		783bp		
2572233227	t3m_01584	Protein_length		260aa		
2572233227	t3m_01584	GC			0.69	

2572233228	t3m_01585	COG_category	[C] Energy production and conversion			
2572233228	t3m_01585	COG2025	Electron transfer flavoprotein, alpha subunit			2.00E-65
2572233228	t3m_01585	pfam01012	ETF			1.80E-22
2572233228	t3m_01585	pfam00766	ETF_alpha			9.60E-34
2572233228	t3m_01585	KO:K03522	electron transfer flavoprotein alpha subunit			0.00E+00
2572233228	t3m_01585	ITERM:01638	electron transfer flavoprotein alpha subunit apoprotein			
2572233228	t3m_01585	Locus_type		CDS		
2572233228	t3m_01585	Product_name		electron transfer flavoprotein alpha subunit apoprotein		
2572233228	t3m_01585	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		
2572233228	t3m_01585	Coordinates		10547..11530(+)		
2572233228	t3m_01585	DNA_length		984bp		
2572233228	t3m_01585	Protein_length		327aa		
2572233228	t3m_01585	GC			0.71	
2572233229	t3m_01586	COG_category	[C] Energy production and conversion			
2572233229	t3m_01586	COG0644	Dehydrogenases (flavoproteins)			4.00E-51
2572233229	t3m_01586	pfam12831	FAD_oxidored			9.50E-09
2572233229	t3m_01586	EC:1.5.5.-	Oxidoreductases. Acting on the CH-NH group of donors. With a quinone or similar compound as ac			
2572233229	t3m_01586	KO:K00313	electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]			0.00E+00
2572233229	t3m_01586	Locus_type		CDS		
2572233229	t3m_01586	Product_name		Dehydrogenases (flavoproteins)		
2572233229	t3m_01586	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		
2572233229	t3m_01586	Coordinates		11594..12895(-)		
2572233229	t3m_01586	DNA_length		1302bp		
2572233229	t3m_01586	Protein_length		433aa		
2572233229	t3m_01586	GC			0.68	
2572233230	t3m_01587	pfam03703	bPH_2			1.40E-16
2572233230	t3m_01587	Locus_type		CDS		
2572233230	t3m_01587	Product_name		Bacterial PH domain		
2572233230	t3m_01587	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		
2572233230	t3m_01587	Coordinates		12951..13592(-)		
2572233230	t3m_01587	DNA_length		642bp		

2572233230	t3m_01587	Protein_length		213aa		
2572233230	t3m_01587	GC			0.64	
2572233230	t3m_01587	Transmembrane		Yes		
2572233231	t3m_01588	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233231	t3m_01588	COG0361	Translation initiation factor 1 (IF-1)			5.00E-15
2572233231	t3m_01588	pfam01176	eIF-1a			8.10E-19
2572233231	t3m_01588	TIGR00523	eukaryotic/archaeal initiation factor 1A			4.00E-31
2572233231	t3m_01588	KO:K03236	translation initiation factor 1A			2.00E-22
2572233231	t3m_01588	ITERM:01957	translation initiation factor 1A (aeIF-1A)			
2572233231	t3m_01588	Locus_type		CDS		
2572233231	t3m_01588	Product_name		translation initiation factor 1A (aeIF-1A)		
2572233231	t3m_01588	Scaffold		t3m_contig_70_566_len_14045_read_count_1043208.44		
2572233231	t3m_01588	Coordinates		13722..14042(+)		
2572233231	t3m_01588	DNA_length		321bp		
2572233231	t3m_01588	Protein_length		107aa		
2572233231	t3m_01588	GC			0.67	
2572233232	t3m_01589	Locus_type		CDS		
2572233232	t3m_01589	Product_name		hypothetical protein		
2572233232	t3m_01589	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233232	t3m_01589	Coordinates		152..727(-)		
2572233232	t3m_01589	DNA_length		576bp		
2572233232	t3m_01589	Protein_length		191aa		
2572233232	t3m_01589	GC			0.71	
2572233233	t3m_01590	pfam00041	fn3			1.40E-05
2572233233	t3m_01590	pfam00041	fn3			9.40E-07
2572233233	t3m_01590	pfam00041	fn3			2.00E-05
2572233233	t3m_01590	pfam00041	fn3			2.50E-06
2572233233	t3m_01590	Locus_type		CDS		
2572233233	t3m_01590	Product_name		Fibronectin type III domain		
2572233233	t3m_01590	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233233	t3m_01590	Coordinates		1168..4545(-)		

2572233233	t3m_01590	DNA_length		3378bp		
2572233233	t3m_01590	Protein_length		1125aa		
2572233233	t3m_01590	GC			0.66	
2572233233	t3m_01590	Transmembrane		Yes		
2572233234	t3m_01591	Locus_type		CDS		
2572233234	t3m_01591	Product_name		hypothetical protein		
2572233234	t3m_01591	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233234	t3m_01591	Coordinates		4958..5167(-)		
2572233234	t3m_01591	DNA_length		210bp		
2572233234	t3m_01591	Protein_length		69aa		
2572233234	t3m_01591	GC			0.66	
2572233234	t3m_01591	Transmembrane		Yes		
2572233235	t3m_01592	Locus_type		CDS		
2572233235	t3m_01592	Product_name		hypothetical protein		
2572233235	t3m_01592	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233235	t3m_01592	Coordinates		5334..5735(-)		
2572233235	t3m_01592	DNA_length		402bp		
2572233235	t3m_01592	Protein_length		133aa		
2572233235	t3m_01592	GC			0.73	
2572233236	t3m_01593	Locus_type		CDS		
2572233236	t3m_01593	Product_name		hypothetical protein		
2572233236	t3m_01593	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233236	t3m_01593	Coordinates		5742..6077(-)		
2572233236	t3m_01593	DNA_length		336bp		
2572233236	t3m_01593	Protein_length		111aa		
2572233236	t3m_01593	GC			0.79	
2572233237	t3m_01594	COG_category	[S] Function unknown			
2572233237	t3m_01594	COG3391	Uncharacterized conserved protein			2.00E-12
2572233237	t3m_01594	TIGR02276	40-residue YVTN family beta-propeller repeat			8.10E-11
2572233237	t3m_01594	Locus_type		CDS		

2572233237	t3m_01594	Product_name		40-residue YVTN family beta-propeller repeat		
2572233237	t3m_01594	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233237	t3m_01594	Coordinates		6074..7237(-)		
2572233237	t3m_01594	DNA_length		1164bp		
2572233237	t3m_01594	Protein_length		387aa		
2572233237	t3m_01594	GC			0.69	
2572233237	t3m_01594	Signal_peptide		Yes		
2572233237	t3m_01594	Transmembrane		Yes		

2572233238	t3m_01595	Locus_type		CDS		
2572233238	t3m_01595	Product_name		hypothetical protein		
2572233238	t3m_01595	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233238	t3m_01595	Coordinates		7251..9728(-)		
2572233238	t3m_01595	DNA_length		2478bp		
2572233238	t3m_01595	Protein_length		825aa		
2572233238	t3m_01595	GC			0.64	
2572233238	t3m_01595	Signal_peptide		Yes		
2572233238	t3m_01595	Transmembrane		Yes		

2572233239	t3m_01596	COG_category	[S] Function unknown			
2572233239	t3m_01596	COG3391	Uncharacterized conserved protein			1.00E-15
2572233239	t3m_01596	pfam00041	fn3			2.80E-09
2572233239	t3m_01596	pfam10282	Lactonase			2.10E-05
2572233239	t3m_01596	TIGR02276	40-residue YVTN family beta-propeller repeat			9.30E-11
2572233239	t3m_01596	Locus_type		CDS		
2572233239	t3m_01596	Product_name		Uncharacterized conserved protein		
2572233239	t3m_01596	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233239	t3m_01596	Coordinates		9764..12394(-)		
2572233239	t3m_01596	DNA_length		2631bp		
2572233239	t3m_01596	Protein_length		876aa		
2572233239	t3m_01596	GC			0.67	
2572233239	t3m_01596	Signal_peptide		Yes		
2572233239	t3m_01596	Transmembrane		Yes		

2572233240	t3m_01597	Locus_type		CDS		
2572233240	t3m_01597	Product_name		hypothetical protein		
2572233240	t3m_01597	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233240	t3m_01597	Coordinates		12555..13100(+)		
2572233240	t3m_01597	DNA_length		546bp		
2572233240	t3m_01597	Protein_length		181aa		
2572233240	t3m_01597	GC			0.67	
2572233241	t3m_01598	Locus_type		CDS		
2572233241	t3m_01598	Product_name		hypothetical protein		
2572233241	t3m_01598	Scaffold		t3m_contig_70_569_len_14038_read_count_992473.45		
2572233241	t3m_01598	Coordinates		13456..13770(+)		
2572233241	t3m_01598	DNA_length		315bp		
2572233241	t3m_01598	Protein_length		104aa		
2572233241	t3m_01598	GC			0.77	
2572233242	t3m_01599	pfam03590	AsnA			5.80E-54
2572233242	t3m_01599	Locus_type		CDS		
2572233242	t3m_01599	Product_name		Aspartate-ammonia ligase		
2572233242	t3m_01599	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233242	t3m_01599	Coordinates		2..730(-)		
2572233242	t3m_01599	DNA_length		729bp		
2572233242	t3m_01599	Protein_length		243aa		
2572233242	t3m_01599	GC			0.65	
2572233243	t3m_01600	Locus_type		CDS		
2572233243	t3m_01600	Product_name		hypothetical protein		
2572233243	t3m_01600	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233243	t3m_01600	Coordinates		952..1656(+)		
2572233243	t3m_01600	DNA_length		705bp		
2572233243	t3m_01600	Protein_length		234aa		
2572233243	t3m_01600	GC			0.64	
2572233244	t3m_01601	Locus_type		CDS		

2572233244	t3m_01601	Product_name		hypothetical protein		
2572233244	t3m_01601	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233244	t3m_01601	Coordinates		1865..2485(+)		
2572233244	t3m_01601	DNA_length		621bp		
2572233244	t3m_01601	Protein_length		206aa		
2572233244	t3m_01601	GC			0.67	

2572233245	t3m_01602	pfam00583	Acetyltransf_1			2.00E-07
2572233245	t3m_01602	Locus_type		CDS		
2572233245	t3m_01602	Product_name		Acetyltransferase (GNAT) family		
2572233245	t3m_01602	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233245	t3m_01602	Coordinates		2554..3117(-)		
2572233245	t3m_01602	DNA_length		564bp		
2572233245	t3m_01602	Protein_length		187aa		
2572233245	t3m_01602	GC			0.68	

2572233246	t3m_01603	COG_category	[E] Amino acid transport and metabolism			
2572233246	t3m_01603	COG_category	[G] Carbohydrate transport and metabolism			
2572233246	t3m_01603	COG_category	[R] General function prediction only			
2572233246	t3m_01603	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily			1.00E-07
2572233246	t3m_01603	pfam00892	EamA			4.60E-12
2572233246	t3m_01603	pfam00892	EamA			4.00E-13
2572233246	t3m_01603	Locus_type		CDS		
2572233246	t3m_01603	Product_name		Permeases of the drug/metabolite transporter (DMT) superfamily		
2572233246	t3m_01603	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233246	t3m_01603	Coordinates		3279..4226(+)		
2572233246	t3m_01603	DNA_length		948bp		
2572233246	t3m_01603	Protein_length		315aa		
2572233246	t3m_01603	GC			0.67	
2572233246	t3m_01603	Transmembrane		Yes		

2572233247	t3m_01604	COG_category	[S] Function unknown			
2572233247	t3m_01604	COG3832	Uncharacterized conserved protein			4.00E-11
2572233247	t3m_01604	pfam08327	AHSA1			1.90E-18

2572233247	t3m_01604	Locus_type	CDS
2572233247	t3m_01604	Product_name	Uncharacterized conserved protein
2572233247	t3m_01604	Scaffold	t3m_contig_70_592_len_13739_read_count_1164878.46
2572233247	t3m_01604	Coordinates	4380..4826(+)
2572233247	t3m_01604	DNA_length	447bp
2572233247	t3m_01604	Protein_length	148aa
2572233247	t3m_01604	GC	0.66

2572233248	t3m_01605	Locus_type	CDS
2572233248	t3m_01605	Product_name	hypothetical protein
2572233248	t3m_01605	Scaffold	t3m_contig_70_592_len_13739_read_count_1164878.46
2572233248	t3m_01605	Coordinates	4863..5324(+)
2572233248	t3m_01605	DNA_length	462bp
2572233248	t3m_01605	Protein_length	153aa
2572233248	t3m_01605	GC	0.65

2572233249	t3m_01606	Locus_type	CDS
2572233249	t3m_01606	Product_name	hypothetical protein
2572233249	t3m_01606	Scaffold	t3m_contig_70_592_len_13739_read_count_1164878.46
2572233249	t3m_01606	Coordinates	5365..6669(-)
2572233249	t3m_01606	DNA_length	1305bp
2572233249	t3m_01606	Protein_length	434aa
2572233249	t3m_01606	GC	0.68
2572233249	t3m_01606	Transmembrane	Yes

2572233250	t3m_01607	Locus_type	CDS
2572233250	t3m_01607	Product_name	hypothetical protein
2572233250	t3m_01607	Scaffold	t3m_contig_70_592_len_13739_read_count_1164878.46
2572233250	t3m_01607	Coordinates	7139..8005(-)
2572233250	t3m_01607	DNA_length	867bp
2572233250	t3m_01607	Protein_length	288aa
2572233250	t3m_01607	GC	0.65

2572233251	t3m_01608	COG_category	[R] General function prediction only

2572233251	t3m_01608	COG3413	Predicted DNA binding protein			2.00E-12
2572233251	t3m_01608	pfam04967	HTH_10			5.30E-13
2572233251	t3m_01608	Locus_type		CDS		
2572233251	t3m_01608	Product_name		Predicted DNA binding protein		
2572233251	t3m_01608	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233251	t3m_01608	Coordinates		8366..9061(+)		
2572233251	t3m_01608	DNA_length		696bp		
2572233251	t3m_01608	Protein_length		231aa		
2572233251	t3m_01608	GC			0.65	
2572233252	t3m_01609	COG_category	[S] Function unknown			
2572233252	t3m_01609	COG2350	Uncharacterized protein conserved in bacteria			4.00E-06
2572233252	t3m_01609	pfam03795	YCII			2.20E-10
2572233252	t3m_01609	Locus_type		CDS		
2572233252	t3m_01609	Product_name		Uncharacterized protein conserved in bacteria		
2572233252	t3m_01609	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233252	t3m_01609	Coordinates		9093..9449(-)		
2572233252	t3m_01609	DNA_length		357bp		
2572233252	t3m_01609	Protein_length		118aa		
2572233252	t3m_01609	GC			0.68	
2572233253	t3m_01610	COG_category	[S] Function unknown			
2572233253	t3m_01610	COG4805	Uncharacterized protein conserved in bacteria			0.00E+00
2572233253	t3m_01610	pfam05960	DUF885			0.00E+00
2572233253	t3m_01610	Locus_type		CDS		
2572233253	t3m_01610	Product_name		Uncharacterized protein conserved in bacteria		
2572233253	t3m_01610	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233253	t3m_01610	Coordinates		9459..11288(-)		
2572233253	t3m_01610	DNA_length		1830bp		
2572233253	t3m_01610	Protein_length		609aa		
2572233253	t3m_01610	GC			0.68	
2572233254	t3m_01611	COG_category	[E] Amino acid transport and metabolism			
2572233254	t3m_01611	COG0346	Lactoylglutathione lyase and related lyases			5.00E-04

2572233254	t3m_01611	pfam12681	Glyoxalase_2			1.30E-14
2572233254	t3m_01611	Locus_type		CDS		
2572233254	t3m_01611	Product_name		Lactoylglutathione lyase and related lyases		
2572233254	t3m_01611	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233254	t3m_01611	Coordinates		11397..11822(+)		
2572233254	t3m_01611	DNA_length		426bp		
2572233254	t3m_01611	Protein_length		141aa		
2572233254	t3m_01611	GC			0.65	
2572233255	t3m_01612	Locus_type		CDS		
2572233255	t3m_01612	Product_name		hypothetical protein		
2572233255	t3m_01612	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233255	t3m_01612	Coordinates		11819..12397(-)		
2572233255	t3m_01612	DNA_length		579bp		
2572233255	t3m_01612	Protein_length		192aa		
2572233255	t3m_01612	GC			0.71	
2572233255	t3m_01612	Transmembrane		Yes		
2572233256	t3m_01613	pfam13912	zf-C2H2_6			5.50E-04
2572233256	t3m_01613	pfam00096	zf-C2H2			2.70E-03
2572233256	t3m_01613	Locus_type		CDS		
2572233256	t3m_01613	Product_name		C2H2-type zinc finger/Zinc finger, C2H2 type		
2572233256	t3m_01613	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		
2572233256	t3m_01613	Coordinates		12674..12901(+)		
2572233256	t3m_01613	DNA_length		228bp		
2572233256	t3m_01613	Protein_length		75aa		
2572233256	t3m_01613	GC			0.67	
2572233257	t3m_01614	COG_category	[S] Function unknown			
2572233257	t3m_01614	COG2764	Uncharacterized protein conserved in bacteria			4.00E-31
2572233257	t3m_01614	pfam12681	Glyoxalase_2			7.90E-14
2572233257	t3m_01614	Locus_type		CDS		
2572233257	t3m_01614	Product_name		Uncharacterized protein conserved in bacteria		
2572233257	t3m_01614	Scaffold		t3m_contig_70_592_len_13739_read_count_1164878.46		

2572233257	t3m_01614	Coordinates		13008..13559(+)	
2572233257	t3m_01614	DNA_length		552bp	
2572233257	t3m_01614	Protein_length		183aa	
2572233257	t3m_01614	GC		0.66	

2572233258	t3m_01615	Locus_type		CDS	
2572233258	t3m_01615	Product_name		hypothetical protein	
2572233258	t3m_01615	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47	
2572233258	t3m_01615	Coordinates		167..649(-)	
2572233258	t3m_01615	DNA_length		483bp	
2572233258	t3m_01615	Protein_length		160aa	
2572233258	t3m_01615	GC		0.66	
2572233258	t3m_01615	Transmembrane		Yes	

2572233259	t3m_01616	Locus_type		CDS	
2572233259	t3m_01616	Product_name		hypothetical protein	
2572233259	t3m_01616	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47	
2572233259	t3m_01616	Coordinates		646..1089(-)	
2572233259	t3m_01616	DNA_length		444bp	
2572233259	t3m_01616	Protein_length		147aa	
2572233259	t3m_01616	GC		0.63	
2572233259	t3m_01616	Transmembrane		Yes	

2572233260	t3m_01617	Locus_type		CDS	
2572233260	t3m_01617	Product_name		hypothetical protein	
2572233260	t3m_01617	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47	
2572233260	t3m_01617	Coordinates		1100..1390(-)	
2572233260	t3m_01617	DNA_length		291bp	
2572233260	t3m_01617	Protein_length		96aa	
2572233260	t3m_01617	GC		0.62	

2572233261	t3m_01618	pfam08448	PAS_4		3.50E-07
2572233261	t3m_01618	Locus_type		CDS	
2572233261	t3m_01618	Product_name		PAS fold	

2572233261	t3m_01618	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47		
2572233261	t3m_01618	Coordinates		1485..1835(-)		
2572233261	t3m_01618	DNA_length		351bp		
2572233261	t3m_01618	Protein_length		116aa		
2572233261	t3m_01618	GC			0.58	
2572233262	t3m_01619	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme			
2572233262	t3m_01619	Metacyc	PWY-5188: tetrapyrrole biosynthesis I (from glutamate)			
2572233262	t3m_01619	COG_category	[H] Coenzyme transport and metabolism			
2572233262	t3m_01619	COG0001	Glutamate-1-semialdehyde aminotransferase			1.00E-102
2572233262	t3m_01619	pfam00202	Aminotran_3			6.70E-56
2572233262	t3m_01619	EC:5.4.3.8	Glutamate-1-semialdehyde 2,1-aminomutase.			
2572233262	t3m_01619	TIGR00713	glutamate-1-semialdehyde-2,1-aminomutase			3.90E-97
2572233262	t3m_01619	KO:K01845	glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]			0.00E+00
2572233262	t3m_01619	Locus_type		CDS		
2572233262	t3m_01619	Product_name		Glutamate-1-semialdehyde aminotransferase		
2572233262	t3m_01619	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47		
2572233262	t3m_01619	Coordinates		2011..3381(-)		
2572233262	t3m_01619	DNA_length		1371bp		
2572233262	t3m_01619	Protein_length		456aa		
2572233262	t3m_01619	GC			0.65	
2572233263	t3m_01620	KEGG_module	M00013: Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA			
2572233263	t3m_01620	Metacyc	PWY-6373: acrylate degradation			
2572233263	t3m_01620	Metacyc	VALDEG-PWY: valine degradation I			
2572233263	t3m_01620	Metacyc	PWY-5642: 2,4-dinitrotoluene degradation			
2572233263	t3m_01620	COG_category	[C] Energy production and conversion			
2572233263	t3m_01620	COG1012	NAD-dependent aldehyde dehydrogenases			1.00E-118
2572233263	t3m_01620	pfam00171	Aldedh			0.00E+00
2572233263	t3m_01620	EC:1.2.1.27	Methylmalonate-semialdehyde dehydrogenase (acylating).			
2572233263	t3m_01620	EC:1.2.1.18	Malonate-semialdehyde dehydrogenase (acetylating).			
2572233263	t3m_01620	TIGR01722	methylmalonic acid semialdehyde dehydrogenase			0.00E+00
2572233263	t3m_01620	KO:K00140	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate			0.00E+00
2572233263	t3m_01620	Locus_type		CDS		

2572233263	t3m_01620	Product_name		methylmalonic acid semialdehyde dehydrogenase	
2572233263	t3m_01620	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47	
2572233263	t3m_01620	Coordinates		3538..4986(+)	
2572233263	t3m_01620	DNA_length		1449bp	
2572233263	t3m_01620	Protein_length		482aa	
2572233263	t3m_01620	GC		0.67	
2572233264	t3m_01621	Metacyc	TAURINEDEG-PWY: taurine degradation III		
2572233264	t3m_01621	COG_category	[E] Amino acid transport and metabolism		
2572233264	t3m_01621	COG0160	4-aminobutyrate aminotransferase and related aminotransferases		2.00E-109
2572233264	t3m_01621	pfam00202	Aminotran_3		5.30E-88
2572233264	t3m_01621	EC:2.6.1.55	Taurine--2-oxoglutarate transaminase.		
2572233264	t3m_01621	KO:K15372	taurine---2-oxoglutarate transaminase [EC:2.6.1.55]		0.00E+00
2572233264	t3m_01621	Locus_type		CDS	
2572233264	t3m_01621	Product_name		4-aminobutyrate aminotransferase and related aminotransferases	
2572233264	t3m_01621	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47	
2572233264	t3m_01621	Coordinates		5005..6351(-)	
2572233264	t3m_01621	DNA_length		1347bp	
2572233264	t3m_01621	Protein_length		448aa	
2572233264	t3m_01621	GC		0.67	
2572233265	t3m_01622	pfam04909	Amidohydro_2		7.80E-41
2572233265	t3m_01622	Locus_type		CDS	
2572233265	t3m_01622	Product_name		Amidohydrolase	
2572233265	t3m_01622	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47	
2572233265	t3m_01622	Coordinates		6413..7282(-)	
2572233265	t3m_01622	DNA_length		870bp	
2572233265	t3m_01622	Protein_length		289aa	
2572233265	t3m_01622	GC		0.65	
2572233266	t3m_01623	KEGG_module	M00033: Ectoine biosynthesis, aspartate => ectoine		
2572233266	t3m_01623	Metacyc	P101-PWY: ectoine biosynthesis		
2572233266	t3m_01623	Metacyc	PWY-6409: pyoverdine I biosynthesis		
2572233266	t3m_01623	Metacyc	PWY-6562: norspermidine biosynthesis		

2572233266	t3m_01623	Metacyc	PWY-761: rhizobactin 1021 biosynthesis		
2572233266	t3m_01623	COG_category	[E] Amino acid transport and metabolism		
2572233266	t3m_01623	COG0160	4-aminobutyrate aminotransferase and related aminotransferases		4.00E-120
2572233266	t3m_01623	pfam00202	Aminotran_3		5.60E-90
2572233266	t3m_01623	EC:2.6.1.76	Diaminobutyrate--2-oxoglutarate transaminase.		
2572233266	t3m_01623	KO:K00836	diaminobutyrate-2-oxoglutarate transaminase [EC:2.6.1.76]		0.00E+00
2572233266	t3m_01623	Locus_type		CDS	
2572233266	t3m_01623	Product_name		4-aminobutyrate aminotransferase and related aminotransferases	
2572233266	t3m_01623	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47	
2572233266	t3m_01623	Coordinates		7841..9352(+)	
2572233266	t3m_01623	DNA_length		1512bp	
2572233266	t3m_01623	Protein_length		503aa	
2572233266	t3m_01623	GC		0.7	
2572233267	t3m_01624	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle		
2572233267	t3m_01624	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2572233267	t3m_01624	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle		
2572233267	t3m_01624	Metacyc	PWY-5677: succinate fermentation to butyrate		
2572233267	t3m_01624	COG_category	[C] Energy production and conversion		
2572233267	t3m_01624	COG1012	NAD-dependent aldehyde dehydrogenases		3.00E-130
2572233267	t3m_01624	pfam00171	Aldedh		0.00E+00
2572233267	t3m_01624	EC:1.2.1.76	Succinate-semialdehyde dehydrogenase (acetylating).		
2572233267	t3m_01624	KO:K15038	succinyl-coA reductase [EC:1.2.1.76]		0.00E+00
2572233267	t3m_01624	Locus_type		CDS	
2572233267	t3m_01624	Product_name		NAD-dependent aldehyde dehydrogenases	
2572233267	t3m_01624	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47	
2572233267	t3m_01624	Coordinates		9368..10852(-)	
2572233267	t3m_01624	DNA_length		1485bp	
2572233267	t3m_01624	Protein_length		494aa	
2572233267	t3m_01624	GC		0.71	
2572233268	t3m_01625	KEGG_module	M00555: Betaine biosynthesis, choline => betaine		
2572233268	t3m_01625	Metacyc	PWY1F-353: glycine betaine biosynthesis III (plants)		
2572233268	t3m_01625	Metacyc	CHOLINE-BETAINE-ANA-PWY: choline degradation I		

2572233268	t3m_01625	Metacyc	PWY-3722: glycine betaine biosynthesis II (Gram-positive bacteria)			
2572233268	t3m_01625	Metacyc	BETSYN-PWY: glycine betaine biosynthesis I (Gram-negative bacteria)			
2572233268	t3m_01625	COG_category	[C] Energy production and conversion			
2572233268	t3m_01625	COG1012	NAD-dependent aldehyde dehydrogenases			0.00E+00
2572233268	t3m_01625	pfam00171	Aldedh			0.00E+00
2572233268	t3m_01625	EC:1.2.1.8	Betaine-aldehyde dehydrogenase.			
2572233268	t3m_01625	KO:K00130	betaine-aldehyde dehydrogenase [EC:1.2.1.8]			0.00E+00
2572233268	t3m_01625	Locus_type		CDS		
2572233268	t3m_01625	Product_name		NAD-dependent aldehyde dehydrogenases		
2572233268	t3m_01625	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47		
2572233268	t3m_01625	Coordinates		10861..12354(-)		
2572233268	t3m_01625	DNA_length		1494bp		
2572233268	t3m_01625	Protein_length		497aa		
2572233268	t3m_01625	GC			0.68	
2572233269	t3m_01626	Locus_type		CDS		
2572233269	t3m_01626	Product_name		hypothetical protein		
2572233269	t3m_01626	Scaffold		t3m_contig_70_638_len_13083_read_count_1168974.47		
2572233269	t3m_01626	Coordinates		12492..13082(+)		
2572233269	t3m_01626	DNA_length		591bp		
2572233269	t3m_01626	Protein_length		197aa		
2572233269	t3m_01626	GC			0.64	
2572233269	t3m_01626	Transmembrane		Yes		
2572233270	t3m_01627	Locus_type		tRNA		
2572233270	t3m_01627	Product_name		tRNA_Ala_CGC		
2572233270	t3m_01627	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233270	t3m_01627	Coordinates		2..73(-)		
2572233270	t3m_01627	DNA_length		72bp		
2572233270	t3m_01627	GC			0.6	
2572233271	t3m_01628	COG_category	[S] Function unknown			
2572233271	t3m_01628	COG4754	Uncharacterized conserved protein			8.00E-19
2572233271	t3m_01628	pfam09821	AAA_assoc_C			1.50E-25

2572233271	t3m_01628	Locus_type		CDS	
2572233271	t3m_01628	Product_name		Uncharacterized conserved protein	
2572233271	t3m_01628	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48	
2572233271	t3m_01628	Coordinates		193..813(-)	
2572233271	t3m_01628	DNA_length		621bp	
2572233271	t3m_01628	Protein_length		206aa	
2572233271	t3m_01628	GC		0.67	
2572233272	t3m_01629	KEGG_module	M00188: NitT/TauT family transport system		
2572233272	t3m_01629	COG_category	[P] Inorganic ion transport and metabolism		
2572233272	t3m_01629	COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase com		3.00E-80
2572233272	t3m_01629	pfam00005	ABC_tran		1.10E-29
2572233272	t3m_01629	KO:K02049	NitT/TauT family transport system ATP-binding protein		0.00E+00
2572233272	t3m_01629	Locus_type		CDS	
2572233272	t3m_01629	Product_name		ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase comp	
2572233272	t3m_01629	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48	
2572233272	t3m_01629	Coordinates		858..1691(-)	
2572233272	t3m_01629	DNA_length		834bp	
2572233272	t3m_01629	Protein_length		277aa	
2572233272	t3m_01629	GC		0.66	
2572233273	t3m_01630	KEGG_module	M00188: NitT/TauT family transport system		
2572233273	t3m_01630	COG_category	[P] Inorganic ion transport and metabolism		
2572233273	t3m_01630	COG4986	ABC-type anion transport system, duplicated permease component		2.00E-76
2572233273	t3m_01630	pfam00528	BPD_transp_1		8.30E-19
2572233273	t3m_01630	pfam00528	BPD_transp_1		2.70E-18
2572233273	t3m_01630	KO:K02050	NitT/TauT family transport system permease protein		0.00E+00
2572233273	t3m_01630	Locus_type		CDS	
2572233273	t3m_01630	Product_name		ABC-type anion transport system, duplicated permease component	
2572233273	t3m_01630	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48	
2572233273	t3m_01630	Coordinates		1704..3437(-)	
2572233273	t3m_01630	DNA_length		1734bp	
2572233273	t3m_01630	Protein_length		577aa	
2572233273	t3m_01630	GC		0.65	

2572233273	t3m_01630	Transmembrane		Yes		
2572233274	t3m_01631	Locus_type		tRNA		
2572233274	t3m_01631	Product_name		tRNA_Gln_CTG		
2572233274	t3m_01631	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233274	t3m_01631	Coordinates		3656..3728(+)		
2572233274	t3m_01631	DNA_length		73bp		
2572233274	t3m_01631	GC			0.63	
2572233275	t3m_01632	pfam00149	Metallophos			4.30E-08
2572233275	t3m_01632	Locus_type		CDS		
2572233275	t3m_01632	Product_name		Calcineurin-like phosphoesterase		
2572233275	t3m_01632	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233275	t3m_01632	Coordinates		3969..4868(+)		
2572233275	t3m_01632	DNA_length		900bp		
2572233275	t3m_01632	Protein_length		299aa		
2572233275	t3m_01632	GC			0.68	
2572233276	t3m_01633	COG_category	[S] Function unknown			
2572233276	t3m_01633	COG2042	Uncharacterized conserved protein			5.00E-42
2572233276	t3m_01633	pfam04068	RLI			7.30E-05
2572233276	t3m_01633	pfam04034	DUF367			2.60E-31
2572233276	t3m_01633	KO:K09140	pre-rRNA-processing protein TSR3			1.10E-26
2572233276	t3m_01633	Locus_type		CDS		
2572233276	t3m_01633	Product_name		Uncharacterized conserved protein		
2572233276	t3m_01633	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233276	t3m_01633	Coordinates		4960..5535(-)		
2572233276	t3m_01633	DNA_length		576bp		
2572233276	t3m_01633	Protein_length		191aa		
2572233276	t3m_01633	GC			0.7	
2572233277	t3m_01634	Metacyc	PWY66-373: sucrose degradation V (mammalian)			
2572233277	t3m_01634	Metacyc	SUCSYN-PWY: sucrose biosynthesis			
2572233277	t3m_01634	Metacyc	P341-PWY: glycolysis V (Pyrococcus)			

2572233277	t3m_01634	Metacyc	P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)		
2572233277	t3m_01634	Metacyc	PWY-1042: glycolysis IV (plant cytosol)		
2572233277	t3m_01634	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)		
2572233277	t3m_01634	Metacyc	CALVIN-PWY: Calvin-Benson-Bassham cycle		
2572233277	t3m_01634	Metacyc	GLUCONEO-PWY: gluconeogenesis I		
2572233277	t3m_01634	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2572233277	t3m_01634	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)		
2572233277	t3m_01634	Metacyc	PWY-5484: glycolysis II (from fructose-6P)		
2572233277	t3m_01634	Metacyc	GLYCOLYSIS: glycolysis I		
2572233277	t3m_01634	COG_category	[G] Carbohydrate transport and metabolism		
2572233277	t3m_01634	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes		6.00E-50
2572233277	t3m_01634	pfam01791	DeoC		4.20E-35
2572233277	t3m_01634	EC:4.1.2.13	Fructose-bisphosphate aldolase.		
2572233277	t3m_01634	KO:K11645	fructose-bisphosphate aldolase, class I [EC:4.1.2.13]		0.00E+00
2572233277	t3m_01634	Locus_type		CDS	
2572233277	t3m_01634	Product_name		DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	
2572233277	t3m_01634	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48	
2572233277	t3m_01634	Coordinates		5498..6346(-)	
2572233277	t3m_01634	DNA_length		849bp	
2572233277	t3m_01634	Protein_length		282aa	
2572233277	t3m_01634	GC		0.67	

2572233278	t3m_01635	COG_category	[P] Inorganic ion transport and metabolism		
2572233278	t3m_01635	COG0053	Predicted Co/Zn/Cd cation transporters		5.00E-24
2572233278	t3m_01635	pfam01545	Cation_efflux		1.60E-40
2572233278	t3m_01635	TIGR01297	cation diffusion facilitator family transporter		5.70E-42
2572233278	t3m_01635	Locus_type		CDS	
2572233278	t3m_01635	Product_name		Predicted Co/Zn/Cd cation transporters	
2572233278	t3m_01635	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48	
2572233278	t3m_01635	Coordinates		6669..7553(+)	
2572233278	t3m_01635	DNA_length		885bp	
2572233278	t3m_01635	Protein_length		294aa	
2572233278	t3m_01635	GC		0.68	
2572233278	t3m_01635	Transmembrane		Yes	

2572233279	t3m_01636	COG_category	[G] Carbohydrate transport and metabolism			
2572233279	t3m_01636	COG2814	Arabinose efflux permease			6.00E-07
2572233279	t3m_01636	pfam07690	MFS_1			2.90E-13
2572233279	t3m_01636	Locus_type		CDS		
2572233279	t3m_01636	Product_name		Arabinose efflux permease		
2572233279	t3m_01636	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233279	t3m_01636	Coordinates		7534..8799(-)		
2572233279	t3m_01636	DNA_length		1266bp		
2572233279	t3m_01636	Protein_length		421aa		
2572233279	t3m_01636	GC			0.68	
2572233279	t3m_01636	Transmembrane		Yes		

2572233280	t3m_01637	Metacyc	PWY-5386: methylglyoxal degradation I			
2572233280	t3m_01637	COG_category	[E] Amino acid transport and metabolism			
2572233280	t3m_01637	COG0346	Lactoylglutathione lyase and related lyases			1.00E-07
2572233280	t3m_01637	pfam00903	Glyoxalase			2.00E-16
2572233280	t3m_01637	EC:4.4.1.5	Lactoylglutathione lyase.			
2572233280	t3m_01637	TIGR00068	lactoylglutathione lyase			1.20E-29
2572233280	t3m_01637	KO:K01759	lactoylglutathione lyase [EC:4.4.1.5]			2.30E-19
2572233280	t3m_01637	Locus_type		CDS		
2572233280	t3m_01637	Product_name		Lactoylglutathione lyase and related lyases		
2572233280	t3m_01637	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233280	t3m_01637	Coordinates		8810..9199(-)		
2572233280	t3m_01637	DNA_length		390bp		
2572233280	t3m_01637	Protein_length		129aa		
2572233280	t3m_01637	GC			0.65	

2572233281	t3m_01638	KEGG_module	M00121: Heme biosynthesis, glutamate => protoheme/siroheme
2572233281	t3m_01638	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes
2572233281	t3m_01638	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes
2572233281	t3m_01638	Metacyc	PWY-5188: tetrapyrrole biosynthesis I (from glutamate)
2572233281	t3m_01638	Metacyc	TRNA-CHARGING-PWY: tRNA charging
2572233281	t3m_01638	IMG_pathway	350: tRNA-dependent glutamine synthesis

2572233281	t3m_01638	IMG_pathway	490: L-glutamate ligation to tRNA(Glu)			
2572233281	t3m_01638	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233281	t3m_01638	COG0008	Glutamyl- and glutaminyl-tRNA synthetases			1.00E-66
2572233281	t3m_01638	pfam03950	tRNA-synt_1c_C			1.80E-20
2572233281	t3m_01638	pfam00749	tRNA-synt_1c			1.30E-52
2572233281	t3m_01638	EC:6.1.1.17	Glutamate--tRNA ligase.			
2572233281	t3m_01638	TIGR00463	glutamyl-tRNA synthetase, archaeal and eukaryotic family			0.00E+00
2572233281	t3m_01638	KO:K01885	glutamyl-tRNA synthetase [EC:6.1.1.17]			0.00E+00
2572233281	t3m_01638	ITERM:00398	glutamyl-tRNA synthetase (EC 6.1.1.17)			
2572233281	t3m_01638	Locus_type		CDS		
2572233281	t3m_01638	Product_name		glutamyl-tRNA synthetase (EC 6.1.1.17)		
2572233281	t3m_01638	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233281	t3m_01638	Coordinates		9251..10981(-)		
2572233281	t3m_01638	DNA_length		1731bp		
2572233281	t3m_01638	Protein_length		576aa		
2572233281	t3m_01638	GC			0.69	

2572233282	t3m_01639	Locus_type		CDS		
2572233282	t3m_01639	Product_name		hypothetical protein		
2572233282	t3m_01639	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233282	t3m_01639	Coordinates		11005..11790(-)		
2572233282	t3m_01639	DNA_length		786bp		
2572233282	t3m_01639	Protein_length		261aa		
2572233282	t3m_01639	GC			0.7	

2572233283	t3m_01640	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233283	t3m_01640	COG2023	RNase P subunit RPR2			4.00E-16
2572233283	t3m_01640	pfam04032	Rpr2			1.80E-14
2572233283	t3m_01640	Locus_type		CDS		
2572233283	t3m_01640	Product_name		RNase P subunit RPR2		
2572233283	t3m_01640	Scaffold		t3m_contig_70_652_len_12777_read_count_1101433.48		
2572233283	t3m_01640	Coordinates		12278..12685(+)		
2572233283	t3m_01640	DNA_length		408bp		
2572233283	t3m_01640	Protein_length		135aa		

2572233283	t3m_01640	GC		0.67
2572233284	t3m_01641	Locus_type	CDS	
2572233284	t3m_01641	Product_name	hypothetical protein	
2572233284	t3m_01641	Scaffold	t3m_contig_70_663_len_12684_read_count_1130802.49	
2572233284	t3m_01641	Coordinates	1..1380(-)	
2572233284	t3m_01641	DNA_length	1380bp	
2572233284	t3m_01641	Protein_length	460aa	
2572233284	t3m_01641	GC		0.63
2572233285	t3m_01642	Locus_type	CDS	
2572233285	t3m_01642	Product_name	hypothetical protein	
2572233285	t3m_01642	Scaffold	t3m_contig_70_663_len_12684_read_count_1130802.49	
2572233285	t3m_01642	Coordinates	1541..1699(+)	
2572233285	t3m_01642	DNA_length	159bp	
2572233285	t3m_01642	Protein_length	52aa	
2572233285	t3m_01642	GC		0.65
2572233286	t3m_01643	Locus_type	CDS	
2572233286	t3m_01643	Product_name	hypothetical protein	
2572233286	t3m_01643	Scaffold	t3m_contig_70_663_len_12684_read_count_1130802.49	
2572233286	t3m_01643	Coordinates	2767..3381(+)	
2572233286	t3m_01643	DNA_length	615bp	
2572233286	t3m_01643	Protein_length	204aa	
2572233286	t3m_01643	GC		0.67
2572233286	t3m_01643	Signal_peptide	Yes	
2572233286	t3m_01643	Transmembrane	Yes	
2572233287	t3m_01644	Locus_type	CDS	
2572233287	t3m_01644	Product_name	hypothetical protein	
2572233287	t3m_01644	Scaffold	t3m_contig_70_663_len_12684_read_count_1130802.49	
2572233287	t3m_01644	Coordinates	3536..4126(+)	
2572233287	t3m_01644	DNA_length	591bp	
2572233287	t3m_01644	Protein_length	196aa	

2572233287	t3m_01644	GC			0.69	
2572233287	t3m_01644	Signal_peptide		Yes		
2572233287	t3m_01644	Transmembrane		Yes		
2572233288	t3m_01645	Locus_type		CDS		
2572233288	t3m_01645	Product_name		hypothetical protein		
2572233288	t3m_01645	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49		
2572233288	t3m_01645	Coordinates		4158..4703(+)		
2572233288	t3m_01645	DNA_length		546bp		
2572233288	t3m_01645	Protein_length		181aa		
2572233288	t3m_01645	GC			0.66	
2572233288	t3m_01645	Transmembrane		Yes		
2572233289	t3m_01646	COG_category	[P] Inorganic ion transport and metabolism			
2572233289	t3m_01646	COG0306	Phosphate/sulphate permeases			4.00E-38
2572233289	t3m_01646	pfam01384	PHO4			1.60E-44
2572233289	t3m_01646	KO:K03306	inorganic phosphate transporter, PiT family			3.50E-41
2572233289	t3m_01646	Locus_type		CDS		
2572233289	t3m_01646	Product_name		Phosphate/sulphate permeases		
2572233289	t3m_01646	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49		
2572233289	t3m_01646	Coordinates		4874..5857(+)		
2572233289	t3m_01646	DNA_length		984bp		
2572233289	t3m_01646	Protein_length		327aa		
2572233289	t3m_01646	GC			0.69	
2572233289	t3m_01646	Transmembrane		Yes		
2572233290	t3m_01647	COG_category	[R] General function prediction only			
2572233290	t3m_01647	COG1741	Pirin-related protein			3.00E-57
2572233290	t3m_01647	pfam02678	Pirin			3.20E-37
2572233290	t3m_01647	pfam05726	Pirin_C			3.10E-29
2572233290	t3m_01647	Locus_type		CDS		
2572233290	t3m_01647	Product_name		Pirin-related protein		
2572233290	t3m_01647	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49		
2572233290	t3m_01647	Coordinates		5950..6825(+)		

2572233290	t3m_01647	DNA_length		876bp	
2572233290	t3m_01647	Protein_length		291aa	
2572233290	t3m_01647	GC		0.66	
2572233291	t3m_01648	COG_category	[P] Inorganic ion transport and metabolism		
2572233291	t3m_01648	COG3376	High-affinity nickel permease		4.00E-92
2572233291	t3m_01648	pfam03824	NicO		1.30E-76
2572233291	t3m_01648	TIGR00802	high-affinity nickel-transporter, HoxN/HupN/NixA family		5.30E-104
2572233291	t3m_01648	KO:K07241	high-affinity nickel-transport protein		0.00E+00
2572233291	t3m_01648	Locus_type		CDS	
2572233291	t3m_01648	Product_name		high-affinity nickel-transporter, HoxN/HupN/NixA family	
2572233291	t3m_01648	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49	
2572233291	t3m_01648	Coordinates		6971..8068(+)	
2572233291	t3m_01648	DNA_length		1098bp	
2572233291	t3m_01648	Protein_length		365aa	
2572233291	t3m_01648	GC		0.65	
2572233291	t3m_01648	Transmembrane		Yes	
2572233292	t3m_01649	COG_category	[K] Transcription		
2572233292	t3m_01649	COG0864	Predicted transcriptional regulators containing the CopG/Arc/MetJ DNA		1.00E-20
2572233292	t3m_01649	pfam08753	NikR_C		3.30E-17
2572233292	t3m_01649	pfam01402	RHH_1		2.40E-06
2572233292	t3m_01649	TIGR02793	nickel-responsive transcriptional regulator NikR		1.60E-26
2572233292	t3m_01649	KO:K07722	CopG family transcriptional regulator, nickel-responsive regulator		1.50E-22
2572233292	t3m_01649	Locus_type		CDS	
2572233292	t3m_01649	Product_name		Predicted transcriptional regulators containing the CopG/Arc/MetJ DNA	
2572233292	t3m_01649	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49	
2572233292	t3m_01649	Coordinates		8065..8523(+)	
2572233292	t3m_01649	DNA_length		459bp	
2572233292	t3m_01649	Protein_length		152aa	
2572233292	t3m_01649	GC		0.71	
2572233293	t3m_01650	COG_category	[E] Amino acid transport and metabolism		
2572233293	t3m_01650	COG2309	Leucyl aminopeptidase (aminopeptidase T)		1.00E-12

2572233293	t3m_01650	pfam02073	Peptidase_M29			4.20E-07
2572233293	t3m_01650	Locus_type		CDS		
2572233293	t3m_01650	Product_name		Leucyl aminopeptidase (aminopeptidase T)		
2572233293	t3m_01650	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49		
2572233293	t3m_01650	Coordinates		8520..9671(+)		
2572233293	t3m_01650	DNA_length		1152bp		
2572233293	t3m_01650	Protein_length		383aa		
2572233293	t3m_01650	GC			0.72	
2572233294	t3m_01651	COG_category	[E] Amino acid transport and metabolism			
2572233294	t3m_01651	COG0685	5,10-methylenetetrahydrofolate reductase			9.00E-10
2572233294	t3m_01651	Locus_type		CDS		
2572233294	t3m_01651	Product_name		5,10-methylenetetrahydrofolate reductase		
2572233294	t3m_01651	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49		
2572233294	t3m_01651	Coordinates		9720..10649(-)		
2572233294	t3m_01651	DNA_length		930bp		
2572233294	t3m_01651	Protein_length		309aa		
2572233294	t3m_01651	GC			0.69	
2572233295	t3m_01652	KEGG_module	M00248: Putative antibiotic transport system			
2572233295	t3m_01652	COG_category	[V] Defense mechanisms			
2572233295	t3m_01652	COG1131	ABC-type multidrug transport system, ATPase component			1.00E-71
2572233295	t3m_01652	pfam00005	ABC_tran			6.00E-28
2572233295	t3m_01652	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2572233295	t3m_01652	Locus_type		CDS		
2572233295	t3m_01652	Product_name		ABC-type multidrug transport system, ATPase component		
2572233295	t3m_01652	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49		
2572233295	t3m_01652	Coordinates		10759..11805(+)		
2572233295	t3m_01652	DNA_length		1047bp		
2572233295	t3m_01652	Protein_length		348aa		
2572233295	t3m_01652	GC			0.67	
2572233296	t3m_01653	pfam12698	ABC2_membrane_3			4.60E-25
2572233296	t3m_01653	Locus_type		CDS		

2572233296	t3m_01653	Product_name		ABC-2 family transporter protein	
2572233296	t3m_01653	Scaffold		t3m_contig_70_663_len_12684_read_count_1130802.49	
2572233296	t3m_01653	Coordinates		11802..12683(+)	
2572233296	t3m_01653	DNA_length		882bp	
2572233296	t3m_01653	Protein_length		294aa	
2572233296	t3m_01653	GC			0.64
2572233296	t3m_01653	Transmembrane		Yes	
2572233297	t3m_01654	Locus_type		CDS	
2572233297	t3m_01654	Product_name		hypothetical protein	
2572233297	t3m_01654	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50	
2572233297	t3m_01654	Coordinates		3..188(+)	
2572233297	t3m_01654	DNA_length		186bp	
2572233297	t3m_01654	Protein_length		61aa	
2572233297	t3m_01654	GC			0.55
2572233298	t3m_01655	Locus_type		CDS	
2572233298	t3m_01655	Product_name		hypothetical protein	
2572233298	t3m_01655	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50	
2572233298	t3m_01655	Coordinates		208..603(+)	
2572233298	t3m_01655	DNA_length		396bp	
2572233298	t3m_01655	Protein_length		131aa	
2572233298	t3m_01655	GC			0.65
2572233299	t3m_01656	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233299	t3m_01656	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins		7.00E-22
2572233299	t3m_01656	pfam13302	Acetyltransf_3		4.90E-23
2572233299	t3m_01656	EC:2.3.1.128	Ribosomal-protein-alanine N-acetyltransferase.		
2572233299	t3m_01656	KO:K00676	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]		2.80E-15
2572233299	t3m_01656	Locus_type		CDS	
2572233299	t3m_01656	Product_name		Acetyltransferases, including N-acetylases of ribosomal proteins	
2572233299	t3m_01656	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50	
2572233299	t3m_01656	Coordinates		610..1161(+)	
2572233299	t3m_01656	DNA_length		552bp	

2572233299	t3m_01656	Protein_length		183aa		
2572233299	t3m_01656	GC			0.69	
2572233300	t3m_01657	COG_category	[R] General function prediction only			
2572233300	t3m_01657	COG2872	Predicted metal-dependent hydrolases related to alanyl-tRNA synthetas			3.00E-47
2572233300	t3m_01657	pfam01411	tRNA-synt_2c			5.00E-10
2572233300	t3m_01657	pfam07973	tRNA_SAD			1.50E-08
2572233300	t3m_01657	Locus_type		CDS		
2572233300	t3m_01657	Product_name		Predicted metal-dependent hydrolases related to alanyl-tRNA synthetas		
2572233300	t3m_01657	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233300	t3m_01657	Coordinates		1121..1876(-)		
2572233300	t3m_01657	DNA_length		756bp		
2572233300	t3m_01657	Protein_length		251aa		
2572233300	t3m_01657	GC			0.72	
2572233301	t3m_01658	KEGG_module	M00295: BRCA1-associated genome surveillance complex (BASC)			
2572233301	t3m_01658	COG_category	[L] Replication, recombination and repair			
2572233301	t3m_01658	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)			2.00E-19
2572233301	t3m_01658	pfam00705	PCNA_N			3.00E-11
2572233301	t3m_01658	KO:K04802	proliferating cell nuclear antigen			0.00E+00
2572233301	t3m_01658	Locus_type		CDS		
2572233301	t3m_01658	Product_name		DNA polymerase sliding clamp subunit (PCNA homolog)		
2572233301	t3m_01658	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233301	t3m_01658	Coordinates		1974..2705(+)		
2572233301	t3m_01658	DNA_length		732bp		
2572233301	t3m_01658	Protein_length		243aa		
2572233301	t3m_01658	GC			0.64	
2572233302	t3m_01659	KEGG_module	M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone			
2572233302	t3m_01659	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			
2572233302	t3m_01659	KEGG_module	M00375: Hydroxypropionate-hydroxybutylate cycle			
2572233302	t3m_01659	KEGG_module	M00373: Ethylmalonyl pathway			
2572233302	t3m_01659	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			
2572233302	t3m_01659	Metacyc	PWY-6883: pyruvate fermentation to butanol II			

2572233302	t3m_01659	Metacyc	PWY66-367: ketogenesis			
2572233302	t3m_01659	Metacyc	ILEUDEG-PWY: isoleucine degradation I			
2572233302	t3m_01659	Metacyc	PWY-922: mevalonate pathway I			
2572233302	t3m_01659	Metacyc	PWY-5741: ethylmalonyl pathway			
2572233302	t3m_01659	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate			
2572233302	t3m_01659	Metacyc	PWY-6583: pyruvate fermentation to butanol I			
2572233302	t3m_01659	Metacyc	ACETOACETATE-DEG-PWY: acetoacetate degradation (to acetyl CoA)			
2572233302	t3m_01659	Metacyc	PWY-6174: mevalonate pathway II (archaea)			
2572233302	t3m_01659	Metacyc	PWY-6876: isopropanol biosynthesis			
2572233302	t3m_01659	Metacyc	PWY-5676: acetyl-CoA fermentation to butyrate II			
2572233302	t3m_01659	Metacyc	PWY-6588: pyruvate fermentation to acetone			
2572233302	t3m_01659	Metacyc	PWY-5789: 3-hydroxypropionate/4-hydroxybutyrate cycle			
2572233302	t3m_01659	Metacyc	P163-PWY: lysine fermentation to acetate and butyrate			
2572233302	t3m_01659	Metacyc	PWY66-368: ketolysis			
2572233302	t3m_01659	Metacyc	PWY1-3: polyhydroxybutyrate biosynthesis			
2572233302	t3m_01659	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis			
2572233302	t3m_01659	Metacyc	PWY-6863: pyruvate fermentation to hexanol			
2572233302	t3m_01659	Metacyc	PWY-7003: glycerol degradation to butanol			
2572233302	t3m_01659	Metacyc	PWY-5177: glutaryl-CoA degradation			
2572233302	t3m_01659	COG_category	[I] Lipid transport and metabolism			
2572233302	t3m_01659	COG0183	Acetyl-CoA acetyltransferase			8.00E-79
2572233302	t3m_01659	pfam00108	Thiolase_N			3.80E-82
2572233302	t3m_01659	pfam02803	Thiolase_C			1.30E-38
2572233302	t3m_01659	EC:2.3.1.9	Acetyl-CoA C-acetyltransferase.			
2572233302	t3m_01659	TIGR01930	acetyl-CoA acetyltransferases			2.10E-125
2572233302	t3m_01659	KO:K00626	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]			0.00E+00
2572233302	t3m_01659	Locus_type		CDS		
2572233302	t3m_01659	Product_name		acetyl-CoA acetyltransferases		
2572233302	t3m_01659	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233302	t3m_01659	Coordinates		2792..3997(+)		
2572233302	t3m_01659	DNA_length		1206bp		
2572233302	t3m_01659	Protein_length		401aa		
2572233302	t3m_01659	GC			0.7	

2572233303	t3m_01660	Metacyc	PWY1G-0: mycothiol biosynthesis			
2572233303	t3m_01660	IMG_pathway	488: L-cysteine ligation to tRNA(Cys)			
2572233303	t3m_01660	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233303	t3m_01660	COG0215	Cysteinyl-tRNA synthetase			1.00E-87
2572233303	t3m_01660	pfam01406	tRNA-synt_1e			8.30E-73
2572233303	t3m_01660	EC:6.3.1.13	L-cysteine:1D-myo-inositol 2-amino-2-deoxy-alpha-D-glucopyranoside ligase.			
2572233303	t3m_01660	KO:K15526	L-cysteine:1D-myo-inositol 2-amino-2-deoxy-alpha-D-glucopyranoside l			0.00E+00
2572233303	t3m_01660	ITERM:00404	cysteinyl-tRNA synthetase (EC 6.1.1.16)			
2572233303	t3m_01660	Locus_type		CDS		
2572233303	t3m_01660	Product_name		cysteinyl-tRNA synthetase (EC 6.1.1.16)		
2572233303	t3m_01660	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233303	t3m_01660	Coordinates		3975..5216(-)		
2572233303	t3m_01660	DNA_length		1242bp		
2572233303	t3m_01660	Protein_length		413aa		
2572233303	t3m_01660	GC			0.72	
2572233304	t3m_01661	pfam01037	AsnC_trans_reg			4.50E-16
2572233304	t3m_01661	Locus_type		CDS		
2572233304	t3m_01661	Product_name		AsnC family		
2572233304	t3m_01661	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233304	t3m_01661	Coordinates		5333..5569(+)		
2572233304	t3m_01661	DNA_length		237bp		
2572233304	t3m_01661	Protein_length		78aa		
2572233304	t3m_01661	GC			0.67	
2572233305	t3m_01662	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233305	t3m_01662	COG1225	Peroxiredoxin			2.00E-40
2572233305	t3m_01662	pfam00578	AhpC-TSA			6.20E-38
2572233305	t3m_01662	EC:1.11.1.15	Peroxiredoxin.			
2572233305	t3m_01662	KO:K03564	peroxiredoxin Q/BCP [EC:1.11.1.15]			8.70E-31
2572233305	t3m_01662	Locus_type		CDS		
2572233305	t3m_01662	Product_name		Peroxiredoxin		
2572233305	t3m_01662	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233305	t3m_01662	Coordinates		5624..6064(+)		

2572233305	t3m_01662	DNA_length		441bp		
2572233305	t3m_01662	Protein_length		146aa		
2572233305	t3m_01662	GC			0.68	

2572233306	t3m_01663	pfam03176	MMPL			1.80E-35
2572233306	t3m_01663	pfam03176	MMPL			3.60E-38
2572233306	t3m_01663	Locus_type		CDS		
2572233306	t3m_01663	Product_name		MMPL family		
2572233306	t3m_01663	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233306	t3m_01663	Coordinates		6054..9143(-)		
2572233306	t3m_01663	DNA_length		3090bp		
2572233306	t3m_01663	Protein_length		1029aa		
2572233306	t3m_01663	GC			0.69	
2572233306	t3m_01663	Transmembrane		Yes		

2572233307	t3m_01664	KEGG_module	M00425: H/ACA ribonucleoprotein complex			
2572233307	t3m_01664	Metacyc	RIBOKIN-PWY: ribose degradation			
2572233307	t3m_01664	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233307	t3m_01664	COG0130	Pseudouridine synthase			4.00E-56
2572233307	t3m_01664	pfam01509	TruB_N			3.30E-10
2572233307	t3m_01664	pfam01472	PUA			5.80E-12
2572233307	t3m_01664	EC:5.4.99.-	Isomerases. Intramolecular transferases (mutases). Transferring other groups.			
2572233307	t3m_01664	TIGR00425	rRNA pseudouridine synthase, putative			1.50E-84
2572233307	t3m_01664	KO:K11131	H/ACA ribonucleoprotein complex subunit 4 [EC:5.4.99.-]			0.00E+00
2572233307	t3m_01664	ITERM:05206	tRNA pseudouridine synthase B (EC 4.2.1.70)			
2572233307	t3m_01664	Locus_type		CDS		
2572233307	t3m_01664	Product_name		tRNA pseudouridine synthase B (EC 4.2.1.70)		
2572233307	t3m_01664	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233307	t3m_01664	Coordinates		9175..10134(-)		
2572233307	t3m_01664	DNA_length		960bp		
2572233307	t3m_01664	Protein_length		319aa		
2572233307	t3m_01664	GC			0.74	

2572233308	t3m_01665	KEGG_module	M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP			

2572233308	t3m_01665	COG_category	[F] Nucleotide transport and metabolism			
2572233308	t3m_01665	COG1102	Cytidylate kinase			2.00E-33
2572233308	t3m_01665	pfam13207	AAA_17			1.10E-10
2572233308	t3m_01665	EC:2.7.4.14	UMP/CMP kinase.			
2572233308	t3m_01665	TIGR02173	cytidylate kinase, putative			6.40E-36
2572233308	t3m_01665	KO:K00945	cytidylate kinase [EC:2.7.4.14]			1.40E-26
2572233308	t3m_01665	Locus_type		CDS		
2572233308	t3m_01665	Product_name		cytidylate kinase, putative		
2572233308	t3m_01665	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233308	t3m_01665	Coordinates		10131..10679(-)		
2572233308	t3m_01665	DNA_length		549bp		
2572233308	t3m_01665	Protein_length		182aa		
2572233308	t3m_01665	GC			0.71	
2572233309	t3m_01666	COG_category	[S] Function unknown			
2572233309	t3m_01666	COG1422	Predicted membrane protein			1.00E-13
2572233309	t3m_01666	pfam01956	DUF106			2.10E-11
2572233309	t3m_01666	Locus_type		CDS		
2572233309	t3m_01666	Product_name		Predicted membrane protein		
2572233309	t3m_01666	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233309	t3m_01666	Coordinates		10676..11527(-)		
2572233309	t3m_01666	DNA_length		852bp		
2572233309	t3m_01666	Protein_length		283aa		
2572233309	t3m_01666	GC			0.66	
2572233309	t3m_01666	Transmembrane		Yes		
2572233310	t3m_01667	pfam00344	SecY			5.60E-69
2572233310	t3m_01667	Locus_type		CDS		
2572233310	t3m_01667	Product_name		SecY translocase		
2572233310	t3m_01667	Scaffold		t3m_contig_70_671_len_12624_read_count_988736.50		
2572233310	t3m_01667	Coordinates		11527..12621(-)		
2572233310	t3m_01667	DNA_length		1095bp		
2572233310	t3m_01667	Protein_length		364aa		
2572233310	t3m_01667	GC			0.66	

2572233310	t3m_01667	Transmembrane		Yes		
2572233311	t3m_01668	pfam04055	Radical_SAM			5.10E-18
2572233311	t3m_01668	Locus_type		CDS		
2572233311	t3m_01668	Product_name		Radical SAM superfamily		
2572233311	t3m_01668	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51		
2572233311	t3m_01668	Coordinates		1..966(+)		
2572233311	t3m_01668	DNA_length		966bp		
2572233311	t3m_01668	Protein_length		321aa		
2572233311	t3m_01668	GC			0.64	
2572233312	t3m_01669	COG_category	[R] General function prediction only			
2572233312	t3m_01669	COG1310	Predicted metal-dependent protease of the PAD1/JAB1 superfamily			9.00E-15
2572233312	t3m_01669	pfam14464	Prok-JAB			5.70E-15
2572233312	t3m_01669	Locus_type		CDS		
2572233312	t3m_01669	Product_name		Predicted metal-dependent protease of the PAD1/JAB1 superfamily		
2572233312	t3m_01669	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51		
2572233312	t3m_01669	Coordinates		996..1529(-)		
2572233312	t3m_01669	DNA_length		534bp		
2572233312	t3m_01669	Protein_length		177aa		
2572233312	t3m_01669	GC			0.71	
2572233313	t3m_01670	Metacyc	NADPHOS-DEPHOS-PWY: NAD phosphorylation and dephosphorylation			
2572233313	t3m_01670	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572233313	t3m_01670	COG_category	[G] Carbohydrate transport and metabolism			
2572233313	t3m_01670	COG0061	Predicted sugar kinase			6.00E-49
2572233313	t3m_01670	pfam01513	NAD_kinase			4.60E-43
2572233313	t3m_01670	EC:2.7.1.23	NAD(+) kinase.			
2572233313	t3m_01670	KO:K00858	NAD+ kinase [EC:2.7.1.23]			2.40E-44
2572233313	t3m_01670	Locus_type		CDS		
2572233313	t3m_01670	Product_name		Predicted sugar kinase		
2572233313	t3m_01670	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51		
2572233313	t3m_01670	Coordinates		1504..2412(-)		
2572233313	t3m_01670	DNA_length		909bp		

2572233313	t3m_01670	Protein_length		302aa	
2572233313	t3m_01670	GC		0.69	
2572233314	t3m_01671	KEGG_module	M00131: Inositol phosphate metabolism, Ins(1,3,4,5)P4 => Ins(1,3,4)P3 => myo-inositol		
2572233314	t3m_01671	Metacyc	PWY-2301: <i>myo</i>-inositol biosynthesis		
2572233314	t3m_01671	Metacyc	PWY-4702: phytate degradation I		
2572233314	t3m_01671	Metacyc	PWY-6363: D-<i>myo</i>-inositol (1,4,5)-trisphosphate degradation		
2572233314	t3m_01671	COG_category	[G] Carbohydrate transport and metabolism		
2572233314	t3m_01671	COG0483	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol n		2.00E-35
2572233314	t3m_01671	pfam00459	Inositol_P		1.70E-32
2572233314	t3m_01671	EC:3.1.3.25	Inositol-phosphate phosphatase.		
2572233314	t3m_01671	KO:K01092	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]		2.10E-39
2572233314	t3m_01671	Locus_type		CDS	
2572233314	t3m_01671	Product_name		Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol m	
2572233314	t3m_01671	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51	
2572233314	t3m_01671	Coordinates		2379..3191(-)	
2572233314	t3m_01671	DNA_length		813bp	
2572233314	t3m_01671	Protein_length		270aa	
2572233314	t3m_01671	GC		0.7	
2572233315	t3m_01672	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233315	t3m_01672	COG1236	Predicted exonuclease of the beta-lactamase fold involved in RNA proc		2.00E-81
2572233315	t3m_01672	pfam07521	RMMBL		7.70E-11
2572233315	t3m_01672	pfam10996	Beta-Casp		7.30E-17
2572233315	t3m_01672	pfam00753	Lactamase_B		7.40E-13
2572233315	t3m_01672	KO:K07577	putative mRNA 3-end processing factor		0.00E+00
2572233315	t3m_01672	Locus_type		CDS	
2572233315	t3m_01672	Product_name		Predicted exonuclease of the beta-lactamase fold involved in RNA proce	
2572233315	t3m_01672	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51	
2572233315	t3m_01672	Coordinates		3277..4509(+)	
2572233315	t3m_01672	DNA_length		1233bp	
2572233315	t3m_01672	Protein_length		410aa	
2572233315	t3m_01672	GC		0.68	

2572233316	t3m_01673	COG_category	[R] General function prediction only			
2572233316	t3m_01673	COG1084	Predicted GTPase			3.00E-54
2572233316	t3m_01673	pfam01926	MMR_HSR1			7.90E-16
2572233316	t3m_01673	TIGR00231	small GTP-binding protein domain			3.90E-13
2572233316	t3m_01673	KO:K06943	nucleolar GTP-binding protein			0.00E+00
2572233316	t3m_01673	Locus_type		CDS		
2572233316	t3m_01673	Product_name		Predicted GTPase		
2572233316	t3m_01673	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51		
2572233316	t3m_01673	Coordinates		4569..5669(-)		
2572233316	t3m_01673	DNA_length		1101bp		
2572233316	t3m_01673	Protein_length		366aa		
2572233316	t3m_01673	GC			0.7	
2572233317	t3m_01674	Metacyc	GLYCLEAV-PWY: glycine cleavage			
2572233317	t3m_01674	COG_category	[E] Amino acid transport and metabolism			
2572233317	t3m_01674	COG0403	Glycine cleavage system protein P (pyridoxal-binding), N-terminal doma			2.00E-109
2572233317	t3m_01674	pfam02347	GDC-P			2.60E-102
2572233317	t3m_01674	EC:1.4.4.2	Glycine dehydrogenase (decarboxylating).			
2572233317	t3m_01674	KO:K00282	glycine dehydrogenase subunit 1 [EC:1.4.4.2]			0.00E+00
2572233317	t3m_01674	Locus_type		CDS		
2572233317	t3m_01674	Product_name		Glycine cleavage system protein P (pyridoxal-binding), N-terminal domai		
2572233317	t3m_01674	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51		
2572233317	t3m_01674	Coordinates		5815..7197(+)		
2572233317	t3m_01674	DNA_length		1383bp		
2572233317	t3m_01674	Protein_length		460aa		
2572233317	t3m_01674	GC			0.7	
2572233318	t3m_01675	Metacyc	GLYCLEAV-PWY: glycine cleavage			
2572233318	t3m_01675	COG_category	[E] Amino acid transport and metabolism			
2572233318	t3m_01675	COG1003	Glycine cleavage system protein P (pyridoxal-binding), C-terminal doma			0.00E+00
2572233318	t3m_01675	pfam02347	GDC-P			4.00E-16
2572233318	t3m_01675	EC:1.4.4.2	Glycine dehydrogenase (decarboxylating).			
2572233318	t3m_01675	KO:K00283	glycine dehydrogenase subunit 2 [EC:1.4.4.2]			0.00E+00
2572233318	t3m_01675	ITERM:02613	glycine dehydrogenase (decarboxylating) beta subunit (EC 1.4.4.2)			

2572233318	t3m_01675	Locus_type		CDS		
2572233318	t3m_01675	Product_name		glycine dehydrogenase (decarboxylating) beta subunit (EC 1.4.4.2)		
2572233318	t3m_01675	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51		
2572233318	t3m_01675	Coordinates		7194..8660(+)		
2572233318	t3m_01675	DNA_length		1467bp		
2572233318	t3m_01675	Protein_length		488aa		
2572233318	t3m_01675	GC			0.68	
2572233319	t3m_01676	COG_category	[E] Amino acid transport and metabolism			
2572233319	t3m_01676	COG0006	Xaa-Pro aminopeptidase			5.00E-69
2572233319	t3m_01676	pfam01321	Creatinase_N			2.00E-04
2572233319	t3m_01676	pfam00557	Peptidase_M24			9.70E-59
2572233319	t3m_01676	EC:3.4.13.9	Xaa-Pro dipeptidase.			
2572233319	t3m_01676	KO:K01271	Xaa-Pro dipeptidase [EC:3.4.13.9]			0.00E+00
2572233319	t3m_01676	Locus_type		CDS		
2572233319	t3m_01676	Product_name		Xaa-Pro aminopeptidase		
2572233319	t3m_01676	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51		
2572233319	t3m_01676	Coordinates		8676..9782(+)		
2572233319	t3m_01676	DNA_length		1107bp		
2572233319	t3m_01676	Protein_length		368aa		
2572233319	t3m_01676	GC			0.68	
2572233320	t3m_01677	KEGG_module	M00345: Formaldehyde assimilation, ribulose monophosphate pathway			
2572233320	t3m_01677	KEGG_module	M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate			
2572233320	t3m_01677	Metacyc	PWY-5484: glycolysis II (from fructose-6P)			
2572233320	t3m_01677	Metacyc	GLYCOLYSIS: glycolysis I			
2572233320	t3m_01677	Metacyc	PWY-1861: formaldehyde assimilation II (RuMP Cycle)			
2572233320	t3m_01677	Metacyc	ANAGLYCOLYSIS-PWY: glycolysis III (glucokinase)			
2572233320	t3m_01677	Metacyc	PWY-1042: glycolysis IV (plant cytosol)			
2572233320	t3m_01677	COG_category	[G] Carbohydrate transport and metabolism			
2572233320	t3m_01677	COG0205	6-phosphofructokinase			7.00E-78
2572233320	t3m_01677	pfam00365	PFK			2.10E-73
2572233320	t3m_01677	EC:2.7.1.11	6-phosphofructokinase.			
2572233320	t3m_01677	KO:K00850	6-phosphofructokinase 1 [EC:2.7.1.11]			0.00E+00

2572233320	t3m_01677	Locus_type		CDS	
2572233320	t3m_01677	Product_name		6-phosphofructokinase	
2572233320	t3m_01677	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51	
2572233320	t3m_01677	Coordinates		9779..10801(+)	
2572233320	t3m_01677	DNA_length		1023bp	
2572233320	t3m_01677	Protein_length		340aa	
2572233320	t3m_01677	GC		0.71	

2572233321	t3m_01678	KEGG_module	M00034: Methionine salvage pathway		
2572233321	t3m_01678	Metacyc	PWY-6755: <i>S</i>-methyl-5-thio-α-D-ribose 1-phosphate degradation I		
2572233321	t3m_01678	Metacyc	PWY-7174: <i>S</i>-methyl-5-thio-α-D-ribose 1-phosphate degradation II		
2572233321	t3m_01678	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233321	t3m_01678	COG0182	Predicted translation initiation factor 2B subunit, eIF-2B alpha/beta/del		6.00E-103
2572233321	t3m_01678	pfam01008	IF-2B		9.20E-62
2572233321	t3m_01678	EC:5.3.1.23	S-methyl-5-thioribose-1-phosphate isomerase.		
2572233321	t3m_01678	TIGR00512	S-methyl-5-thioribose-1-phosphate isomerase		2.30E-117
2572233321	t3m_01678	TIGR00524	eIF-2B alpha/beta/delta-related uncharacterized proteins		8.10E-98
2572233321	t3m_01678	KO:K08963	methylthioribose-1-phosphate isomerase [EC:5.3.1.23]		0.00E+00
2572233321	t3m_01678	ITERM:02585	translation initiation factor 2B subunit I family (IF-2BI)		
2572233321	t3m_01678	Locus_type		CDS	
2572233321	t3m_01678	Product_name		translation initiation factor 2B subunit I family (IF-2BI)	
2572233321	t3m_01678	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51	
2572233321	t3m_01678	Coordinates		10811..11803(+)	
2572233321	t3m_01678	DNA_length		993bp	
2572233321	t3m_01678	Protein_length		330aa	
2572233321	t3m_01678	GC		0.72	

2572233322	t3m_01679	Locus_type		CDS	
2572233322	t3m_01679	Product_name		hypothetical protein	
2572233322	t3m_01679	Scaffold		t3m_contig_70_707_len_12253_read_count_885831.51	
2572233322	t3m_01679	Coordinates		11830..11982(-)	
2572233322	t3m_01679	DNA_length		153bp	
2572233322	t3m_01679	Protein_length		50aa	
2572233322	t3m_01679	GC		0.65	

2572233322	t3m_01679	Transmembrane		Yes		
2572233323	t3m_01680	pfam13522	GATase_6			1.10E-14
2572233323	t3m_01680	Locus_type		CDS		
2572233323	t3m_01680	Product_name		Glutamine amidotransferase domain		
2572233323	t3m_01680	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233323	t3m_01680	Coordinates		2..451(-)		
2572233323	t3m_01680	DNA_length		450bp		
2572233323	t3m_01680	Protein_length		150aa		
2572233323	t3m_01680	GC			0.69	
2572233324	t3m_01681	KEGG_module	M00179: Ribosome, archaea			
2572233324	t3m_01681	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233324	t3m_01681	COG2058	Ribosomal protein L12E/L44/L45/RPP1/RPP2			2.00E-07
2572233324	t3m_01681	pfam00428	Ribosomal_60s			1.10E-13
2572233324	t3m_01681	TIGR03685	50S ribosomal protein L12P			1.70E-37
2572233324	t3m_01681	KO:K02869	large subunit ribosomal protein L12			6.00E-27
2572233324	t3m_01681	Locus_type		CDS		
2572233324	t3m_01681	Product_name		LSU ribosomal protein L12AE		
2572233324	t3m_01681	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233324	t3m_01681	Coordinates		537..851(-)		
2572233324	t3m_01681	DNA_length		315bp		
2572233324	t3m_01681	Protein_length		104aa		
2572233324	t3m_01681	GC			0.68	
2572233325	t3m_01682	KEGG_module	M00179: Ribosome, archaea			
2572233325	t3m_01682	KEGG_module	M00178: Ribosome, bacteria			
2572233325	t3m_01682	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233325	t3m_01682	COG0244	Ribosomal protein L10			2.00E-18
2572233325	t3m_01682	pfam00466	Ribosomal_L10			8.70E-12
2572233325	t3m_01682	KO:K02864	large subunit ribosomal protein L10			0.00E+00
2572233325	t3m_01682	ITERM:00276	LSU ribosomal protein L10P			
2572233325	t3m_01682	Locus_type		CDS		
2572233325	t3m_01682	Product_name		LSU ribosomal protein L10P		

2572233325	t3m_01682	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52	
2572233325	t3m_01682	Coordinates		883..1743(-)	
2572233325	t3m_01682	DNA_length		861bp	
2572233325	t3m_01682	Protein_length		286aa	
2572233325	t3m_01682	GC		0.7	
2572233326	t3m_01683	KEGG_module	M00178: Ribosome, bacteria		
2572233326	t3m_01683	KEGG_module	M00179: Ribosome, archaea		
2572233326	t3m_01683	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233326	t3m_01683	COG0081	Ribosomal protein L1		4.00E-41
2572233326	t3m_01683	pfam00687	Ribosomal_L1		1.20E-42
2572233326	t3m_01683	KO:K02863	large subunit ribosomal protein L1		0.00E+00
2572233326	t3m_01683	ITERM:00163	LSU ribosomal protein L1P		
2572233326	t3m_01683	Locus_type		CDS	
2572233326	t3m_01683	Product_name		LSU ribosomal protein L1P	
2572233326	t3m_01683	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52	
2572233326	t3m_01683	Coordinates		1754..2383(-)	
2572233326	t3m_01683	DNA_length		630bp	
2572233326	t3m_01683	Protein_length		209aa	
2572233326	t3m_01683	GC		0.66	
2572233327	t3m_01684	KEGG_module	M00177: Ribosome, eukaryotes		
2572233327	t3m_01684	KEGG_module	M00179: Ribosome, archaea		
2572233327	t3m_01684	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233327	t3m_01684	COG1631	Ribosomal protein L44E		1.00E-23
2572233327	t3m_01684	pfam00935	Ribosomal_L44		8.80E-28
2572233327	t3m_01684	KO:K02929	large subunit ribosomal protein L44e		8.30E-28
2572233327	t3m_01684	ITERM:00274	LSU ribosomal protein L44E		
2572233327	t3m_01684	Locus_type		CDS	
2572233327	t3m_01684	Product_name		LSU ribosomal protein L44E	
2572233327	t3m_01684	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52	
2572233327	t3m_01684	Coordinates		2636..2920(+)	
2572233327	t3m_01684	DNA_length		285bp	
2572233327	t3m_01684	Protein_length		94aa	

2572233327	t3m_01684	GC			0.66	
2572233328	t3m_01685	KEGG_module	M00177: Ribosome, eukaryotes			
2572233328	t3m_01685	KEGG_module	M00179: Ribosome, archaea			
2572233328	t3m_01685	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233328	t3m_01685	COG2051	Ribosomal protein S27E			2.00E-12
2572233328	t3m_01685	pfam01667	Ribosomal_S27e			7.00E-20
2572233328	t3m_01685	KO:K02978	small subunit ribosomal protein S27e			1.10E-11
2572233328	t3m_01685	Locus_type		CDS		
2572233328	t3m_01685	Product_name		SSU ribosomal protein S27E		
2572233328	t3m_01685	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233328	t3m_01685	Coordinates		2931..3107(+)		
2572233328	t3m_01685	DNA_length		177bp		
2572233328	t3m_01685	Protein_length		58aa		
2572233328	t3m_01685	GC			0.7	
2572233329	t3m_01686	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233329	t3m_01686	COG1093	Translation initiation factor 2, alpha subunit (eIF-2alpha)			7.00E-74
2572233329	t3m_01686	pfam07541	EIF_2_alpha			5.40E-22
2572233329	t3m_01686	pfam00575	S1			8.90E-15
2572233329	t3m_01686	KO:K03237	translation initiation factor 2 subunit 1			0.00E+00
2572233329	t3m_01686	ITERM:01963	translation initiation factor 2 subunit alpha (aeIF-2a)			
2572233329	t3m_01686	Locus_type		CDS		
2572233329	t3m_01686	Product_name		translation initiation factor 2 subunit alpha (aeIF-2a)		
2572233329	t3m_01686	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233329	t3m_01686	Coordinates		3127..3903(+)		
2572233329	t3m_01686	DNA_length		777bp		
2572233329	t3m_01686	Protein_length		258aa		
2572233329	t3m_01686	GC			0.66	
2572233330	t3m_01687	KEGG_module	M00425: H/ACA ribonucleoprotein complex			
2572233330	t3m_01687	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233330	t3m_01687	COG2260	Predicted Zn-ribbon RNA-binding protein			1.00E-09
2572233330	t3m_01687	pfam04135	Nop10p			5.30E-18

2572233330	t3m_01687	KO:K11130	H/ACA ribonucleoprotein complex subunit 3			6.60E-10
2572233330	t3m_01687	Locus_type		CDS		
2572233330	t3m_01687	Product_name		Predicted Zn-ribbon RNA-binding protein		
2572233330	t3m_01687	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233330	t3m_01687	Coordinates		3900..4085(+)		
2572233330	t3m_01687	DNA_length		186bp		
2572233330	t3m_01687	Protein_length		61aa		
2572233330	t3m_01687	GC			0.69	

2572233331	t3m_01688	COG_category	[S] Function unknown			
2572233331	t3m_01688	COG4860	Uncharacterized protein conserved in archaea			3.00E-30
2572233331	t3m_01688	pfam09824	ArsR			7.40E-38
2572233331	t3m_01688	Locus_type		CDS		
2572233331	t3m_01688	Product_name		Uncharacterized protein conserved in archaea		
2572233331	t3m_01688	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233331	t3m_01688	Coordinates		4088..4615(+)		
2572233331	t3m_01688	DNA_length		528bp		
2572233331	t3m_01688	Protein_length		175aa		
2572233331	t3m_01688	GC			0.64	

2572233332	t3m_01689	COG_category	[S] Function unknown			
2572233332	t3m_01689	COG1303	Uncharacterized protein conserved in archaea			6.00E-47
2572233332	t3m_01689	pfam01994	Trm56			2.20E-34
2572233332	t3m_01689	EC:2.1.1.206	tRNA (cytidine(56)-2'-O)-methyltransferase.			
2572233332	t3m_01689	KO:K07254	tRNA (cytidine56-2'-O)-methyltransferase [EC:2.1.1.206]			1.90E-42
2572233332	t3m_01689	Locus_type		CDS		
2572233332	t3m_01689	Product_name		Uncharacterized protein conserved in archaea		
2572233332	t3m_01689	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233332	t3m_01689	Coordinates		4569..5144(+)		
2572233332	t3m_01689	DNA_length		576bp		
2572233332	t3m_01689	Protein_length		191aa		
2572233332	t3m_01689	GC			0.73	

2572233333	t3m_01690	KEGG_module	M00095: C5 isoprenoid biosynthesis, mevalonate pathway			

2572233333	t3m_01690	Metacyc	PWY-6174: mevalonate pathway II (archaea)			
2572233333	t3m_01690	Metacyc	PWY-922: mevalonate pathway I			
2572233333	t3m_01690	IMG_pathway	178: Mevalonate pathway for isopentenyl pyrophopsphate synthesis			
2572233333	t3m_01690	IMG_pathway	591: Archaeal mevalonate pathway for isopentenyl pyrophosphate synthesis			
2572233333	t3m_01690	COG_category	[I] Lipid transport and metabolism			
2572233333	t3m_01690	COG1577	Mevalonate kinase			5.00E-39
2572233333	t3m_01690	pfam00288	GHMP_kinases_N			1.60E-13
2572233333	t3m_01690	pfam08544	GHMP_kinases_C			9.60E-10
2572233333	t3m_01690	EC:2.7.1.36	Mevalonate kinase.			
2572233333	t3m_01690	TIGR00549	mevalonate kinase			5.90E-52
2572233333	t3m_01690	KO:K00869	mevalonate kinase [EC:2.7.1.36]			2.30E-40
2572233333	t3m_01690	ITERM:00464	mevalonate kinase (EC 2.7.1.36)			
2572233333	t3m_01690	Locus_type		CDS		
2572233333	t3m_01690	Product_name		mevalonate kinase (EC 2.7.1.36)		
2572233333	t3m_01690	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233333	t3m_01690	Coordinates		5141..6112(+)		
2572233333	t3m_01690	DNA_length		972bp		
2572233333	t3m_01690	Protein_length		323aa		
2572233333	t3m_01690	GC			0.73	
2572233334	t3m_01691	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233334	t3m_01691	COG0012	Predicted GTPase, probable translation factor			1.00E-76
2572233334	t3m_01691	pfam01926	MMR_HSR1			6.40E-18
2572233334	t3m_01691	pfam08438	MMR_HSR1_C			5.40E-29
2572233334	t3m_01691	Locus_type		CDS		
2572233334	t3m_01691	Product_name		Predicted GTPase, probable translation factor		
2572233334	t3m_01691	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233334	t3m_01691	Coordinates		6136..7332(-)		
2572233334	t3m_01691	DNA_length		1197bp		
2572233334	t3m_01691	Protein_length		398aa		
2572233334	t3m_01691	GC			0.69	
2572233335	t3m_01692	COG_category	[S] Function unknown			
2572233335	t3m_01692	COG2096	Uncharacterized conserved protein			1.00E-43

2572233335	t3m_01692	pfam01923	Cob_adeno_trans		6.50E-51
2572233335	t3m_01692	TIGR00636	ATP:cob(I)alamin adenosyltransferase		3.40E-51
2572233335	t3m_01692	Locus_type		CDS	
2572233335	t3m_01692	Product_name		ATP:cob(I)alamin adenosyltransferase	
2572233335	t3m_01692	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52	
2572233335	t3m_01692	Coordinates		7355..7930(-)	
2572233335	t3m_01692	DNA_length		576bp	
2572233335	t3m_01692	Protein_length		191aa	
2572233335	t3m_01692	GC		0.7	
2572233336	t3m_01693	Locus_type		CDS	
2572233336	t3m_01693	Product_name		hypothetical protein	
2572233336	t3m_01693	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52	
2572233336	t3m_01693	Coordinates		8098..8451(-)	
2572233336	t3m_01693	DNA_length		354bp	
2572233336	t3m_01693	Protein_length		117aa	
2572233336	t3m_01693	GC		0.71	
2572233337	t3m_01694	Locus_type		CDS	
2572233337	t3m_01694	Product_name		hypothetical protein	
2572233337	t3m_01694	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52	
2572233337	t3m_01694	Coordinates		8802..9128(-)	
2572233337	t3m_01694	DNA_length		327bp	
2572233337	t3m_01694	Protein_length		108aa	
2572233337	t3m_01694	GC		0.61	
2572233338	t3m_01695	Locus_type		CDS	
2572233338	t3m_01695	Product_name		hypothetical protein	
2572233338	t3m_01695	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52	
2572233338	t3m_01695	Coordinates		9347..9592(-)	
2572233338	t3m_01695	DNA_length		246bp	
2572233338	t3m_01695	Protein_length		81aa	
2572233338	t3m_01695	GC		0.56	
2572233338	t3m_01695	Transmembrane		Yes	

2572233339	t3m_01696	Locus_type		CDS		
2572233339	t3m_01696	Product_name		hypothetical protein		
2572233339	t3m_01696	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233339	t3m_01696	Coordinates		10191..11108(+)		
2572233339	t3m_01696	DNA_length		918bp		
2572233339	t3m_01696	Protein_length		305aa		
2572233339	t3m_01696	GC			0.66	
2572233339	t3m_01696	Transmembrane		Yes		
2572233340	t3m_01697	Locus_type		CDS		
2572233340	t3m_01697	Product_name		hypothetical protein		
2572233340	t3m_01697	Scaffold		t3m_contig_70_752_len_11779_read_count_862950.52		
2572233340	t3m_01697	Coordinates		11110..11778(+)		
2572233340	t3m_01697	DNA_length		669bp		
2572233340	t3m_01697	Protein_length		223aa		
2572233340	t3m_01697	GC			0.68	
2572233340	t3m_01697	Transmembrane		Yes		
2572233341	t3m_01698	KEGG_module	M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP			
2572233341	t3m_01698	Metacyc	PWY-6125: guanosine nucleotides <i>de novo</i> biosynthesis			
2572233341	t3m_01698	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2572233341	t3m_01698	COG_category	[F] Nucleotide transport and metabolism			
2572233341	t3m_01698	COG0518	GMP synthase - Glutamine amidotransferase domain			1.00E-39
2572233341	t3m_01698	pfam00117	GATase			1.90E-30
2572233341	t3m_01698	EC:6.3.5.2	GMP synthase (glutamine-hydrolyzing).			
2572233341	t3m_01698	TIGR00888	GMP synthase (glutamine-hydrolyzing), N-terminal domain or A subunit			6.80E-52
2572233341	t3m_01698	KO:K01951	GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]			1.40E-45
2572233341	t3m_01698	Locus_type		CDS		
2572233341	t3m_01698	Product_name		GMP synthase - Glutamine amidotransferase domain		
2572233341	t3m_01698	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53		
2572233341	t3m_01698	Coordinates		3..539(+)		
2572233341	t3m_01698	DNA_length		537bp		
2572233341	t3m_01698	Protein_length		178aa		

2572233341	t3m_01698	GC			0.71	
2572233342	t3m_01699	Locus_type		CDS		
2572233342	t3m_01699	Product_name		hypothetical protein		
2572233342	t3m_01699	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53		
2572233342	t3m_01699	Coordinates		586..2139(+)		
2572233342	t3m_01699	DNA_length		1554bp		
2572233342	t3m_01699	Protein_length		517aa		
2572233342	t3m_01699	GC			0.72	
2572233343	t3m_01700	Locus_type		CDS		
2572233343	t3m_01700	Product_name		hypothetical protein		
2572233343	t3m_01700	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53		
2572233343	t3m_01700	Coordinates		2266..2667(+)		
2572233343	t3m_01700	DNA_length		402bp		
2572233343	t3m_01700	Protein_length		133aa		
2572233343	t3m_01700	GC			0.7	
2572233344	t3m_01701	Metacyc	PWY-6482: diphthamide biosynthesis			
2572233344	t3m_01701	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233344	t3m_01701	COG1798	Diphthamide biosynthesis methyltransferase			6.00E-56
2572233344	t3m_01701	pfam00590	TP_methylase			5.00E-17
2572233344	t3m_01701	EC:2.1.1.98	Diphthine synthase.			
2572233344	t3m_01701	TIGR00522	diphthine synthase			5.70E-60
2572233344	t3m_01701	KO:K00586	diphthine synthase [EC:2.1.1.98]			4.40E-42
2572233344	t3m_01701	Locus_type		CDS		
2572233344	t3m_01701	Product_name		diphthine synthase		
2572233344	t3m_01701	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53		
2572233344	t3m_01701	Coordinates		2664..3461(-)		
2572233344	t3m_01701	DNA_length		798bp		
2572233344	t3m_01701	Protein_length		265aa		
2572233344	t3m_01701	GC			0.71	
2572233345	t3m_01702	COG_category	[T] Signal transduction mechanisms			

2572233345	t3m_01702	COG0589	Universal stress protein UspA and related nucleotide-binding proteins		6.00E-05
2572233345	t3m_01702	pfam00582	Usp		2.30E-14
2572233345	t3m_01702	Locus_type		CDS	
2572233345	t3m_01702	Product_name		Universal stress protein UspA and related nucleotide-binding proteins	
2572233345	t3m_01702	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53	
2572233345	t3m_01702	Coordinates		3476..4285(-)	
2572233345	t3m_01702	DNA_length		810bp	
2572233345	t3m_01702	Protein_length		269aa	
2572233345	t3m_01702	GC		0.71	
2572233346	t3m_01703	COG_category	[P] Inorganic ion transport and metabolism		
2572233346	t3m_01703	COG2156	K+-transporting ATPase, c chain		1.00E-32
2572233346	t3m_01703	pfam02669	KdpC		8.70E-30
2572233346	t3m_01703	EC:3.6.3.12	Potassium-transporting ATPase.		
2572233346	t3m_01703	TIGR00681	K+-transporting ATPase, C subunit		8.00E-34
2572233346	t3m_01703	KO:K01548	K+-transporting ATPase ATPase C chain [EC:3.6.3.12]		3.30E-26
2572233346	t3m_01703	Locus_type		CDS	
2572233346	t3m_01703	Product_name		K+-transporting ATPase, c chain	
2572233346	t3m_01703	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53	
2572233346	t3m_01703	Coordinates		4288..4968(-)	
2572233346	t3m_01703	DNA_length		681bp	
2572233346	t3m_01703	Protein_length		226aa	
2572233346	t3m_01703	GC		0.64	
2572233346	t3m_01703	Transmembrane		Yes	
2572233347	t3m_01704	COG_category	[P] Inorganic ion transport and metabolism		
2572233347	t3m_01704	COG2216	High-affinity K+ transport system, ATPase chain B		0.00E+00
2572233347	t3m_01704	pfam00122	E1-E2_ATPase		1.00E-33
2572233347	t3m_01704	pfam00702	Hydrolase		1.30E-34
2572233347	t3m_01704	EC:3.6.3.12	Potassium-transporting ATPase.		
2572233347	t3m_01704	TIGR01497	K+-transporting ATPase, B subunit		0.00E+00
2572233347	t3m_01704	TIGR01494	ATPase, P-type (transporting), HAD superfamily, subfamily IC		3.30E-34
2572233347	t3m_01704	KO:K01547	K+-transporting ATPase ATPase B chain [EC:3.6.3.12]		0.00E+00
2572233347	t3m_01704	Locus_type		CDS	

2572233347	t3m_01704	Product_name		K+-transporting ATPase, B subunit		
2572233347	t3m_01704	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53		
2572233347	t3m_01704	Coordinates		4965..7100(-)		
2572233347	t3m_01704	DNA_length		2136bp		
2572233347	t3m_01704	Protein_length		711aa		
2572233347	t3m_01704	GC			0.66	
2572233347	t3m_01704	Transmembrane		Yes		
2572233348	t3m_01705	COG_category	[P] Inorganic ion transport and metabolism			
2572233348	t3m_01705	COG2060	K+-transporting ATPase, A chain			3.00E-127
2572233348	t3m_01705	pfam03814	KdpA			0.00E+00
2572233348	t3m_01705	EC:3.6.3.12	Potassium-transporting ATPase.			
2572233348	t3m_01705	TIGR00680	K+-transporting ATPase, KdpA			1.20E-130
2572233348	t3m_01705	KO:K01546	K+-transporting ATPase ATPase A chain [EC:3.6.3.12]			0.00E+00
2572233348	t3m_01705	Locus_type		CDS		
2572233348	t3m_01705	Product_name		K+-transporting ATPase, KdpA		
2572233348	t3m_01705	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53		
2572233348	t3m_01705	Coordinates		7102..8814(-)		
2572233348	t3m_01705	DNA_length		1713bp		
2572233348	t3m_01705	Protein_length		570aa		
2572233348	t3m_01705	GC			0.64	
2572233348	t3m_01705	Transmembrane		Yes		
2572233349	t3m_01706	COG_category	[L] Replication, recombination and repair			
2572233349	t3m_01706	COG1111	ERCC4-like helicases			5.00E-121
2572233349	t3m_01706	pfam00271	Helicase_C			5.90E-19
2572233349	t3m_01706	pfam00270	DEAD			3.00E-20
2572233349	t3m_01706	Locus_type		CDS		
2572233349	t3m_01706	Product_name		ERCC4-like helicases		
2572233349	t3m_01706	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53		
2572233349	t3m_01706	Coordinates		9024..10694(-)		
2572233349	t3m_01706	DNA_length		1671bp		
2572233349	t3m_01706	Protein_length		556aa		
2572233349	t3m_01706	GC			0.69	

2572233350	t3m_01707	Locus_type		CDS		
2572233350	t3m_01707	Product_name		hypothetical protein		
2572233350	t3m_01707	Scaffold		t3m_contig_70_764_len_11651_read_count_1037928.53		
2572233350	t3m_01707	Coordinates		10810..11649(-)		
2572233350	t3m_01707	DNA_length		840bp		
2572233350	t3m_01707	Protein_length		279aa		
2572233350	t3m_01707	GC			0.66	

2572233351	t3m_01708	COG_category	[L] Replication, recombination and repair			
2572233351	t3m_01708	COG0675	Transposase and inactivated derivatives			6.00E-20
2572233351	t3m_01708	pfam01385	OrfB_IS605			3.80E-12
2572233351	t3m_01708	pfam07282	OrfB_Zn_ribbon			1.40E-20
2572233351	t3m_01708	TIGR01766	transposase, IS605 OrfB family, central region			1.50E-18
2572233351	t3m_01708	TIGR01765	transposase, putative, N-terminal domain			1.60E-09
2572233351	t3m_01708	Locus_type		CDS		
2572233351	t3m_01708	Product_name		transposase, IS605 OrfB family, central region		
2572233351	t3m_01708	Scaffold		t3m_contig_70_813_len_11090_read_count_917376.54		
2572233351	t3m_01708	Coordinates		1..1146(-)		
2572233351	t3m_01708	DNA_length		1146bp		
2572233351	t3m_01708	Protein_length		381aa		
2572233351	t3m_01708	GC			0.66	

2572233352	t3m_01709	COG_category	[L] Replication, recombination and repair			
2572233352	t3m_01709	COG1943	Transposase and inactivated derivatives			2.00E-26
2572233352	t3m_01709	pfam01797	Y1_Tnp			1.80E-34
2572233352	t3m_01709	KO:K07491	putative transposase			2.20E-32
2572233352	t3m_01709	Locus_type		CDS		
2572233352	t3m_01709	Product_name		Transposase and inactivated derivatives		
2572233352	t3m_01709	Scaffold		t3m_contig_70_813_len_11090_read_count_917376.54		
2572233352	t3m_01709	Coordinates		1185..1619(+)		
2572233352	t3m_01709	DNA_length		435bp		
2572233352	t3m_01709	Protein_length		144aa		
2572233352	t3m_01709	GC			0.63	

2572233353	t3m_01710	pfam08706	D5_N		4.40E-07
2572233353	t3m_01710	TIGR01613	phage/plasmid primase, P4 family, C-terminal domain		1.40E-53
2572233353	t3m_01710	Locus_type		CDS	
2572233353	t3m_01710	Product_name		phage/plasmid primase, P4 family, C-terminal domain	
2572233353	t3m_01710	Scaffold		t3m_contig_70_813_len_11090_read_count_917376.54	
2572233353	t3m_01710	Coordinates		2303..5155(+)	
2572233353	t3m_01710	DNA_length		2853bp	
2572233353	t3m_01710	Protein_length		950aa	
2572233353	t3m_01710	GC		0.66	
2572233354	t3m_01711	Locus_type		CDS	
2572233354	t3m_01711	Product_name		hypothetical protein	
2572233354	t3m_01711	Scaffold		t3m_contig_70_813_len_11090_read_count_917376.54	
2572233354	t3m_01711	Coordinates		5281..5481(+)	
2572233354	t3m_01711	DNA_length		201bp	
2572233354	t3m_01711	Protein_length		66aa	
2572233354	t3m_01711	GC		0.75	
2572233355	t3m_01712	Locus_type		CDS	
2572233355	t3m_01712	Product_name		hypothetical protein	
2572233355	t3m_01712	Scaffold		t3m_contig_70_813_len_11090_read_count_917376.54	
2572233355	t3m_01712	Coordinates		5478..6095(+)	
2572233355	t3m_01712	DNA_length		618bp	
2572233355	t3m_01712	Protein_length		205aa	
2572233355	t3m_01712	GC		0.69	
2572233356	t3m_01713	Locus_type		CDS	
2572233356	t3m_01713	Product_name		hypothetical protein	
2572233356	t3m_01713	Scaffold		t3m_contig_70_813_len_11090_read_count_917376.54	
2572233356	t3m_01713	Coordinates		6092..7102(+)	
2572233356	t3m_01713	DNA_length		1011bp	
2572233356	t3m_01713	Protein_length		336aa	
2572233356	t3m_01713	GC		0.6	

2572233357	t3m_01714	Locus_type	CDS
2572233357	t3m_01714	Product_name	hypothetical protein
2572233357	t3m_01714	Scaffold	t3m_contig_70_813_len_11090_read_count_917376.54
2572233357	t3m_01714	Coordinates	7833..9401(+)
2572233357	t3m_01714	DNA_length	1569bp
2572233357	t3m_01714	Protein_length	522aa
2572233357	t3m_01714	GC	0.63
2572233357	t3m_01714	Signal_peptide	Yes
2572233357	t3m_01714	Transmembrane	Yes

2572233358	t3m_01715	Locus_type	CDS
2572233358	t3m_01715	Product_name	hypothetical protein
2572233358	t3m_01715	Scaffold	t3m_contig_70_813_len_11090_read_count_917376.54
2572233358	t3m_01715	Coordinates	9850..10086(+)
2572233358	t3m_01715	DNA_length	237bp
2572233358	t3m_01715	Protein_length	78aa
2572233358	t3m_01715	GC	0.62

2572233359	t3m_01716	Locus_type	CDS
2572233359	t3m_01716	Product_name	hypothetical protein
2572233359	t3m_01716	Scaffold	t3m_contig_70_813_len_11090_read_count_917376.54
2572233359	t3m_01716	Coordinates	10264..10476(+)
2572233359	t3m_01716	DNA_length	213bp
2572233359	t3m_01716	Protein_length	70aa
2572233359	t3m_01716	GC	0.65

2572233360	t3m_01717	Locus_type	CDS
2572233360	t3m_01717	Product_name	hypothetical protein
2572233360	t3m_01717	Scaffold	t3m_contig_70_813_len_11090_read_count_917376.54
2572233360	t3m_01717	Coordinates	10473..10808(+)
2572233360	t3m_01717	DNA_length	336bp
2572233360	t3m_01717	Protein_length	111aa
2572233360	t3m_01717	GC	0.72

2572233361	t3m_01718	Locus_type		CDS	
2572233361	t3m_01718	Product_name		hypothetical protein	
2572233361	t3m_01718	Scaffold		t3m_contig_70_813_len_11090_read_count_917376.54	
2572233361	t3m_01718	Coordinates		10805..11089(+)	
2572233361	t3m_01718	DNA_length		285bp	
2572233361	t3m_01718	Protein_length		95aa	
2572233361	t3m_01718	GC		0.68	
2572233361	t3m_01718	Transmembrane		Yes	
2572233362	t3m_01719	pfam01849	NAC		7.70E-17
2572233362	t3m_01719	TIGR00264	alpha-NAC-related protein		1.50E-22
2572233362	t3m_01719	Locus_type		CDS	
2572233362	t3m_01719	Product_name		NAC domain	
2572233362	t3m_01719	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55	
2572233362	t3m_01719	Coordinates		1..204(-)	
2572233362	t3m_01719	DNA_length		204bp	
2572233362	t3m_01719	Protein_length		68aa	
2572233362	t3m_01719	GC		0.67	
2572233363	t3m_01720	COG_category	[R] General function prediction only		
2572233363	t3m_01720	COG0517	FOG: CBS domain		4.00E-08
2572233363	t3m_01720	pfam00571	CBS		8.70E-10
2572233363	t3m_01720	pfam00571	CBS		9.70E-10
2572233363	t3m_01720	pfam00571	CBS		1.40E-08
2572233363	t3m_01720	Locus_type		CDS	
2572233363	t3m_01720	Product_name		FOG: CBS domain	
2572233363	t3m_01720	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55	
2572233363	t3m_01720	Coordinates		218..1438(-)	
2572233363	t3m_01720	DNA_length		1221bp	
2572233363	t3m_01720	Protein_length		406aa	
2572233363	t3m_01720	GC		0.7	
2572233364	t3m_01721	COG_category	[R] General function prediction only		

2572233364	t3m_01721	COG0456	Acetyltransferases		3.00E-16
2572233364	t3m_01721	pfam00583	Acetyltransf_1		1.50E-14
2572233364	t3m_01721	EC:2.3.1.128	Ribosomal-protein-alanine N-acetyltransferase.		
2572233364	t3m_01721	KO:K03789	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]		3.30E-24
2572233364	t3m_01721	ITERM:02526	[SSU ribosomal protein S18P]-alanine acetyltransferase (EC 2.3.1.128)		
2572233364	t3m_01721	Locus_type		CDS	
2572233364	t3m_01721	Product_name		[SSU ribosomal protein S18P]-alanine acetyltransferase (EC 2.3.1.128)	
2572233364	t3m_01721	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55	
2572233364	t3m_01721	Coordinates		1528..2010(-)	
2572233364	t3m_01721	DNA_length		483bp	
2572233364	t3m_01721	Protein_length		160aa	
2572233364	t3m_01721	GC		0.68	
2572233365	t3m_01722	COG_category	[R] General function prediction only		
2572233365	t3m_01722	COG1938	Archaeal enzymes of ATP-grasp superfamily		8.00E-35
2572233365	t3m_01722	pfam09754	PAC2		1.60E-32
2572233365	t3m_01722	KO:K06869	uncharacterized protein		1.90E-34
2572233365	t3m_01722	Locus_type		CDS	
2572233365	t3m_01722	Product_name		Archaeal enzymes of ATP-grasp superfamily	
2572233365	t3m_01722	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55	
2572233365	t3m_01722	Coordinates		2018..2794(-)	
2572233365	t3m_01722	DNA_length		777bp	
2572233365	t3m_01722	Protein_length		258aa	
2572233365	t3m_01722	GC		0.67	
2572233366	t3m_01723	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572233366	t3m_01723	COG_category	[G] Carbohydrate transport and metabolism		
2572233366	t3m_01723	COG0451	Nucleoside-diphosphate-sugar epimerases		4.00E-31
2572233366	t3m_01723	pfam01370	Epimerase		6.00E-22
2572233366	t3m_01723	ITERM:00477	UDP-sulfoquinovose synthase (EC 3.13.1.1)		
2572233366	t3m_01723	Locus_type		CDS	
2572233366	t3m_01723	Product_name		UDP-sulfoquinovose synthase (EC 3.13.1.1)	
2572233366	t3m_01723	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55	
2572233366	t3m_01723	Coordinates		2922..4172(+)	

2572233366	t3m_01723	DNA_length		1251bp	
2572233366	t3m_01723	Protein_length		416aa	
2572233366	t3m_01723	GC		0.67	
2572233367	t3m_01724	KEGG_module	M00549: Nucleotide sugar biosynthesis, glucose => UDP-glucose		
2572233367	t3m_01724	KEGG_module	M00362: Nucleotide sugar biosynthesis, prokaryotes		
2572233367	t3m_01724	KEGG_module	M00361: Nucleotide sugar biosynthesis, eukaryotes		
2572233367	t3m_01724	KEGG_module	M00129: Ascorbate biosynthesis, animals, glucose-1P => ascorbate		
2572233367	t3m_01724	Metacyc	SUCSYN-PWY: sucrose biosynthesis		
2572233367	t3m_01724	Metacyc	PWY3DJ-35471: L-ascorbate biosynthesis IV		
2572233367	t3m_01724	Metacyc	COLANSYN-PWY: colanic acid building blocks biosynthesis		
2572233367	t3m_01724	Metacyc	PWY-3801: sucrose degradation VI (anaerobic)		
2572233367	t3m_01724	Metacyc	PWY-6527: stachyose degradation		
2572233367	t3m_01724	Metacyc	PWY-3821: galactose degradation III		
2572233367	t3m_01724	Metacyc	PWY-6981: chitin biosynthesis		
2572233367	t3m_01724	Metacyc	PWY-621: sucrose degradation III		
2572233367	t3m_01724	Metacyc	PWY-5067: glycogen biosynthesis II (from UDP-D-Glucose)		
2572233367	t3m_01724	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572233367	t3m_01724	COG1209	dTDP-glucose pyrophosphorylase		8.00E-39
2572233367	t3m_01724	pfam00483	NTP_transferase		3.10E-19
2572233367	t3m_01724	EC:2.7.7.9	UTP--glucose-1-phosphate uridylyltransferase.		
2572233367	t3m_01724	KO:K00963	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]		1.70E-42
2572233367	t3m_01724	Locus_type		CDS	
2572233367	t3m_01724	Product_name		dTDP-glucose pyrophosphorylase	
2572233367	t3m_01724	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55	
2572233367	t3m_01724	Coordinates		4181..5059(+)	
2572233367	t3m_01724	DNA_length		879bp	
2572233367	t3m_01724	Protein_length		292aa	
2572233367	t3m_01724	GC		0.69	
2572233368	t3m_01725	KEGG_module	M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine		
2572233368	t3m_01725	Metacyc	DAPLYSINESYN-PWY: lysine biosynthesis I		
2572233368	t3m_01725	COG_category	[E] Amino acid transport and metabolism		
2572233368	t3m_01725	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase ar		1.00E-51

2572233368	t3m_01725	pfam01546	Peptidase_M20			5.60E-29
2572233368	t3m_01725	pfam07687	M20_dimer			2.30E-25
2572233368	t3m_01725	EC:3.5.1.18	Succinyl-diaminopimelate desuccinylase.			
2572233368	t3m_01725	KO:K01439	succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]			6.40E-40
2572233368	t3m_01725	Locus_type		CDS		
2572233368	t3m_01725	Product_name		Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase an		
2572233368	t3m_01725	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55		
2572233368	t3m_01725	Coordinates		5143..6222(+)		
2572233368	t3m_01725	DNA_length		1080bp		
2572233368	t3m_01725	Protein_length		359aa		
2572233368	t3m_01725	GC			0.68	
2572233369	t3m_01726	Metacyc	PWY1G-0: mycothiol biosynthesis			
2572233369	t3m_01726	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572233369	t3m_01726	COG0438	Glycosyltransferase			3.00E-45
2572233369	t3m_01726	pfam00534	Glycos_transf_1			7.20E-43
2572233369	t3m_01726	pfam13579	Glyco_trans_4_4			4.20E-24
2572233369	t3m_01726	EC:2.4.1.250	D-inositol-3-phosphate glycosyltransferase.			
2572233369	t3m_01726	KO:K15521	D-inositol-3-phosphate glycosyltransferase [EC:2.4.1.250]			1.30E-41
2572233369	t3m_01726	Locus_type		CDS		
2572233369	t3m_01726	Product_name		Glycosyltransferase		
2572233369	t3m_01726	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55		
2572233369	t3m_01726	Coordinates		6287..7471(+)		
2572233369	t3m_01726	DNA_length		1185bp		
2572233369	t3m_01726	Protein_length		394aa		
2572233369	t3m_01726	GC			0.72	
2572233370	t3m_01727	COG_category	[M] Cell wall/membrane/envelope biogenesis			
2572233370	t3m_01727	COG0438	Glycosyltransferase			1.00E-37
2572233370	t3m_01727	pfam13579	Glyco_trans_4_4			2.20E-20
2572233370	t3m_01727	pfam00534	Glycos_transf_1			2.90E-32
2572233370	t3m_01727	Locus_type		CDS		
2572233370	t3m_01727	Product_name		Glycosyltransferase		
2572233370	t3m_01727	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55		

2572233370	t3m_01727	Coordinates		7468..8625(+)		
2572233370	t3m_01727	DNA_length		1158bp		
2572233370	t3m_01727	Protein_length		385aa		
2572233370	t3m_01727	GC			0.73	
2572233371	t3m_01728	Metacyc	ASPARTATE-DEG1-PWY: aspartate degradation I			
2572233371	t3m_01728	Metacyc	PWY-6643: coenzyme M biosynthesis II			
2572233371	t3m_01728	Metacyc	PWY-7117: C4 photosynthetic carbon assimilation cycle, PEPCK type			
2572233371	t3m_01728	Metacyc	ASPARTATESYN-PWY: aspartate biosynthesis			
2572233371	t3m_01728	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)			
2572233371	t3m_01728	Metacyc	PWY-6638: sulfolactate degradation III			
2572233371	t3m_01728	Metacyc	PWY-6642: (<i>R</i>)-cysteate degradation			
2572233371	t3m_01728	Metacyc	GLUTDEG-PWY: glutamate degradation II			
2572233371	t3m_01728	Metacyc	MALATE-ASPARTATE-SHUTTLE-PWY: aspartate degradation II			
2572233371	t3m_01728	Metacyc	PWY-7115: C4 photosynthetic carbon assimilation cycle, NAD-ME type			
2572233371	t3m_01728	Metacyc	PWY-6318: phenylalanine degradation IV (mammalian, via side chain)			
2572233371	t3m_01728	COG_category	[E] Amino acid transport and metabolism			
2572233371	t3m_01728	COG0436	Aspartate/tyrosine/aromatic aminotransferase			6.00E-92
2572233371	t3m_01728	pfam00155	Aminotran_1_2			2.20E-65
2572233371	t3m_01728	EC:2.6.1.1	Aspartate transaminase.			
2572233371	t3m_01728	KO:K00812	aspartate aminotransferase [EC:2.6.1.1]			0.00E+00
2572233371	t3m_01728	Locus_type		CDS		
2572233371	t3m_01728	Product_name		Aspartate/tyrosine/aromatic aminotransferase		
2572233371	t3m_01728	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55		
2572233371	t3m_01728	Coordinates		8741..9871(-)		
2572233371	t3m_01728	DNA_length		1131bp		
2572233371	t3m_01728	Protein_length		376aa		
2572233371	t3m_01728	GC			0.68	
2572233372	t3m_01729	KEGG_module	M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP			
2572233372	t3m_01729	Metacyc	PWY-841: purine nucleotides <i>de novo</i> biosynthesis II			
2572233372	t3m_01729	Metacyc	PWY-6126: adenosine nucleotides <i>de novo</i> biosynthesis			
2572233372	t3m_01729	IMG_pathway	236: AMP anabolism via adenylosuccinate			
2572233372	t3m_01729	COG_category	[F] Nucleotide transport and metabolism			

2572233372	t3m_01729	COG0104	Adenylosuccinate synthase			1.00E-113
2572233372	t3m_01729	pfam00709	Adenylsucc_synt			5.90E-117
2572233372	t3m_01729	EC:6.3.4.4	Adenylosuccinate synthase.			
2572233372	t3m_01729	TIGR00184	adenylosuccinate synthase			1.70E-108
2572233372	t3m_01729	KO:K01939	adenylosuccinate synthase [EC:6.3.4.4]			0.00E+00
2572233372	t3m_01729	ITERM:00630	Adenylosuccinate synthetase (EC 6.3.4.4)			
2572233372	t3m_01729	Locus_type		CDS		
2572233372	t3m_01729	Product_name		Adenylosuccinate synthetase (EC 6.3.4.4)		
2572233372	t3m_01729	Scaffold		t3m_contig_70_820_len_11056_read_count_891743.55		
2572233372	t3m_01729	Coordinates		10025..11053(+)		
2572233372	t3m_01729	DNA_length		1029bp		
2572233372	t3m_01729	Protein_length		343aa		
2572233372	t3m_01729	GC			0.7	
2572233373	t3m_01730	Locus_type		CDS		
2572233373	t3m_01730	Product_name		hypothetical protein		
2572233373	t3m_01730	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233373	t3m_01730	Coordinates		3..602(-)		
2572233373	t3m_01730	DNA_length		600bp		
2572233373	t3m_01730	Protein_length		200aa		
2572233373	t3m_01730	GC			0.67	
2572233374	t3m_01731	COG_category	[R] General function prediction only			
2572233374	t3m_01731	COG0433	Predicted ATPase			1.00E-39
2572233374	t3m_01731	pfam01935	DUF87			7.40E-31
2572233374	t3m_01731	Locus_type		CDS		
2572233374	t3m_01731	Product_name		Predicted ATPase		
2572233374	t3m_01731	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233374	t3m_01731	Coordinates		728..2188(+)		
2572233374	t3m_01731	DNA_length		1461bp		
2572233374	t3m_01731	Protein_length		486aa		
2572233374	t3m_01731	GC			0.67	
2572233375	t3m_01732	Locus_type		CDS		

2572233375	t3m_01732	Product_name		hypothetical protein		
2572233375	t3m_01732	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233375	t3m_01732	Coordinates		2198..2440(+)		
2572233375	t3m_01732	DNA_length		243bp		
2572233375	t3m_01732	Protein_length		80aa		
2572233375	t3m_01732	GC			0.63	
2572233376	t3m_01733	Metacyc	PWY-5988: wound-induced proteolysis I			
2572233376	t3m_01733	Metacyc	PWY-6018: seed germination protein turnover			
2572233376	t3m_01733	COG_category	[E] Amino acid transport and metabolism			
2572233376	t3m_01733	COG0260	Leucyl aminopeptidase			4.00E-123
2572233376	t3m_01733	pfam00883	Peptidase_M17			5.30E-106
2572233376	t3m_01733	pfam02789	Peptidase_M17_N			3.80E-21
2572233376	t3m_01733	EC:3.4.11.1	Leucyl aminopeptidase.			
2572233376	t3m_01733	KO:K01255	leucyl aminopeptidase [EC:3.4.11.1]			0.00E+00
2572233376	t3m_01733	Locus_type		CDS		
2572233376	t3m_01733	Product_name		Leucyl aminopeptidase		
2572233376	t3m_01733	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233376	t3m_01733	Coordinates		2508..4040(-)		
2572233376	t3m_01733	DNA_length		1533bp		
2572233376	t3m_01733	Protein_length		510aa		
2572233376	t3m_01733	GC			0.69	
2572233377	t3m_01734	pfam04472	DUF552			7.70E-12
2572233377	t3m_01734	KO:K09152	hypothetical protein			1.00E-20
2572233377	t3m_01734	Locus_type		CDS		
2572233377	t3m_01734	Product_name		Protein of unknown function (DUF552)		
2572233377	t3m_01734	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233377	t3m_01734	Coordinates		4062..4439(-)		
2572233377	t3m_01734	DNA_length		378bp		
2572233377	t3m_01734	Protein_length		125aa		
2572233377	t3m_01734	GC			0.6	
2572233378	t3m_01735	pfam04981	NMD3			2.70E-35

2572233378	t3m_01735	Locus_type		CDS		
2572233378	t3m_01735	Product_name		NMD3 family		
2572233378	t3m_01735	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233378	t3m_01735	Coordinates		4492..5280(-)		
2572233378	t3m_01735	DNA_length		789bp		
2572233378	t3m_01735	Protein_length		262aa		
2572233378	t3m_01735	GC			0.71	
2572233379	t3m_01736	COG_category	[S] Function unknown			
2572233379	t3m_01736	COG2412	Uncharacterized conserved protein			3.00E-20
2572233379	t3m_01736	pfam04242	DUF424			4.10E-19
2572233379	t3m_01736	KO:K09148	hypothetical protein			1.80E-15
2572233379	t3m_01736	Locus_type		CDS		
2572233379	t3m_01736	Product_name		Uncharacterized conserved protein		
2572233379	t3m_01736	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233379	t3m_01736	Coordinates		5353..5667(-)		
2572233379	t3m_01736	DNA_length		315bp		
2572233379	t3m_01736	Protein_length		104aa		
2572233379	t3m_01736	GC			0.72	
2572233380	t3m_01737	IMG_pathway	436: Archaeal replication initiation			
2572233380	t3m_01737	COG_category	[L] Replication, recombination and repair			
2572233380	t3m_01737	COG1241	Predicted ATPase involved in replication control, Cdc46/Mcm family			0.00E+00
2572233380	t3m_01737	pfam00493	MCM			2.30E-125
2572233380	t3m_01737	EC:3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid anhydrides; involved in cellular and subcellul			
2572233380	t3m_01737	KO:K10726	replicative DNA helicase Mcm [EC:3.6.4.-]			0.00E+00
2572233380	t3m_01737	ITERM:00094	replicative DNA helicase Mcm (EC 3.6.1.-)			
2572233380	t3m_01737	Locus_type		CDS		
2572233380	t3m_01737	Product_name		replicative DNA helicase Mcm (EC 3.6.1.-)		
2572233380	t3m_01737	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233380	t3m_01737	Coordinates		5735..7852(-)		
2572233380	t3m_01737	DNA_length		2118bp		
2572233380	t3m_01737	Protein_length		705aa		
2572233380	t3m_01737	GC			0.69	

2572233381	t3m_01738	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572233381	t3m_01738	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572233381	t3m_01738	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572233381	t3m_01738	IMG_pathway	349: tRNA-dependent asparagine synthesis			
2572233381	t3m_01738	IMG_pathway	489: L-aspartate ligation to tRNA(Asp)			
2572233381	t3m_01738	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233381	t3m_01738	COG0017	Aspartyl/asparaginyl-tRNA synthetases			3.00E-101
2572233381	t3m_01738	pfam00152	tRNA-synt_2			6.30E-83
2572233381	t3m_01738	EC:6.1.1.12	Aspartate--tRNA ligase.			
2572233381	t3m_01738	TIGR00458	nondiscriminating aspartyl-tRNA synthetase			1.40E-122
2572233381	t3m_01738	KO:K01876	aspartyl-tRNA synthetase [EC:6.1.1.12]			0.00E+00
2572233381	t3m_01738	ITERM:00393	aspartyl-tRNA synthetase (EC 6.1.1.12)			
2572233381	t3m_01738	Locus_type		CDS		
2572233381	t3m_01738	Product_name		aspartyl-tRNA synthetase (EC 6.1.1.12)		
2572233381	t3m_01738	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56		
2572233381	t3m_01738	Coordinates		7871..8971(-)		
2572233381	t3m_01738	DNA_length		1101bp		
2572233381	t3m_01738	Protein_length		366aa		
2572233381	t3m_01738	GC			0.69	

2572233382	t3m_01739	KEGG_module	M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP	
2572233382	t3m_01739	Metacyc	PWY-7176: UTP and CTP <i>de novo</i> biosynthesis	
2572233382	t3m_01739	Metacyc	PWY-7177: UTP and CTP dephosphorylation II	
2572233382	t3m_01739	Metacyc	PWY-7185: UTP and CTP dephosphorylation I	
2572233382	t3m_01739	IMG_pathway	324: CTP synthesis	
2572233382	t3m_01739	COG_category	[F] Nucleotide transport and metabolism	
2572233382	t3m_01739	COG0504	CTP synthase (UTP-ammonia lyase)	0.00E+00
2572233382	t3m_01739	pfam06418	CTP_synth_N	1.60E-88
2572233382	t3m_01739	pfam00117	GATase	1.30E-40
2572233382	t3m_01739	EC:6.3.4.2	CTP synthase.	
2572233382	t3m_01739	TIGR00337	CTP synthase	0.00E+00
2572233382	t3m_01739	KO:K01937	CTP synthase [EC:6.3.4.2]	0.00E+00
2572233382	t3m_01739	ITERM:01398	CTP synthase (EC 6.3.4.2)	

2572233382	t3m_01739	Locus_type		CDS	
2572233382	t3m_01739	Product_name		CTP synthase (EC 6.3.4.2)	
2572233382	t3m_01739	Scaffold		t3m_contig_70_870_len_10624_read_count_814288.56	
2572233382	t3m_01739	Coordinates		9153..10622(-)	
2572233382	t3m_01739	DNA_length		1470bp	
2572233382	t3m_01739	Protein_length		489aa	
2572233382	t3m_01739	GC		0.68	
2572233383	t3m_01740	Metacyc	LIPA-CORESYN-PWY: Lipid A-core biosynthesis		
2572233383	t3m_01740	Metacyc	SPHINGOLIPID-SYN-PWY: sphingolipid biosynthesis (yeast)		
2572233383	t3m_01740	Metacyc	PWY-6577: farnesylcysteine salvage pathway		
2572233383	t3m_01740	Metacyc	PWY-6626: CDP-2-glycerol biosynthesis		
2572233383	t3m_01740	Metacyc	PWY-7077: <i>N</i>-acetyl-D-galactosamine degradation		
2572233383	t3m_01740	Metacyc	PWY-6682: dehydrophos biosynthesis		
2572233383	t3m_01740	Metacyc	PWY-5107: phytol salvage pathway		
2572233383	t3m_01740	Metacyc	PWY-5129: sphingolipid biosynthesis (plants)		
2572233383	t3m_01740	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233383	t3m_01740	COG1859	RNA:NAD 2'-phosphotransferase		9.00E-49
2572233383	t3m_01740	pfam01885	PTS_2-RNA		6.40E-35
2572233383	t3m_01740	EC:2.7.1.-	Transferases. Transferring phosphorous-containing groups. Phosphotransferases with an alcohol g		
2572233383	t3m_01740	KO:K07559	putative RNA 2'-phosphotransferase [EC:2.7.1.-]		0.00E+00
2572233383	t3m_01740	Locus_type		CDS	
2572233383	t3m_01740	Product_name		RNA:NAD 2'-phosphotransferase	
2572233383	t3m_01740	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57	
2572233383	t3m_01740	Coordinates		1..603(+)	
2572233383	t3m_01740	DNA_length		603bp	
2572233383	t3m_01740	Protein_length		200aa	
2572233383	t3m_01740	GC		0.67	
2572233384	t3m_01741	COG_category	[M] Cell wall/membrane/envelope biogenesis		
2572233384	t3m_01741	COG0463	Glycosyltransferases involved in cell wall biogenesis		9.00E-19
2572233384	t3m_01741	pfam00535	Glycos_transf_2		1.20E-23
2572233384	t3m_01741	Locus_type		CDS	
2572233384	t3m_01741	Product_name		Glycosyltransferases involved in cell wall biogenesis	

2572233384	t3m_01741	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57		
2572233384	t3m_01741	Coordinates		662..1804(-)		
2572233384	t3m_01741	DNA_length		1143bp		
2572233384	t3m_01741	Protein_length		380aa		
2572233384	t3m_01741	GC			0.69	
2572233384	t3m_01741	Transmembrane		Yes		
2572233385	t3m_01742	KEGG_module	M00413: FA core complex			
2572233385	t3m_01742	COG_category	[L] Replication, recombination and repair			
2572233385	t3m_01742	COG1111	ERCC4-like helicases			0.00E+00
2572233385	t3m_01742	pfam00271	Helicase_C			3.30E-20
2572233385	t3m_01742	pfam00270	DEAD			5.40E-18
2572233385	t3m_01742	KO:K10896	fanconi anemia group M protein			0.00E+00
2572233385	t3m_01742	Locus_type		CDS		
2572233385	t3m_01742	Product_name		ERCC4-like helicases		
2572233385	t3m_01742	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57		
2572233385	t3m_01742	Coordinates		1866..3470(+)		
2572233385	t3m_01742	DNA_length		1605bp		
2572233385	t3m_01742	Protein_length		534aa		
2572233385	t3m_01742	GC			0.7	
2572233386	t3m_01743	KEGG_module	M00053: Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP			
2572233386	t3m_01743	COG_category	[F] Nucleotide transport and metabolism			
2572233386	t3m_01743	COG0756	dUTPase			3.00E-25
2572233386	t3m_01743	pfam00692	dUTPase			6.40E-17
2572233386	t3m_01743	EC:3.6.1.23	dUTP diphosphatase.			
2572233386	t3m_01743	TIGR00576	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)			2.20E-33
2572233386	t3m_01743	KO:K01520	dUTP pyrophosphatase [EC:3.6.1.23]			6.80E-22
2572233386	t3m_01743	Locus_type		CDS		
2572233386	t3m_01743	Product_name		dUTPase		
2572233386	t3m_01743	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57		
2572233386	t3m_01743	Coordinates		3467..3883(-)		
2572233386	t3m_01743	DNA_length		417bp		
2572233386	t3m_01743	Protein_length		138aa		

2572233386	t3m_01743	GC			0.71	
2572233387	t3m_01744	COG_category	[R] General function prediction only			
2572233387	t3m_01744	COG3413	Predicted DNA binding protein			1.00E-10
2572233387	t3m_01744	pfam04967	HTH_10			5.70E-13
2572233387	t3m_01744	Locus_type		CDS		
2572233387	t3m_01744	Product_name		Predicted DNA binding protein		
2572233387	t3m_01744	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57		
2572233387	t3m_01744	Coordinates		3936..4670(-)		
2572233387	t3m_01744	DNA_length		735bp		
2572233387	t3m_01744	Protein_length		244aa		
2572233387	t3m_01744	GC			0.69	
2572233388	t3m_01745	KEGG_module	M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone			
2572233388	t3m_01745	Metacyc	PWY-6627: salinosporamide A biosynthesis			
2572233388	t3m_01745	Metacyc	PWY-6585: 2-tridecanone biosynthesis			
2572233388	t3m_01745	Metacyc	PWY-5826: hypoglycin biosynthesis			
2572233388	t3m_01745	Metacyc	PWY3O-19: ubiquinol-6 biosynthesis (eukaryotic)			
2572233388	t3m_01745	Metacyc	PWY-6708: ubiquinol-8 biosynthesis (prokaryotic)			
2572233388	t3m_01745	Metacyc	PWY-7007: methyl ketone biosynthesis			
2572233388	t3m_01745	Metacyc	PWY-5163: <I>p</I>-cumate degradation to 2-oxopent-4-enoate			
2572233388	t3m_01745	Metacyc	PWY-5873: ubiquinol-7 biosynthesis (eukaryotic)			
2572233388	t3m_01745	Metacyc	PWY-5872: ubiquinol-10 biosynthesis (eukaryotic)			
2572233388	t3m_01745	Metacyc	PWY-5856: ubiquinol-9 biosynthesis (prokaryotic)			
2572233388	t3m_01745	Metacyc	PWY-5870: ubiquinol-8 biosynthesis (eukaryotic)			
2572233388	t3m_01745	Metacyc	PWY-181: photorespiration			
2572233388	t3m_01745	Metacyc	PWY-3385: choline biosynthesis I			
2572233388	t3m_01745	Metacyc	PWY-5871: ubiquinol-9 biosynthesis (eukaryotic)			
2572233388	t3m_01745	Metacyc	PWY-5855: ubiquinol-7 biosynthesis (prokaryotic)			
2572233388	t3m_01745	Metacyc	PWY-5857: ubiquinol-10 biosynthesis (prokaryotic)			
2572233388	t3m_01745	Metacyc	PWY-5113: UDP-D-apiose biosynthesis (from UDP-D-glucuronate)			
2572233388	t3m_01745	Metacyc	PWY-6559: spermidine biosynthesis II			
2572233388	t3m_01745	COG_category	[H] Coenzyme transport and metabolism			
2572233388	t3m_01745	COG0043	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxyl			0.00E+00

2572233388	t3m_01745	pfam01977	UbiD			0.00E+00
2572233388	t3m_01745	EC:4.1.1.-	Lyases. Carbon-carbon lyases. Carboxy-lyases.			
2572233388	t3m_01745	TIGR00148	UbiD family decarboxylase			0.00E+00
2572233388	t3m_01745	TIGR03701	menaquinone biosynthesis decarboxylase, SCO4490 family			0.00E+00
2572233388	t3m_01745	KO:K03182	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiD [EC:4.1.1.-]			0.00E+00
2572233388	t3m_01745	Locus_type		CDS		
2572233388	t3m_01745	Product_name		menaquinone biosynthesis decarboxylase, SCO4490 family		
2572233388	t3m_01745	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57		
2572233388	t3m_01745	Coordinates		4751..6232(+)		
2572233388	t3m_01745	DNA_length		1482bp		
2572233388	t3m_01745	Protein_length		493aa		
2572233388	t3m_01745	GC			0.68	

2572233389	t3m_01746	KEGG_module	M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone
2572233389	t3m_01746	Metacyc	PWY-5133: cohumulone biosynthesis
2572233389	t3m_01746	Metacyc	PWY-5068: chlorophyll cycle
2572233389	t3m_01746	Metacyc	PWY-702: methionine biosynthesis II
2572233389	t3m_01746	Metacyc	PWY-4681: kievitone biosynthesis
2572233389	t3m_01746	Metacyc	PWY-5365: linear furanocoumarin biosynthesis
2572233389	t3m_01746	Metacyc	PWY-5132: humulone biosynthesis
2572233389	t3m_01746	Metacyc	PWY-5064: chlorophyll <i>a</i> biosynthesis II
2572233389	t3m_01746	Metacyc	PWY-5027: phylloquinol biosynthesis
2572233389	t3m_01746	Metacyc	PWY-6262: demethylmenaquinol-8 biosynthesis II
2572233389	t3m_01746	Metacyc	PWY-2681: <i>trans</i>-zeatin biosynthesis
2572233389	t3m_01746	Metacyc	PWY-5770: phenazine-1-carboxylate biosynthesis
2572233389	t3m_01746	Metacyc	PWY-4502: wighteone and luteone biosynthesis
2572233389	t3m_01746	Metacyc	PWY-6403: carrageenan biosynthesis
2572233389	t3m_01746	Metacyc	PWY-6834: spermidine biosynthesis III
2572233389	t3m_01746	Metacyc	PWY-5808: hyperforin and adhyperforin biosynthesis
2572233389	t3m_01746	Metacyc	PWY-5135: xanthohumol biosynthesis
2572233389	t3m_01746	Metacyc	PWY-5802: alizarin biosynthesis
2572233389	t3m_01746	Metacyc	PWY-7169: hyperxanthone E biosynthesis
2572233389	t3m_01746	Metacyc	PWY-6936: seleno-amino acid biosynthesis
2572233389	t3m_01746	Metacyc	PWY-5893: tridecaprenyl diphosphate biosynthesis

2572233389	t3m_01746	Metacyc	PWY-5817: dodecaprenyl diphosphate biosynthesis		
2572233389	t3m_01746	Metacyc	PWY-6793: demethylmenaquinol-8 biosynthesis III		
2572233389	t3m_01746	Metacyc	PWY-6681: neurosporaxanthin biosynthesis		
2572233389	t3m_01746	Metacyc	PWY-5816: all <i>trans</i> undecaprenyl diphosphate biosynthesis		
2572233389	t3m_01746	IMG_pathway	209: Ubiquinone biosynthesis		
2572233389	t3m_01746	COG_category	[H] Coenzyme transport and metabolism		
2572233389	t3m_01746	COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferase		3.00E-26
2572233389	t3m_01746	pfam01040	UbiA		3.10E-30
2572233389	t3m_01746	EC:2.5.1.-	Transferases. Transferring alkyl or aryl groups, other than methyl groups. Transferring alkyl or aryl		
2572233389	t3m_01746	TIGR01475	putative 4-hydroxybenzoate polyprenyltransferase		4.20E-61
2572233389	t3m_01746	KO:K03179	4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]		3.70E-41
2572233389	t3m_01746	ITERM:00553	4-hydroxybenzoate polyprenyltransferase (EC 2.5.1.39)		
2572233389	t3m_01746	Locus_type		CDS	
2572233389	t3m_01746	Product_name		4-hydroxybenzoate polyprenyltransferase (EC 2.5.1.39)	
2572233389	t3m_01746	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57	
2572233389	t3m_01746	Coordinates		6229..7119(+)	
2572233389	t3m_01746	DNA_length		891bp	
2572233389	t3m_01746	Protein_length		296aa	
2572233389	t3m_01746	GC		0.69	
2572233389	t3m_01746	Transmembrane		Yes	
2572233390	t3m_01747	Locus_type		CDS	
2572233390	t3m_01747	Product_name		hypothetical protein	
2572233390	t3m_01747	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57	
2572233390	t3m_01747	Coordinates		7189..7539(+)	
2572233390	t3m_01747	DNA_length		351bp	
2572233390	t3m_01747	Protein_length		116aa	
2572233390	t3m_01747	GC		0.7	
2572233391	t3m_01748	Metacyc	PWY-6720: toyocamycin biosynthesis		
2572233391	t3m_01748	Metacyc	PWY-7018: paromomycin biosynthesis		
2572233391	t3m_01748	Metacyc	PWY-5800: xylan biosynthesis		
2572233391	t3m_01748	Metacyc	PWY-7015: ribostamycin biosynthesis		
2572233391	t3m_01748	Metacyc	PWY-5381: pyridine nucleotide cycling (plants)		

2572233391	t3m_01748	Metacyc	PWY-7025: gentamicin biosynthesis			
2572233391	t3m_01748	Metacyc	HISTSYN-PWY: histidine biosynthesis			
2572233391	t3m_01748	Metacyc	PWY-6148: tetrahydromethanopterin biosynthesis			
2572233391	t3m_01748	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233391	t3m_01748	COG1549	Queuine tRNA-ribosyltransferases, contain PUA domain			8.00E-69
2572233391	t3m_01748	pfam01472	PUA			8.40E-08
2572233391	t3m_01748	pfam14810	TGT_C2			7.90E-08
2572233391	t3m_01748	EC:2.4.2.-	Transferases. Glycosyltransferases. Pentosyltransferases.			
2572233391	t3m_01748	KO:K07557	archaeosine tRNA-ribosyltransferase [EC:2.4.2.-]			0.00E+00
2572233391	t3m_01748	Locus_type		CDS		
2572233391	t3m_01748	Product_name		Queuine tRNA-ribosyltransferases, contain PUA domain		
2572233391	t3m_01748	Scaffold		t3m_contig_70_1041_len_9416_read_count_811947.57		
2572233391	t3m_01748	Coordinates		7580..9415(+)		
2572233391	t3m_01748	DNA_length		1836bp		
2572233391	t3m_01748	Protein_length		612aa		
2572233391	t3m_01748	GC			0.71	

2572233392	t3m_01749	Locus_type		CDS		
2572233392	t3m_01749	Product_name		hypothetical protein		
2572233392	t3m_01749	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233392	t3m_01749	Coordinates		3..518(+)		
2572233392	t3m_01749	DNA_length		516bp		
2572233392	t3m_01749	Protein_length		171aa		
2572233392	t3m_01749	GC			0.63	
2572233392	t3m_01749	Transmembrane		Yes		

2572233393	t3m_01750	COG_category	[R] General function prediction only			
2572233393	t3m_01750	COG1926	Predicted phosphoribosyltransferases			1.00E-53
2572233393	t3m_01750	pfam00156	Pribosyltran			2.70E-27
2572233393	t3m_01750	Locus_type		CDS		
2572233393	t3m_01750	Product_name		Predicted phosphoribosyltransferases		
2572233393	t3m_01750	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233393	t3m_01750	Coordinates		611..1291(+)		
2572233393	t3m_01750	DNA_length		681bp		

2572233393	t3m_01750	Protein_length		226aa		
2572233393	t3m_01750	GC			0.73	
2572233394	t3m_01751	COG_category	[R] General function prediction only			
2572233394	t3m_01751	COG0517	FOG: CBS domain			2.00E-12
2572233394	t3m_01751	pfam00571	CBS			3.60E-17
2572233394	t3m_01751	pfam00571	CBS			8.20E-16
2572233394	t3m_01751	Locus_type		CDS		
2572233394	t3m_01751	Product_name		FOG: CBS domain		
2572233394	t3m_01751	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233394	t3m_01751	Coordinates		1384..1941(+)		
2572233394	t3m_01751	DNA_length		558bp		
2572233394	t3m_01751	Protein_length		185aa		
2572233394	t3m_01751	GC			0.67	
2572233395	t3m_01752	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233395	t3m_01752	COG1765	Predicted redox protein, regulator of disulfide bond formation			3.00E-08
2572233395	t3m_01752	pfam02566	OsmC			6.70E-12
2572233395	t3m_01752	Locus_type		CDS		
2572233395	t3m_01752	Product_name		Predicted redox protein, regulator of disulfide bond formation		
2572233395	t3m_01752	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233395	t3m_01752	Coordinates		1981..2403(-)		
2572233395	t3m_01752	DNA_length		423bp		
2572233395	t3m_01752	Protein_length		140aa		
2572233395	t3m_01752	GC			0.71	
2572233396	t3m_01753	pfam13847	Methyltransf_31			2.20E-14
2572233396	t3m_01753	Locus_type		CDS		
2572233396	t3m_01753	Product_name		Methyltransferase domain		
2572233396	t3m_01753	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233396	t3m_01753	Coordinates		2469..3083(-)		
2572233396	t3m_01753	DNA_length		615bp		
2572233396	t3m_01753	Protein_length		204aa		
2572233396	t3m_01753	GC			0.69	

2572233397	t3m_01754	Locus_type		CDS		
2572233397	t3m_01754	Product_name		hypothetical protein		
2572233397	t3m_01754	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233397	t3m_01754	Coordinates		3422..3892(-)		
2572233397	t3m_01754	DNA_length		471bp		
2572233397	t3m_01754	Protein_length		156aa		
2572233397	t3m_01754	GC			0.64	
2572233397	t3m_01754	Transmembrane		Yes		
2572233398	t3m_01755	COG_category	[C] Energy production and conversion			
2572233398	t3m_01755	COG_category	[R] General function prediction only			
2572233398	t3m_01755	COG0604	NADPH:quinone reductase and related Zn-dependent oxidoreductases			3.00E-39
2572233398	t3m_01755	pfam08240	ADH_N			1.40E-10
2572233398	t3m_01755	pfam00107	ADH_zinc_N			3.90E-09
2572233398	t3m_01755	Locus_type		CDS		
2572233398	t3m_01755	Product_name		NADPH:quinone reductase and related Zn-dependent oxidoreductases		
2572233398	t3m_01755	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233398	t3m_01755	Coordinates		3997..4947(+)		
2572233398	t3m_01755	DNA_length		951bp		
2572233398	t3m_01755	Protein_length		316aa		
2572233398	t3m_01755	GC			0.69	
2572233399	t3m_01756	pfam09360	zf-CDGSH			9.30E-14
2572233399	t3m_01756	Locus_type		CDS		
2572233399	t3m_01756	Product_name		Iron-binding zinc finger CDGSH type		
2572233399	t3m_01756	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233399	t3m_01756	Coordinates		5042..5218(-)		
2572233399	t3m_01756	DNA_length		177bp		
2572233399	t3m_01756	Protein_length		58aa		
2572233399	t3m_01756	GC			0.61	
2572233400	t3m_01757	COG_category	[C] Energy production and conversion			
2572233400	t3m_01757	COG1042	Acyl-CoA synthetase (NDP forming)			0.00E+00

2572233400	t3m_01757	pfam13549	ATP-grasp_5			2.90E-84
2572233400	t3m_01757	pfam13380	CoA_binding_2			1.70E-21
2572233400	t3m_01757	pfam13607	Succ_CoA_lig			1.00E-56
2572233400	t3m_01757	pfam13302	Acetyltransf_3			1.00E-10
2572233400	t3m_01757	TIGR02717	acetyl coenzyme A synthetase (ADP forming), alpha domain			0.00E+00
2572233400	t3m_01757	KO:K09181	hypothetical protein			0.00E+00
2572233400	t3m_01757	Locus_type		CDS		
2572233400	t3m_01757	Product_name		Acyl-CoA synthetase (NDP forming)		
2572233400	t3m_01757	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233400	t3m_01757	Coordinates		5427..8216(+)		
2572233400	t3m_01757	DNA_length		2790bp		
2572233400	t3m_01757	Protein_length		929aa		
2572233400	t3m_01757	GC			0.65	

2572233401	t3m_01758	Locus_type		CDS		
2572233401	t3m_01758	Product_name		hypothetical protein		
2572233401	t3m_01758	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233401	t3m_01758	Coordinates		8334..8675(-)		
2572233401	t3m_01758	DNA_length		342bp		
2572233401	t3m_01758	Protein_length		113aa		
2572233401	t3m_01758	GC			0.64	

2572233402	t3m_01759	pfam01467	CTP_transf_2			1.80E-11
2572233402	t3m_01759	TIGR00125	cytidyltransferase-like domain			8.20E-17
2572233402	t3m_01759	Locus_type		CDS		
2572233402	t3m_01759	Product_name		cytidyltransferase-like domain		
2572233402	t3m_01759	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233402	t3m_01759	Coordinates		8878..9252(-)		
2572233402	t3m_01759	DNA_length		375bp		
2572233402	t3m_01759	Protein_length		124aa		
2572233402	t3m_01759	GC			0.61	

2572233403	t3m_01760	Locus_type		tRNA		
2572233403	t3m_01760	Product_name		tRNA_Ala_CGC		

2572233403	t3m_01760	Scaffold		t3m_contig_70_1050_len_9331_read_count_809888.58		
2572233403	t3m_01760	Coordinates		9264..9330(-)		
2572233403	t3m_01760	DNA_length		67bp		
2572233403	t3m_01760	GC			0.58	
2572233404	t3m_01761	pfam00361	Oxidored_q1			4.40E-18
2572233404	t3m_01761	Locus_type		CDS		
2572233404	t3m_01761	Product_name		NADH-Ubiquinone/plastoquinone (complex I), various chains		
2572233404	t3m_01761	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59		
2572233404	t3m_01761	Coordinates		1..615(+)		
2572233404	t3m_01761	DNA_length		615bp		
2572233404	t3m_01761	Protein_length		204aa		
2572233404	t3m_01761	GC			0.7	
2572233404	t3m_01761	Transmembrane		Yes		
2572233405	t3m_01762	COG_category	[C] Energy production and conversion			
2572233405	t3m_01762	COG0644	Dehydrogenases (flavoproteins)			3.00E-41
2572233405	t3m_01762	pfam01494	FAD_binding_3			9.20E-08
2572233405	t3m_01762	TIGR02032	geranylgeranyl reductase family			5.20E-61
2572233405	t3m_01762	ITERM:05619	2,3-di-O-geranylgeranylglyceryl phosphate reductase (EC 1.3.99.-)			
2572233405	t3m_01762	Locus_type		CDS		
2572233405	t3m_01762	Product_name		2,3-di-O-geranylgeranylglyceryl phosphate reductase (EC 1.3.99.-)		
2572233405	t3m_01762	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59		
2572233405	t3m_01762	Coordinates		623..1723(+)		
2572233405	t3m_01762	DNA_length		1101bp		
2572233405	t3m_01762	Protein_length		366aa		
2572233405	t3m_01762	GC			0.73	
2572233406	t3m_01763	Metacyc	PWY-5783: octaprenyl diphosphate biosynthesis			
2572233406	t3m_01763	COG_category	[H] Coenzyme transport and metabolism			
2572233406	t3m_01763	COG0142	Geranylgeranyl pyrophosphate synthase			2.00E-60
2572233406	t3m_01763	pfam00348	polyprenyl_synt			7.90E-52
2572233406	t3m_01763	EC:2.5.1.90	All-trans-octaprenyl-diphosphate synthase.			
2572233406	t3m_01763	KO:K02523	octaprenyl-diphosphate synthase [EC:2.5.1.90]			0.00E+00

2572233406	t3m_01763	Locus_type		CDS	
2572233406	t3m_01763	Product_name		Geranylgeranyl pyrophosphate synthase	
2572233406	t3m_01763	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59	
2572233406	t3m_01763	Coordinates		1720..2775(+)	
2572233406	t3m_01763	DNA_length		1056bp	
2572233406	t3m_01763	Protein_length		351aa	
2572233406	t3m_01763	GC		0.7	
2572233407	t3m_01764	Locus_type		CDS	
2572233407	t3m_01764	Product_name		hypothetical protein	
2572233407	t3m_01764	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59	
2572233407	t3m_01764	Coordinates		2842..3309(+)	
2572233407	t3m_01764	DNA_length		468bp	
2572233407	t3m_01764	Protein_length		155aa	
2572233407	t3m_01764	GC		0.66	
2572233407	t3m_01764	Transmembrane		Yes	
2572233408	t3m_01765	COG_category	[R] General function prediction only		
2572233408	t3m_01765	COG0388	Predicted amidohydrolase		2.00E-38
2572233408	t3m_01765	pfam00795	CN_hydrolase		2.10E-21
2572233408	t3m_01765	Locus_type		CDS	
2572233408	t3m_01765	Product_name		Predicted amidohydrolase	
2572233408	t3m_01765	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59	
2572233408	t3m_01765	Coordinates		3309..4166(+)	
2572233408	t3m_01765	DNA_length		858bp	
2572233408	t3m_01765	Protein_length		285aa	
2572233408	t3m_01765	GC		0.72	
2572233409	t3m_01766	COG_category	[L] Replication, recombination and repair		
2572233409	t3m_01766	COG1389	DNA topoisomerase VI, subunit B		0.00E+00
2572233409	t3m_01766	pfam02518	HATPase_c		3.40E-10
2572233409	t3m_01766	pfam09239	Topo-VIb_trans		6.90E-56
2572233409	t3m_01766	EC:5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).		
2572233409	t3m_01766	TIGR01052	DNA topoisomerase VI, B subunit		0.00E+00

2572233409	t3m_01766	KO:K03167	DNA topoisomerase VI subunit B [EC:5.99.1.3]			0.00E+00
2572233409	t3m_01766	Locus_type		CDS		
2572233409	t3m_01766	Product_name		DNA topoisomerase VI, B subunit		
2572233409	t3m_01766	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59		
2572233409	t3m_01766	Coordinates		4191..6215(+)		
2572233409	t3m_01766	DNA_length		2025bp		
2572233409	t3m_01766	Protein_length		674aa		
2572233409	t3m_01766	GC			0.69	
2572233410	t3m_01767	COG_category	[L] Replication, recombination and repair			
2572233410	t3m_01767	COG1697	DNA topoisomerase VI, subunit A			5.00E-101
2572233410	t3m_01767	pfam04406	TP6A_N			2.20E-14
2572233410	t3m_01767	EC:5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).			
2572233410	t3m_01767	KO:K03166	DNA topoisomerase VI subunit A [EC:5.99.1.3]			0.00E+00
2572233410	t3m_01767	Locus_type		CDS		
2572233410	t3m_01767	Product_name		DNA topoisomerase VI, subunit A		
2572233410	t3m_01767	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59		
2572233410	t3m_01767	Coordinates		6175..7317(+)		
2572233410	t3m_01767	DNA_length		1143bp		
2572233410	t3m_01767	Protein_length		380aa		
2572233410	t3m_01767	GC			0.65	
2572233411	t3m_01768	COG_category	[G] Carbohydrate transport and metabolism			
2572233411	t3m_01768	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Prote			1.00E-34
2572233411	t3m_01768	pfam00230	MIP			4.50E-46
2572233411	t3m_01768	TIGR00861	MIP family channel proteins			1.50E-50
2572233411	t3m_01768	KO:K06188	aquaporin Z			9.80E-45
2572233411	t3m_01768	Locus_type		CDS		
2572233411	t3m_01768	Product_name		Glycerol uptake facilitator and related permeases (Major Intrinsic Protei		
2572233411	t3m_01768	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59		
2572233411	t3m_01768	Coordinates		7384..8118(+)		
2572233411	t3m_01768	DNA_length		735bp		
2572233411	t3m_01768	Protein_length		244aa		
2572233411	t3m_01768	GC			0.67	

2572233411	t3m_01768	Transmembrane		Yes	

2572233412	t3m_01769	Locus_type		CDS	
2572233412	t3m_01769	Product_name		hypothetical protein	
2572233412	t3m_01769	Scaffold		t3m_contig_70_1156_len_8766_read_count_661841.59	
2572233412	t3m_01769	Coordinates		8136..8552(-)	
2572233412	t3m_01769	DNA_length		417bp	
2572233412	t3m_01769	Protein_length		138aa	
2572233412	t3m_01769	GC		0.7	

2572233413	t3m_01770	COG_category	[R] General function prediction only		
2572233413	t3m_01770	COG1011	Predicted hydrolase (HAD superfamily)		1.00E-26
2572233413	t3m_01770	pfam13419	HAD_2		2.70E-28
2572233413	t3m_01770	TIGR01549	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third m		3.00E-10
2572233413	t3m_01770	TIGR01509	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third m		1.30E-11
2572233413	t3m_01770	KO:K07025	putative hydrolase of the HAD superfamily		7.50E-27
2572233413	t3m_01770	Locus_type		CDS	
2572233413	t3m_01770	Product_name		haloacid dehalogenase superfamily, subfamily IA, variant 3 with third m	
2572233413	t3m_01770	Scaffold		t3m_contig_70_1173_len_8710_read_count_677408.60	
2572233413	t3m_01770	Coordinates		163..894(-)	
2572233413	t3m_01770	DNA_length		732bp	
2572233413	t3m_01770	Protein_length		243aa	
2572233413	t3m_01770	GC		0.69	

2572233414	t3m_01771	COG_category	[K] Transcription		
2572233414	t3m_01771	COG0195	Transcription elongation factor		2.00E-15
2572233414	t3m_01771	TIGR01952	NusA family KH domain protein, archaeal		3.10E-36
2572233414	t3m_01771	KO:K02600	N utilization substance protein A		7.10E-23
2572233414	t3m_01771	Locus_type		CDS	
2572233414	t3m_01771	Product_name		NusA family KH domain protein, archaeal	
2572233414	t3m_01771	Scaffold		t3m_contig_70_1173_len_8710_read_count_677408.60	
2572233414	t3m_01771	Coordinates		977..1402(-)	
2572233414	t3m_01771	DNA_length		426bp	
2572233414	t3m_01771	Protein_length		141aa	

2572233414	t3m_01771	GC			0.64	
2572233415	t3m_01772	KEGG_module	M00179: Ribosome, archaea			
2572233415	t3m_01772	KEGG_module	M00177: Ribosome, eukaryotes			
2572233415	t3m_01772	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233415	t3m_01772	COG1911	Ribosomal protein L30E			4.00E-19
2572233415	t3m_01772	pfam01248	Ribosomal_L7Ae			1.10E-14
2572233415	t3m_01772	KO:K02908	large subunit ribosomal protein L30e			8.70E-17
2572233415	t3m_01772	ITERM:00256	LSU ribosomal protein L30E			
2572233415	t3m_01772	Locus_type		CDS		
2572233415	t3m_01772	Product_name		LSU ribosomal protein L30E		
2572233415	t3m_01772	Scaffold		t3m_contig_70_1173_len_8710_read_count_677408.60		
2572233415	t3m_01772	Coordinates		1421..1708(-)		
2572233415	t3m_01772	DNA_length		288bp		
2572233415	t3m_01772	Protein_length		95aa		
2572233415	t3m_01772	GC			0.69	
2572233416	t3m_01773	KEGG_module	M00184: RNA polymerase, archaea			
2572233416	t3m_01773	pfam04998	RNA_pol_Rpb1_5			1.00E-49
2572233416	t3m_01773	EC:2.7.7.6	DNA-directed RNA polymerase.			
2572233416	t3m_01773	TIGR02389	DNA-directed RNA polymerase, subunit A''			0.00E+00
2572233416	t3m_01773	KO:K03042	DNA-directed RNA polymerase subunit A" [EC:2.7.7.6]			0.00E+00
2572233416	t3m_01773	Locus_type		CDS		
2572233416	t3m_01773	Product_name		DNA-directed RNA polymerase, subunit A''		
2572233416	t3m_01773	Scaffold		t3m_contig_70_1173_len_8710_read_count_677408.60		
2572233416	t3m_01773	Coordinates		1714..3021(-)		
2572233416	t3m_01773	DNA_length		1308bp		
2572233416	t3m_01773	Protein_length		435aa		
2572233416	t3m_01773	GC			0.69	
2572233417	t3m_01774	KEGG_module	M00184: RNA polymerase, archaea			
2572233417	t3m_01774	COG_category	[K] Transcription			
2572233417	t3m_01774	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit			0.00E+00
2572233417	t3m_01774	pfam04983	RNA_pol_Rpb1_3			1.70E-28

2572233417	t3m_01774	pfam00623	RNA_pol_Rpb1_2			4.80E-58
2572233417	t3m_01774	pfam04997	RNA_pol_Rpb1_1			5.80E-28
2572233417	t3m_01774	pfam04997	RNA_pol_Rpb1_1			6.70E-54
2572233417	t3m_01774	pfam05000	RNA_pol_Rpb1_4			1.70E-27
2572233417	t3m_01774	pfam04998	RNA_pol_Rpb1_5			2.60E-29
2572233417	t3m_01774	EC:2.7.7.6	DNA-directed RNA polymerase.			
2572233417	t3m_01774	TIGR02390	DNA-directed RNA polymerase subunit A'			0.00E+00
2572233417	t3m_01774	KO:K03041	DNA-directed RNA polymerase subunit A' [EC:2.7.7.6]			0.00E+00
2572233417	t3m_01774	Locus_type		CDS		
2572233417	t3m_01774	Product_name		DNA-directed RNA polymerase, subunit A' (EC 2.7.7.6)		
2572233417	t3m_01774	Scaffold		t3m_contig_70_1173_len_8710_read_count_677408.60		
2572233417	t3m_01774	Coordinates		3018..5816(-)		
2572233417	t3m_01774	DNA_length		2799bp		
2572233417	t3m_01774	Protein_length		932aa		
2572233417	t3m_01774	GC			0.68	

2572233418	t3m_01775	KEGG_module	M00184: RNA polymerase, archaea			
2572233418	t3m_01775	COG_category	[K] Transcription			
2572233418	t3m_01775	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit			0.00E+00
2572233418	t3m_01775	pfam04563	RNA_pol_Rpb2_1			2.10E-06
2572233418	t3m_01775	pfam04566	RNA_pol_Rpb2_4			1.40E-18
2572233418	t3m_01775	pfam04560	RNA_pol_Rpb2_7			9.30E-24
2572233418	t3m_01775	pfam04565	RNA_pol_Rpb2_3			1.50E-25
2572233418	t3m_01775	pfam00562	RNA_pol_Rpb2_6			2.30E-118
2572233418	t3m_01775	pfam04561	RNA_pol_Rpb2_2			6.40E-17
2572233418	t3m_01775	pfam04567	RNA_pol_Rpb2_5			1.30E-11
2572233418	t3m_01775	EC:2.7.7.6	DNA-directed RNA polymerase.			
2572233418	t3m_01775	TIGR03670	DNA-directed RNA polymerase subunit B			0.00E+00
2572233418	t3m_01775	KO:K13798	DNA-directed RNA polymerase subunit B [EC:2.7.7.6]			0.00E+00
2572233418	t3m_01775	Locus_type		CDS		
2572233418	t3m_01775	Product_name		DNA-directed RNA polymerase, subunit B" (EC 2.7.7.6)/DNA-directed RN		
2572233418	t3m_01775	Scaffold		t3m_contig_70_1173_len_8710_read_count_677408.60		
2572233418	t3m_01775	Coordinates		5827..8709(-)		
2572233418	t3m_01775	DNA_length		2883bp		

2572233418	t3m_01775	Protein_length	960aa
2572233418	t3m_01775	GC	0.68

2572233419	t3m_01776	Locus_type	CDS
2572233419	t3m_01776	Product_name	hypothetical protein
2572233419	t3m_01776	Scaffold	t3m_contig_70_1259_len_8374_read_count_746448.61
2572233419	t3m_01776	Coordinates	92..394(-)
2572233419	t3m_01776	DNA_length	303bp
2572233419	t3m_01776	Protein_length	100aa
2572233419	t3m_01776	GC	0.66
2572233419	t3m_01776	Transmembrane	Yes

2572233420	t3m_01777	Locus_type	CDS
2572233420	t3m_01777	Product_name	hypothetical protein
2572233420	t3m_01777	Scaffold	t3m_contig_70_1259_len_8374_read_count_746448.61
2572233420	t3m_01777	Coordinates	439..1056(-)
2572233420	t3m_01777	DNA_length	618bp
2572233420	t3m_01777	Protein_length	205aa
2572233420	t3m_01777	GC	0.66
2572233420	t3m_01777	Transmembrane	Yes

2572233421	t3m_01778	KEGG_module	M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone
2572233421	t3m_01778	Metacyc	PWY-6559: spermidine biosynthesis II
2572233421	t3m_01778	Metacyc	PWY-5872: ubiquinol-10 biosynthesis (eukaryotic)
2572233421	t3m_01778	Metacyc	PWY-5873: ubiquinol-7 biosynthesis (eukaryotic)
2572233421	t3m_01778	Metacyc	PWY-5856: ubiquinol-9 biosynthesis (prokaryotic)
2572233421	t3m_01778	Metacyc	PWY-5855: ubiquinol-7 biosynthesis (prokaryotic)
2572233421	t3m_01778	Metacyc	PWY-181: photorespiration
2572233421	t3m_01778	Metacyc	PWY-5857: ubiquinol-10 biosynthesis (prokaryotic)
2572233421	t3m_01778	Metacyc	PWY-5871: ubiquinol-9 biosynthesis (eukaryotic)
2572233421	t3m_01778	Metacyc	PWY-7007: methyl ketone biosynthesis
2572233421	t3m_01778	Metacyc	PWY-5113: UDP-D-apiose biosynthesis (from UDP-D-glucuronate)
2572233421	t3m_01778	Metacyc	PWY-6585: 2-tridecanone biosynthesis
2572233421	t3m_01778	Metacyc	PWY-5870: ubiquinol-8 biosynthesis (eukaryotic)

2572233421	t3m_01778	Metacyc	PWY-5163: <I>p</I>-cumate degradation to 2-oxopent-4-enoate		
2572233421	t3m_01778	Metacyc	PWY-5826: hypoglycin biosynthesis		
2572233421	t3m_01778	Metacyc	PWY-6627: salinosporamide A biosynthesis		
2572233421	t3m_01778	Metacyc	PWY-3385: choline biosynthesis I		
2572233421	t3m_01778	Metacyc	PWY3O-19: ubiquinol-6 biosynthesis (eukaryotic)		
2572233421	t3m_01778	Metacyc	PWY-6708: ubiquinol-8 biosynthesis (prokaryotic)		
2572233421	t3m_01778	COG_category	[H] Coenzyme transport and metabolism		
2572233421	t3m_01778	COG0163	3-polyprenyl-4-hydroxybenzoate decarboxylase		1.00E-57
2572233421	t3m_01778	pfam02441	Flavoprotein		2.50E-30
2572233421	t3m_01778	EC:4.1.1.-	Lyases. Carbon-carbon lyases. Carboxy-lyases.		
2572233421	t3m_01778	TIGR00421	polyprenyl P-hydroxybenzoate and phenylacrylic acid decarboxylases		4.60E-63
2572233421	t3m_01778	KO:K03186	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiX [EC:4.1.1.-]		0.00E+00
2572233421	t3m_01778	Locus_type		CDS	
2572233421	t3m_01778	Product_name		polyprenyl P-hydroxybenzoate and phenylacrylic acid decarboxylases	
2572233421	t3m_01778	Scaffold		t3m_contig_70_1259_len_8374_read_count_746448.61	
2572233421	t3m_01778	Coordinates		1053..1628(-)	
2572233421	t3m_01778	DNA_length		576bp	
2572233421	t3m_01778	Protein_length		191aa	
2572233421	t3m_01778	GC		0.69	

2572233422	t3m_01779	COG_category	[R] General function prediction only		
2572233422	t3m_01779	COG3975	Predicted protease with the C-terminal PDZ domain		1.00E-111
2572233422	t3m_01779	pfam13180	PDZ_2		7.80E-09
2572233422	t3m_01779	pfam05299	Peptidase_M61		7.40E-37
2572233422	t3m_01779	Locus_type		CDS	
2572233422	t3m_01779	Product_name		Predicted protease with the C-terminal PDZ domain	
2572233422	t3m_01779	Scaffold		t3m_contig_70_1259_len_8374_read_count_746448.61	
2572233422	t3m_01779	Coordinates		1802..3571(-)	
2572233422	t3m_01779	DNA_length		1770bp	
2572233422	t3m_01779	Protein_length		589aa	
2572233422	t3m_01779	GC		0.66	

2572233423	t3m_01780	Locus_type		CDS	
2572233423	t3m_01780	Product_name		hypothetical protein	

2572233423	t3m_01780	Scaffold		t3m_contig_70_1259_len_8374_read_count_746448.61		
2572233423	t3m_01780	Coordinates		3570..3842(+)		
2572233423	t3m_01780	DNA_length		273bp		
2572233423	t3m_01780	Protein_length		90aa		
2572233423	t3m_01780	GC			0.66	
2572233424	t3m_01781	KEGG_module	M00248: Putative antibiotic transport system			
2572233424	t3m_01781	COG_category	[V] Defense mechanisms			
2572233424	t3m_01781	COG1131	ABC-type multidrug transport system, ATPase component			3.00E-81
2572233424	t3m_01781	pfam00005	ABC_tran			8.10E-32
2572233424	t3m_01781	TIGR01188	daunorubicin resistance ABC transporter ATP-binding subunit			2.60E-108
2572233424	t3m_01781	KO:K09687	antibiotic transport system ATP-binding protein			0.00E+00
2572233424	t3m_01781	Locus_type		CDS		
2572233424	t3m_01781	Product_name		daunorubicin resistance ABC transporter ATP-binding subunit		
2572233424	t3m_01781	Scaffold		t3m_contig_70_1259_len_8374_read_count_746448.61		
2572233424	t3m_01781	Coordinates		4058..5071(+)		
2572233424	t3m_01781	DNA_length		1014bp		
2572233424	t3m_01781	Protein_length		337aa		
2572233424	t3m_01781	GC			0.68	
2572233425	t3m_01782	KEGG_module	M00248: Putative antibiotic transport system			
2572233425	t3m_01782	COG_category	[V] Defense mechanisms			
2572233425	t3m_01782	COG0842	ABC-type multidrug transport system, permease component			3.00E-04
2572233425	t3m_01782	pfam01061	ABC2_membrane			2.70E-22
2572233425	t3m_01782	KO:K09686	antibiotic transport system permease protein			4.20E-35
2572233425	t3m_01782	Locus_type		CDS		
2572233425	t3m_01782	Product_name		ABC-type multidrug transport system, permease component		
2572233425	t3m_01782	Scaffold		t3m_contig_70_1259_len_8374_read_count_746448.61		
2572233425	t3m_01782	Coordinates		5068..5916(+)		
2572233425	t3m_01782	DNA_length		849bp		
2572233425	t3m_01782	Protein_length		282aa		
2572233425	t3m_01782	GC			0.65	
2572233425	t3m_01782	Transmembrane		Yes		

2572233426	t3m_01783	Locus_type		CDS		
2572233426	t3m_01783	Product_name		hypothetical protein		
2572233426	t3m_01783	Scaffold		t3m_contig_70_1259_len_8374_read_count_746448.61		
2572233426	t3m_01783	Coordinates		5921..6469(-)		
2572233426	t3m_01783	DNA_length		549bp		
2572233426	t3m_01783	Protein_length		182aa		
2572233426	t3m_01783	GC			0.7	
2572233427	t3m_01784	COG_category	[R] General function prediction only			
2572233427	t3m_01784	COG1964	Predicted Fe-S oxidoreductases			1.00E-130
2572233427	t3m_01784	pfam04055	Radical_SAM			2.50E-15
2572233427	t3m_01784	pfam13394	Fer4_14			5.20E-06
2572233427	t3m_01784	Locus_type		CDS		
2572233427	t3m_01784	Product_name		Predicted Fe-S oxidoreductases		
2572233427	t3m_01784	Scaffold		t3m_contig_70_1259_len_8374_read_count_746448.61		
2572233427	t3m_01784	Coordinates		6713..8371(+)		
2572233427	t3m_01784	DNA_length		1659bp		
2572233427	t3m_01784	Protein_length		553aa		
2572233427	t3m_01784	GC			0.64	
2572233428	t3m_01785	COG_category	[R] General function prediction only			
2572233428	t3m_01785	COG2018	Uncharacterized distant relative of homeotic protein bithoraxoid			5.00E-11
2572233428	t3m_01785	pfam03259	Robl_LC7			4.50E-10
2572233428	t3m_01785	Locus_type		CDS		
2572233428	t3m_01785	Product_name		Uncharacterized distant relative of homeotic protein bithoraxoid		
2572233428	t3m_01785	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62		
2572233428	t3m_01785	Coordinates		131..487(+)		
2572233428	t3m_01785	DNA_length		357bp		
2572233428	t3m_01785	Protein_length		118aa		
2572233428	t3m_01785	GC			0.66	
2572233429	t3m_01786	pfam13641	Glyco_tranf_2_3			7.50E-24
2572233429	t3m_01786	Locus_type		CDS		
2572233429	t3m_01786	Product_name		Glycosyltransferase like family 2		

2572233429	t3m_01786	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62		
2572233429	t3m_01786	Coordinates		566..1417(-)		
2572233429	t3m_01786	DNA_length		852bp		
2572233429	t3m_01786	Protein_length		283aa		
2572233429	t3m_01786	GC			0.68	
2572233430	t3m_01787	COG_category	[S] Function unknown			
2572233430	t3m_01787	COG1873	Uncharacterized conserved protein			2.00E-06
2572233430	t3m_01787	pfam05239	PRC			6.70E-11
2572233430	t3m_01787	Locus_type		CDS		
2572233430	t3m_01787	Product_name		Uncharacterized conserved protein		
2572233430	t3m_01787	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62		
2572233430	t3m_01787	Coordinates		1407..1649(-)		
2572233430	t3m_01787	DNA_length		243bp		
2572233430	t3m_01787	Protein_length		80aa		
2572233430	t3m_01787	GC			0.61	
2572233431	t3m_01788	KEGG_module	M00177: Ribosome, eukaryotes			
2572233431	t3m_01788	KEGG_module	M00179: Ribosome, archaea			
2572233431	t3m_01788	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233431	t3m_01788	COG1727	Ribosomal protein L18E			3.00E-27
2572233431	t3m_01788	pfam00828	Ribosomal_L18e			2.80E-14
2572233431	t3m_01788	KO:K02883	large subunit ribosomal protein L18e			2.50E-24
2572233431	t3m_01788	Locus_type		CDS		
2572233431	t3m_01788	Product_name		Ribosomal protein L18E		
2572233431	t3m_01788	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62		
2572233431	t3m_01788	Coordinates		1816..2181(+)		
2572233431	t3m_01788	DNA_length		366bp		
2572233431	t3m_01788	Protein_length		121aa		
2572233431	t3m_01788	GC			0.66	
2572233432	t3m_01789	KEGG_module	M00178: Ribosome, bacteria			
2572233432	t3m_01789	KEGG_module	M00179: Ribosome, archaea			
2572233432	t3m_01789	COG_category	[J] Translation, ribosomal structure and biogenesis			

2572233432	t3m_01789	COG0102	Ribosomal protein L13		5.00E-21
2572233432	t3m_01789	pfam00572	Ribosomal_L13		2.60E-20
2572233432	t3m_01789	TIGR01077	ribosomal protein L13, archaeal/eukaryotic		3.30E-45
2572233432	t3m_01789	KO:K02871	large subunit ribosomal protein L13		7.80E-33
2572233432	t3m_01789	ITERM:00230	LSU ribosomal protein L13P		
2572233432	t3m_01789	Locus_type		CDS	
2572233432	t3m_01789	Product_name		LSU ribosomal protein L13P	
2572233432	t3m_01789	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62	
2572233432	t3m_01789	Coordinates		2174..2614(+)	
2572233432	t3m_01789	DNA_length		441bp	
2572233432	t3m_01789	Protein_length		146aa	
2572233432	t3m_01789	GC		0.72	
2572233433	t3m_01790	KEGG_module	M00179: Ribosome, archaea		
2572233433	t3m_01790	KEGG_module	M00178: Ribosome, bacteria		
2572233433	t3m_01790	COG_category	[J] Translation, ribosomal structure and biogenesis		
2572233433	t3m_01790	COG0103	Ribosomal protein S9		1.00E-30
2572233433	t3m_01790	pfam00380	Ribosomal_S9		4.80E-34
2572233433	t3m_01790	TIGR03627	archaeal ribosomal protein S9P		2.90E-60
2572233433	t3m_01790	KO:K02996	small subunit ribosomal protein S9		2.10E-40
2572233433	t3m_01790	Locus_type		CDS	
2572233433	t3m_01790	Product_name		SSU ribosomal protein S9P	
2572233433	t3m_01790	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62	
2572233433	t3m_01790	Coordinates		2611..3018(+)	
2572233433	t3m_01790	DNA_length		408bp	
2572233433	t3m_01790	Protein_length		135aa	
2572233433	t3m_01790	GC		0.7	
2572233434	t3m_01791	KEGG_module	M00184: RNA polymerase, archaea		
2572233434	t3m_01791	COG_category	[K] Transcription		
2572233434	t3m_01791	COG1644	DNA-directed RNA polymerase, subunit N (RpoN/RPB10)		3.00E-22
2572233434	t3m_01791	pfam01194	RNA_pol_N		3.30E-30
2572233434	t3m_01791	EC:2.7.7.6	DNA-directed RNA polymerase.		
2572233434	t3m_01791	KO:K03058	DNA-directed RNA polymerase subunit N [EC:2.7.7.6]		3.70E-19

2572233434	t3m_01791	ITERM:01913	DNA-directed RNA polymerase, subunit N (EC 2.7.7.6)			
2572233434	t3m_01791	Locus_type		CDS		
2572233434	t3m_01791	Product_name		DNA-directed RNA polymerase, subunit N (EC 2.7.7.6)		
2572233434	t3m_01791	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62		
2572233434	t3m_01791	Coordinates		3038..3235(+)		
2572233434	t3m_01791	DNA_length		198bp		
2572233434	t3m_01791	Protein_length		65aa		
2572233434	t3m_01791	GC			0.7	
2572233435	t3m_01792	Locus_type		CDS		
2572233435	t3m_01792	Product_name		hypothetical protein		
2572233435	t3m_01792	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62		
2572233435	t3m_01792	Coordinates		3380..6760(-)		
2572233435	t3m_01792	DNA_length		3381bp		
2572233435	t3m_01792	Protein_length		1126aa		
2572233435	t3m_01792	GC			0.65	
2572233435	t3m_01792	Signal_peptide		Yes		
2572233435	t3m_01792	Transmembrane		Yes		
2572233436	t3m_01793	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233436	t3m_01793	COG0464	ATPases of the AAA+ class			2.00E-114
2572233436	t3m_01793	pfam00004	AAA			6.10E-48
2572233436	t3m_01793	pfam00004	AAA			4.30E-25
2572233436	t3m_01793	Locus_type		CDS		
2572233436	t3m_01793	Product_name		ATPases of the AAA+ class		
2572233436	t3m_01793	Scaffold		t3m_contig_70_1281_len_8301_read_count_711995.62		
2572233436	t3m_01793	Coordinates		6875..8299(-)		
2572233436	t3m_01793	DNA_length		1425bp		
2572233436	t3m_01793	Protein_length		474aa		
2572233436	t3m_01793	GC			0.68	
2572233437	t3m_01794	KEGG_module	M00335: Sec (secretion) system			
2572233437	t3m_01794	COG_category	[U] Intracellular trafficking, secretion, and vesicular transport			
2572233437	t3m_01794	COG0552	Signal recognition particle GTPase			1.00E-92

2572233437	t3m_01794	pfam00448	SRP54			3.50E-74
2572233437	t3m_01794	pfam02881	SRP54_N			8.40E-10
2572233437	t3m_01794	TIGR00064	signal recognition particle-docking protein FtsY			1.20E-101
2572233437	t3m_01794	KO:K03110	fused signal recognition particle receptor			0.00E+00
2572233437	t3m_01794	ITERM:02712	signal recognition particle-docking protein FtsY			
2572233437	t3m_01794	Locus_type		CDS		
2572233437	t3m_01794	Product_name		signal recognition particle-docking protein FtsY		
2572233437	t3m_01794	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233437	t3m_01794	Coordinates		91..1104(+)		
2572233437	t3m_01794	DNA_length		1014bp		
2572233437	t3m_01794	Protein_length		337aa		
2572233437	t3m_01794	GC			0.68	
2572233438	t3m_01795	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233438	t3m_01795	COG0565	rRNA methylase			1.00E-46
2572233438	t3m_01795	pfam00588	SpoU_methylase			3.60E-29
2572233438	t3m_01795	TIGR00050	RNA methyltransferase, TrmH family, group 1			2.30E-55
2572233438	t3m_01795	Locus_type		CDS		
2572233438	t3m_01795	Product_name		RNA methyltransferase, TrmH family, group 1		
2572233438	t3m_01795	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233438	t3m_01795	Coordinates		1101..1844(+)		
2572233438	t3m_01795	DNA_length		744bp		
2572233438	t3m_01795	Protein_length		247aa		
2572233438	t3m_01795	GC			0.69	
2572233439	t3m_01796	Locus_type		CDS		
2572233439	t3m_01796	Product_name		hypothetical protein		
2572233439	t3m_01796	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233439	t3m_01796	Coordinates		1831..2247(+)		
2572233439	t3m_01796	DNA_length		417bp		
2572233439	t3m_01796	Protein_length		138aa		
2572233439	t3m_01796	GC			0.7	
2572233440	t3m_01797	KEGG_module	M00179: Ribosome, archaea			

2572233440	t3m_01797	KEGG_module	M00177: Ribosome, eukaryotes			
2572233440	t3m_01797	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233440	t3m_01797	COG1632	Ribosomal protein L15E			2.00E-48
2572233440	t3m_01797	pfam00827	Ribosomal_L15e			1.10E-72
2572233440	t3m_01797	KO:K02877	large subunit ribosomal protein L15e			0.00E+00
2572233440	t3m_01797	ITERM:00233	LSU ribosomal protein L15E			
2572233440	t3m_01797	Locus_type		CDS		
2572233440	t3m_01797	Product_name		LSU ribosomal protein L15E		
2572233440	t3m_01797	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233440	t3m_01797	Coordinates		2330..2920(+)		
2572233440	t3m_01797	DNA_length		591bp		
2572233440	t3m_01797	Protein_length		196aa		
2572233440	t3m_01797	GC			0.69	

2572233441	t3m_01798	COG_category	[L] Replication, recombination and repair			
2572233441	t3m_01798	COG1658	Small primase-like proteins (Toprim domain)			1.00E-12
2572233441	t3m_01798	pfam13662	Toprim_4			1.60E-07
2572233441	t3m_01798	Locus_type		CDS		
2572233441	t3m_01798	Product_name		Small primase-like proteins (Toprim domain)		
2572233441	t3m_01798	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233441	t3m_01798	Coordinates		2910..3440(-)		
2572233441	t3m_01798	DNA_length		531bp		
2572233441	t3m_01798	Protein_length		176aa		
2572233441	t3m_01798	GC			0.72	

2572233442	t3m_01799	COG_category	[S] Function unknown			
2572233442	t3m_01799	COG1711	Uncharacterized protein conserved in archaea			9.00E-05
2572233442	t3m_01799	Locus_type		CDS		
2572233442	t3m_01799	Product_name		hypothetical protein		
2572233442	t3m_01799	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233442	t3m_01799	Coordinates		3506..4156(+)		
2572233442	t3m_01799	DNA_length		651bp		
2572233442	t3m_01799	Protein_length		216aa		
2572233442	t3m_01799	GC			0.7	

2572233443	t3m_01800	COG_category	[S] Function unknown			
2572233443	t3m_01800	COG1565	Uncharacterized conserved protein			8.00E-49
2572233443	t3m_01800	pfam02636	Methyltransf_28			3.30E-39
2572233443	t3m_01800	Locus_type		CDS		
2572233443	t3m_01800	Product_name		Uncharacterized conserved protein		
2572233443	t3m_01800	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233443	t3m_01800	Coordinates		4149..5297(-)		
2572233443	t3m_01800	DNA_length		1149bp		
2572233443	t3m_01800	Protein_length		382aa		
2572233443	t3m_01800	GC			0.72	
2572233444	t3m_01801	COG_category	[R] General function prediction only			
2572233444	t3m_01801	COG2047	Uncharacterized protein (ATP-grasp superfamily)			4.00E-77
2572233444	t3m_01801	pfam09754	PAC2			1.20E-48
2572233444	t3m_01801	TIGR00162	TIGR00162 family protein			1.80E-82
2572233444	t3m_01801	Locus_type		CDS		
2572233444	t3m_01801	Product_name		Uncharacterized protein (ATP-grasp superfamily)		
2572233444	t3m_01801	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233444	t3m_01801	Coordinates		5309..6094(-)		
2572233444	t3m_01801	DNA_length		786bp		
2572233444	t3m_01801	Protein_length		261aa		
2572233444	t3m_01801	GC			0.67	
2572233445	t3m_01802	COG_category	[T] Signal transduction mechanisms			
2572233445	t3m_01802	COG0467	RecA-superfamily ATPases implicated in signal transduction			8.00E-12
2572233445	t3m_01802	pfam06745	KaiC			1.40E-10
2572233445	t3m_01802	Locus_type		CDS		
2572233445	t3m_01802	Product_name		RecA-superfamily ATPases implicated in signal transduction		
2572233445	t3m_01802	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233445	t3m_01802	Coordinates		6162..6926(-)		
2572233445	t3m_01802	DNA_length		765bp		
2572233445	t3m_01802	Protein_length		254aa		
2572233445	t3m_01802	GC			0.68	

2572233446	t3m_01803	pfam06745	KaiC			1.50E-05
2572233446	t3m_01803	Locus_type		CDS		
2572233446	t3m_01803	Product_name		KaiC		
2572233446	t3m_01803	Scaffold		t3m_contig_70_1517_len_7421_read_count_590785.63		
2572233446	t3m_01803	Coordinates		6929..7420(-)		
2572233446	t3m_01803	DNA_length		492bp		
2572233446	t3m_01803	Protein_length		163aa		
2572233446	t3m_01803	GC			0.64	
2572233447	t3m_01804	Locus_type		CDS		
2572233447	t3m_01804	Product_name		hypothetical protein		
2572233447	t3m_01804	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233447	t3m_01804	Coordinates		1..312(-)		
2572233447	t3m_01804	DNA_length		312bp		
2572233447	t3m_01804	Protein_length		104aa		
2572233447	t3m_01804	GC			0.7	
2572233448	t3m_01805	pfam00156	Pribosyltran			3.20E-13
2572233448	t3m_01805	TIGR01134	amidophosphoribosyltransferase			6.70E-79
2572233448	t3m_01805	Locus_type		CDS		
2572233448	t3m_01805	Product_name		Phosphoribosyl transferase domain		
2572233448	t3m_01805	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233448	t3m_01805	Coordinates		280..1023(+)		
2572233448	t3m_01805	DNA_length		744bp		
2572233448	t3m_01805	Protein_length		247aa		
2572233448	t3m_01805	GC			0.69	
2572233449	t3m_01806	pfam01798	Nop			7.30E-22
2572233449	t3m_01806	KO:K14564	nucleolar protein 56			9.70E-17
2572233449	t3m_01806	Locus_type		CDS		
2572233449	t3m_01806	Product_name		Putative snoRNA binding domain		
2572233449	t3m_01806	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233449	t3m_01806	Coordinates		1027..1950(+)		

2572233449	t3m_01806	DNA_length		924bp		
2572233449	t3m_01806	Protein_length		307aa		
2572233449	t3m_01806	GC			0.74	

2572233450	t3m_01807	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233450	t3m_01807	COG1889	Fibrillarin-like rRNA methylase			3.00E-45
2572233450	t3m_01807	pfam01269	Fibrillarin			1.70E-51
2572233450	t3m_01807	KO:K04795	fibrillarin-like pre-rRNA processing protein			1.30E-35
2572233450	t3m_01807	Locus_type		CDS		
2572233450	t3m_01807	Product_name		Fibrillarin-like rRNA methylase		
2572233450	t3m_01807	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233450	t3m_01807	Coordinates		1947..2720(+)		
2572233450	t3m_01807	DNA_length		774bp		
2572233450	t3m_01807	Protein_length		257aa		
2572233450	t3m_01807	GC			0.73	

2572233451	t3m_01808	pfam02824	TGS			8.10E-11
2572233451	t3m_01808	Locus_type		CDS		
2572233451	t3m_01808	Product_name		TGS domain		
2572233451	t3m_01808	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233451	t3m_01808	Coordinates		2677..3228(-)		
2572233451	t3m_01808	DNA_length		552bp		
2572233451	t3m_01808	Protein_length		183aa		
2572233451	t3m_01808	GC			0.68	

2572233452	t3m_01809	Locus_type		CDS		
2572233452	t3m_01809	Product_name		hypothetical protein		
2572233452	t3m_01809	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233452	t3m_01809	Coordinates		3214..3924(+)		
2572233452	t3m_01809	DNA_length		711bp		
2572233452	t3m_01809	Protein_length		236aa		
2572233452	t3m_01809	GC			0.67	

2572233453	t3m_01810	COG_category	[R] General function prediction only			

2572233453	t3m_01810	COG0433	Predicted ATPase			5.00E-07
2572233453	t3m_01810	pfam12846	AAA_10			7.60E-17
2572233453	t3m_01810	Locus_type		CDS		
2572233453	t3m_01810	Product_name		Predicted ATPase		
2572233453	t3m_01810	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233453	t3m_01810	Coordinates		3921..6284(+)		
2572233453	t3m_01810	DNA_length		2364bp		
2572233453	t3m_01810	Protein_length		787aa		
2572233453	t3m_01810	GC			0.71	

2572233454	t3m_01811	COG_category	[T] Signal transduction mechanisms			
2572233454	t3m_01811	COG0467	RecA-superfamily ATPases implicated in signal transduction			3.00E-31
2572233454	t3m_01811	pfam06745	KaiC			1.80E-52
2572233454	t3m_01811	Locus_type		CDS		
2572233454	t3m_01811	Product_name		RecA-superfamily ATPases implicated in signal transduction		
2572233454	t3m_01811	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233454	t3m_01811	Coordinates		6401..7123(+)		
2572233454	t3m_01811	DNA_length		723bp		
2572233454	t3m_01811	Protein_length		240aa		
2572233454	t3m_01811	GC			0.67	

2572233455	t3m_01812	Locus_type		CDS		
2572233455	t3m_01812	Product_name		hypothetical protein		
2572233455	t3m_01812	Scaffold		t3m_contig_70_1550_len_7292_read_count_487136.64		
2572233455	t3m_01812	Coordinates		7127..7291(+)		
2572233455	t3m_01812	DNA_length		165bp		
2572233455	t3m_01812	Protein_length		55aa		
2572233455	t3m_01812	GC			0.72	

2572233456	t3m_01813	pfam10431	ClpB_D2-small			1.50E-22
2572233456	t3m_01813	pfam07724	AAA_2			1.40E-54
2572233456	t3m_01813	Locus_type		CDS		
2572233456	t3m_01813	Product_name		C-terminal, D2-small domain, of ClpB protein/AAA domain (Cdc48 subfa		
2572233456	t3m_01813	Scaffold		t3m_contig_70_1921_len_6375_read_count_464708.65		

2572233456	t3m_01813	Coordinates		3..1592(+)		
2572233456	t3m_01813	DNA_length		1590bp		
2572233456	t3m_01813	Protein_length		529aa		
2572233456	t3m_01813	GC			0.68	

2572233457	t3m_01814	pfam03144	GTP_EFTU_D2			1.00E-10
2572233457	t3m_01814	Locus_type		CDS		
2572233457	t3m_01814	Product_name		Elongation factor Tu domain 2		
2572233457	t3m_01814	Scaffold		t3m_contig_70_1921_len_6375_read_count_464708.65		
2572233457	t3m_01814	Coordinates		1589..2524(+)		
2572233457	t3m_01814	DNA_length		936bp		
2572233457	t3m_01814	Protein_length		311aa		
2572233457	t3m_01814	GC			0.71	

2572233458	t3m_01815	KEGG_module	M00343: Archaeal proteasome			
2572233458	t3m_01815	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233458	t3m_01815	COG1222	ATP-dependent 26S proteasome regulatory subunit			0.00E+00
2572233458	t3m_01815	pfam00004	AAA			4.10E-42
2572233458	t3m_01815	TIGR01242	26S proteasome subunit P45 family			0.00E+00
2572233458	t3m_01815	KO:K03420	proteasome regulatory subunit			0.00E+00
2572233458	t3m_01815	Locus_type		CDS		
2572233458	t3m_01815	Product_name		Proteasome-activating nucleotidase		
2572233458	t3m_01815	Scaffold		t3m_contig_70_1921_len_6375_read_count_464708.65		
2572233458	t3m_01815	Coordinates		2576..3781(-)		
2572233458	t3m_01815	DNA_length		1206bp		
2572233458	t3m_01815	Protein_length		401aa		
2572233458	t3m_01815	GC			0.68	

2572233459	t3m_01816	Metacyc	PWY-6654: phosphopantothenate biosynthesis III			
2572233459	t3m_01816	IMG_pathway	116: Coenzyme A biosynthesis			
2572233459	t3m_01816	COG_category	[R] General function prediction only			
2572233459	t3m_01816	COG1829	Predicted archaeal kinase (sugar kinase superfamily)			1.00E-39
2572233459	t3m_01816	EC:2.7.1.169	Pantoate kinase.			
2572233459	t3m_01816	KO:K06982	pantoate kinase [EC:2.7.1.169]			3.70E-29

2572233459	t3m_01816	ITERM:00184	pantothenate kinase (EC 2.7.1.33)			
2572233459	t3m_01816	Locus_type		CDS		
2572233459	t3m_01816	Product_name		pantothenate kinase (EC 2.7.1.33)		
2572233459	t3m_01816	Scaffold		t3m_contig_70_1921_len_6375_read_count_464708.65		
2572233459	t3m_01816	Coordinates		3876..4784(+)		
2572233459	t3m_01816	DNA_length		909bp		
2572233459	t3m_01816	Protein_length		302aa		
2572233459	t3m_01816	GC			0.73	
2572233460	t3m_01817	KEGG_module	M00179: Ribosome, archaea			
2572233460	t3m_01817	KEGG_module	M00177: Ribosome, eukaryotes			
2572233460	t3m_01817	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233460	t3m_01817	COG0197	Ribosomal protein L16/L10E			2.00E-23
2572233460	t3m_01817	pfam00252	Ribosomal_L16			3.10E-26
2572233460	t3m_01817	TIGR00279	ribosomal protein L10.e			1.00E-59
2572233460	t3m_01817	KO:K02866	large subunit ribosomal protein L10e			2.70E-42
2572233460	t3m_01817	Locus_type		CDS		
2572233460	t3m_01817	Product_name		LSU ribosomal protein L10AE		
2572233460	t3m_01817	Scaffold		t3m_contig_70_1921_len_6375_read_count_464708.65		
2572233460	t3m_01817	Coordinates		4880..5365(+)		
2572233460	t3m_01817	DNA_length		486bp		
2572233460	t3m_01817	Protein_length		161aa		
2572233460	t3m_01817	GC			0.67	
2572233461	t3m_01818	COG_category	[T] Signal transduction mechanisms			
2572233461	t3m_01818	COG0589	Universal stress protein UspA and related nucleotide-binding proteins			7.00E-18
2572233461	t3m_01818	pfam00582	Usp			2.50E-31
2572233461	t3m_01818	Locus_type		CDS		
2572233461	t3m_01818	Product_name		Universal stress protein UspA and related nucleotide-binding proteins		
2572233461	t3m_01818	Scaffold		t3m_contig_70_1921_len_6375_read_count_464708.65		
2572233461	t3m_01818	Coordinates		5346..5816(-)		
2572233461	t3m_01818	DNA_length		471bp		
2572233461	t3m_01818	Protein_length		156aa		
2572233461	t3m_01818	GC			0.67	

2572233462	t3m_01819	KEGG_module	M00032: Lysine degradation, lysine => saccharopine => acetoacetyl-CoA		
2572233462	t3m_01819	KEGG_module	M00013: Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA		
2572233462	t3m_01819	KEGG_module	M00087: beta-Oxidation		
2572233462	t3m_01819	Metacyc	PWY-5109: 2-methylbutyrate biosynthesis		
2572233462	t3m_01819	Metacyc	PWY-7094: fatty acid salvage		
2572233462	t3m_01819	Metacyc	PWY-7007: methyl ketone biosynthesis		
2572233462	t3m_01819	Metacyc	PWY-735: jasmonic acid biosynthesis		
2572233462	t3m_01819	Metacyc	VALDEG-PWY: valine degradation I		
2572233462	t3m_01819	Metacyc	PWY0-321: phenylacetate degradation I (aerobic)		
2572233462	t3m_01819	Metacyc	PWY-5138: unsaturated, even numbered fatty acid β-oxidation		
2572233462	t3m_01819	Metacyc	PWY-6435: 4-hydroxybenzoate biosynthesis V		
2572233462	t3m_01819	Metacyc	ILEUDEG-PWY: isoleucine degradation I		
2572233462	t3m_01819	Metacyc	PWY-5136: fatty acid β-oxidation II (peroxisome)		
2572233462	t3m_01819	Metacyc	PWY-7046: 4-coumarate degradation (anaerobic)		
2572233462	t3m_01819	Metacyc	PWY66-391: fatty acid β-oxidation VI (peroxisome)		
2572233462	t3m_01819	Metacyc	FAO-PWY: fatty acid β-oxidation I		
2572233462	t3m_01819	COG_category	[I] Lipid transport and metabolism		
2572233462	t3m_01819	COG1024	Enoyl-CoA hydratase/carnithine racemase		7.00E-52
2572233462	t3m_01819	pfam00378	ECH		7.50E-66
2572233462	t3m_01819	EC:4.2.1.17	Enoyl-CoA hydratase.		
2572233462	t3m_01819	KO:K01692	enoyl-CoA hydratase [EC:4.2.1.17]		0.00E+00
2572233462	t3m_01819	Locus_type		CDS	
2572233462	t3m_01819	Product_name		Enoyl-CoA hydratase/carnithine racemase	
2572233462	t3m_01819	Scaffold		t3m_contig_70_1923_len_6371_read_count_527639.66	
2572233462	t3m_01819	Coordinates		60..953(-)	
2572233462	t3m_01819	DNA_length		894bp	
2572233462	t3m_01819	Protein_length		297aa	
2572233462	t3m_01819	GC		0.67	
2572233463	t3m_01820	pfam01798	Nop		2.70E-37
2572233463	t3m_01820	Locus_type		CDS	
2572233463	t3m_01820	Product_name		Putative snoRNA binding domain	
2572233463	t3m_01820	Scaffold		t3m_contig_70_1923_len_6371_read_count_527639.66	

2572233463	t3m_01820	Coordinates		983..2053(+)		
2572233463	t3m_01820	DNA_length		1071bp		
2572233463	t3m_01820	Protein_length		356aa		
2572233463	t3m_01820	GC			0.7	
2572233464	t3m_01821	pfam00578	AhpC-TSA			1.00E-20
2572233464	t3m_01821	Locus_type		CDS		
2572233464	t3m_01821	Product_name		AhpC/TSA family		
2572233464	t3m_01821	Scaffold		t3m_contig_70_1923_len_6371_read_count_527639.66		
2572233464	t3m_01821	Coordinates		2015..2542(-)		
2572233464	t3m_01821	DNA_length		528bp		
2572233464	t3m_01821	Protein_length		175aa		
2572233464	t3m_01821	GC			0.66	
2572233465	t3m_01822	COG_category	[H] Coenzyme transport and metabolism			
2572233465	t3m_01822	COG0095	Lipoate-protein ligase A			2.00E-16
2572233465	t3m_01822	pfam03099	BPL_LplA_LipB			6.60E-09
2572233465	t3m_01822	Locus_type		CDS		
2572233465	t3m_01822	Product_name		Lipoate-protein ligase A		
2572233465	t3m_01822	Scaffold		t3m_contig_70_1923_len_6371_read_count_527639.66		
2572233465	t3m_01822	Coordinates		2599..3336(+)		
2572233465	t3m_01822	DNA_length		738bp		
2572233465	t3m_01822	Protein_length		245aa		
2572233465	t3m_01822	GC			0.69	
2572233466	t3m_01823	Metacyc	PWY-6753: <i>S</i>-methyl-5'-thioadenosine degradation III			
2572233466	t3m_01823	COG_category	[F] Nucleotide transport and metabolism			
2572233466	t3m_01823	COG_category	[R] General function prediction only			
2572233466	t3m_01823	COG0402	Cytosine deaminase and related metal-dependent hydrolases			2.00E-79
2572233466	t3m_01823	pfam01979	Amidohydro_1			1.40E-47
2572233466	t3m_01823	EC:3.5.4.31	S-methyl-5'-thioadenosine deaminase.			
2572233466	t3m_01823	EC:3.5.4.28	S-adenosylhomocysteine deaminase.			
2572233466	t3m_01823	KO:K12960	5-methylthioadenosine/S-adenosylhomocysteine deaminase [EC:3.5.4.3			0.00E+00
2572233466	t3m_01823	Locus_type		CDS		

2572233466	t3m_01823	Product_name		Cytosine deaminase and related metal-dependent hydrolases		
2572233466	t3m_01823	Scaffold		t3m_contig_70_1923_len_6371_read_count_527639.66		
2572233466	t3m_01823	Coordinates		3353..4669(-)		
2572233466	t3m_01823	DNA_length		1317bp		
2572233466	t3m_01823	Protein_length		438aa		
2572233466	t3m_01823	GC			0.69	
2572233467	t3m_01824	COG_category	[L] Replication, recombination and repair			
2572233467	t3m_01824	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subu			0.00E+00
2572233467	t3m_01824	pfam00204	DNA_gyraseB			4.10E-57
2572233467	t3m_01824	pfam00986	DNA_gyraseB_C			2.90E-24
2572233467	t3m_01824	pfam01751	Toprim			5.90E-27
2572233467	t3m_01824	EC:5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).			
2572233467	t3m_01824	KO:K02470	DNA gyrase subunit B [EC:5.99.1.3]			0.00E+00
2572233467	t3m_01824	Locus_type		CDS		
2572233467	t3m_01824	Product_name		DNA gyrase subunit B (EC 5.99.1.3)		
2572233467	t3m_01824	Scaffold		t3m_contig_70_1923_len_6371_read_count_527639.66		
2572233467	t3m_01824	Coordinates		4765..6369(-)		
2572233467	t3m_01824	DNA_length		1605bp		
2572233467	t3m_01824	Protein_length		534aa		
2572233467	t3m_01824	GC			0.67	
2572233468	t3m_01825	Locus_type		CDS		
2572233468	t3m_01825	Product_name		hypothetical protein		
2572233468	t3m_01825	Scaffold		t3m_contig_70_2198_len_5839_read_count_452084.67		
2572233468	t3m_01825	Coordinates		194..418(-)		
2572233468	t3m_01825	DNA_length		225bp		
2572233468	t3m_01825	Protein_length		74aa		
2572233468	t3m_01825	GC			0.69	
2572233469	t3m_01826	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)			
2572233469	t3m_01826	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle			
2572233469	t3m_01826	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate			
2572233469	t3m_01826	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)			

2572233469	t3m_01826	Metacyc	PWY-5538: pyruvate fermentation to acetate VI			
2572233469	t3m_01826	Metacyc	PWY-5690: TCA cycle II (eukaryotic)			
2572233469	t3m_01826	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572233469	t3m_01826	Metacyc	PWY-5392: reductive TCA cycle II			
2572233469	t3m_01826	Metacyc	PWY-5537: pyruvate fermentation to acetate V			
2572233469	t3m_01826	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)			
2572233469	t3m_01826	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2572233469	t3m_01826	Metacyc	PWY-6728: methylaspartate cycle			
2572233469	t3m_01826	Metacyc	P23-PWY: reductive TCA cycle I			
2572233469	t3m_01826	Metacyc	TCA: TCA cycle I (prokaryotic)			
2572233469	t3m_01826	COG_category	[C] Energy production and conversion			
2572233469	t3m_01826	COG0074	Succinyl-CoA synthetase, alpha subunit			2.00E-111
2572233469	t3m_01826	pfam02629	CoA_binding			5.20E-25
2572233469	t3m_01826	pfam00549	Ligase_CoA			1.40E-17
2572233469	t3m_01826	EC:6.2.1.5	Succinate--CoA ligase (ADP-forming).			
2572233469	t3m_01826	TIGR01019	succinyl-CoA synthetase, alpha subunit			0.00E+00
2572233469	t3m_01826	KO:K01902	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]			0.00E+00
2572233469	t3m_01826	Locus_type		CDS		
2572233469	t3m_01826	Product_name		succinyl-CoA synthetase, alpha subunit		
2572233469	t3m_01826	Scaffold		t3m_contig_70_2198_len_5839_read_count_452084.67		
2572233469	t3m_01826	Coordinates		415..1296(-)		
2572233469	t3m_01826	DNA_length		882bp		
2572233469	t3m_01826	Protein_length		293aa		
2572233469	t3m_01826	GC			0.7	

2572233470	t3m_01827	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle
2572233470	t3m_01827	KEGG_module	M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate
2572233470	t3m_01827	KEGG_module	M00009: Citrate cycle (TCA cycle, Krebs cycle)
2572233470	t3m_01827	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)
2572233470	t3m_01827	Metacyc	PWY-5537: pyruvate fermentation to acetate V
2572233470	t3m_01827	Metacyc	PWY-5392: reductive TCA cycle II
2572233470	t3m_01827	Metacyc	PWY-5538: pyruvate fermentation to acetate VI
2572233470	t3m_01827	Metacyc	P23-PWY: reductive TCA cycle I
2572233470	t3m_01827	Metacyc	PWY-5913: TCA cycle VI (obligate autotrophs)

2572233470	t3m_01827	Metacyc	PWY-5690: TCA cycle II (eukaryotic)			
2572233470	t3m_01827	Metacyc	PWY-6728: methylaspartate cycle			
2572233470	t3m_01827	Metacyc	TCA: TCA cycle I (prokaryotic)			
2572233470	t3m_01827	Metacyc	P42-PWY: incomplete reductive TCA cycle			
2572233470	t3m_01827	Metacyc	PWY-6969: TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)			
2572233470	t3m_01827	COG_category	[C] Energy production and conversion			
2572233470	t3m_01827	COG0045	Succinyl-CoA synthetase, beta subunit			2.00E-101
2572233470	t3m_01827	pfam08442	ATP-grasp_2			9.30E-53
2572233470	t3m_01827	pfam00549	Ligase_CoA			1.30E-13
2572233470	t3m_01827	EC:6.2.1.5	Succinate--CoA ligase (ADP-forming).			
2572233470	t3m_01827	TIGR01016	succinyl-CoA synthetase, beta subunit			7.50E-112
2572233470	t3m_01827	KO:K01903	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]			0.00E+00
2572233470	t3m_01827	Locus_type		CDS		
2572233470	t3m_01827	Product_name		Succinyl-CoA synthetase, beta subunit		
2572233470	t3m_01827	Scaffold		t3m_contig_70_2198_len_5839_read_count_452084.67		
2572233470	t3m_01827	Coordinates		1293..2426(-)		
2572233470	t3m_01827	DNA_length		1134bp		
2572233470	t3m_01827	Protein_length		377aa		
2572233470	t3m_01827	GC			0.69	
2572233471	t3m_01828	COG_category	[P] Inorganic ion transport and metabolism			
2572233471	t3m_01828	COG0428	Predicted divalent heavy-metal cations transporter			3.00E-05
2572233471	t3m_01828	KO:K07238	zinc transporter, ZIP family			8.30E-30
2572233471	t3m_01828	Locus_type		CDS		
2572233471	t3m_01828	Product_name		Predicted divalent heavy-metal cations transporter		
2572233471	t3m_01828	Scaffold		t3m_contig_70_2198_len_5839_read_count_452084.67		
2572233471	t3m_01828	Coordinates		2620..3390(+)		
2572233471	t3m_01828	DNA_length		771bp		
2572233471	t3m_01828	Protein_length		256aa		
2572233471	t3m_01828	GC			0.63	
2572233471	t3m_01828	Transmembrane		Yes		
2572233472	t3m_01829	KEGG_module	M00120: Coenzyme A biosynthesis, pantothenate => CoA			
2572233472	t3m_01829	Metacyc	COA-PWY: coenzyme A biosynthesis			

2572233472	t3m_01829	COG_category	[H] Coenzyme transport and metabolism			
2572233472	t3m_01829	COG0452	Phosphopantothenoylcysteine synthetase/decarboxylase			1.00E-69
2572233472	t3m_01829	pfam02441	Flavoprotein			5.20E-28
2572233472	t3m_01829	pfam04127	DFP			9.70E-36
2572233472	t3m_01829	EC:6.3.2.5	Phosphopantothenate--cysteine ligase.			
2572233472	t3m_01829	EC:4.1.1.36	Phosphopantothenoylcysteine decarboxylase.			
2572233472	t3m_01829	TIGR00521	phosphopantothenoylcysteine decarboxylase / phosphopantothenate--			1.30E-87
2572233472	t3m_01829	KO:K13038	phosphopantothenoylcysteine decarboxylase / phosphopantothenate--			0.00E+00
2572233472	t3m_01829	Locus_type		CDS		
2572233472	t3m_01829	Product_name		phosphopantothenoylcysteine decarboxylase / phosphopantothenate--		
2572233472	t3m_01829	Scaffold		t3m_contig_70_2198_len_5839_read_count_452084.67		
2572233472	t3m_01829	Coordinates		3445..4743(-)		
2572233472	t3m_01829	DNA_length		1299bp		
2572233472	t3m_01829	Protein_length		432aa		
2572233472	t3m_01829	GC			0.71	
2572233473	t3m_01830	COG_category	[R] General function prediction only			
2572233473	t3m_01830	COG0546	Predicted phosphatases			2.00E-18
2572233473	t3m_01830	pfam13419	HAD_2			2.70E-15
2572233473	t3m_01830	Locus_type		CDS		
2572233473	t3m_01830	Product_name		Predicted phosphatases		
2572233473	t3m_01830	Scaffold		t3m_contig_70_2198_len_5839_read_count_452084.67		
2572233473	t3m_01830	Coordinates		4742..5713(+)		
2572233473	t3m_01830	DNA_length		972bp		
2572233473	t3m_01830	Protein_length		323aa		
2572233473	t3m_01830	GC			0.7	
2572233474	t3m_01831	pfam00627	UBA			9.40E-06
2572233474	t3m_01831	Locus_type		CDS		
2572233474	t3m_01831	Product_name		UBA/TS-N domain		
2572233474	t3m_01831	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		
2572233474	t3m_01831	Coordinates		3..206(+)		
2572233474	t3m_01831	DNA_length		204bp		
2572233474	t3m_01831	Protein_length		67aa		

2572233474	t3m_01831	GC			0.77	
2572233475	t3m_01832	Metacyc	PWY-6383: mono-<i>trans</i>, poly-<i>cis</i> decaprenyl phosphate biosynthesis			
2572233475	t3m_01832	Metacyc	PWY-6797: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (archaea)			
2572233475	t3m_01832	Metacyc	PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I			
2572233475	t3m_01832	Metacyc	PWY-7206: pyrimidine deoxyribonucleotides dephosphorylation			
2572233475	t3m_01832	Metacyc	PWY-6502: oxidized GTP and dGTP detoxification			
2572233475	t3m_01832	Metacyc	PWY-6575: juvenile hormone III biosynthesis I			
2572233475	t3m_01832	COG_category	[F] Nucleotide transport and metabolism			
2572233475	t3m_01832	COG1051	ADP-ribose pyrophosphatase			1.00E-04
2572233475	t3m_01832	pfam00293	NUDIX			7.90E-13
2572233475	t3m_01832	EC:3.6.1.-	Hydrolases. Acting on acid anhydrides. In phosphorous-containing anhydrides.			
2572233475	t3m_01832	KO:K08310	dATP pyrophosphohydrolase [EC:3.6.1.-]			6.60E-15
2572233475	t3m_01832	Locus_type		CDS		
2572233475	t3m_01832	Product_name		ADP-ribose pyrophosphatase		
2572233475	t3m_01832	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		
2572233475	t3m_01832	Coordinates		206..655(+)		
2572233475	t3m_01832	DNA_length		450bp		
2572233475	t3m_01832	Protein_length		149aa		
2572233475	t3m_01832	GC			0.69	
2572233476	t3m_01833	Locus_type		CDS		
2572233476	t3m_01833	Product_name		hypothetical protein		
2572233476	t3m_01833	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		
2572233476	t3m_01833	Coordinates		677..1102(-)		
2572233476	t3m_01833	DNA_length		426bp		
2572233476	t3m_01833	Protein_length		141aa		
2572233476	t3m_01833	GC			0.7	
2572233477	t3m_01834	pfam01866	Diphthamide_syn			1.10E-51
2572233477	t3m_01834	TIGR00322	diphthamide biosynthesis enzyme Dph1/Dph2 domain			4.30E-45
2572233477	t3m_01834	Locus_type		CDS		
2572233477	t3m_01834	Product_name		Putative diphthamide synthesis protein		
2572233477	t3m_01834	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		

2572233477	t3m_01834	Coordinates		1103..1741(+)		
2572233477	t3m_01834	DNA_length		639bp		
2572233477	t3m_01834	Protein_length		212aa		
2572233477	t3m_01834	GC			0.69	
2572233478	t3m_01835	TIGR00304	TIGR00304 family protein			1.80E-11
2572233478	t3m_01835	Locus_type		CDS		
2572233478	t3m_01835	Product_name		hypothetical protein		
2572233478	t3m_01835	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		
2572233478	t3m_01835	Coordinates		1768..2196(+)		
2572233478	t3m_01835	DNA_length		429bp		
2572233478	t3m_01835	Protein_length		142aa		
2572233478	t3m_01835	GC			0.69	
2572233478	t3m_01835	Transmembrane		Yes		
2572233479	t3m_01836	COG_category	[H] Coenzyme transport and metabolism			
2572233479	t3m_01836	COG0311	Predicted glutamine amidotransferase involved in pyridoxine biosynthe			4.00E-56
2572233479	t3m_01836	pfam01174	SNO			2.20E-41
2572233479	t3m_01836	EC:2.6.-	Transferases. Transferring nitrogenous groups.			
2572233479	t3m_01836	TIGR03800	pyridoxal 5'-phosphate synthase, glutaminase subunit Pdx2			3.50E-58
2572233479	t3m_01836	KO:K08681	glutamine amidotransferase [EC:2.6.-.-]			7.70E-44
2572233479	t3m_01836	Locus_type		CDS		
2572233479	t3m_01836	Product_name		pyridoxal 5'-phosphate synthase, glutaminase subunit Pdx2		
2572233479	t3m_01836	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		
2572233479	t3m_01836	Coordinates		2156..2794(-)		
2572233479	t3m_01836	DNA_length		639bp		
2572233479	t3m_01836	Protein_length		212aa		
2572233479	t3m_01836	GC			0.7	
2572233480	t3m_01837	Metacyc	PWY-5074: mevalonate degradation			
2572233480	t3m_01837	IMG_pathway	178: Mevalonate pathway for isopentenyl pyrophopsphate synthesis			
2572233480	t3m_01837	IMG_pathway	591: Archaeal mevalonate pathway for isopentenyl pyrophosphate synthesis			
2572233480	t3m_01837	COG_category	[I] Lipid transport and metabolism			
2572233480	t3m_01837	COG1257	Hydroxymethylglutaryl-CoA reductase			3.00E-107

2572233480	t3m_01837	pfam00368	HMG-CoA_red			6.40E-91
2572233480	t3m_01837	EC:1.1.1.88	Hydroxymethylglutaryl-CoA reductase.			
2572233480	t3m_01837	TIGR00532	hydroxymethylglutaryl-CoA reductase, degradative			0.00E+00
2572233480	t3m_01837	KO:K00054	hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]			0.00E+00
2572233480	t3m_01837	ITERM:00463	3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34)			
2572233480	t3m_01837	Locus_type		CDS		
2572233480	t3m_01837	Product_name		3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34)		
2572233480	t3m_01837	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		
2572233480	t3m_01837	Coordinates		2791..4095(-)		
2572233480	t3m_01837	DNA_length		1305bp		
2572233480	t3m_01837	Protein_length		434aa		
2572233480	t3m_01837	GC			0.67	
2572233481	t3m_01838	COG_category	[O] Posttranslational modification, protein turnover, chaperones			
2572233481	t3m_01838	COG0576	Molecular chaperone GrpE (heat shock protein)			6.00E-24
2572233481	t3m_01838	pfam01025	GrpE			4.30E-33
2572233481	t3m_01838	KO:K03687	molecular chaperone GrpE			1.40E-20
2572233481	t3m_01838	Locus_type		CDS		
2572233481	t3m_01838	Product_name		Molecular chaperone GrpE (heat shock protein)		
2572233481	t3m_01838	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		
2572233481	t3m_01838	Coordinates		4099..4668(-)		
2572233481	t3m_01838	DNA_length		570bp		
2572233481	t3m_01838	Protein_length		189aa		
2572233481	t3m_01838	GC			0.69	
2572233482	t3m_01839	pfam02518	HATPase_c			1.30E-12
2572233482	t3m_01839	Locus_type		CDS		
2572233482	t3m_01839	Product_name		Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase		
2572233482	t3m_01839	Scaffold		t3m_contig_70_2516_len_5342_read_count_446082.68		
2572233482	t3m_01839	Coordinates		4989..5339(+)		
2572233482	t3m_01839	DNA_length		351bp		
2572233482	t3m_01839	Protein_length		117aa		
2572233482	t3m_01839	GC			0.65	

2572233483	t3m_01840	pfam00361	Oxidored_q1			1.20E-31
2572233483	t3m_01840	Locus_type		CDS		
2572233483	t3m_01840	Product_name		NADH-Ubiquinone/plastoquinone (complex I), various chains		
2572233483	t3m_01840	Scaffold		t3m_contig_70_3071_len_4659_read_count_381100.69		
2572233483	t3m_01840	Coordinates		3..1037(-)		
2572233483	t3m_01840	DNA_length		1035bp		
2572233483	t3m_01840	Protein_length		345aa		
2572233483	t3m_01840	GC			0.68	
2572233483	t3m_01840	Transmembrane		Yes		
2572233484	t3m_01841	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2572233484	t3m_01841	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation			
2572233484	t3m_01841	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)			
2572233484	t3m_01841	Metacyc	PWY-3781: aerobic respiration (cytochrome c)			
2572233484	t3m_01841	Metacyc	PWY-6692: Fe(II) oxidation			
2572233484	t3m_01841	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer			
2572233484	t3m_01841	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			
2572233484	t3m_01841	COG_category	[C] Energy production and conversion			
2572233484	t3m_01841	COG1008	NADH:ubiquinone oxidoreductase subunit 4 (chain M)			3.00E-101
2572233484	t3m_01841	pfam00361	Oxidored_q1			4.30E-66
2572233484	t3m_01841	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).			
2572233484	t3m_01841	TIGR01972	proton-translocating NADH-quinone oxidoreductase, chain M			0.00E+00
2572233484	t3m_01841	KO:K00342	NADH-quinone oxidoreductase subunit M [EC:1.6.5.3]			0.00E+00
2572233484	t3m_01841	Locus_type		CDS		
2572233484	t3m_01841	Product_name		proton-translocating NADH-quinone oxidoreductase, chain M		
2572233484	t3m_01841	Scaffold		t3m_contig_70_3071_len_4659_read_count_381100.69		
2572233484	t3m_01841	Coordinates		1042..2529(-)		
2572233484	t3m_01841	DNA_length		1488bp		
2572233484	t3m_01841	Protein_length		495aa		
2572233484	t3m_01841	GC			0.67	
2572233484	t3m_01841	Transmembrane		Yes		
2572233485	t3m_01842	KEGG_module	M00144: NADH:quinone oxidoreductase, prokaryotes			
2572233485	t3m_01842	Metacyc	PWY0-1335: NADH to cytochrome <i>bo</i> oxidase electron transfer			

2572233485	t3m_01842	Metacyc	PWY-5083: NAD/NADH phosphorylation and dephosphorylation		
2572233485	t3m_01842	Metacyc	PWY-3781: aerobic respiration (cytochrome c)		
2572233485	t3m_01842	Metacyc	PWY0-1334: NADH to cytochrome <i>bd</i> oxidase electron transfer		
2572233485	t3m_01842	Metacyc	PWY-4302: aerobic respiration (alternative oxidase pathway)		
2572233485	t3m_01842	Metacyc	PWY-6692: Fe(II) oxidation		
2572233485	t3m_01842	COG_category	[C] Energy production and conversion		
2572233485	t3m_01842	COG_category	[P] Inorganic ion transport and metabolism		
2572233485	t3m_01842	COG1009	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+		2.00E-112
2572233485	t3m_01842	pfam00361	Oxidored_q1		4.20E-73
2572233485	t3m_01842	pfam00662	Oxidored_q1_N		2.20E-13
2572233485	t3m_01842	EC:1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).		
2572233485	t3m_01842	TIGR01974	proton-translocating NADH-quinone oxidoreductase, chain L		0.00E+00
2572233485	t3m_01842	KO:K00341	NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]		0.00E+00
2572233485	t3m_01842	Locus_type		CDS	
2572233485	t3m_01842	Product_name		proton-translocating NADH-quinone oxidoreductase, chain L	
2572233485	t3m_01842	Scaffold		t3m_contig_70_3071_len_4659_read_count_381100.69	
2572233485	t3m_01842	Coordinates		2522..4435(-)	
2572233485	t3m_01842	DNA_length		1914bp	
2572233485	t3m_01842	Protein_length		637aa	
2572233485	t3m_01842	GC		0.68	
2572233485	t3m_01842	Transmembrane		Yes	
2572233486	t3m_01843	Metacyc	PWY-6545: pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis III		
2572233486	t3m_01843	COG_category	[F] Nucleotide transport and metabolism		
2572233486	t3m_01843	COG1351	Predicted alternative thymidylate synthase		7.00E-45
2572233486	t3m_01843	pfam02511	Thy1		9.70E-59
2572233486	t3m_01843	EC:2.1.1.148	Thymidylate synthase (FAD).		
2572233486	t3m_01843	TIGR02170	thymidylate synthase, flavin-dependent		2.20E-63
2572233486	t3m_01843	KO:K03465	thymidylate synthase (FAD) [EC:2.1.1.148]		0.00E+00
2572233486	t3m_01843	Locus_type		CDS	
2572233486	t3m_01843	Product_name		Predicted alternative thymidylate synthase	
2572233486	t3m_01843	Scaffold		t3m_contig_70_3526_len_4237_read_count_356275.70	
2572233486	t3m_01843	Coordinates		130..1035(-)	
2572233486	t3m_01843	DNA_length		906bp	

2572233486	t3m_01843	Protein_length		301aa		
2572233486	t3m_01843	GC			0.67	
2572233487	t3m_01844	KEGG_module	M00360: Aminoacyl-tRNA biosynthesis, prokaryotes			
2572233487	t3m_01844	KEGG_module	M00359: Aminoacyl-tRNA biosynthesis, eukaryotes			
2572233487	t3m_01844	Metacyc	TRNA-CHARGING-PWY: tRNA charging			
2572233487	t3m_01844	IMG_pathway	498: L-methionine ligation to tRNA(Met)			
2572233487	t3m_01844	COG_category	[J] Translation, ribosomal structure and biogenesis			
2572233487	t3m_01844	COG0143	Methionyl-tRNA synthetase			0.00E+00
2572233487	t3m_01844	pfam09334	tRNA-synt_1g			2.60E-127
2572233487	t3m_01844	pfam01588	tRNA_bind			2.50E-19
2572233487	t3m_01844	EC:6.1.1.10	Methionine--tRNA ligase.			
2572233487	t3m_01844	TIGR00398	methionyl-tRNA synthetase			2.60E-129
2572233487	t3m_01844	KO:K01874	methionyl-tRNA synthetase [EC:6.1.1.10]			0.00E+00
2572233487	t3m_01844	ITERM:00402	methionyl-tRNA synthetase (EC 6.1.1.10)			
2572233487	t3m_01844	Locus_type		CDS		
2572233487	t3m_01844	Product_name		methionyl-tRNA synthetase (EC 6.1.1.10)		
2572233487	t3m_01844	Scaffold		t3m_contig_70_3526_len_4237_read_count_356275.70		
2572233487	t3m_01844	Coordinates		1165..3435(+)		
2572233487	t3m_01844	DNA_length		2271bp		
2572233487	t3m_01844	Protein_length		756aa		
2572233487	t3m_01844	GC			0.69	
2572233488	t3m_01845	COG_category	[R] General function prediction only			
2572233488	t3m_01845	COG0613	Predicted metal-dependent phosphoesterases (PHP family)			2.00E-16
2572233488	t3m_01845	pfam13263	PHP_C			6.70E-14
2572233488	t3m_01845	pfam02811	PHP			2.70E-09
2572233488	t3m_01845	Locus_type		CDS		
2572233488	t3m_01845	Product_name		Predicted metal-dependent phosphoesterases (PHP family)		
2572233488	t3m_01845	Scaffold		t3m_contig_70_3526_len_4237_read_count_356275.70		
2572233488	t3m_01845	Coordinates		3435..4112(+)		
2572233488	t3m_01845	DNA_length		678bp		
2572233488	t3m_01845	Protein_length		225aa		
2572233488	t3m_01845	GC			0.71	

2572233489	t3m_01846	Locus_type		CDS		
2572233489	t3m_01846	Product_name		hypothetical protein		
2572233489	t3m_01846	Scaffold		t3m_contig_70_3763_len_4052_read_count_334737.71		
2572233489	t3m_01846	Coordinates		164..616(-)		
2572233489	t3m_01846	DNA_length		453bp		
2572233489	t3m_01846	Protein_length		150aa		
2572233489	t3m_01846	GC			0.71	

2572233490	t3m_01847	COG_category	[P] Inorganic ion transport and metabolism			
2572233490	t3m_01847	COG0475	Kef-type K+ transport systems, membrane components			5.00E-24
2572233490	t3m_01847	pfam00999	Na_H_Exchanger			2.60E-44
2572233490	t3m_01847	ITERM:06565	transporter, CPA2 family (TC 2.A.37)			
2572233490	t3m_01847	Locus_type		CDS		
2572233490	t3m_01847	Product_name		transporter, CPA2 family (TC 2.A.37)		
2572233490	t3m_01847	Scaffold		t3m_contig_70_3763_len_4052_read_count_334737.71		
2572233490	t3m_01847	Coordinates		809..2128(+)		
2572233490	t3m_01847	DNA_length		1320bp		
2572233490	t3m_01847	Protein_length		439aa		
2572233490	t3m_01847	GC			0.66	
2572233490	t3m_01847	Transmembrane		Yes		

2572233491	t3m_01848	COG_category	[E] Amino acid transport and metabolism			
2572233491	t3m_01848	COG0560	Phosphoserine phosphatase			2.00E-17
2572233491	t3m_01848	pfam12710	HAD			7.30E-07
2572233491	t3m_01848	Locus_type		CDS		
2572233491	t3m_01848	Product_name		Phosphoserine phosphatase		
2572233491	t3m_01848	Scaffold		t3m_contig_70_3763_len_4052_read_count_334737.71		
2572233491	t3m_01848	Coordinates		2285..2938(+)		
2572233491	t3m_01848	DNA_length		654bp		
2572233491	t3m_01848	Protein_length		217aa		
2572233491	t3m_01848	GC			0.69	

2572233492	t3m_01849	Locus_type		CDS		

2572233492	t3m_01849	Product_name		hypothetical protein	
2572233492	t3m_01849	Scaffold		t3m_contig_70_3763_len_4052_read_count_334737.71	
2572233492	t3m_01849	Coordinates		2999..3577(+)	
2572233492	t3m_01849	DNA_length		579bp	
2572233492	t3m_01849	Protein_length		192aa	
2572233492	t3m_01849	GC		0.7	
2572233493	t3m_01850	Locus_type		CDS	
2572233493	t3m_01850	Product_name		hypothetical protein	
2572233493	t3m_01850	Scaffold		t3m_contig_70_3763_len_4052_read_count_334737.71	
2572233493	t3m_01850	Coordinates		3865..4050(+)	
2572233493	t3m_01850	DNA_length		186bp	
2572233493	t3m_01850	Protein_length		62aa	
2572233493	t3m_01850	GC		0.65	
2572233494	t3m_01851	pfam06418	CTP_synth_N		2.20E-42
2572233494	t3m_01851	Locus_type		CDS	
2572233494	t3m_01851	Product_name		CTP synthase N-terminus	
2572233494	t3m_01851	Scaffold		t3m_contig_70_3977_len_3906_read_count_317865.72	
2572233494	t3m_01851	Coordinates		2..232(-)	
2572233494	t3m_01851	DNA_length		231bp	
2572233494	t3m_01851	Protein_length		77aa	
2572233494	t3m_01851	GC		0.65	
2572233495	t3m_01852	COG_category	[L] Replication, recombination and repair		
2572233495	t3m_01852	COG0675	Transposase and inactivated derivatives		2.00E-15
2572233495	t3m_01852	pfam07282	OrfB_Zn_ribbon		1.40E-19
2572233495	t3m_01852	TIGR01766	transposase, IS605 OrfB family, central region		1.10E-11
2572233495	t3m_01852	KO:K07496	putative transposase		1.00E-23
2572233495	t3m_01852	Locus_type		CDS	
2572233495	t3m_01852	Product_name		Transposase and inactivated derivatives	
2572233495	t3m_01852	Scaffold		t3m_contig_70_3977_len_3906_read_count_317865.72	
2572233495	t3m_01852	Coordinates		643..1776(+)	
2572233495	t3m_01852	DNA_length		1134bp	

2572233495	t3m_01852	Protein_length		377aa		
2572233495	t3m_01852	GC			0.64	
2572233496	t3m_01853	COG_category	[H] Coenzyme transport and metabolism			
2572233496	t3m_01853	COG_category	[C] Energy production and conversion			
2572233496	t3m_01853	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductase			3.00E-41
2572233496	t3m_01853	pfam10418	DHODB_Fe-S_bind			7.20E-12
2572233496	t3m_01853	pfam00970	FAD_binding_6			2.30E-05
2572233496	t3m_01853	pfam00175	NAD_binding_1			1.40E-09
2572233496	t3m_01853	KO:K02823	dihydroorotate dehydrogenase electron transfer subunit			0.00E+00
2572233496	t3m_01853	Locus_type		CDS		
2572233496	t3m_01853	Product_name		2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases		
2572233496	t3m_01853	Scaffold		t3m_contig_70_3977_len_3906_read_count_317865.72		
2572233496	t3m_01853	Coordinates		1844..2620(-)		
2572233496	t3m_01853	DNA_length		777bp		
2572233496	t3m_01853	Protein_length		258aa		
2572233496	t3m_01853	GC			0.7	
2572233497	t3m_01854	KEGG_module	M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP			
2572233497	t3m_01854	COG_category	[F] Nucleotide transport and metabolism			
2572233497	t3m_01854	COG0167	Dihydroorotate dehydrogenase			3.00E-69
2572233497	t3m_01854	pfam01180	DHO_dh			2.10E-57
2572233497	t3m_01854	EC:1.3.98.1	Dihydroorotate oxidase (fumarate).			
2572233497	t3m_01854	TIGR01037	dihydroorotate dehydrogenase (subfamily 1) family protein			8.30E-99
2572233497	t3m_01854	KO:K00226	dihydroorotate dehydrogenase (fumarate) [EC:1.3.98.1]			0.00E+00
2572233497	t3m_01854	Locus_type		CDS		
2572233497	t3m_01854	Product_name		dihydroorotate oxidase B, catalytic subunit (EC 1.3.3.1)		
2572233497	t3m_01854	Scaffold		t3m_contig_70_3977_len_3906_read_count_317865.72		
2572233497	t3m_01854	Coordinates		2679..3611(-)		
2572233497	t3m_01854	DNA_length		933bp		
2572233497	t3m_01854	Protein_length		310aa		
2572233497	t3m_01854	GC			0.71	
2572233498	t3m_01855	pfam02861	Clp_N			1.00E-11

2572233498	t3m_01855	Locus_type		CDS		
2572233498	t3m_01855	Product_name		Clp amino terminal domain		
2572233498	t3m_01855	Scaffold		t3m_contig_70_3977_len_3906_read_count_317865.72		
2572233498	t3m_01855	Coordinates		3667..3903(+)		
2572233498	t3m_01855	DNA_length		237bp		
2572233498	t3m_01855	Protein_length		79aa		
2572233498	t3m_01855	GC			0.73	

2572233499	t3m_01856	pfam00496	SBP_bac_5			2.00E-05
2572233499	t3m_01856	Locus_type		CDS		
2572233499	t3m_01856	Product_name		Bacterial extracellular solute-binding proteins, family 5 Middle		
2572233499	t3m_01856	Scaffold		t3m_contig_70_4636_len_3511_read_count_360663.73		
2572233499	t3m_01856	Coordinates		3..590(-)		
2572233499	t3m_01856	DNA_length		588bp		
2572233499	t3m_01856	Protein_length		196aa		
2572233499	t3m_01856	GC			0.64	
2572233499	t3m_01856	Transmembrane		Yes		

2572233500	t3m_01857	COG_category	[E] Amino acid transport and metabolism			
2572233500	t3m_01857	COG1748	Saccharopine dehydrogenase and related proteins			7.00E-43
2572233500	t3m_01857	pfam03435	Saccharop_dh			5.50E-41
2572233500	t3m_01857	Locus_type		CDS		
2572233500	t3m_01857	Product_name		Saccharopine dehydrogenase and related proteins		
2572233500	t3m_01857	Scaffold		t3m_contig_70_4636_len_3511_read_count_360663.73		
2572233500	t3m_01857	Coordinates		900..1976(+)		
2572233500	t3m_01857	DNA_length		1077bp		
2572233500	t3m_01857	Protein_length		358aa		
2572233500	t3m_01857	GC			0.69	

2572233501	t3m_01858	COG_category	[E] Amino acid transport and metabolism			
2572233501	t3m_01858	COG0747	ABC-type dipeptide transport system, periplasmic component			8.00E-23
2572233501	t3m_01858	pfam00496	SBP_bac_5			3.60E-28
2572233501	t3m_01858	Locus_type		CDS		
2572233501	t3m_01858	Product_name		Bacterial extracellular solute-binding proteins, family 5 Middle		

2572233501	t3m_01858	Scaffold		t3m_contig_70_4636_len_3511_read_count_360663.73	
2572233501	t3m_01858	Coordinates		2140..3510(-)	
2572233501	t3m_01858	DNA_length		1371bp	
2572233501	t3m_01858	Protein_length		456aa	
2572233501	t3m_01858	GC		0.64	
2572233502	t3m_01859	TIGR02179	2-oxoacid:acceptor oxidoreductase, delta subunit, pyruvate/2-ketoisova		4.10E-23
2572233502	t3m_01859	Locus_type		CDS	
2572233502	t3m_01859	Product_name		hypothetical protein	
2572233502	t3m_01859	Scaffold		t3m_contig_70_7868_len_2417_read_count_208576.74	
2572233502	t3m_01859	Coordinates		1..156(+)	
2572233502	t3m_01859	DNA_length		156bp	
2572233502	t3m_01859	Protein_length		51aa	
2572233502	t3m_01859	GC		0.58	
2572233503	t3m_01860	KEGG_module	M00310: Pyruvate:ferredoxin oxidoreductase		
2572233503	t3m_01860	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA		
2572233503	t3m_01860	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)		
2572233503	t3m_01860	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle		
2572233503	t3m_01860	Metacyc	PWY-7003: glycerol degradation to butanol		
2572233503	t3m_01860	Metacyc	PWY-6863: pyruvate fermentation to hexanol		
2572233503	t3m_01860	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2572233503	t3m_01860	Metacyc	PWY-5392: reductive TCA cycle II		
2572233503	t3m_01860	Metacyc	PWY-5493: reductive monocarboxylic acid cycle		
2572233503	t3m_01860	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)		
2572233503	t3m_01860	Metacyc	PWY-5538: pyruvate fermentation to acetate VI		
2572233503	t3m_01860	Metacyc	PWY-5483: pyruvate fermentation to acetate III		
2572233503	t3m_01860	Metacyc	P23-PWY: reductive TCA cycle I		
2572233503	t3m_01860	Metacyc	PWY-5600: pyruvate fermentation to acetate VII		
2572233503	t3m_01860	Metacyc	P142-PWY: pyruvate fermentation to acetate I		
2572233503	t3m_01860	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)		
2572233503	t3m_01860	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate		
2572233503	t3m_01860	Metacyc	PWY-6583: pyruvate fermentation to butanol I		
2572233503	t3m_01860	Metacyc	PWY-6876: isopropanol biosynthesis		

2572233503	t3m_01860	Metacyc	PWY-6587: pyruvate fermentation to ethanol III		
2572233503	t3m_01860	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)		
2572233503	t3m_01860	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2572233503	t3m_01860	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2572233503	t3m_01860	COG_category	[C] Energy production and conversion		
2572233503	t3m_01860	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o		8.00E-76
2572233503	t3m_01860	pfam01855	POR_N		2.90E-65
2572233503	t3m_01860	EC:1.2.7.1	Pyruvate synthase.		
2572233503	t3m_01860	KO:K00169	pyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.1]		0.00E+00
2572233503	t3m_01860	Locus_type		CDS	
2572233503	t3m_01860	Product_name		Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin ox	
2572233503	t3m_01860	Scaffold		t3m_contig_70_7868_len_2417_read_count_208576.74	
2572233503	t3m_01860	Coordinates		170..1348(+)	
2572233503	t3m_01860	DNA_length		1179bp	
2572233503	t3m_01860	Protein_length		392aa	
2572233503	t3m_01860	GC		0.68	

2572233504	t3m_01861	KEGG_module	M00310: Pyruvate:ferredoxin oxidoreductase
2572233504	t3m_01861	KEGG_module	M00173: Reductive citric acid cycle (Arnon-Buchanan cycle)
2572233504	t3m_01861	KEGG_module	M00374: Dicarboxylate-hydroxybutyrate cycle
2572233504	t3m_01861	KEGG_module	M00307: Pyruvate oxidation, pyruvate => acetyl-CoA
2572233504	t3m_01861	Metacyc	PWY-6863: pyruvate fermentation to hexanol
2572233504	t3m_01861	Metacyc	PWY-6587: pyruvate fermentation to ethanol III
2572233504	t3m_01861	Metacyc	PWY-6876: isopropanol biosynthesis
2572233504	t3m_01861	Metacyc	PWY-6583: pyruvate fermentation to butanol I
2572233504	t3m_01861	Metacyc	PWY-5392: reductive TCA cycle II
2572233504	t3m_01861	Metacyc	PWY-7003: glycerol degradation to butanol
2572233504	t3m_01861	Metacyc	CENTFERM-PWY: pyruvate fermentation to butanoate
2572233504	t3m_01861	Metacyc	PWY-6142: gluconeogenesis II (<i>Methanobacterium thermoautotrophicum</i>)
2572233504	t3m_01861	Metacyc	PWY-5600: pyruvate fermentation to acetate VII
2572233504	t3m_01861	Metacyc	P142-PWY: pyruvate fermentation to acetate I
2572233504	t3m_01861	Metacyc	NPGLUCAT-PWY: Entner-Doudoroff pathway II (non-phosphorylative)
2572233504	t3m_01861	Metacyc	PWY-5483: pyruvate fermentation to acetate III
2572233504	t3m_01861	Metacyc	PWY-5493: reductive monocarboxylic acid cycle

2572233504	t3m_01861	Metacyc	P23-PWY: reductive TCA cycle I		
2572233504	t3m_01861	Metacyc	P42-PWY: incomplete reductive TCA cycle		
2572233504	t3m_01861	Metacyc	PWY-5497: purine nucleobases degradation II (anaerobic)		
2572233504	t3m_01861	Metacyc	PWY-6588: pyruvate fermentation to acetone		
2572233504	t3m_01861	Metacyc	PWY-5538: pyruvate fermentation to acetate VI		
2572233504	t3m_01861	Metacyc	GLUDEG-II-PWY: glutamate degradation VII (to butanoate)		
2572233504	t3m_01861	COG_category	[C] Energy production and conversion		
2572233504	t3m_01861	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin o		1.00E-61
2572233504	t3m_01861	pfam02775	TPP_enzyme_C		1.50E-18
2572233504	t3m_01861	EC:1.2.7.1	Pyruvate synthase.		
2572233504	t3m_01861	KO:K00170	pyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.1]		0.00E+00
2572233504	t3m_01861	Locus_type		CDS	
2572233504	t3m_01861	Product_name		ketoisovalerate ferredoxin oxidoreductase, beta subunit (EC 1.2.7.7)	
2572233504	t3m_01861	Scaffold		t3m_contig_70_7868_len_2417_read_count_208576.74	
2572233504	t3m_01861	Coordinates		1341..2285(+)	
2572233504	t3m_01861	DNA_length		945bp	
2572233504	t3m_01861	Protein_length		314aa	
2572233504	t3m_01861	GC		0.69	
2572233505	t3m_01862	Locus_type		tRNA	
2572233505	t3m_01862	Product_name		tRNA_Met_CAT	
2572233505	t3m_01862	Scaffold		t3m_contig_70_7868_len_2417_read_count_208576.74	
2572233505	t3m_01862	Coordinates		2313..2415(+)	
2572233505	t3m_01862	DNA_length		103bp	
2572233505	t3m_01862	GC		0.6	