

Table S1. Physicochemical characteristics of sampling points

	Temperature (°C)	pH	Dissolved O ₂ (mg/L)	H ₂ S (mg/L)	Fe ²⁺ (mg/L)	Salinity (‰)
Upper stream	74	2.6	0.3	<d.l.	0.4	<0.1
Middle stream	57	2.2	0.8	14	3.1	<0.1
Lower stream	46	2.1	3.4	0.5	3.0	<0.1

Table S2. Utilization of organic compounds

Tested compounds	Growth
<i>Sugars (final 0.5% w/v)</i>	
D-Arabinose	-
D-Fructose	-
D-Galactose	-
D-Glucose	-
Lactose	-
Maltose	-
Mannose	-
D-Ribose	-
Sucrose	-
D-Xylose	-
Soluble starch	-
<i>Organic acids (final 0.2% w/v)</i>	
Acetate	-
Butyrate	-
Citrate	-
Formate	-
Fumarate	-
L-Lactate	-
L-Malate	-
Propionate	-
Pyruvate	-
Succinate	-
<i>Alcohol or others (final 0.2% w/v)</i>	
Methanol	-
Ethanol	-
Formamide	-
Methylamine	-
Trimethylamine	-
Gelatin	-
<i>Organic compounds (final 0.05% w/v)</i>	
Beef extract	+
Casamino acids	-
Peptone	++
Malt extract	++
Tryptone	-

Table S3. List of the 43 marker proteins used for the genome tree construction

Pfam/TIGRfam ID	Function
PF00164.20	Ribosomal protein S12/S23
PF00177.16	Ribosomal protein S7p/S5e
PF00181.18	Ribosomal Proteins L2, RNA binding domain
PF00189.15	Ribosomal protein S3, C-terminal domain
PF00203.16	Ribosomal protein S19
PF00237.14	Ribosomal protein L22p/L17e
PF00238.14	Ribosomal protein L14p/L23e
PF00252.13	Ribosomal protein L16p/L10e
PF00276.15	Ribosomal protein L23
PF00281.14	Ribosomal protein L5
PF00297.17	Ribosomal protein L3
PF00298.14	Ribosomal protein L11, RNA binding domain
PF00312.17	Ribosomal protein S15
PF00318.15	Ribosomal protein S2
PF00333.15	Ribosomal protein S5, N-terminal domain
PF00366.15	Ribosomal protein S17
PF00380.14	Ribosomal protein S9/S16
PF00410.14	Ribosomal protein S8
PF00411.14	Ribosomal protein S11
PF00466.15	Ribosomal protein L10
PF00562.23	RNA polymerase Rpb2, domain 6
PF00572.13	Ribosomal protein L13
PF00573.17	Ribosomal protein L4/L1 family
PF00623.15	RNA polymerase Rpb1, domain 2
PF00673.16	ribosomal L5P family C-terminus
PF00687.16	Ribosomal protein L1p/L10e family
PF00831.18	Ribosomal L29 protein
PF00861.17	Ribosomal L18 of archaea, bacteria, mitoch. and chloroplast
PF01192.17	RNA polymerase Rpb6
PF01509.13	TruB family pseudouridylate synthase (N terminal domain)
PF02978.14	Signal peptide binding domain
PF03719.10	Ribosomal protein S5, C-terminal domain
PF03946.9	Ribosomal protein L11, N-terminal domain
PF03947.13	Ribosomal Proteins L2, C-terminal domain
PF04560.15	RNA polymerase Rpb2, domain 7
PF04561.9	RNA polymerase Rpb2, domain 2
PF04563.10	RNA polymerase beta subunit
PF04565.11	RNA polymerase Rpb2, domain 3
PF04997.7	RNA polymerase Rpb1, domain 1
PF05000.12	RNA polymerase Rpb1, domain 4
PF11987.3	Translation-initiation factor 2
TIGR00344	alanine--tRNA ligase
TIGR00422	valine--tRNA ligase

Table S4. List of all CDSs

Locus_tag	AA Length	feature	Annotation	Ecnumber	KEGG ID	Taxonomic classification by MEGAN	COG category	MEROPS ID	eggNOG ID	Transporter	Subcellular location	Gene ID in Fig. 3
NAS2_0001	407	CDS	ORC1-type DNA replication protein		K10725	Thaumarchaeota	L		0FBCM@creNOG,COG1474@NOG,arCOG00467@arNOG		Cytoplasmic	
NAS2_0002	382	CDS	Archaea DNA polymerase II small subunit	2.7.7.7	K02323	Thaumarchaeota	L		1CBKA@thaNOG,COG1311@NOG,arCOG04455@arNOG		Cytoplasmic	
NAS2_0003	397	CDS	Transporter			TACK group	G		02TQH@arNOG,0FFUZ@creNOG,0XQ3C@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0004	356	CDS	Tungstate ABC transporter, periplasmic substrate-binding protein WpA		K15495	Thaumarchaeota	P		0FD93@creNOG,COG0725@NOG,arCOG00219@arNOG	Transporter (ABC)	CytoplasmicMembrane	
NAS2_0005	258	CDS	Tungstate ABC transporter, permease protein WpB		K15496	Thaumarchaeota	P		0FBZU@creNOG,COG0555@NOG,arCOG00164@arNOG	Transporter (ABC)	CytoplasmicMembrane	
NAS2_0006	197	CDS	ABC transporter ATP-binding protein		K06861	Thaumarchaeota	G		0FCEM@creNOG,COG1120@NOG,arCOG00198@arNOG	Transporter (ABC)	multiples	
NAS2_0007		tRNA	tRNA-Val									
NAS2_0008	495	CDS	L-Proline/Glycine betaine transporter ProP		K08176	TACK group	G		0FB90@creNOG,0XQKC@NOG,arCOG02682@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0009		tRNA	tRNA-Ala									
NAS2_0010	175	CDS	Small heat shock protein		K13993	Thaumarchaeota	O		COG0071@NOG,arCOG01833@arNOG		Cytoplasmic	
NAS2_0011	711	CDS	DinG family ATP-dependent helicase CPE1197		K10844	Archaea	L		0FC3V@creNOG,COG1199@NOG,arCOG00770@arNOG		Cytoplasmic	
NAS2_0012	85	CDS	Uncharacterized protein		K09700	Thaumarchaeota			0KU51@eurNOG,1CCX6@theNOG,COG3461@NOG,arCOG03350@arNOG		Cytoplasmic	
NAS2_0013	244	CDS	DedA protein			Thaumarchaeota			0KT41@eurNOG,0WRY5@metNOG,COG0586@NOG,arCOG03117@arNOG		CytoplasmicMembrane	
NAS2_0014	346	CDS	hypothetical protein			Thaumarchaeota					Unknown	
NAS2_0015	93	CDS	hypothetical protein		K07166	Thaumarchaeota	E		0FCWW@creNOG,COG3830@NOG,arCOG04941@arNOG		Cytoplasmic	
NAS2_0016	462	CDS	hypothetical protein		K09157	Thaumarchaeota			0KR0Z@eurNOG,0WK45@methaNOG,COG2848@NOG,arCOG04321@arNOG		Cytoplasmic	
NAS2_0017		tRNA	tRNA-Thr									
NAS2_0018	320	CDS	Thiamine-monophosphate kinase	2.7.4.16	K00946	Archaea	H		COG0611@NOG,arCOG00638@arNOG		Cytoplasmic	
NAS2_0019	71	CDS	Transcriptional regulator, AsnC family			Thaumarchaeota	K		0FCVX@creNOG,COG1522@NOG,arCOG01117@arNOG		Cytoplasmic	
NAS2_0020	441	CDS	OB-fold nucleic acid binding domain protein		K06932	Thaumarchaeota			0KS42@eurNOG,1CEC9@thermNOG,COG1571@arNOG,arCOG01115@arNOG		Cytoplasmic	
NAS2_0021	547	CDS	CTP synthase	6.3.4.2	K01937	Thaumarchaeota	F	MER0065772	0KRTS@eurNOG,1CE24@thermNOG,COG0504@NOG,arCOG00063@arNOG		Cytoplasmic	
NAS2_0022	292	CDS	Serine/threonine-protein kinase RIO2	2.7.11.1	K07179	Thaumarchaeota	T		0FBWT@creNOG,COG0478@NOG,arCOG01181@arNOG		Cytoplasmic	
NAS2_0023	86	CDS	Putative snRNP Sm-like protein		K04796	Thaumarchaeota	K		1CC5l@thaNOG,COG1958@NOG,arCOG00998@arNOG		Cytoplasmic	
NAS2_0024	369	CDS	hypothetical protein			Thaumarchaeota	L		0KTV7@eurNOG,0WN5H@methaNOG,COG3385@NOG,arCOG06160@arNOG		Cytoplasmic	
NAS2_0025	428	CDS	putative sugar transport protein			Thaumarchaeota	G	MER0011529	0KW3U@eurNOG,0XP7l@NOG,1CD64@theNOG,arCOG02691@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0026	264	CDS	Aliphatic amidase AmiE	3.5.1.4		cellular organisms			0FC6P@creNOG,COG0388@NOG,arCOG00082@arNOG		Cytoplasmic	
NAS2_0027	552	CDS	N-methylhydantoinase B	3.5.2.14	K01474	Archaea	E		0FBZ@creNOG,COG0146@NOG,arCOG01512@arNOG		Cytoplasmic	
NAS2_0028	669	CDS	N-methylhydantoinase A	3.5.2.14	K01473	Crenarchaeota	E		0FAZT@creNOG,COG0145@NOG,arCOG01511@arNOG		Cytoplasmic	
NAS2_0029	218	CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic	
NAS2_0030	477	CDS	Replication factor A		K07466	Thaumarchaeota	L		1CBRS@thaNOG,COG1599@NOG,arCOG01510@arNOG		Cytoplasmic	
NAS2_0031		tRNA	tRNA-Met									
NAS2_0032	310	CDS	5-methyltetrahydropteroyltrimethylglutamate-- homocysteine methyltransferase	2.1.1.14	K00549	Thaumarchaeota	E		0FC2C@creNOG,COG0620@NOG,arCOG01877@arNOG		Cytoplasmic	
NAS2_0033	346	CDS	5-methyltetrahydropteroyltrimethylglutamate-- homocysteine methyltransferase	2.1.1.14	K00549	Archaea	E		0KRMF@eurNOG,1CCCN@theNOG,COG0620@NOG,arCOG01876@arNOG		Cytoplasmic	
NAS2_0034	207	CDS	hypothetical protein		K03752	Thaumarchaeota	H		0FF38@creNOG,COG0746@NOG,arCOG01872@arNOG		Cytoplasmic	
NAS2_0035	1245	CDS	DNA reverse gyrase		K03170	Thaumarchaeota	L		0FAWW@creNOG,COG1110@NOG,arCOG01526@arNOG		Cytoplasmic	
NAS2_0036	195	CDS	Archaeal transcription factor E		K03136	Thaumarchaeota	K		1CBS3@thaNOG,COG1675@NOG,arCOG04270@arNOG		Cytoplasmic	
NAS2_0037	365	CDS	GTP-binding protein HflX		K03665	cellular organisms			0KRZQ@eurNOG,1CE5B@thermNOG,COG2262@NOG,arCOG00353@arNOG		Unknown	
NAS2_0038	142	CDS	Uncharacterized HTH-type transcriptional regulator		K03627	Archaea	K		0FCS2@creNOG,COG1813@NOG,arCOG01863@arNOG		Cytoplasmic	
NAS2_0039	171	CDS	archaeosine tRNA-ribosyltransferase		K07398	Thaumarchaeota	J		1CBPB@thaNOG,COG1370@NOG,arCOG00991@arNOG		Cytoplasmic	
NAS2_0040	58	CDS	hypothetical protein								Cytoplasmic	
NAS2_0041	296	CDS	Methionine aminopeptidase	3.4.11.18	K01265	Archaea	J	MER0274347	0FBP8@creNOG,COG0024@NOG,arCOG01001@arNOG		Cytoplasmic	Peptidase
NAS2_0042	155	CDS	Phosphopantetheine adenylyltransferase, type II eukaryotic		K02201	Archaea	H		0KT5l@eurNOG,0WRZ2@metNOG,COG1019@NOG,COG1986@NOG,arCOG01221@arNOG,arCOG01223@arNOG		Cytoplasmic	
NAS2_0043	506	CDS	Phenylalanyl-tRNA synthetase alpha chain	6.1.1.20	K01889	Archaea	J		0KRFM@eurNOG,0WRCV@metNOG,COG0016@NOG,arCOG00410@arNOG		Cytoplasmic	
NAS2_0044	529	CDS	Phenylalanyl-tRNA synthetase beta chain	6.1.1.20	K01890	Archaea	J		1CBG3@thaNOG,COG0072@NOG,arCOG00412@arNOG		Cytoplasmic	
NAS2_0045	742	CDS	Pyrophosphate-energized proton pump	3.6.1.1	K15987	Crenarchaeota	C		0FBHQ@creNOG,COG3808@NOG,arCOG04949@arNOG	Transporter (Other)	CytoplasmicMembrane	
NAS2_0046	95	CDS	Acylphosphate phosphohydrolase	3.6.1.7	K01512	cellular organisms			0FD23@creNOG,COG1254@NOG,arCOG01674@arNOG		Cytoplasmic	
NAS2_0047	141	CDS	DNA-binding protein ttx		K09714	Archaea	K		0KBTB@eurNOG,0WMFH@methaNOG,COG1356@NOG,arCOG04554@arNOG		Cytoplasmic	
NAS2_0048	331	CDS	tRNA/RNA cytosine-C5-methylase			Crenarchaeota	J		0FBX7@creNOG,COG0144@NOG,arCOG00973@arNOG		Cytoplasmic	
NAS2_0049	163	CDS	UPF0113 protein		K07565	Thaumarchaeota	J		COG1374@NOG,arCOG00993@arNOG		Cytoplasmic	
NAS2_0050	312	CDS	Threonine synthase	4.2.3.1	K01733	Thaumarchaeota	E		0KRFG@eurNOG,1CCMQ@theNOG,COG0498@NOG,arCOG01434@arNOG		Cytoplasmic	
NAS2_0051	359	CDS	Protein often near L-alanine-DL-glutamate epimerase			Thaumarchaeota			0FEIT@creNOG,COG3387@NOG,arCOG02828@arNOG		Cytoplasmic	
NAS2_0052	478	CDS	hypothetical protein			Thaumarchaeota			0KS6E@eurNOG,102GU@NOG,arCOG05346@arNOG		Cytoplasmic	
NAS2_0053	163	CDS	PhnO protein			Korarchaeota	K		COG0454@NOG,arCOG00826@arNOG		Cytoplasmic	
NAS2_0054	245	CDS	Uroporphyrinogen-III methyltransferase	2.1.1.107	K02303	Crenarchaeota	H		0FBRD@creNOG,COG0007@NOG,arCOG00644@arNOG		Unknown	
NAS2_0055	419	CDS	Glutamate-1-semialdehyde aminotransferase	5.4.3.8	K01845	Crenarchaeota	H		0FB29@creNOG,COG0001@NOG,arCOG00918@arNOG		Cytoplasmic	
NAS2_0056	336	CDS	Porphobilinogen synthase	4.2.1.24	K01698	Thaumarchaeota	H		0FBD8@creNOG,COG0113@NOG,arCOG04308@arNOG		Cytoplasmic	
NAS2_0057	403	CDS	Radical SAM domain heme biosynthesis protein			Thaumarchaeota			0FB0M@creNOG,COG0535@NOG,arCOG00938@arNOG		Cytoplasmic	
NAS2_0058	306	CDS	Heme biosynthesis protein related to NirD and NirG			Archaea	K		0FBMA@creNOG,COG1522@NOG,arCOG01628@arNOG		Cytoplasmic	
NAS2_0059	285	CDS	Porphobilinogen deaminase	2.5.1.61	K01749	cellular organisms	H		0KRTW@eurNOG,COG0181@NOG,arCOG04299@arNOG		Cytoplasmic	
NAS2_0060	230	CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic	
NAS2_0061	223	CDS	Siroheme synthase	1.3.1.76	K02304	Thaumarchaeota	H		0FCHT@creNOG,COG1648@NOG,arCOG01044@arNOG		Cytoplasmic	
NAS2_0062	343	CDS	Radical SAM domain heme biosynthesis protein			Thaumarchaeota			0FB8Y@eurNOG,COG0535@NOG,arCOG00938@arNOG		Cytoplasmic	
NAS2_0063	306	CDS	Proteolytic protease htpX homolog		K03799	TACK group	O	MER0349317	0FBD4@creNOG,COG0501@NOG,arCOG01331@arNOG		CytoplasmicMembrane	Peptidase
NAS2_0064	60	CDS	hypothetical protein								Cytoplasmic	
NAS2_0065	428	CDS	Transposase ISC1476		K07496	root;	L		0FCI7@creNOG,COG0675@NOG,arCOG00683@arNOG		Cytoplasmic	
NAS2_0066	155	CDS	NUDIX hydrolase			Thaumarchaeota	F		0FC8E@creNOG,COG1051@NOG,arCOG01075@arNOG		Unknown	
NAS2_0067		tRNA	tRNA-Pro									
NAS2_0068	111	CDS	hypothetical protein			Thaumarchaeota			111Fi@NOG,1CBXE@thaNOG,arCOG08641@arNOG		Cytoplasmic	
NAS2_0069	442	CDS	hypothetical protein			DPANN					Unknown	
NAS2_0070	379	CDS	Molybdopterin biosynthesis protein MoeA		K03750	Thaumarchaeota	H		0FBBR@creNOG,COG0303@NOG,arCOG00216@arNOG		Cytoplasmic	
NAS2_0071	139	CDS	Archaease			Thaumarchaeota			0FCN8@creNOG,COG1371@NOG,arCOG04055@arNOG		Cytoplasmic	
NAS2_0072	341	CDS	hypothetical protein		K00939	Thaumarchaeota	F		0FC3B@creNOG,0Y7XC@NOG,arCOG01048@arNOG		Cytoplasmic	
NAS2_0073	462	CDS	Phosphomannomutase	5.4.2.8	K15778	Thaumarchaeota	G		0KS9R@eurNOG,0WNKY@methaNOG,COG1109@NOG,arCOG00767@arNOG		Cytoplasmic	PGM
NAS2_0074	69	CDS	hypothetical protein			Thaumarchaeota			0KTY0@eurNOG,COG1342@NOG,arCOG02238@arNOG		Unknown	
NAS2_0075	163	CDS	hypothetical protein			Thaumarchaeota			0FD98@creNOG,12AY9@theNOG,arCOG08011@arNOG		CytoplasmicMembrane	
NAS2_0076	103	CDS	Twin-arginine translocation protein TatA		K03116	Thaumarchaeota	U		0FD48@creNOG,COG1826@NOG,arCOG02694@arNOG		Cytoplasmic	
NAS2_0077	48	CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic	
NAS2_0078	416	CDS	Histidyl-tRNA synthetase	6.1.1.21	K01892	Thaumarchaeota	J		1CBPV@thaNOG,COG0124@NOG,arCOG00404@arNOG		Cytoplasmic	
NAS2_0079	323	CDS	Replication factor C small subunit		K04801	Thaumarchaeota	L		0FB2l@creNOG,COG0470@NOG,arCOG00469@arNOG		Cytoplasmic	
NAS2_0080	196	CDS	hypothetical protein			Thaumarchaeota					Unknown	
NAS2_0081	695	CDS	DNA replication helicase protein MCM		K10726	Thaumarchaeota	L		1CBP5@thaNOG,COG1241@NOG,arCOG00439@arNOG		Cytoplasmic	
NAS2_0082		tRNA	tRNA-Lys									
NAS2_0083	397	CDS	permease			Euryarchaeota	G		0KSJ9@eurNOG,1CDSQ@thermNOG,COG0477@NOG,arCOG00132@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0084		tRNA	tRNA-Asp									
NAS2_0085	539	CDS	Acetyl-coenzyme A synthetase	6.2.1.1	K00666	Archaea	I		0FBCJ@creNOG,COG0318@NOG,arCOG00856@arNOG		Cytoplasmic	
NAS2_0086	112	CDS	hypothetical protein			Thaumarchaeota	I				Cytoplasmic	

NAS2_0087	664 CDS	3-hydroxyacyl-CoA dehydrogenase	4.2.1.17	K15016	Archaea	I	MER1073108	02TCS@arNOG,0KRK0@eurNOG,1CCG8@theNOG,COG1024@arNOG,COG1250@arNOG,arCOG00249@arNOG	Cytoplasmic	ECAH
NAS2_0088	400 CDS	3-ketoacyl-CoA thiolase	2.3.1.16	K00626	Archaea	I		0KRUZ@eurNOG,1CCBI@theNOG,COG0183@arNOG,arCOG01282@arNOG	Cytoplasmic	ATO
NAS2_0089	370 CDS	Butyryl-CoA dehydrogenase	1.3.99.2		Thaumarchaeota	I		0KRZR@eurNOG,1CCJM@theNOG,COG1960@arNOG,arCOG01708@arNOG	Cytoplasmic	ACADH
NAS2_0090	346 CDS	Butyryl-CoA dehydrogenase	1.3.8.1		Thaumarchaeota	I		0KTZH@eurNOG,1CCZT@theNOG,COG1960@arNOG,arCOG06973@arNOG	Cytoplasmic	ACADH
NAS2_0091	122 CDS	hypothetical protein			Thaumarchaeota	Q		0KY2S@eurNOG,1CD4N@theNOG,COG2050@arNOG,arCOG00777@arNOG	Cytoplasmic	
NAS2_0092	369 CDS	hypothetical protein			Thaumarchaeota	L		0KTW7@eurNOG,0WN5H@methaNOG,COG3385@arNOG,arCOG06160@arNOG	Cytoplasmic	
NAS2_0093	383 CDS	Butyryl-CoA dehydrogenase	1.3.99.2		Crenarchaeota	I		0FBDW@creNOG,COG1960@arNOG,arCOG01707@arNOG	Cytoplasmic	ACADH
NAS2_0094	rRNA	rRNA-Phe								
NAS2_0095	rRNA	rRNA-Tip								
NAS2_0096	rRNA	rRNA-Pro								
NAS2_0097	180 CDS	2-oxoglutarate synthase subunit KorC		K00177	Thaumarchaeota	C			Cytoplasmic	OFOR
NAS2_0098	260 CDS	2-oxoglutarate oxidoreductase, beta subunit	1.2.7.3	K00175	Thaumarchaeota	C		02TE4@arNOG,0KRGW@eurNOG,0WK87@methaNOG,COG1013@arNOG,COG1014@arNOG,arCOG01600@arNOG	Cytoplasmic	OFOR
NAS2_0099	351 CDS	2-oxoglutarate oxidoreductase, alpha subunit	1.2.7.3		Thaumarchaeota	C		0KREH@eurNOG,0WK06@methaNOG,COG0674@arNOG,arCOG01607@arNOG	Cytoplasmic	OFOR
NAS2_0100	93 CDS	2-oxoglutarate oxidoreductase, delta subunit	1.2.7.3		cellular organisms	C		0KTV0@eurNOG,0WMVP@methaNOG,COG1146@arNOG,arCOG00960@arNOG	Cytoplasmic	OFOR
NAS2_0101	rRNA	rRNA-Thr								
NAS2_0102	677 CDS	Acetyl-CoA synthetase (ADP-forming) alpha and beta chains		K09181	Thaumarchaeota	C		COG1042@arNOG,arCOG01340@arNOG	Unknown	
NAS2_0103	382 CDS	2-methylcitrate synthase	2.3.3.5	K01647	Thaumarchaeota	C		0KRNU@eurNOG,1CCCEM@theNOG,COG0372@arNOG,arCOG04237@arNOG	Cytoplasmic	CS
NAS2_0104	243 CDS	Methylisocitrate lyase	4.1.3.30	K03417	Thaumarchaeota	G		0FB9M@creNOG,COG2513@arNOG,arCOG00581@arNOG	Cytoplasmic	
NAS2_0105	430 CDS	2-methylcitrate dehydratase	4.2.1.79	K01720	Crenarchaeota			0FAWW@creNOG,COG2079@arNOG,arCOG04285@arNOG	Cytoplasmic	
NAS2_0106	rRNA	rRNA-Pro								
NAS2_0107	584 CDS	Ribonucleotide reductase of class III, large subunit	1.17.4.2	K21636	Thaumarchaeota			1CBBU@thaNOG,COG1328@arNOG,arCOG00734@arNOG,arCOG04889@arNOG	Cytoplasmic	
NAS2_0108	117 CDS	Nascent polypeptide-associated complex protein		K03626	Thaumarchaeota	K		0KUJ8@eurNOG,COG1308@arNOG,arCOG04061@arNOG	Cytoplasmic	
NAS2_0109	241 CDS	hypothetical protein		K07176	Thaumarchaeota	T		0FC4S@creNOG,COG2112@arNOG,arCOG01182@arNOG	Cytoplasmic	
NAS2_0110	447 CDS	rRNA nucleotidyltransferase, archaeal type	2.7.7.21	K07558	Thaumarchaeota	J		COG1746@arNOG,arCOG04249@arNOG	Cytoplasmic	
NAS2_0111	184 CDS	2'-5' RNA ligase		K01975	Thaumarchaeota	J		0FCCT@creNOG,COG1514@arNOG,arCOG01736@arNOG	Cytoplasmic	
NAS2_0112	189 CDS	Dephospho-CoA kinase archaeal, predicted	2.7.1.24		Thaumarchaeota	H		1CBJT@thaNOG,COG0237@arNOG,arCOG01045@arNOG	Cytoplasmic	
NAS2_0113	131 CDS	hypothetical protein		K09736	Thaumarchaeota			0FCK7@creNOG,COG1931@arNOG,arCOG01043@arNOG	Cytoplasmic	
NAS2_0114	294 CDS	Ribonuclease Z	3.1.26.11	K00784	Thaumarchaeota			0FC7E@creNOG,COG1234@arNOG,arCOG00501@arNOG	Cytoplasmic	
NAS2_0115	325 CDS	rRNA-(G10-N2) methyltransferase		K07446	Thaumarchaeota	L		0KSOG@eurNOG,0WKU9@methaNOG,COG1041@arNOG,arCOG00047@arNOG	Cytoplasmic	
NAS2_0116	241 CDS	Aerobic carbon monoxide dehydrogenase molybdenum cofactor insertion protein C		K07402	Thaumarchaeota	O		0FC02@creNOG,COG1975@arNOG,arCOG01929@arNOG	Cytoplasmic	
NAS2_0117	189 CDS	Transposase ISC1476		K07496	Crenarchaeota	L		0FCI7@creNOG,COG0675@arNOG,arCOG00683@arNOG	Cytoplasmic	
NAS2_0118	117 CDS	Transposase ISC1476			Thaumarchaeota	L		0FCI7@creNOG,COG0675@arNOG,arCOG00683@arNOG	Cytoplasmic	
NAS2_0119	250 CDS	hypothetical protein			Thaumarchaeota				Unknown	
NAS2_0120	67 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0121	254 CDS	hypothetical protein		K06883	Thaumarchaeota			1CBCR@thaNOG,COG1100@arNOG,arCOG01225@arNOG	Unknown	
NAS2_0122	126 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0123	197 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0124	535 CDS	(R)-citramalate synthase	2.3.1.182	K01649	Thaumarchaeota	E		0M1N8@eurNOG,0XW8Q@arNOG,1CETT@thermNOG,arCOG02103@arNOG	Cytoplasmic	
NAS2_0125	558 CDS	Dihydroxy-acid dehydratase	4.2.1.9	K01687	cellular organisms			0FAY6@creNOG,COG0119@arNOG,arCOG02092@arNOG	Cytoplasmic	
NAS2_0126	564 CDS	Acetolactate synthase large subunit	2.2.1.6	K01652	cellular organisms	E		0KRH7@eurNOG,COG0129@arNOG,arCOG04045@arNOG	Cytoplasmic	
NAS2_0127	163 CDS	Acetolactate synthase small subunit	2.2.1.6	K01653	Thaumarchaeota	E		0KRBJ@eurNOG,COG0028@arNOG,arCOG01998@arNOG	Cytoplasmic	
NAS2_0128	398 CDS	Ketol-acid reductoisomerase	1.1.1.86	K00053	cellular organisms	E		0KT20@eurNOG,COG0440@arNOG,arCOG04445@arNOG	Cytoplasmic	
NAS2_0129	526 CDS	2-isopropylmalate synthase	2.3.3.13	K01649	Archaea	E		0FBM1@creNOG,COG0059@arNOG,arCOG04465@arNOG	Cytoplasmic	
NAS2_0130	322 CDS	3-isopropylmalate dehydrogenase	1.1.1.85	K00052	Thaumarchaeota	E		1CB2V@thaNOG,COG0119@arNOG,arCOG02092@arNOG	Cytoplasmic	
NAS2_0131	274 CDS	DNA double-strand break repair Rad50 ATPase			Thaumarchaeota			0FBBF@creNOG,COG0473@arNOG,arCOG01163@arNOG	Cytoplasmic	
NAS2_0132	373 CDS	Uncharacterized protein		K08975	Archaea			1CBN8@thaNOG,COG2237@arNOG,arCOG04151@arNOG	CytoplasmicMembrane	
NAS2_0133	268 CDS	Undecaprenyl diphosphate synthase	2.5.1.31	K15888	Archaea	I		0FB1C@creNOG,COG0020@arNOG,arCOG01532@arNOG	Cytoplasmic	
NAS2_0134	326 CDS	COG1801: Uncharacterized conserved protein			Thaumarchaeota			0KTRP@eurNOG,1CDTQ@thermNOG,COG1801@arNOG,arCOG04291@arNOG	Cytoplasmic	
NAS2_0135	233 CDS	hypothetical protein			Thaumarchaeota			1100Q@arNOG,1CBSF@thaNOG,arCOG08773@arNOG	Cytoplasmic	
NAS2_0136	223 CDS	Multiple antibiotic resistance protein marC		K05595	Thaumarchaeota	U		0FC0F@creNOG,COG2095@arNOG,arCOG01997@arNOG	CytoplasmicMembrane	
NAS2_0137	210 CDS	Ribonuclease HII	3.1.26.4	K03470	Archaea	L		0KSZR@eurNOG,1CE44@thermNOG,COG0164@arNOG,arCOG04121@arNOG	Cytoplasmic	
NAS2_0138	179 CDS	Hypothetical ATP-binding protein, containing DUF265 domain		K06928	Archaea	F		0FD01@creNOG,COG1618@arNOG,arCOG01034@arNOG	Cytoplasmic	
NAS2_0139	rRNA	rRNA-Leu								
NAS2_0140	427 CDS	Arsenic efflux pump protein			Archaea	P		0FBJG@creNOG,COG1055@arNOG,arCOG00238@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_0141	809 CDS	Lead, cadmium, zinc and mercury transporting ATPase	3.6.3.4	K01535	Thaumarchaeota	P		0FBBG@creNOG,COG0474@arNOG,arCOG01578@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0142	rRNA	rRNA-Ala								
NAS2_0143	130 CDS	SSU ribosomal protein S8e		K02995	Thaumarchaeota	J		02HSX@arNOG,0KTXN@eurNOG,COG2007@arNOG,arCOG04154@arNOG	Cytoplasmic	
NAS2_0144	92 CDS	hypothetical protein		K03105	Thaumarchaeota	U			Cytoplasmic	
NAS2_0145	80 CDS	hypothetical protein		K07569	Thaumarchaeota	J			Cytoplasmic	
NAS2_0146	300 CDS	Transcription initiation factor B		K03124	Thaumarchaeota	K		COG1405@arNOG,arCOG01981@arNOG	Cytoplasmic	
NAS2_0147	128 CDS	hypothetical protein			Thaumarchaeota	K		COG1522@arNOG,arCOG04153@arNOG	Cytoplasmic	
NAS2_0148	209 CDS	Cell division protein FtsJ		K02427	Thaumarchaeota	J		0KRBK@eurNOG,0WKNN@methaNOG,COG0293@arNOG,COG3269@arNOG,arCOG00079@arNOG	Cytoplasmic	
NAS2_0149	359 CDS	rRNA N2,N2-dimethyl(Guanine26-N2)-methyltransferase	2.1.1.32	K00555	Thaumarchaeota	J		0FBWZ@creNOG,COG1867@arNOG,arCOG01219@arNOG	Cytoplasmic	
NAS2_0150	rRNA	rRNA-Leu								
NAS2_0151	254 CDS	N5-methyltetrahydromethanopterin:coenzyme M methyltransferase sub	2.1.1.86	K00577	Archaea	H		0KRBX@eurNOG,0WQ5A@methaNOG,COG0294@arNOG,arCOG01978@arNOG	CytoplasmicMembrane	
NAS2_0152	rRNA	Small Subunit Ribosomal RNA								
NAS2_0153	rRNA	Large Subunit Ribosomal RNA								
NAS2_0154	410 CDS	Tryptophanyl-tRNA synthetase	6.1.1.2	K01867	Archaea	J		0FB1W@creNOG,COG0180@arNOG,arCOG01887@arNOG	Cytoplasmic	
NAS2_0155	72 CDS	hypothetical protein			Archaea				Cytoplasmic	
NAS2_0156	226 CDS	Uridine monophosphate kinase	2.7.4.22	K09903	Thaumarchaeota	F		0FC8Y@creNOG,COG0528@arNOG,arCOG00858@arNOG	Cytoplasmic	
NAS2_0157	424 CDS	Eukaryotic peptide chain release factor subunit 1		K03265	Thaumarchaeota	J		1CBN0@thaNOG,COG1503@arNOG,arCOG01742@arNOG	Cytoplasmic	
NAS2_0158	790 CDS	Valyl-tRNA synthetase	6.1.1.9	K01873	Archaea	J		0FAZR@creNOG,COG0525@arNOG,arCOG00808@arNOG	Cytoplasmic	
NAS2_0159	325 CDS	Ornithine cyclodeaminase	4.3.1.12	K19244	cellular organisms	E		0KRWJ@eurNOG,0WJYT@methaNOG,COG2423@arNOG,arCOG01035@arNOG	Cytoplasmic	
NAS2_0160	41 CDS	hypothetical protein			Not assigned				Cytoplasmic	
NAS2_0161	103 CDS	Transcription factor S		K03057	Thaumarchaeota	K	MER0069149	0FCMG@creNOG,COG1594@arNOG,arCOG00579@arNOG	Cytoplasmic	
NAS2_0162	93 CDS	hypothetical protein		K03056	cellular organisms	K			Cytoplasmic	
NAS2_0163	185 CDS	RNA-binding protein, containing S1 domain		K07573	Archaea	J		0FCYN@creNOG,COG1096@arNOG,arCOG00676@arNOG	Cytoplasmic	
NAS2_0164	346 CDS	diphtheria toxin resistance protein		K07561	Archaea	J		1CBIG@thaNOG,COG1736@arNOG,arCOG04112@arNOG	Cytoplasmic	
NAS2_0165	169 CDS	LSU ribosomal protein L10e		K02866	Archaea	J		0FBY2@creNOG,COG0197@arNOG,arCOG04113@arNOG	Cytoplasmic	
NAS2_0166	260 CDS	rRNA-Cm32/Urn32 methyltransferase			Archaea	J		0KRWG@eurNOG,1CCRH@theNOG,COG0565@arNOG,arCOG01018@arNOG	Cytoplasmic	
NAS2_0167	40 CDS	hypothetical protein			No hits				Cytoplasmic	
NAS2_0168	rRNA	rRNA-Gly								
NAS2_0169	359 CDS	putative cell division protein		K06965	Thaumarchaeota			0FBIG@creNOG,COG1537@arNOG,arCOG01741@arNOG	Cytoplasmic	
NAS2_0170	724 CDS	Translation elongation factor 2		K03234	Archaea	J		0FB3P@creNOG,COG0480@arNOG,arCOG01559@arNOG	Cytoplasmic	
NAS2_0171	455 CDS	Non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (N/1.2.1.9		K15038	Crenarchaeota	C		0FBG9@creNOG,COG1012@arNOG,arCOG01252@arNOG	Cytoplasmic	
NAS2_0172	rRNA	rRNA-Ser								
NAS2_0173	59 CDS	CBS domain protein			Crenarchaeota		MER0231653	02TZE@arNOG,0FFWW@creNOG,0ZX5J@arNOG	Unknown	
NAS2_0174	rRNA	rRNA-Arg								
NAS2_0175	rRNA	rRNA-Arg								

NAS2_0176	246 CDS	Proteasome subunit alpha	3.4.25.1	K03432	Thaumarchaeota	O	MER0080948	1CBAI@thaNOG,COG0638@NOG,arCOG00971@arNOG	Cytoplasmic	Peptidase
NAS2_0177	326 CDS	Methylthioribose-1-phosphate isomerase	5.3.1.23	K08963	cellular organisms	J		0KRAC@eurNOG,0WPZA@methNOG,COG0182@NOG,arCOG01123@arNOG	Cytoplasmic	
NAS2_0178	230 CDS	Shwachman-Bodian-Diamond syndrome protein		K14574	Archaea	J		1CBGY@thaNOG,COG1500@NOG,arCOG04187@arNOG	Cytoplasmic	
NAS2_0179	243 CDS	Probable exosome complex RNA-binding protein 1		K03679	Thaumarchaeota	J		1CBA8@thaNOG,COG1097@NOG,arCOG00678@arNOG	Unknown	
NAS2_0180	218 CDS	Ribonuclease PH	2.7.7.56	K11600	Thaumarchaeota	J		0FB7Q@creNOG,COG0689@NOG,arCOG01575@arNOG	Cytoplasmic	
NAS2_0181	283 CDS	Probable exosome complex exonuclease 2		K12589	Thaumarchaeota	J		1CB3Y@thaNOG,COG2123@NOG,arCOG01574@arNOG	Cytoplasmic	
NAS2_0182	68 CDS	LSU ribosomal protein L37Ae		K02921	Thaumarchaeota	J		1CC8V@thaNOG,COG1997@NOG,arCOG04208@arNOG	Cytoplasmic	
NAS2_0183	80 CDS	hypothetical protein							Cytoplasmic	
NAS2_0184	118 CDS	Prefoldin beta subunit		K04798	Thaumarchaeota	O		1CBZQ@thaNOG,COG1382@NOG,arCOG01342@arNOG	Cytoplasmic	
NAS2_0185	330 CDS	Conserved protein			Bathyarchaeota			0FCPW@creNOG,COG0618@NOG,arCOG01565@arNOG	Unknown	
NAS2_0186	229 CDS	ATPase component N1kO of energizing module of nickel ECF transporter		K16786	Thaumarchaeota			02TIP@arNOG,0FFTZ@creNOG,COG1122@NOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0187	163 CDS	hypothetical protein			Thaumarchaeota				Transporter (ABC)	Cytoplasmic
NAS2_0188	205 CDS	Transmembrane component of general energizing module of ECF transporters		K16785	Thaumarchaeota	P		COG0619@arNOG,arCOG02250@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0189	271 CDS	putative ABC transporter ATP-binding protein			Thaumarchaeota			0KRWZ@eurNOG,0WQFK@methNOG,COG1122@NOG,arCOG00202@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0190	112 CDS	hypothetical protein			Thaumarchaeota			0KV81@eurNOG,0YST6@NOG,arCOG08221@arNOG	Unknown	
NAS2_0191	83 CDS	no similarity			Thaumarchaeota			0KVPD@eurNOG,0Y2IG@NOG,1CD34@theNOG,arCOG05390@arNOG	Cytoplasmic	
NAS2_0192	64 CDS	hypothetical protein			Thaumarchaeota	L			Unknown	
NAS2_0193	486 CDS	Dihydropyrimidine dehydrogenase	1.8.1.4	K00382	Thaumarchaeota	C		0FBA8@creNOG,COG1249@NOG,arCOG01068@arNOG	Cytoplasmic	
NAS2_0194	155 CDS	hypothetical protein			Thaumarchaeota			1114B@NOG,1CBWN@thaNOG,arCOG08723@arNOG	Cytoplasmic	
NAS2_0195	125 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0196	43 CDS	hypothetical protein			Not assigned				Cytoplasmic	
NAS2_0197	116 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0198	349 CDS	V-type ATP synthase subunit C	3.6.3.14	K02119	Thaumarchaeota	C		1CB40@thaNOG,COG1527@NOG,arCOG02459@arNOG	CytoplasmicMembrane	ATPase
NAS2_0199	677 CDS	V-type ATP synthase subunit I	3.6.3.14	K02123	Thaumarchaeota	C		1CBHJ@thaNOG,COG1269@NOG,arCOG04138@arNOG	Transporter ATPase?	CytoplasmicMembrane
NAS2_0200	98 CDS	ATP synthase subunit F	3.6.3.14	K02122	Thaumarchaeota	C		1CC5K@thaNOG,COG1436@NOG,arCOG04102@arNOG	Transporter ATPase?	Cytoplasmic
NAS2_0201	214 CDS	V-type ATP synthase subunit E	3.6.3.14	K02121	Thaumarchaeota	C		1CBOS@thaNOG,COG1390@NOG,arCOG00869@arNOG	Transporter ATPase?	Cytoplasmic
NAS2_0202	594 CDS	V-type ATP synthase subunit A	3.6.3.14	K02117	Archaea	C		1CBMZ@thaNOG,COG1155@NOG,arCOG00868@arNOG	multiple	ATPase
NAS2_0203	476 CDS	V-type ATP synthase subunit B	3.6.3.14	K02118	Archaea	C		0FB55@creNOG,COG1156@NOG,arCOG00865@arNOG	Cytoplasmic	ATPase
NAS2_0204	214 CDS	V-type ATP synthase subunit D	3.6.3.14	K02120	Thaumarchaeota	C		1CB4W@thaNOG,COG1394@NOG,arCOG04101@arNOG	Cytoplasmic	ATPase
NAS2_0205	57 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0206	90 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0207	260 CDS	hypothetical protein			Archaea				Cytoplasmic	
NAS2_0208	225 CDS	Function Code: 15.3 Other Categories: Transposon-related functions			Thaumarchaeota	L		0KUY3@eurNOG,COG3316@NOG,arCOG02134@arNOG	Cytoplasmic	
NAS2_0209	87 CDS	V-type ATP synthase subunit K	3.6.3.14	K02124	Thaumarchaeota	C			Transporter ATPase?	CytoplasmicMembrane
NAS2_0210	48 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0211	351 CDS	Menquinone-specific polyprenyl reductase			Thaumarchaeota	C		1CB3T@thaNOG,COG0644@NOG,arCOG00570@arNOG	Cytoplasmic	
NAS2_0212	411 CDS	Adenosylhomocysteinase	3.3.1.1	K01251	cellular organisms	F		0FAX3@creNOG,COG0499@NOG,arCOG04137@arNOG	Cytoplasmic	
NAS2_0213	428 CDS	S-adenosylhomocysteine deaminase	3.5.4.28	K12960	Archaea	H	MER0211949	02HD4@arcNOG,0KRC1@eurNOG,COG0402@NOG,arCOG00695@arNOG	Cytoplasmic	
NAS2_0214	458 CDS	putative tRNA N6-threonylcarbamoyladenine 2-methylthiotransferase			Thaumarchaeota	J		0KRAT@eurNOG,COG0621@NOG,arCOG01358@arNOG	Cytoplasmic	
NAS2_0215	274 CDS	hypothetical protein			Thaumarchaeota				CytoplasmicMembrane	
NAS2_0216	139 CDS	Eukaryotic translation initiation factor 2 beta subunit		K03238	Thaumarchaeota	J		0KT01@eurNOG,1CDVN@thermNOG,COG1601@NOG,arCOG01640@arNOG	Cytoplasmic	
NAS2_0217	102 CDS	hypothetical protein		K09148	Thaumarchaeota			0FCPN@creNOG,COG2412@NOG,arCOG04051@arNOG	Cytoplasmic	
NAS2_0218	37 CDS	hypothetical protein			No hits				Unknown	
NAS2_0219	80 CDS	Translation initiation factor 1A		K03236	Thaumarchaeota	J		0KTNN@eurNOG,COG0361@NOG,arCOG01179@arNOG	Cytoplasmic	
NAS2_0220	260 CDS	Serine/threonine-protein kinase RIO1	2.7.11.1	K07178	Thaumarchaeota	T		1CB6U@thaNOG,COG1718@NOG,arCOG01180@arNOG	Cytoplasmic	
NAS2_0221	205 CDS	Putative RNA-binding protein COG1094		K06961	Thaumarchaeota			1CBAH@thaNOG,COG1094@NOG,arCOG04150@arNOG	Cytoplasmic	
NAS2_0222	507 CDS	DNA topoisomerase VI subunit B	5.99.1.3	K03167	Thaumarchaeota	L		0FAX4@creNOG,COG1389@NOG,arCOG01165@arNOG	Cytoplasmic	
NAS2_0223	358 CDS	DNA topoisomerase VI subunit A	5.99.1.3	K03166	Thaumarchaeota	L		1CBFQ@thaNOG,COG1697@NOG,arCOG04143@arNOG	Unknown	
NAS2_0224		tRNA								
NAS2_0225		tRNA-Met								
NAS2_0226	404 CDS	Transcriptional regulator with GntR family domain	2.6.1.1		Thaumarchaeota	K		0FBRV@creNOG,COG1167@NOG,arCOG00492@arNOG	Cytoplasmic	
NAS2_0227	318 CDS	Oriblone cyclodeaminase	4.3.1.12		Thaumarchaeota	E		0KRWJ@eurNOG,COG2423@NOG,arCOG01035@arNOG	Cytoplasmic	
NAS2_0228	350 CDS	Phosphate regulatory protein-like			Thaumarchaeota	P		0FBEW@creNOG,COG0704@NOG,arCOG00318@arNOG	Cytoplasmic	
NAS2_0229	628 CDS	Indolepyruvate oxidoreductase subunit IorA	1.2.7.8	K00179	Archaea	C		0KRBD@eurNOG,1CD96@theNOG,COG4231@NOG,arCOG01609@arNOG	Cytoplasmic	
NAS2_0230	209 CDS	Indolepyruvate oxidoreductase subunit IorB	1.2.7.8	K00180	Euryarchaeota	C		0KV3D@eurNOG,1CDFP@theNOG,COG1014@NOG,arCOG01602@arNOG	Cytoplasmic	
NAS2_0231	59 CDS	hypothetical protein			No hits				Unknown	
NAS2_0232	476 CDS	RNA-2',3'-Phosphate-5'-OH ligase		K14415	Thaumarchaeota			0FBB8@creNOG,COG1690@NOG,arCOG04246@arNOG	Cytoplasmic	
NAS2_0233	132 CDS	tRNA-intron endonuclease	3.1.27.9	K01170	Thaumarchaeota	J		1CB3U@thaNOG,COG1676@NOG,arCOG01701@arNOG	Cytoplasmic	
NAS2_0234	279 CDS	(S)-2,3-di-O-geranylgeranylglycerol phosphate synthase		K17105	Thaumarchaeota	H		02GXT@arcNOG,0KTG2@eurNOG,COG0382@NOG,arCOG00476@arNOG	CytoplasmicMembrane	
NAS2_0235	416 CDS	Replication factor C large subunit		K04800	Thaumarchaeota	L		1CB2R@thaNOG,COG0470@NOG,arCOG00470@arNOG	CytoplasmicMembrane	
NAS2_0236		tRNA								
NAS2_0237	369 CDS	putative transposase			Thaumarchaeota	L		0KTV7@eurNOG,0WN5H@methaNOG,COG3385@NOG,arCOG06160@arNOG	Cytoplasmic	
NAS2_0238	160 CDS	Xanthine-guanine phosphoribosyltransferase	2.4.2.22	K07101	Thaumarchaeota			0FCPU@creNOG,COG2236@NOG,arCOG00040@arNOG	Cytoplasmic	
NAS2_0239	95 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0240	85 CDS	DNA-directed RNA polymerase subunit H	2.7.7.6	K03053	cellular organisms	K		0FCW5@creNOG,COG02012@NOG,arCOG04258@arNOG	Cytoplasmic	
NAS2_0241	1120 CDS	DNA-directed RNA polymerase subunit B	2.7.7.6	K13798	Thaumarchaeota	K	MER0195833	1CBEC@thaNOG,COG0085@NOG,arCOG01782@arNOG	Cytoplasmic	
NAS2_0242	1271 CDS	DNA-directed RNA polymerase subunit A'	2.7.7.6	K03041	cellular organisms	K		02UA2@arNOG,1CBSR@thaNOG,COG0086@NOG,arCOG04257@arNOG	Cytoplasmic	
NAS2_0243	122 CDS	hypothetical protein			Thaumarchaeota				Unknown	
NAS2_0244	144 CDS	NusA protein homolog, archaeal		K02600	Thaumarchaeota	K		0FC9X@creNOG,COG0195@NOG,arCOG01780@arNOG	Cytoplasmic	
NAS2_0245	148 CDS	SSU ribosomal protein S23e		K02950	Thaumarchaeota	J		0FC6K@creNOG,COG0048@NOG,arCOG04255@arNOG	Cytoplasmic	
NAS2_0246	206 CDS	SSU ribosomal protein S5e		K02992	Thaumarchaeota	J		0FAZX@creNOG,COG0049@NOG,arCOG04254@arNOG	Cytoplasmic	
NAS2_0247	443 CDS	Translation elongation factor 1 alpha subunit		K03231	Thaumarchaeota	J		0FB9H@creNOG,COG5256@NOG,arCOG01561@arNOG	Cytoplasmic	
NAS2_0248	154 CDS	N-terminal acetyltransferase complex subunit			Thaumarchaeota	K		0FCGY@creNOG,COG0454@NOG,arCOG00826@arNOG	Cytoplasmic	
NAS2_0249	442 CDS	NADP-dependent malic enzyme	1.1.1.40	K00027	Archaea	C		0FB3G@creNOG,COG0281@NOG,arCOG00853@arNOG	Cytoplasmic	MAE
NAS2_0250		tRNA-Lys								
NAS2_0251	91 CDS	Translation elongation factor 1 beta subunit		K03232	Thaumarchaeota	J		0FCMF@creNOG,COG2092@NOG,arCOG01988@arNOG	Unknown	
NAS2_0252	355 CDS	Predicted Zn-ribbon RNA-binding protein with a function in translation	1.3.1.83	K07580	Thaumarchaeota	J		0FDEP@creNOG,COG2888@NOG,arCOG01989@arNOG	Unknown	
NAS2_0253	355 CDS	Geranylgeranyl diphosphate reductase			Thaumarchaeota	C		0KRTN@eurNOG,0WQ1F@methNOG,COG0644@NOG,arCOG00570@arNOG	Cytoplasmic	
NAS2_0254	124 CDS	Peptidyl-tRNA hydrolase, archaeal type	3.1.1.29	K04794	Thaumarchaeota			0FC11@creNOG,COG1990@NOG,arCOG04228@arNOG	Cytoplasmic	
NAS2_0255	376 CDS	tRNA pseudouridine 13 synthase		K06176	Thaumarchaeota			1CBMM@thaNOG,COG0585@NOG,arCOG04252@arNOG	Unknown	
NAS2_0256	347 CDS	Diphthine synthase	2.1.1.98	K02015	Thaumarchaeota	J		1CBDG@thaNOG,COG1798@NOG,arCOG01224@arNOG,arCOG04161@arNOG	Cytoplasmic	
NAS2_0257	720 CDS	Cell division protein FtsH		K13525	Thaumarchaeota	O	MER0269263	0FBAP@creNOG,COG0464@NOG,arCOG01308@arNOG	Cytoplasmic	
NAS2_0258	92 CDS	hypothetical protein			Thaumarchaeota				Cytoplasmic	
NAS2_0259	342 CDS	Flap structure-specific endonuclease		K04799	Thaumarchaeota	L		0FB8P@creNOG,COG0258@NOG,arCOG04050@arNOG	Cytoplasmic	
NAS2_0260	235 CDS	Protein-L-isoaspartate O-methyltransferase	2.1.1.77	K00573	Thaumarchaeota	O		0FBGE@creNOG,COG2518@NOG,arCOG00976@arNOG	Cytoplasmic	
NAS2_0261	114 CDS	Uncharacterized protein		K09738	Thaumarchaeota			COG2090@NOG,arCOG04171@arNOG	Unknown	
NAS2_0262	210 CDS	hypothetical protein			Thaumarchaeota			0FCVA@creNOG,0ZXD4@NOG,arCOG01806@arNOG	Cytoplasmic	
NAS2_0263	402 CDS	Argininosuccinate synthase	6.3.4.5	K01940	Thaumarchaeota	E		0KRGT@eurNOG,COG0137@NOG,arCOG00112@arNOG	Cytoplasmic	
NAS2_0264	493 CDS	Argininosuccinate lyase	4.3.2.1	K01755	Thaumarchaeota	E		0KRV2@eurNOG,0WKBJ@methaNOG,COG0165@NOG,arCOG01748@arNOG	Cytoplasmic	

NAS2_0265	61 CDS	Lysine Biosynthetic Amino Acid Carrier Protein LysW		K05826	Thaumarchaeota			02TR0@arNOG,0XXG3@NOG		Cytoplasmic
NAS2_0266	289 CDS	Alpha-aminoacidate-LysW ligase LysX		K05827	Thaumarchaeota	J		1CB79@thaNOG,COG0189@NOG,arCOG01589@arNOG		Cytoplasmic
NAS2_0267	355 CDS	N-acetyl-gamma-glutamyl-phosphate reductase	1.2,1.38	K05829	Thaumarchaeota	E		0FB8K@creNOG,COG0002@NOG,arCOG00495@arNOG		Cytoplasmic
NAS2_0268	269 CDS	Acetylglutamate kinase	2.7,2.8	K05828	Archaea	E		1CBM1@thaNOG,COG0548@NOG,arCOG00862@arNOG		Unknown
NAS2_0269	404 CDS	N-acetyl-lysine aminotransferase	2.6,1.11	K05830	Archaea	E		1CBRT@thaNOG,COG4992@NOG,arCOG00914@arNOG		Cytoplasmic
NAS2_0270	138 CDS	HTH-type transcriptional regulator LysM			Thaumarchaeota	K		1CBWH@thaNOG,COG1522@NOG,arCOG01580@arNOG		Cytoplasmic
NAS2_0271	401 CDS	2-isopropylmalate synthase	2.3,3.13	K01649	Archaea	E		1CBX3@thaNOG,COG0119@NOG,arCOG0092@arNOG		Cytoplasmic
NAS2_0272	285 CDS	Lysine biosynthesis protein LysX		K05827	Archaea	J		0KTPN@eurNOG,1CD91@thaNOG,COG0189@NOG,arCOG01589@arNOG		Cytoplasmic
NAS2_0273	373 CDS	N-acetyl-lysine deacetylase		K05831	Thaumarchaeota	E	MER0841676	0KTHT@eurNOG,1CD8N@thaNOG,COG0624@NOG,arCOG01107@arNOG		Unknown
NAS2_0274	115 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_0275	191 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_0276	155 CDS	Uncharacterized protein		K07581	Thaumarchaeota	J		0FCWR@creNOG,COG1325@NOG,arCOG01042@arNOG		Cytoplasmic
NAS2_0277	337 CDS	TsaDKae1/Qn7 protein		K01409	Archaea	O		1CB4C@thaNOG,COG0533@NOG,arCOG01183@arNOG		Cytoplasmic
NAS2_0278	213 CDS	p53-regulating protein kinase		K08851	Thaumarchaeota	T		0FCA5@creNOG,COG3642@NOG,arCOG01185@arNOG		Cytoplasmic
NAS2_0279	154 CDS	Xanthosine/inosine triphosphate pyrophosphatase		K02428	Archaea	F		0FC91@creNOG,COG0127@NOG,arCOG04184@arNOG		Cytoplasmic
NAS2_0280	122 CDS	SSU ribosomal protein S13e		K02956	Thaumarchaeota	J		0KSZT@eurNOG,COG0184@NOG,arCOG04185@arNOG		Cytoplasmic
NAS2_0281	419 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_0282	81 CDS	hypothetical protein			Thaumarchaeota					Unknown
NAS2_0283	217 CDS	SSU ribosomal protein S3Ae		K02984	Thaumarchaeota	J		0FB82@creNOG,COG1890@NOG,arCOG04186@arNOG		Cytoplasmic
NAS2_0284	401 CDS	GTP-binding and nucleic acid-binding protein YchF		K06942	Archaea	J		0FAY8@creNOG,COG0012@NOG,arCOG00357@arNOG		Cytoplasmic
NAS2_0285	315 CDS	D-3-phosphoglycerate dehydrogenase	1.1,1.95	K00058	Thaumarchaeota	E		0FAXN@creNOG,COG0111@NOG,arCOG01754@arNOG		Cytoplasmic
NAS2_0286	154 CDS	LSU ribosomal protein L15e		K02877	Archaea	J		0FB7W@creNOG,COG1632@NOG,arCOG04209@arNOG		Cytoplasmic
NAS2_0287	207 CDS	FMN adenylyltransferase, type 3 archaeal	2.7,7.2	K14656	Thaumarchaeota	M		1CB2l@thaNOG,COG0615@NOG,arCOG01222@arNOG		Cytoplasmic
NAS2_0288	194 CDS	Uncharacterized protein		K07477	Thaumarchaeota	J		1CBHF@thaNOG,COG2178@NOG,arCOG04318@arNOG		Cytoplasmic
NAS2_0289	450 CDS	Proteasome subunit beta	3.4,25.1	K03433	Thaumarchaeota	O	MER1093937	0FC1D@creNOG,COG0638@NOG,arCOG00970@arNOG		Cytoplasmic
NAS2_0290	46 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_0291	170 CDS	Nicotinamide-nucleotide adenylyltransferase, NadM family	2.7,7.1	K00952	Thaumarchaeota	H		0FC6l@creNOG,COG1056@NOG,arCOG00972@arNOG		Cytoplasmic
NAS2_0292	397 CDS	Serine-glyoxylate aminotransferase	2.6,1.45		Thaumarchaeota	E		1CBJj@thaNOG,COG0075@NOG,arCOG00082@arNOG		Cytoplasmic
NAS2_0293	298 CDS	FKBP-type peptidyl-prolyl cis-trans isomerase SlpA	5.2,1.8		Thaumarchaeota	O		1CBSl@thaNOG,COG1047@NOG,arCOG00980@arNOG		Cytoplasmic
NAS2_0294	342 CDS	Glycerol-1-phosphate dehydrogenase [NAD(P)]	1.1,1.261	K00096	Archaea	J		0FB7A@creNOG,COG0371@NOG,arCOG00982@arNOG		Cytoplasmic
NAS2_0295	220 CDS	Proteasome subunit beta	3.4,25.1	K03433	Thaumarchaeota	O	MER0121838	0FC3F@creNOG,COG0638@NOG,arCOG00970@arNOG		Cytoplasmic
NAS2_0296	639 CDS	Protein similar to polyadenylation specificity factor, MJ1236 type		K07041	Thaumarchaeota			1CBE5@thaNOG,COG1782@NOG,arCOG00543@arNOG		Unknown
NAS2_0297	92 CDS	hypothetical protein		K09152	Thaumarchaeota			1CC1S@thaNOG,COG2450@NOG,arCOG02283@arNOG		Cytoplasmic
NAS2_0298	142 CDS	conserved protein with predicted RNA binding PUA domain		K07575	Thaumarchaeota	J		0FCXG@creNOG,COG2016@NOG,arCOG00985@arNOG		Cytoplasmic
NAS2_0299	72 CDS	Putative snRNP Sm-like protein		K04796	Thaumarchaeota	K		0FD0R@creNOG,COG1958@NOG,arCOG00998@arNOG		Cytoplasmic
NAS2_0300	86 CDS	Transposase ISC1476			Thaumarchaeota	L		0FCI7@creNOG,COG0675@NOG,arCOG00683@arNOG		Cytoplasmic
NAS2_0301	52 CDS	LSU ribosomal protein L37e		K02922	Thaumarchaeota	J		0KYIE@eurNOG,COG2126@NOG,arCOG04126@arNOG		Cytoplasmic
NAS2_0302	176 CDS	Adenine phosphoribosyltransferase	2.4,2.7	K00759	Thaumarchaeota	F		1CBNU@thaNOG,COG0503@NOG,arCOG00030@arNOG		Cytoplasmic
NAS2_0303	irRNA	irRNA-ile								
NAS2_0304	321 CDS	LSU ribosomal protein L3e		K02906	Archaea	J		0FAZQ@creNOG,COG0087@NOG,arCOG04070@arNOG		Cytoplasmic
NAS2_0305	267 CDS	LSU ribosomal protein L1e		K02930	Archaea	J		0FBEO@creNOG,COG0058@NOG,arCOG04071@arNOG		Cytoplasmic
NAS2_0306	88 CDS	LSU ribosomal protein L23Ae		K02892	cellular organisms	J		0KHUV@eurNOG,1CF3Y@thermNOG,COG0089@NOG,arCOG04072@arNOG		Cytoplasmic
NAS2_0307	242 CDS	LSU ribosomal protein L8e		K02886	Thaumarchaeota	J		1CBIB@thaNOG,COG0090@NOG,arCOG04067@arNOG		Cytoplasmic
NAS2_0308	128 CDS	SSU ribosomal protein S15e		K02965	Thaumarchaeota	J		0KT47@eurNOG,1CEUI@thermNOG,COG0185@NOG,arCOG04099@arNOG		Cytoplasmic
NAS2_0309	128 CDS	hypothetical protein			Thaumarchaeota			0XTWE@NOG,1C8YF@thaNOG,arCOG05529@arNOG		Cytoplasmic
NAS2_0310	280 CDS	COG2106 Methylase		K09142	Archaea			02HGD@arNOG,0KTHK@eurNOG,COG2106@NOG,arCOG04069@arNOG		Cytoplasmic
NAS2_0311	128 CDS	LSU ribosomal protein L17e		K02890	Thaumarchaeota	J		0KT2J@eurNOG,COG0091@NOG,arCOG04098@arNOG		Cytoplasmic
NAS2_0312	208 CDS	SSU ribosomal protein S3e		K02982	Thaumarchaeota	J		0KRSH@eurNOG,0WKN0@methaNOG,COG0092@NOG,arCOG04097@arNOG		Cytoplasmic
NAS2_0313	57 CDS	hypothetical protein		K02904	Thaumarchaeota	J				Cytoplasmic
NAS2_0314	85 CDS	hypothetical protein		K03538	Thaumarchaeota					Cytoplasmic
NAS2_0315	115 CDS	SSU ribosomal protein S11e		K02961	Thaumarchaeota	J		0FCM6@creNOG,COG0186@NOG,arCOG04096@arNOG		Cytoplasmic
NAS2_0316	142 CDS	LSU ribosomal protein L23e		K02874	root;	J		1CBUJ@thaNOG,COG0093@NOG,arCOG04095@arNOG		Cytoplasmic
NAS2_0317	125 CDS	LSU ribosomal protein L26e		K02875	Thaumarchaeota	J		0FCMl@creNOG,COG0198@NOG,arCOG04094@arNOG		Cytoplasmic
NAS2_0318	125 CDS	LSU ribosomal protein S4e		K02987	Thaumarchaeota	J		1CB42@thaNOG,COG01471@NOG,arCOG04093@arNOG		Cytoplasmic
NAS2_0319	196 CDS	LSU ribosomal protein L11e		K02931	Archaea	J		0FBU4@creNOG,COG0094@NOG,arCOG04092@arNOG		Cytoplasmic
NAS2_0320	54 CDS	SSU ribosomal protein S29e		K02954	Thaumarchaeota	J		0FD5V@creNOG,COG0199@NOG,arCOG00782@arNOG		Cytoplasmic
NAS2_0321	131 CDS	SSU ribosomal protein S15Ae		K02994	Thaumarchaeota	J		1CBVT@thaNOG,COG0096@NOG,arCOG04091@arNOG		Cytoplasmic
NAS2_0322	190 CDS	LSU ribosomal protein L9e		K02933	Thaumarchaeota	J		0KTC6@eurNOG,1CDQ8@thermNOG,COG0097@NOG,arCOG04090@arNOG		Cytoplasmic
NAS2_0323	126 CDS	LSU ribosomal protein L32e		K02912	Archaea	J		0KTY5@eurNOG,1CES3@thermNOG,COG1717@NOG,arCOG00781@arNOG		Cytoplasmic
NAS2_0324	142 CDS	LSU ribosomal protein L19e		K02885	Archaea	J		0FC7D@creNOG,COG2147@NOG,arCOG04089@arNOG		Cytoplasmic
NAS2_0325	159 CDS	LSU ribosomal protein L5e		K02881	TACK group	J		0FBZZ@creNOG,COG0256@NOG,arCOG04088@arNOG		Cytoplasmic
NAS2_0326	189 CDS	SSU ribosomal protein S2e		K02988	root;	J		1CBS5@thaNOG,COG0098@NOG,arCOG04087@arNOG		Cytoplasmic
NAS2_0327	161 CDS	LSU ribosomal protein L7e		K02907	root;	J		0KTH0@eurNOG,COG1841@NOG,arCOG04086@arNOG		Cytoplasmic
NAS2_0328	150 CDS	LSU ribosomal protein L27Ae		K02876	Thaumarchaeota	J		0FCGZ@creNOG,COG0200@NOG,arCOG00779@arNOG		Cytoplasmic
NAS2_0329	466 CDS	Preprotein translocase secY subunit		K03076	Thaumarchaeota	U		1CBND@thaNOG,COG2001@NOG,arCOG04169@arNOG		CytoplasmicMembrane
NAS2_0330	184 CDS	Adenylate kinase, archaeal type	2.7,4.3	K00939	Archaea	F		0KSRP@eurNOG,1CCTM@thaNOG,COG2019@NOG,arCOG01039@arNOG		Cytoplasmic
NAS2_0331	167 CDS	hypothetical protein			Bathymarchaeota					CytoplasmicMembrane
NAS2_0332	196 CDS	Cytidylate kinase	2.7,4.25	K00945	Thaumarchaeota	F		1CBAX@thaNOG,COG1102@NOG,arCOG01037@arNOG		Cytoplasmic
NAS2_0333	355 CDS	irRNA pseudouridine 55 synthase	4.2,1.70	K11131	Thaumarchaeota	J		0FB4Q@creNOG,COG0130@NOG,arCOG00987@arNOG		Cytoplasmic
NAS2_0334	irRNA	irRNA-Ser								
NAS2_0335	98 CDS	hypothetical protein			Thaumarchaeota					Unknown
NAS2_0336	101 CDS	hypothetical protein			Thaumarchaeota	K		0FDAZ@creNOG,COG5625@NOG,arCOG04189@arNOG		CytoplasmicMembrane
NAS2_0337	255 CDS	Glucose-1-phosphate thymidyltransferase	2.7,7.24	K00973	Thaumarchaeota	M		0KT30@eurNOG,COG1208@NOG,arCOG00666@arNOG		CytoplasmicMembrane
NAS2_0338	141 CDS	Ferredoxin			Archaea	C		0KTHJ@eurNOG,1CCS0@thaNOG,COG1146@NOG,arCOG04548@arNOG		Cytoplasmic
NAS2_0339	393 CDS	Uncharacterized protein		K09123	Thaumarchaeota			0KRCE@eurNOG,0WKE7@methaNOG,COG1679@NOG,arCOG04278@arNOG		Unknown
NAS2_0340	584 CDS	Glucosamine-fructose-6-phosphate aminotransferase [isomerizing]	2.6,1.16	K00820	Archaea	M	MER0070556	0KRF5@eurNOG,1CDV7@thermNOG,COG0449@NOG,arCOG00057@arNOG		Cytoplasmic
NAS2_0341	317 CDS	hypothetical protein			Archaea					Cytoplasmic
NAS2_0342	160 CDS	SSU ribosomal protein S18e		K02952	Archaea	J		0FC36@creNOG,COG0099@NOG,arCOG01722@arNOG		Cytoplasmic
NAS2_0343	168 CDS	SSU ribosomal protein S9e		K02966	TACK group	J		0FC64@creNOG,COG0522@NOG,arCOG04239@arNOG		Cytoplasmic
NAS2_0344	140 CDS	SSU ribosomal protein S14e		K02948	Archaea	J		1CBZN@thaNOG,COG0100@NOG,arCOG04240@arNOG		Cytoplasmic
NAS2_0345	264 CDS	DNA-directed RNA polymerase subunit D	2.7,7.6	K03047	TACK group	K		0FBJB@creNOG,COG0202@NOG,arCOG04241@arNOG		Cytoplasmic
NAS2_0346	117 CDS	LSU ribosomal protein L18e		K02883	Archaea	J		0FCJU@creNOG,COG1727@NOG,arCOG00780@arNOG		Cytoplasmic
NAS2_0347	147 CDS	LSU ribosomal protein L13Ae		K02871	Archaea	J		1CBV2@thaNOG,COG0102@NOG,arCOG04242@arNOG		Cytoplasmic
NAS2_0348	135 CDS	SSU ribosomal protein S16e		K02996	Archaea	J		1CBPJ@thaNOG,COG0103@NOG,arCOG04243@arNOG		Cytoplasmic
NAS2_0349	42 CDS	hypothetical protein			Not assigned					Extracellular
NAS2_0350	59 CDS	DNA-directed RNA polymerase subunit N	2.7,7.6	K03058	Archaea	K		0FD6Z@creNOG,COG1644@NOG,arCOG04244@arNOG		Cytoplasmic
NAS2_0351	414 CDS	Enolase	4.2,1.11	K01689	Archaea	G		0FB6C@creNOG,COG0148@NOG,arCOG01169@arNOG		Cytoplasmic
NAS2_0352	217 CDS	SSU ribosomal protein Sae		K02967	Thaumarchaeota	J		1CBPQ@thaNOG,COG0052@NOG,arCOG04245@arNOG		Cytoplasmic
NAS2_0353	280 CDS	Candidate gene for the hypothesized phosphomevalonate decarboxylase, COG1355	K06990	Archaea				0KRQ7@eurNOG,COG1355@NOG,arCOG01728@arNOG		Unknown

NAS2_0354	306 CDS	Mevalonate kinase	2.7.1.36	K00869	Archaea	I	0FBU3@creNOG,COG1577@NOG,arCOG01028@arNOG	Cytoplasmic	
NAS2_0355	245 CDS	Isopentenyl phosphate kinase		K06981	cellular organisms		0KSPV@eurNOG,COG1608@NOG,arCOG00860@arNOG	Unknown	
NAS2_0356	356 CDS	Isopentenyl-diphosphate delta-isomerase, FMN-dependent	5.3.3.2	K01823	Archaea	C	0FB0D@creNOG,COG1304@NOG,arCOG00613@arNOG	Cytoplasmic	
NAS2_0357	339 CDS	Dimethylallyltransferase	2.5.1.1	K13787	TACK group	H	0FBMR@creNOG,COG0142@NOG,arCOG01726@arNOG	Cytoplasmic	
NAS2_0358	590 CDS	Glutamyl-tRNA synthetase	6.1.1.24	K01885	Archaea	J	0KRKE@eurNOG,1CEB0@thermNOG,COG0008@NOG,arCOG04302@arNOG	Cytoplasmic	
NAS2_0359	117 CDS	LSU ribosomal protein L7Ae		K02936	Archaea	J	0FBZQ@creNOG,COG1358@NOG,arCOG01751@arNOG	Cytoplasmic	
NAS2_0360	55 CDS	SSU ribosomal protein S28e		K02979	Archaea	J	0FCP0@creNOG,COG2053@NOG,arCOG04314@arNOG	Cytoplasmic	
NAS2_0361	67 CDS	LSU ribosomal protein L24e		K02896	Archaea	J	0FCWC@creNOG,COG2075@NOG,arCOG01950@arNOG	Cytoplasmic	
NAS2_0362	171 CDS	Nucleoside diphosphate kinase	2.7.4.6	K00940	cellular organisms	F	0KT13@eurNOG,1CCV8@theNOG,COG0105@NOG,arCOG04313@arNOG	Cytoplasmic	
NAS2_0363	594 CDS	Translation initiation factor 2		K03243	Archaea	J	0FAYS@creNOG,COG0532@NOG,arCOG01560@arNOG	Cytoplasmic	
NAS2_0364	127 CDS	SSU ribosomal protein S6e		K02991	Archaea	J	0KTVY@eurNOG,COG2125@NOG,arCOG01946@arNOG	Cytoplasmic	
NAS2_0365	414 CDS	Eukaryotic translation initiation factor 2 gamma subunit		K03242	Archaea	J	1CB57@thaNOG,COG5257@NOG,arCOG01563@arNOG	Cytoplasmic	
NAS2_0366	134 CDS	hypothetical protein		K07158	Archaea			Cytoplasmic	
NAS2_0367	814 CDS	Thermopsin precursor	3.4.23.42	K01385	Crenarchaeota		MER0324275 0FAZ6@creNOG,10GSG@NOG,arCOG02511@arNOG,arCOG03672@arNOG	Extracellular	Peptidase
NAS2_0368	193 CDS	DNA-directed RNA polymerase subunit E'	2.7.7.6	K03049	TACK group	K	1CBN2@thaNOG,COG1095@NOG,arCOG00675@arNOG	Cytoplasmic	
NAS2_0369	62 CDS	DNA-directed RNA polymerase subunit E''		K03050	Archaea	K	1CC6J@thaNOG,COG2093@NOG,arCOG04077@arNOG	Cytoplasmic	
NAS2_0370	155 CDS	UPF0218 protein		K09735	Archaea	J	0KSZA@eurNOG,0RH9W@halNOG,COG1909@NOG,arCOG04076@arNOG	Cytoplasmic	
NAS2_0371	132 CDS	hypothetical protein		K02974	Archaea			Unknown	
NAS2_0372	320 CDS	Carbamate kinase	2.7.2.2	K00926	Archaea	E	0KS3@eurNOG,1CEB2@thermNOG,COG0549@NOG,arCOG00863@arNOG	Cytoplasmic	
NAS2_0373	224 CDS	hypothetical protein		Archaea			1114D@NOG,1CBQN@thaNOG,arCOG08681@arNOG	Cytoplasmic	
NAS2_0374	544 CDS	222aa long hypothetical protein		Archaea			0FDCV@creNOG,COG3642@NOG,arCOG01185@arNOG	Cytoplasmic	
NAS2_0375	73 CDS	SSU ribosomal protein S27Ae		K02977	cellular organisms	J	0KV5T@eurNOG,0WR5S@methNOG,COG1998@NOG,arCOG04183@arNOG	Cytoplasmic	
NAS2_0376	201 CDS	hypothetical protein		Crenarchaeota			0FBVY@creNOG,COG5493@NOG,arCOG01422@arNOG	Cytoplasmic	
NAS2_0377	699 CDS	Conserved protein		Archaea				Unknown	
NAS2_0378	1333 CDS	1082aa long hypothetical protein		Archaea	O	MER0182072 0FBJP@creNOG,COG4934@NOG,arCOG03665@arNOG	CytoplasmicMembrane	Peptidase	
NAS2_0379	68 CDS	hypothetical protein		Not assigned				CytoplasmicMembrane	
NAS2_0380	208 CDS	hypothetical protein		Crenarchaeota	N			CytoplasmicMembrane	
NAS2_0381	169 CDS	Ribosomal-protein-S18p-alanine acetyltransferase		K03789	Thaumarchaeota		0FC3Y@creNOG,COG0456@NOG,arCOG00833@arNOG	Cytoplasmic	
NAS2_0382	721 CDS	Cell division protein FtsH		K13525	Thaumarchaeota	O	1CBCC@thaNOG,COG0464@NOG,arCOG01308@arNOG	Cytoplasmic	
NAS2_0383	574 CDS	Lyxyl-tRNA synthetase	6.1.1.6	K04566	Archaea	J	1CBNP@thaNOG,COG1384@NOG,arCOG00485@arNOG	Cytoplasmic	
NAS2_0384	194 CDS	GMP synthase [glutamine-hydrolyzing] subunit A		K01951	Thaumarchaeota	F	MER0183716 0KSUX@eurNOG,0WM2P@methaNOG,COG1339@NOG,arCOG01904@arNOG	Cytoplasmic	
NAS2_0385	268 CDS	DNA-binding HTH domain in riboflavin kinase		K07732	Archaea	H		Cytoplasmic	
NAS2_0386	190 CDS	hypothetical protein		TACK group				CytoplasmicMembrane	
NAS2_0387	200 CDS	Fumarate hydratase class I, aerobic	4.2.1.32	K01678	Archaea	C	0FB39@creNOG,COG1838@NOG,arCOG04406@arNOG	Cytoplasmic	FUM
NAS2_0388	301 CDS	Fumarate hydratase class I, aerobic	4.2.1.2	K01677	Archaea	C	0FBNY@creNOG,COG1951@NOG,arCOG04407@arNOG	Cytoplasmic	FUM
NAS2_0389	497 CDS	Radical SAM domain protein		TACK group			0FB54@creNOG,COG1032@NOG,arCOG01356@arNOG	Unknown	
NAS2_0390	523 CDS	Radical SAM domain heme biosynthesis protein		Thaumarchaeota			0FAZ4@creNOG,COG0535@NOG,arCOG00940@arNOG	Cytoplasmic	
NAS2_0391	514 CDS	Glycogen phosphorylase	2.4.1.1	K00688	Crenarchaeota	G	0FB5I@creNOG,COG0058@NOG,arCOG01421@arNOG	Unknown	
NAS2_0392	488 CDS	Alpha-amylase	3.2.1.1	K07405	Archaea	G	0FB3@creNOG,COG1449@NOG,arCOG03278@arNOG	Extracellular	
NAS2_0393	681 CDS	hypothetical protein		Thaumarchaeota	G		COG3408@NOG,arCOG03287@arNOG	Unknown	
NAS2_0394	77 CDS	hypothetical protein		Not assigned				Cytoplasmic	
NAS2_0395	187 CDS	hypothetical protein		Not assigned				Unknown	
NAS2_0396	411 CDS	Glycosyltransferase		cellular organisms	M		0FCH9@creNOG,COG0438@NOG,arCOG01403@arNOG	Cytoplasmic	
NAS2_0397	412 CDS	Glycosyltransferase		Archaea	M		02TBJ@arNOG,0M20T@eurNOG,0WPM9@methaNOG,COG0438@NOG	Unknown	
NAS2_0398	tRNA	tRNA-Arg							
NAS2_0399	153 CDS	hypothetical protein		Crenarchaeota			0FDPA@creNOG,0Y508@NOG,arCOG05683@arNOG	Unknown	
NAS2_0400	634 CDS	Arginyl-tRNA synthetase	6.1.1.19	K01887	Thaumarchaeota	J	1CB2S@thaNOG,COG0018@NOG,arCOG00487@arNOG	Cytoplasmic	
NAS2_0401	40 CDS	hypothetical protein		Not assigned				Cytoplasmic	
NAS2_0402	371 CDS	S-adenosylhomocysteine deaminase	3.5.4.28	K12960	Thaumarchaeota	F	MER0861776 COG0402@NOG,arCOG00695@arNOG	Cytoplasmic	
NAS2_0403	562 CDS	Succinate dehydrogenase flavoprotein subunit	1.3.99.1	K00239	cellular organisms	C	0FB6Z@creNOG,COG1053@NOG,arCOG00571@arNOG	CytoplasmicMembrane	SDH
NAS2_0404	157 CDS	Succinate dehydrogenase cytochrome b-556 subunit		K00241	Thaumarchaeota	C	0FC2W@creNOG,COG2009@NOG,arCOG02244@arNOG	CytoplasmicMembrane	SDH
NAS2_0405	119 CDS	Succinate dehydrogenase hydrophobic membrane anchor protein		K00242	Thaumarchaeota	C	0Y5DW@NOG,1CC3B@thaNOG,arCOG04162@arNOG	CytoplasmicMembrane	SDH
NAS2_0406	302 CDS	Succinate dehydrogenase iron-sulfur protein	1.3.99.1	K00240	Thaumarchaeota	C	1CBH7@thaNOG,COG0479@NOG,arCOG00962@arNOG	CytoplasmicMembrane	SDH
NAS2_0407	851 CDS	Archaeal DNA polymerase I	2.7.7.7	K02319	Thaumarchaeota	L	0FAZ4@creNOG,COG0417@NOG,arCOG00328@arNOG	Cytoplasmic	
NAS2_0408	359 CDS	Tyrosyl-tRNA synthetase	6.1.1.1	K01866	Thaumarchaeota	J	0FB5C@creNOG,COG0162@NOG,arCOG01886@arNOG	Cytoplasmic	
NAS2_0409	46 CDS	hypothetical protein		K03059	Archaea	K		Cytoplasmic	
NAS2_0410	347 CDS	Hydroxymethylglutaryl-CoA synthase	2.3.3.10	K01641	Archaea	I	0FAYU@creNOG,COG3425@NOG,arCOG01767@arNOG	Cytoplasmic	
NAS2_0411	378 CDS	nonspecific lipid-transfer protein		K00626	cellular organisms	I	0FBDC@creNOG,COG0183@NOG,arCOG01278@arNOG	Cytoplasmic	
NAS2_0412	132 CDS	conserved protein associated with acetyl-CoA C-acyltransferase		K07068	Archaea		0FCCA@creNOG,COG1545@NOG,arCOG01285@arNOG	Cytoplasmic	
NAS2_0413	184 CDS	ADP-ribose pyrophosphatase	3.6.1.13	K01515	cellular organisms	L	0FCGD@creNOG,COG0494@NOG,arCOG01073@arNOG	Cytoplasmic	
NAS2_0414	279 CDS	5-nucleotidase SurE	3.1.3.5	K03787	cellular organisms	F	0FBSR@creNOG,COG0496@NOG,arCOG02303@arNOG	Cytoplasmic	
NAS2_0415	88 CDS	hypothetical protein		Not assigned				CytoplasmicMembrane	
NAS2_0416	221 CDS	NADPH-dependent F420 reductase		K06988	TACK group		0KTEJ@eurNOG,COG2085@NOG,arCOG00457@arNOG	Unknown	
NAS2_0417	120 CDS	hypothetical protein		Not assigned				Cytoplasmic	
NAS2_0418	267 CDS	Agmatinase	3.5.3.11	K01480	Archaea	E	0FB7E@creNOG,COG0010@NOG,arCOG01700@arNOG	Cytoplasmic	
NAS2_0419	152 CDS	MutT/nudix family protein		cellular organisms	L		0FCP@creNOG,COG0494@NOG,arCOG01072@arNOG	Cytoplasmic	
NAS2_0420	231 CDS	Endonuclease III	4.2.99.18	K10773	TACK group	L	0FBV8@creNOG,COG0177@NOG,arCOG00459@arNOG	Cytoplasmic	
NAS2_0421	631 CDS	Threonyl-tRNA synthetase	6.1.1.3	K01868	TACK group	J	02H1Y@arNOG,0KRJ9@eurNOG,COG0441@NOG,arCOG00401@arNOG	Cytoplasmic	
NAS2_0422	295 CDS	Serine/threonine-protein phosphatase PP2A catalytic subunit	3.1.3.16		TACK group	T	0FB5D@creNOG,COG0639@NOG,arCOG01143@arNOG	Cytoplasmic	
NAS2_0423	184 CDS	hypothetical protein		Thaumarchaeota	L			Cytoplasmic	
NAS2_0424	328 CDS	hypothetical protein		K07097	Thaumarchaeota		0FC0W@creNOG,COG2404@NOG,arCOG00423@arNOG	Cytoplasmic	
NAS2_0425	112 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic	
NAS2_0426	325 CDS	hypothetical protein		Archaea			0KXFD@eurNOG,0RG0Y@halNOG,COG0546@NOG,arCOG04692@arNOG	Cytoplasmic	
NAS2_0427	274 CDS	hypothetical protein		Thaumarchaeota				Unknown	
NAS2_0428	329 CDS	Transcription initiation factor B		K03124	Thaumarchaeota	K	1CB4G@thaNOG,COG1405@NOG,arCOG01981@arNOG	Cytoplasmic	
NAS2_0429	108 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic	
NAS2_0430	176 CDS	hypothetical protein		K01494	Thaumarchaeota	F		Cytoplasmic	
NAS2_0431	103 CDS	Translation initiation factor SUI1-related protein		K03113	Thaumarchaeota	J	0KTD5@eurNOG,0WMCX@methaNOG,COG0023@NOG,arCOG04223@arNOG	Cytoplasmic	
NAS2_0432	193 CDS	hypothetical protein		Not assigned				CytoplasmicMembrane	
NAS2_0433	95 CDS	hypothetical protein		Archaea				Cytoplasmic	
NAS2_0434	123 CDS	hypothetical protein		Archaea			02HVM@arNOG,0KYRH@eurNOG,COG0727@NOG,arCOG02579@arNOG	Cytoplasmic	
NAS2_0435	189 CDS	Nicotinamide	3.5.1.19	K06940	Thaumarchaeota	Q	0FBUB@creNOG,COG1335@NOG,arCOG01943@arNOG	Cytoplasmic	
NAS2_0436	253 CDS	FIG006285: ICC-like protein phosphoesterase		K06953	Thaumarchaeota		COG1407@NOG,arCOG01150@arNOG	Cytoplasmic	
NAS2_0437	tRNA	tRNA-Thr							
NAS2_0438	455 CDS	Sugar transport protein		Thaumarchaeota	G		0KSGN@eurNOG,0XR5P@NOG,1CCMT@theNOG,arCOG02687@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_0439	146 CDS	Dinitrogenase iron-molybdenum cofactor biosynthesis		Archaea			0KTVN@eurNOG,1CEXA@thermNOG,COG1433@NOG,arCOG02734@arNOG	Cytoplasmic	
NAS2_0440	270 CDS	hypothetical protein		Thaumarchaeota			0M1W1@eurNOG,1CFCG@thermNOG,COG2512@NOG,arCOG00374@arNOG	Unknown	
NAS2_0441	381 CDS	Transport protein, permease		Crenarchaeota	G		0FBYI@creNOG,COG0477@NOG,arCOG00141@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_0442	301 CDS	UDP-glucose 4-epimerase	5.1.3.2	K01784	Crenarchaeota	M	0FAXU@creNOG,COG0451@NOG,arCOG01369@arNOG	Cytoplasmic	

NAS2_0443	473 CDS	UbiD family decarboxylase associated with menaquinone via futasiosine	K03182	Crenarchaeota	H	0FBEM@creNOG,COG0043@NOG,arCOG01671@arNOG			Cytoplasmic
NAS2_0444	386 CDS	hypothetical protein		Crenarchaeota				Transporter (MFS)	CytoplasmicMembrane
NAS2_0445	314 CDS	Menaquinone via futasiosine polyprenyltransferase	K02548	Thaumarchaeota	H	0FCD9@creNOG,COG1575@NOG,arCOG00480@arNOG			CytoplasmicMembrane
NAS2_0446	258 CDS	hypothetical protein		Not assigned					CytoplasmicMembrane
NAS2_0447	305 CDS	3-hydroxyisobutyrate dehydrogenase	1.1.1.31	K00020	cellular organisms	I	0FBSP@creNOG,COG2084@NOG,arCOG00247@arNOG		Unknown
NAS2_0448	401 CDS	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K15016	Crenarchaeota		0FB17@creNOG,COG1024@NOG,COG1250@NOG,arCOG00249@arNOG		Cytoplasmic
NAS2_0449	385 CDS	Aspartate aminotransferase	2.6.1.1	K10907	Archaea	E	0KRFG@eurNOG,1CEN6@eurNOG,COG0436@arNOG,arCOG01130@arNOG		Unknown
NAS2_0450	493 CDS	Sarcosine oxidase alpha subunit	1.5.3.1	K00302	Archaea		02H6@creNOG,0KVV3@eurNOG,COG00446@NOG,arCOG01294@arNOG		AT (Family I)
NAS2_0451	180 CDS	putative polyferredoxin		Crenarchaeota	C	0KTZC@eurNOG,COG1142@NOG,arCOG05744@arNOG			Cytoplasmic
NAS2_0452	105 CDS	hypothetical protein		cellular organisms	E				Cytoplasmic
NAS2_0453	373 CDS	Sarcosine oxidase beta subunit	1.5.3.1	K00303	Thaumarchaeota	E	02GWZ@arcNOG,0KTSM@eurNOG,COG0685@NOG,arCOG00755@arNOG		Cytoplasmic
NAS2_0454	230 CDS	hypothetical protein		Archaea					Cytoplasmic
NAS2_0455	251 CDS	COG2047: Uncharacterized protein		TACK group		0KRVG@eurNOG,0WKM8@methaNOG,COG2047@NOG,arCOG00348@arNOG			Cytoplasmic
NAS2_0456	511 CDS	Uncharacterized protein		Crenarchaeota	C	0FBP3@creNOG,COG1032@NOG,arCOG01355@arNOG			Cytoplasmic
NAS2_0457	246 CDS	Phosphoesterase		Thaumarchaeota		0KSC6@eurNOG,0WK10@methaNOG,COG1407@NOG,arCOG01150@arNOG			Cytoplasmic
NAS2_0458	359 CDS	RNA 3'-terminal phosphate cyclase	6.5.1.4	K01974	TACK group	A	0FB1A@creNOG,COG0430@NOG,arCOG04125@arNOG		Cytoplasmic
NAS2_0459	408 CDS	Nicotinate phosphoribosyltransferase	2.4.2.11	K00763	Thaumarchaeota	H	0KS6H@eurNOG,1CDS8@thermNOG,COG1488@NOG,arCOG01481@arNOG		Cytoplasmic
NAS2_0460	172 CDS	hypothetical protein		Thaumarchaeota		0KRJL@eurNOG,COG1793@NOG,arCOG01347@arNOG			CytoplasmicMembrane
NAS2_0461	546 CDS	ATP-dependent DNA ligase	6.5.1.1	K10747	cellular organisms	L	1CB3T@thaNOG,COG0644@NOG,arCOG00570@arNOG		Cytoplasmic
NAS2_0462	342 CDS	Menaquinone-specific polyprenyl reductase		Crenarchaeota		0FB1K@creNOG,COG0446@NOG,arCOG01069@arNOG			Cytoplasmic
NAS2_0463	456 CDS	FAD-dependent pyridine nucleotide-disulphide oxidoreductase		K18367	Crenarchaeota		0KRFG@eurNOG,0WKCH@methaNOG,COG0436@NOG,arCOG01130@arNOG		Nsr
NAS2_0464	380 CDS	Aspartate aminotransferase	2.6.1.1	K00812	root;	E			AT (Family I)
NAS2_0465	52 CDS	hypothetical protein		Not assigned					Cytoplasmic
NAS2_0466	109 CDS	Methionyl-tRNA synthetase	6.1.1.10	K06878	cellular organisms	J	1CBZK@thaNOG,COG0073@NOG,arCOG01136@arNOG		Cytoplasmic
NAS2_0467	395 CDS	amidohydrolase		K12960	Thaumarchaeota	F	COG0402@NOG,arCOG00695@arNOG		Cytoplasmic
NAS2_0468	416 CDS	rRNA and rRNA cytosine-C5-methylase Type 1		K03500	Thaumarchaeota	J	0FB5Z@creNOG,COG0144@NOG,arCOG00975@arNOG		Cytoplasmic
NAS2_0469	178 CDS	Adenylate cyclase	4.6.1.1	K05873	Archaea	F	0FCY1@creNOG,COG1437@NOG,arCOG01723@arNOG		Cytoplasmic
NAS2_0470	422 CDS	hypothetical protein		Archaea		0FBMD@creNOG,COG1341@NOG,arCOG04127@arNOG			Cytoplasmic
NAS2_0471	147 CDS	CBS domain protein		cellular organisms		02HKH@eurNOG,0KTGA@eurNOG,COG0517@NOG,arCOG00606@arNOG			Cytoplasmic
NAS2_0472	475 CDS	DNA helicase		Archaea	L	0KRJL@eurNOG,COG1061@NOG,arCOG009874@arNOG			Cytoplasmic
NAS2_0473	455 CDS	hypothetical protein		Archaea		0KSRK@eurNOG,COG3372@NOG,arCOG04356@arNOG			Cytoplasmic
NAS2_0474	349 CDS	phosphate regulatory protein homolog		Thaumarchaeota	P	0KR94@eurNOG,0WKD.J@methaNOG,COG0704@NOG,arCOG00318@arNOG			Cytoplasmic
NAS2_0475	368 CDS	Cytosolic Fe-S cluster assembling factor NBP35		K03593	cellular organisms	D	1CBHE@thaNOG,COG0489@NOG,arCOG00585@arNOG		CytoplasmicMembrane
NAS2_0476	262 CDS	Coenzyme F420-0-L-glutamate ligase		K12234	cellular organisms		0KSS3@eurNOG,0WRVN@metNOG,COG1478@NOG,arCOG02714@arNOG		Cytoplasmic
NAS2_0477	312 CDS	Lactyl (2) diphospho-(5')guanosine:7,8-didemethyl-8-hydroxy-5'-deazariboflavin 2-ph	K11212	cellular organisms		0KS1M@eurNOG,COG0391@NOG,arCOG04395@arNOG			Cytoplasmic
NAS2_0478	77 CDS	hypothetical protein		Not assigned					CytoplasmicMembrane
NAS2_0479	317 CDS	Deoxyhypusine synthase	2.5.1.46	K00809	Archaea	O	0FBP9@creNOG,COG1899@NOG,arCOG04142@arNOG		Cytoplasmic
NAS2_0480	339 CDS	Galactose-1-phosphate uridylyltransferase	2.7.7.10	K00965	Thaumarchaeota	G	1CB1A@thaNOG,COG1085@NOG,arCOG00422@arNOG		Cytoplasmic
NAS2_0481	223 CDS	Xanthine-guanine phosphoribosyltransferase	2.4.2.22	K07101	Archaea		0FCPU@creNOG,COG2236@NOG,arCOG00040@arNOG		Unknown
NAS2_0482	421 CDS	Adenylosuccinate synthetase	6.3.4.4	K01939	cellular organisms	F	0KREU@eurNOG,1CDDV@therNOG,COG0104@NOG,arCOG04387@arNOG		Cytoplasmic
NAS2_0483	470 CDS	Adenylosuccinate lyase	4.3.2.2	K01756	cellular organisms	F	0FBZ1@creNOG,COG0015@NOG,arCOG01747@arNOG		Cytoplasmic
NAS2_0484	110 CDS	hypothetical protein		Archaea	J				Unknown
NAS2_0485	121 CDS	hypothetical protein		Archaea					Unknown
NAS2_0486	49 CDS	hypothetical protein		Not assigned					Cytoplasmic
NAS2_0487	412 CDS	Diaminopimelate decarboxylase	4.1.1.20	K01586	Archaea	E	0KRVR@eurNOG,0WQB0@methNOG,COG0019@NOG,arCOG02268@arNOG		Cytoplasmic
NAS2_0488	69 CDS	hypothetical protein		Thaumarchaeota					Cytoplasmic
NAS2_0489	420 CDS	2,3-bisphosphoglycerate-independent phosphoglycerate mutase, arch	5.4.2.1	K15635	cellular organisms	G	0FB5X@creNOG,COG3635@NOG,arCOG01696@arNOG		PGAM
NAS2_0490	60 CDS	hypothetical protein		No hits					Cytoplasmic
NAS2_0491	431 CDS	Aspartyl-tRNA synthetase	6.1.1.23	K01876	Thaumarchaeota	J	1CBGC@thaNOG,COG0017@NOG,arCOG00406@arNOG		Cytoplasmic
NAS2_0492	90 CDS	hypothetical protein		K02435	Thaumarchaeota	U			Cytoplasmic
NAS2_0493	476 CDS	Aspartyl-tRNA(Asn) amidotransferase subunit A	6.3.5.7	K02433	cellular organisms	J	0FB0E@creNOG,COG0154@NOG,arCOG01717@arNOG		Cytoplasmic
NAS2_0494	342 CDS	Radical SAM superfamily protein		Thaumarchaeota	L	0KSTY@eurNOG,0WN4.J@methaNOG,COG1533@NOG,arCOG01290@arNOG			Cytoplasmic
NAS2_0495	498 CDS	Aspartyl-tRNA(Asn) amidotransferase subunit B	6.3.5.6	K02434	Thaumarchaeota	L	0FB4F@creNOG,COG0064@NOG,arCOG01719@arNOG		Cytoplasmic
NAS2_0496	465 CDS	hypothetical protein		K07496	root;	J	0FC7J@creNOG,COG0675@NOG,arCOG00693@arNOG		Cytoplasmic
NAS2_0497	227 CDS	methyltransferase		K03183	Archaea	H	1CB3C@thaNOG,COG2226@NOG,arCOG04348@arNOG		CytoplasmicMembrane
NAS2_0498	280 CDS	NAD(P)HX epimerase		K17758,K177	Archaea	G	1CB60@thaNOG,COG0063@NOG,arCOG00018@arNOG		Cytoplasmic
NAS2_0499	141 CDS	Uncharacterized protein		Thaumarchaeota		0FCC1@creNOG,COG0432@NOG,arCOG04214@arNOG			Cytoplasmic
NAS2_0500	414 CDS	Phosphopantothenoacylcysteine decarboxylase	6.3.2.5	K13038	cellular organisms	H	0FBJJ@creNOG,COG0452@NOG,arCOG01704@arNOG		Cytoplasmic
NAS2_0501	248 CDS	Aliphatic amidase AmiE	3.5.1.4	Archaea		0FDR1@creNOG,COG0388@NOG,arCOG00062@arNOG			Cytoplasmic
NAS2_0502	191 CDS	hypothetical protein		Archaea					CytoplasmicMembrane
NAS2_0503	353 CDS	hypothetical protein		TACK group		0FBGI@creNOG,COG0535@NOG,arCOG00938@arNOG			Unknown
NAS2_0504	382 CDS	Alcohol dehydrogenase	1.1.1.1	Thaumarchaeota	C	0FBUG@creNOG,COG1454@NOG,arCOG00984@arNOG			Cytoplasmic
NAS2_0505	378 CDS	6-phospho-3-hexuloisomerase		Thaumarchaeota		0FBX3@creNOG,COG0794@NOG,arCOG00088@arNOG			Cytoplasmic
NAS2_0506	133 CDS	PsaD-like protein involved in Fe-S cluster assembly		K08094	Thaumarchaeota		0FCIQ@creNOG,COG2151@NOG,arCOG01845@arNOG		Cytoplasmic
NAS2_0507	317 CDS	Hexokinase	2.7.1.1	K00845	Archaea	G	0FBZ2@creNOG,COG1940@NOG,arCOG04280@arNOG		GLK
NAS2_0508	200 CDS	hypothetical protein		Not assigned					Cytoplasmic
NAS2_0509	112 CDS	hypothetical protein		Not assigned					Unknown
NAS2_0510	133 CDS	Uncharacterized protein		Crenarchaeota	L	0FD06@creNOG,COG1591@NOG,arCOG00919@arNOG			Cytoplasmic
NAS2_0511	183 CDS	ATP-Cob(I)alamin adenosyltransferase	2.5.1.17	K00798	Crenarchaeota		0FD6S@creNOG,COG2096@NOG,arCOG00489@arNOG		Unknown
NAS2_0512	419 CDS	Cysteine desulfurase	2.8.1.7	K11717	cellular organisms	E	0KRW5@eurNOG,0WK4V@methaNOG,COG0520@NOG,arCOG00065@arNOG		Cytoplasmic
NAS2_0513	424 CDS	Acetylornithine deacetylase	3.5.1.16	K01438	cellular organisms	E	0KBW9@eurNOG,COG0624@NOG,arCOG01107@arNOG		Unknown
NAS2_0514	448 CDS	L-Proline/Glycine betaine transporter ProP		Thaumarchaeota	G	0XQKC@NOG,arCOG02682@arNOG		Transporter (MFS)	CytoplasmicMembrane
NAS2_0515	308 CDS	Malate dehydrogenase	1.1.1.37	K00024	Archaea	C	0FBQ3@creNOG,COG0039@NOG,arCOG00246@arNOG		Cytoplasmic
NAS2_0516	169 CDS	Biotin synthesis protein BioC		cellular organisms	C	0FCWJ@creNOG,120R6@NOG,arCOG03773@arNOG			Unknown
NAS2_0517	386 CDS	Hypothetical radical SAM family enzyme in heat shock gene cluster		Bacteria	Q	0KVIN@eurNOG,1CDDF@theNOG,COG1032@NOG,arCOG01363@arNOG			Cytoplasmic
NAS2_0518	128 CDS	hypothetical protein		Thaumarchaeota		COG4345@NOG,arCOG03772@arNOG			Cytoplasmic
NAS2_0519	269 CDS	5'-methylthioadenosine phosphorylase	2.4.2.28	K00772	Crenarchaeota	F	0FB12@creNOG,COG0005@NOG,arCOG001327@arNOG		Cytoplasmic
NAS2_0520	358 CDS	Menaquinone via futasiosine step 3		Crenarchaeota	H	0FBHE@creNOG,COG1060@NOG,arCOG00656@arNOG			Cytoplasmic
NAS2_0521	360 CDS	hypothetical protein		Thaumarchaeota	H	0FB4G@creNOG,COG1060@NOG,arCOG00656@arNOG			Cytoplasmic
NAS2_0522	241 CDS	Menaquinone via futasiosine step 1		Crenarchaeota		0FCOG@creNOG,COG1427@NOG,arCOG00655@arNOG			Cytoplasmic
NAS2_0523	266 CDS	Menaquinone via futasiosine step 4		Crenarchaeota		0FBNX@creNOG,COG2107@NOG,arCOG00654@arNOG			Cytoplasmic
NAS2_0524	252 CDS	ABC-type multidrug transport system, permease component		K01992	Crenarchaeota	V	0FCS9@creNOG,COG0842@NOG,arCOG01469@arNOG		Transporter (ABC)
NAS2_0525	309 CDS	ABC transporter, ATP binding protein related protein		K01990	Archaea	V	0FBNH@creNOG,COG1131@NOG,arCOG00194@arNOG		Transporter (ABC)
NAS2_0526	262 CDS	CBS domain protein		Thaumarchaeota		0FC7I@creNOG,COG0517@NOG,arCOG00600@arNOG			Unknown
NAS2_0527	384 CDS	3-ketoacyl-CoA thiolase	2.3.1.16	K00626	Thaumarchaeota	I	0KRB2@eurNOG,0WRRD@metNOG,COG0183@NOG,arCOG01278@arNOG		Cytoplasmic
NAS2_0528	135 CDS	hypothetical protein		K07068	Archaea		0KXT2@eurNOG,COG1545@NOG,arCOG01285@arNOG		ATO
NAS2_0529	216 CDS	hypothetical protein		Archaea		0KSYB@eurNOG,COG3382@NOG,arCOG04250@arNOG			Cytoplasmic
NAS2_0530	353 CDS	Isocitrate dehydrogenase [NAD]	1.1.1.41	K00030	cellular organisms	E	02H12@creNOG,0KRW7@eurNOG,COG0473@NOG,arCOG01163@arNOG		IDH
NAS2_0531	165 CDS	Conserved protein		Thaumarchaeota	T	0FCXZ@creNOG,COG2453@NOG,arCOG03413@arNOG			Cytoplasmic

NAS2_0532	111 CDS	mannose-6-phosphate isomerase			Euryarchaeota			0FCIW@creNOG,COG1917@NOG,arCOG02994@arNOG		Cytoplasmic	
NAS2_0533	921 CDS	Leucyl-RNA synthetase	6.1.1.4	K01869	Crenarchaeota	J		0FAWK@creNOG,COG0495@NOG,arCOG00809@arNOG		Cytoplasmic	
NAS2_0534	427 CDS	Inorganic phosphate transporter		K08368	Archaea	G		0KSMU@eurNOG,0XQKC@NOG,1CCHU@theNOG,arCOG02682@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0535	540 CDS	DNA repair helicase Rad3		K10844	Crenarchaeota	L		0FC3V@creNOG,COG1199@NOG,arCOG00770@arNOG		Cytoplasmic	
NAS2_0536	451 CDS	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase			TACK group	M		0FBHU@creNOG,COG0677@NOG,arCOG00252@arNOG		Cytoplasmic	
NAS2_0537	384 CDS	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase			cellular organisms	E		0KR8V@eurNOG,COG0399@NOG,arCOG00118@arNOG		Cytoplasmic	
NAS2_0538	233 CDS	Nitroreductase family protein			cellular organisms	C		0FDN5@creNOG,COG0778@NOG,arCOG00288@arNOG		CytoplasmicMembrane	
NAS2_0539	144 CDS	hypothetical protein			cellular organisms	E				Cytoplasmic	
NAS2_0540	596 CDS	ATP-dependent DNA ligase	6.5.1.1	K10747	Archaea	L		0FB5F@creNOG,COG1793@NOG,arCOG01347@arNOG		Cytoplasmic	
NAS2_0541	309 CDS	Cation transport protein			cellular organisms	P		COG0053@NOG,arCOG01480@arNOG		CytoplasmicMembrane	
NAS2_0542	217 CDS	Formaldehyde activating enzyme		K13812	Archaea	G		0KRAA@eurNOG,0WKAE@methaNOG,COG0269@NOG,COG1795@NOG,arCOG00053@arNOG,arCOG00103@arNOG	Transporter (Other)	Cytoplasmic	
NAS2_0543	219 CDS	Phosphate transport regulator		K07220	Thaumarchaeota	P		1CB92@thaNOG,COG1392@NOG,arCOG02640@arNOG		Cytoplasmic	
NAS2_0544	182 CDS	tRNA-intron endonuclease		K01170	Archaea	J		0FCE1@creNOG,COG1676@NOG,arCOG01701@arNOG		Cytoplasmic	
NAS2_0545	253 CDS	hypothetical protein	3.1.27.9		Crenarchaeota	O		0FBP1@creNOG,COG5494@NOG,arCOG04235@arNOG		Cytoplasmic	
NAS2_0546	140 CDS	hypothetical protein			cellular organisms	Q		0FCE5@creNOG,COG0500@NOG,arCOG01631@arNOG		Cytoplasmic	
NAS2_0547	399 CDS	Glucose-1-phosphate thymidyllyltransferase	2.7.7.24		Archaea	M		COG1208@NOG,arCOG05599@arNOG		Cytoplasmic	
NAS2_0548	234 CDS	Mannose-1-phosphate guanylyltransferase	5.4.2.8	K00966	Thaumarchaeota	M		1CBCK@thaNOG,COG1208@NOG,arCOG00663@arNOG		Cytoplasmic	
NAS2_0549	254 CDS	hypothetical protein			Thaumarchaeota			COG0630@NOG,arCOG01817@arNOG		Cytoplasmic	
NAS2_0550	539 CDS	Flagella-related protein Flal		K07332	Thaumarchaeota	U		0KSD8@eurNOG,0RF6P@halNOG,COG2064@NOG,arCOG01808@arNOG		CytoplasmicMembrane	
NAS2_0551	379 CDS	hypothetical protein		K07333	TACK group	U		COG2064@NOG,arCOG01808@arNOG		CytoplasmicMembrane	
NAS2_0552	259 CDS	hypothetical protein		K07333	Archaea	U		0FD8F@creNOG,0YRWU@NOG,arCOG06883@arNOG		Cytoplasmic	
NAS2_0553	298 CDS	hypothetical protein			TACK group			0FBVQ@creNOG,COG0717@NOG,arCOG04048@arNOG		Cytoplasmic	
NAS2_0554	160 CDS	Deoxycytidine triphosphate deaminase	3.5.4.13	K01494	root;	F		0KST7A@eurNOG,0WRGI@metNOG,COG1415@NOG,arCOG04253@arNOG		Cytoplasmic	
NAS2_0555	380 CDS	hypothetical protein		K09003	cellular organisms			0KTUH@eurNOG,COG1215@NOG,arCOG01389@arNOG		Cytoplasmic	
NAS2_0556	433 CDS	glycosyl transferase, group 2 family protein			cellular organisms	M		0FCJ3@creNOG,COG2110@NOG,arCOG04225@arNOG		CytoplasmicMembrane	
NAS2_0557	173 CDS	COG2110, Macro domain, possibly ADP-ribose binding module			cellular organisms			0KR9V@eurNOG,0WRCC@metNOG,COG0136@NOG,arCOG00494@arNOG		Cytoplasmic	
NAS2_0558	353 CDS	Aspartate-semialdehyde dehydrogenase	1.2.1.11	K00133	Thaumarchaeota	E		0KRDD@eurNOG,0WK3T@methaNOG,COG1830@NOG,arCOG04044@arNOG		Cytoplasmic	FBA
NAS2_0559	263 CDS	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase		K16306	Archaea	G		COG1465@NOG,arCOG04353@arNOG		Cytoplasmic	
NAS2_0560	335 CDS	3,7-dideoxy-D-threo-hepto-2, 6-diulsonate synthase		K11646	cellular organisms	E		1CB8Q@thaNOG,COG0710@NOG,arCOG02097@arNOG		Cytoplasmic	
NAS2_0561	240 CDS	3-dehydroquinate dehydratase I	4.2.1.10	K03785	Thaumarchaeota	E		COG0517@NOG,arCOG00606@arNOG		Cytoplasmic	
NAS2_0562	141 CDS	MaoC family protein			Archaea			0KRZ8@eurNOG,COG0169@NOG,arCOG01033@arNOG		Cytoplasmic	
NAS2_0563	283 CDS	Shikimate 5-dehydrogenase I alpha	1.1.1.25	K00014	cellular organisms	E		0KR9G@eurNOG,COG1685@NOG,arCOG01025@arNOG		Unknown	
NAS2_0564	277 CDS	Shikimate kinase II	2.7.1.71	K00891	Archaea	E		COG128@NOG,arCOG04134@arNOG		Unknown	
NAS2_0565	415 CDS	5-Enolpyruvylshikimate-3-phosphate synthase	2.5.1.19	K00800	Archaea	E		COG0082@NOG,arCOG04133@arNOG		Unknown	
NAS2_0566	387 CDS	Chorismate synthase	4.2.3.5	K01736	cellular organisms	E		0KTAE@eurNOG,1CEMX@thermNOG,COG0537@NOG,arCOG00419@arNOG		Cytoplasmic	
NAS2_0567	430 CDS	hypothetical protein			Archaea	E		0FC8B@creNOG,COG0131@NOG,arCOG04398@arNOG		Unknown	
NAS2_0568	168 CDS	HIT family protein		K19710	cellular organisms	F				Cytoplasmic	
NAS2_0569	212 CDS	Imidazoleglycerol-phosphate dehydratase	4.2.1.19	K01693	cellular organisms	E		0FBES@creNOG,COG0731@NOG,arCOG04174@arNOG		Cytoplasmic	
NAS2_0570	303 CDS	hypothetical protein			TACK group			0KR9J@eurNOG,1CCUW@theNOG,COG0457@NOG,arCOG03038@arNOG		Unknown	
NAS2_0571	365 CDS	Fe-S oxidoreductase		K15449	Archaea	C		0FC05@creNOG,COG2428@NOG,arCOG04202@arNOG		Cytoplasmic	
NAS2_0572	285 CDS	GTP cyclohydrolase III			Bacteria			0FB4B@creNOG,COG0402@NOG,arCOG00692@arNOG		Unknown	
NAS2_0573	221 CDS	GTP cyclohydrolase III	3.5.4.29	K08096	Archaea	F	MER0182099	0FCBD@creNOG,COG1985@NOG,arCOG01484@arNOG		CytoplasmicMembrane	
NAS2_0574	373 CDS	Adenosine deaminase	3.5.4.4		Archaea			COG1402@NOG,arCOG04536@arNOG		Unknown	
NAS2_0575	207 CDS	5-amino-6-(5-phosphoribosylamino)uracil reductase	1.1.1.193	K14654	Crenarchaeota	H		0KR6E@eurNOG,COG1060@NOG,arCOG00657@arNOG		Unknown	
NAS2_0576	215 CDS	Creatinine amidohydrolase	3.5.2.10	K01470	Archaea			0KRH1@eurNOG,0WRN5@metNOG,COG1060@NOG,arCOG00656@arNOG		Cytoplasmic	
NAS2_0577	386 CDS	7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase subunit 1		K11779	Crenarchaeota	H		COG2050@NOG,arCOG00777@arNOG		Cytoplasmic	
NAS2_0578	377 CDS	7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase subunit 1		K11781	Crenarchaeota	H		0FC0H@creNOG,COG1573@NOG,arCOG00905@arNOG		Cytoplasmic	
NAS2_0579	139 CDS	hypothetical protein		K02614	cellular organisms					Cytoplasmic	
NAS2_0580	221 CDS	Uracil-DNA glycosylase, family 4		K02334	TACK group	L				Cytoplasmic	
NAS2_0581	150 CDS	hypothetical protein			Crenarchaeota					CytoplasmicMembrane	
NAS2_0582	409 CDS	hypothetical protein			Thaumarchaeota			0FB4K@creNOG,COG0037@NOG,arCOG00042@arNOG		CytoplasmicMembrane	
NAS2_0583	66 CDS	tRNA(U54)-2-thioribothymidine synthetase			Crenarchaeota	D				Cytoplasmic	
NAS2_0584	150 CDS	hypothetical protein			Crenarchaeota					CytoplasmicMembrane	
NAS2_0585	395 CDS	hypothetical protein			Thaumarchaeota					Unknown	
NAS2_0586	320 CDS	tRNA(U54)-2-thioribothymidine synthetase			Crenarchaeota	D		0FB4K@creNOG,COG0037@NOG,arCOG00042@arNOG		Cytoplasmic	
NAS2_0587	134 CDS	Transcriptional regulator, PadR family			Thaumarchaeota	K		0FFIW@creNOG,COG1695@NOG,arCOG00001@arNOG		Cytoplasmic	
NAS2_0588	337 CDS	hypothetical protein		K09157	Crenarchaeota			0FCAQ@creNOG,COG2848@NOG,arCOG04321@arNOG		Unknown	
NAS2_0589	189 CDS	PAP2 family protein		K19302	cellular organisms	I				CytoplasmicMembrane	
NAS2_0590	164 CDS	hypothetical protein			No hits					Unknown	
NAS2_0591	370 CDS	Dihydropterolate synthase	2.5.1.15	K00796	Archaea	H		COG0294@NOG,arCOG02817@arNOG		Cytoplasmic	
NAS2_0592	111 CDS	Periplasmic divalent cation tolerance protein CutA		K03926	cellular organisms	P		0FCX0@creNOG,COG1324@NOG,arCOG04231@arNOG		Cytoplasmic	
NAS2_0593	1010 CDS	Pyruvate.phosphate dikinase	2.7.9.1	K01006	Crenarchaeota	G		0KRR9@eurNOG,0WKT1@methaNOG,COG0574@NOG,arCOG01111@arNOG		Cytoplasmic	PPDK
NAS2_0594	178 CDS	ThiJ/PlpI family protein		K05520	cellular organisms			0FBST@creNOG,COG0693@NOG,arCOG00769@arNOG		Cytoplasmic	Peptidase
NAS2_0595	894 CDS	Aconitate hydratase	4.2.1.3	K01681	cellular organisms	C	MER0066439	0FAWT@creNOG,COG1048@NOG,arCOG01697@arNOG		Cytoplasmic	ACO
NAS2_0596	154 CDS	hypothetical protein			Not assigned					Cytoplasmic	
NAS2_0597	227 CDS	hypothetical protein			Crenarchaeota			0FCJN@creNOG,COG4344@NOG,arCOG03698@arNOG		Cytoplasmic	
NAS2_0598	225 CDS	7,8 dihydropterolate synthase		K06897	Crenarchaeota			0FCPM@creNOG,COG1237@NOG,arCOG00503@arNOG		Cytoplasmic	
NAS2_0599	146 CDS	COG1720: Uncharacterized conserved protein			Crenarchaeota			0FCKK@creNOG,COG1720@NOG,arCOG00761@arNOG		Unknown	
NAS2_0600	249 CDS	Molybdenum transport ATP-binding protein ModC		K09138	cellular organisms			0KTHE@eurNOG,0WN0J@methaNOG,COG2014@NOG,arCOG03216@arNOG		Cytoplasmic	
NAS2_0601	237 CDS	Cytoplasmic chaperone TorD			Bacteria			0KXXN@eurNOG,COG3381@NOG,arCOG01506@arNOG		Cytoplasmic	
NAS2_0602	143 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic	
NAS2_0603	74 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic	
NAS2_0604	941 CDS	Anaerobic dimethyl sulfoxide reductase chain A	1.8.5.3	K07812	Thaumarchaeota	C		0KVQX@eurNOG,COG0243@NOG,arCOG01491@arNOG		multples	MoCo
NAS2_0605	282 CDS	Tetrahiolate reductase subunit B			Thaumarchaeota	C		0KUS3@eurNOG,COG0437@NOG,arCOG01500@arNOG		Cytoplasmic	
NAS2_0606	92 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic	
NAS2_0607	384 CDS	Niacin transporter NiaP		K08369	Euryarchaeota	G		0FDST@creNOG,0XQKC@NOG,arCOG02682@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0608	684 CDS	Anaerobic dehydrogenases, typically selenocysteine-containing			Bacteria	C		02H6A@arcdNOG,0KVQX@eurNOG,COG0243@NOG,arCOG01491@arNOG		Cytoplasmic	MoCo
NAS2_0609	147 CDS	hypothetical protein			Archaea					Unknown	
NAS2_0610	148 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic	
NAS2_0611	388 CDS	major facilitator superfamily MFS_1			Archaea	G		02U7S@arNOG,0FFYH@creNOG,0ZNSM@NOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0612	375 CDS	Succinyl-CoA ligase [ADP-forming] beta chain	6.2.1.5	K01903	cellular organisms	C		0FB8F@creNOG,COG0045@NOG,arCOG01337@arNOG		Cytoplasmic	SUC
NAS2_0613	294 CDS	Succinyl-CoA ligase [ADP-forming] alpha chain	6.2.1.5	K01902	cellular organisms	C		0FBDE@creNOG,COG0074@NOG,arCOG01339@arNOG		Cytoplasmic	SUC
NAS2_0614	246 CDS	ABC transport system ATP-binding protein PA		K02049	Archaea	P		0FBH7@creNOG,COG1116@NOG,arCOG00193@arNOG	Transporter (ABC)	CytoplasmicMembrane	
NAS2_0615	543 CDS	ABC transporter permease protein		K02050	P Archaea	P		0KSKJ@eurNOG,1CCED@theNOG,COG4986@NOG,arCOG00174@arNOG	Transporter (ABC)	CytoplasmicMembrane	
NAS2_0616	501 CDS	Sugar transport related protein			TACK group	G		0FCE9@creNOG,0XR5P@NOG,arCOG02687@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0617	406 CDS	Ammonium transporter		K03320	cellular organisms	T		0KRDI@eurNOG,0WKFI@methaNOG,COG0004@arNOG,arCOG04397@arNOG	Transporter (Other)	CytoplasmicMembrane	
NAS2_0618	113 CDS	Nitrogen regulatory protein P-II		K04751	cellular organisms	E		0KTXY@eurNOG,0WMJA@methaNOG,COG0347@NOG,arCOG02305@arNOG		CytoplasmicMembrane	
NAS2_0619	292 CDS	Phosphate regulatory protein-like			Archaea	P		0FCB1@creNOG,COG0704@NOG,arCOG00318@arNOG		Cytoplasmic	
NAS2_0620	382 CDS	General substrate transporter			Archaea	G		COG477@NOG,arCOG00130@arNOG	Transporter (MFS)	CytoplasmicMembrane	

NAS2_0621	202 CDS	UPF0098 protein	K06910	cellular organisms	MERO277777	0FCAl@creNOG,COG1881@NOG,arCOG04702@arNOG	Cytoplasmic	
NAS2_0622	157 CDS	hypothetical protein		Archaea			Cytoplasmic	
NAS2_0623	726 CDS	Anaerobic dehydrogenases, typically selenocysteine-containing		Bacteria	C	02H6A@arcNOG,0KVQX@eurNOG,COG0243@NOG,arCOG01491@arNOG	multiple	MoCo
NAS2_0624	150 CDS	hypothetical protein		Bacteria			Cytoplasmic	
NAS2_0625	129 CDS	hypothetical protein		Crenarchaeota		0FD2G@creNOG,COG1917@NOG,arCOG02994@arNOG	Unknown	
NAS2_0626	719 CDS	Anaerobic dehydrogenases, typically selenocysteine-containing		Bacteria	C	02H6A@arcNOG,0KVQX@eurNOG,COG0243@NOG,arCOG01491@arNOG	Cytoplasmic	MoCo
NAS2_0627	223 CDS	Alkyl hydroperoxide reductase subunit C-like protein	K03386	Crenarchaeota	O	0FB8@creNOG,COG0450@NOG,arCOG00312@arNOG	Cytoplasmic	
NAS2_0628	253 CDS	hypothetical protein		Thaumarchaeota		0FDBM@creNOG,11JNK@NOG,arCOG01424@arNOG	Cytoplasmic	
NAS2_0629	224 CDS	Thiaminase II	3.5.99.2	Crenarchaeota	K	0FC4E@creNOG,COG0819@NOG,arCOG01128@arNOG	Cytoplasmic	
NAS2_0630	233 CDS	Methyltransferase TM1293	K03707	Crenarchaeota	Q	0FBW2@creNOG,COG0500@NOG,arCOG01773@arNOG	Cytoplasmic	
NAS2_0631	188 CDS	hypothetical protein		Archaea	M		Unknown	
NAS2_0632	121 CDS	hypothetical protein		cellular organisms			CytoplasmicMembrane	
NAS2_0633	199 CDS	Isochorismatase	3.3.2.1	Archaea	Q	0KT6C@eurNOG,1CCRY@theNOG,COG1335@NOG,arCOG01943@arNOG	Unknown	
NAS2_0634	48 CDS	hypothetical protein		Not assigned			Cytoplasmic	
NAS2_0635	331 CDS	FIG01318144: Rieske (2Fe-2S) domain-containing protein		Bacteria	P		Cytoplasmic	
NAS2_0636	390 CDS	hypothetical protein		Crenarchaeota			Transporter (MFS)	
NAS2_0637	910 CDS	Anaerobic dimethyl sulfoxide reductase chain A	1.8.5.3	Thaumarchaeota	C	0KVQX@eurNOG,COG0243@NOG,arCOG01491@arNOG	CytoplasmicMembrane	MoCo
NAS2_0638	153 CDS	hypothetical protein		Not assigned			multiple	
NAS2_0639	141 CDS	hypothetical protein		Extracellular			Unknown	
NAS2_0640	187 CDS	hypothetical protein		Crenarchaeota			Cytoplasmic	
NAS2_0641	200 CDS	hypothetical protein		Crenarchaeota			Cytoplasmic	
NAS2_0642	406 CDS	Glycosyl transferase, family 2		Euryarchaeota	M	0KTUH@eurNOG,0RIG6@halNOG,COG1215@NOG,arCOG01389@arNOG	CytoplasmicMembrane	
NAS2_0643	342 CDS	hypothetical protein		Euryarchaeota		0FD8F@creNOG,0YRWU@NOG,arCOG06883@arNOG	Cytoplasmic	
NAS2_0644	254 CDS	hypothetical protein		Archaea			Cytoplasmic	
NAS2_0645	390 CDS	Cystathionine gamma-synthase	2.5.1.48	Archaea	E	0FB25@creNOG,COG0626@NOG,arCOG00060@arNOG	Cytoplasmic	
NAS2_0646	246 CDS	hypothetical protein		cellular organisms			Cytoplasmic	
NAS2_0647	249 CDS	hypothetical protein		cellular organisms		11YBY@NOG,arCOG01149@arNOG	Cytoplasmic	
NAS2_0648	136 CDS	hypothetical protein		Not assigned			Cytoplasmic	
NAS2_0649	132 CDS	hypothetical protein		Archaea		10ZS4@NOG,1CBVP@thaNOG,arCOG08677@arNOG	Cytoplasmic	
NAS2_0650	224 CDS	hypothetical protein		Not assigned			Cytoplasmic	
NAS2_0651	339 CDS	hypothetical protein		Bacteria			Cytoplasmic	
NAS2_0652	176 CDS	hypothetical protein		Not assigned			Cytoplasmic	
NAS2_0653	124 CDS	hypothetical protein		Not assigned		0FCIX@creNOG,11PIW@NOG,arCOG06964@arNOG	CytoplasmicMembrane	
NAS2_0654	281 CDS	hypothetical protein		Crenarchaeota	MERO221182		Unknown	Peptidase
NAS2_0655	454 CDS	hypothetical protein		Not assigned			CytoplasmicMembrane	
NAS2_0656	222 CDS	Phosphoglycolate phosphatase, archaeal type	3.1.3.18	Crenarchaeota		0FC0Y@creNOG,COG0561@NOG,arCOG01213@arNOG	Cytoplasmic	
NAS2_0657	167 CDS	hypothetical protein		Not assigned			Cytoplasmic	
NAS2_0658	160 CDS	hypothetical protein		Not assigned			CytoplasmicMembrane	
NAS2_0659	303 CDS	hypothetical protein		Thaumarchaeota			Cytoplasmic	
NAS2_0660	529 CDS	Cellulose synthase (UDP-forming)	2.4.1.12	Thaumarchaeota	M	0KTCX@eurNOG,1CDEH@theNOG,COG1215@NOG,arCOG01391@arNOG	CytoplasmicMembrane	
NAS2_0661	134 CDS	hypothetical protein	K00694	Thaumarchaeota	K		Cytoplasmic	
NAS2_0662	282 CDS	Transcription initiation factor B	K03892	cellular organisms			Unknown	
NAS2_0663	156 CDS	hypothetical protein	K03124	Thaumarchaeota	K	0M1RV@eurNOG,1CEIZ@themNOG,COG1405@NOG,arCOG01981@arNOG	CytoplasmicMembrane	
NAS2_0664	156 CDS	hypothetical protein		Thaumarchaeota			Cytoplasmic	
NAS2_0665	384 CDS	hypothetical protein		Archaea			CytoplasmicMembrane	
NAS2_0666	118 CDS	hypothetical protein		Not assigned			Unknown	
NAS2_0667	150 CDS	hypothetical protein		Not assigned			Unknown	
NAS2_0668	637 CDS	TrsE-like protein		Thaumarchaeota	U	0FD1N@creNOG,126FB@NOG,arCOG04035@arNOG,arCOG07496@arNOG	CytoplasmicMembrane	
NAS2_0669	166 CDS	hypothetical protein		Crenarchaeota		0FDAJ@creNOG,128UT@NOG,arCOG05320@arNOG	CytoplasmicMembrane	
NAS2_0670	169 CDS	hypothetical protein		Archaea			Unknown	
NAS2_0671	349 CDS	luciferase-like		Thaumarchaeota	C	0KWNR@eurNOG,COG2141@NOG,arCOG02410@arNOG	Cytoplasmic	
NAS2_0672	130 CDS	hypothetical protein		Not assigned			Cytoplasmic	
NAS2_0673	344 CDS	hypothetical protein		Thaumarchaeota			Cytoplasmic	
NAS2_0674	633 CDS	hypothetical protein	K07333	Thaumarchaeota	U	0FD28@creNOG,COG2064@NOG,arCOG01808@arNOG	CytoplasmicMembrane	
NAS2_0675	651 CDS	hypothetical protein		cellular organisms	I	MERO725280	0ZWP5@NOG,arCOG06935@arNOG	Unknown
NAS2_0676	724 CDS	Conserved domain protein		Crenarchaeota		0FDGA@creNOG,COG0433@NOG,arCOG04816@arNOG	Unknown	
NAS2_0677	70 CDS	hypothetical protein		Not assigned			Cytoplasmic	
NAS2_0678	214 CDS	hypothetical protein		Not assigned			CytoplasmicMembrane	
NAS2_0679	578 CDS	hypothetical protein		Thaumarchaeota			CytoplasmicMembrane	
NAS2_0680	252 CDS	hypothetical protein		Not assigned			Unknown	
NAS2_0681	200 CDS	hypothetical protein		Not assigned			CytoplasmicMembrane	
NAS2_0682	105 CDS	hypothetical protein		Not assigned			Cytoplasmic	
NAS2_0683	101 CDS	hypothetical protein	K04796	cellular organisms	K		Cytoplasmic	
NAS2_0684	127 CDS	hypothetical protein		Bacteria			Cytoplasmic	
NAS2_0685	183 CDS	hypothetical protein		cellular organisms		0FCD2@creNOG,11IVC@NOG,arCOG06034@arNOG	Cytoplasmic	
NAS2_0686	156 CDS	Ruberythrin		Crenarchaeota	C	0FC0E@creNOG,COG1592@NOG,arCOG01097@arNOG	Cytoplasmic	
NAS2_0687	39 CDS	hypothetical protein		No hits			Unknown	
NAS2_0688	60 CDS	hypothetical protein		Archaea		0FFDR@creNOG,COG3369@NOG,arCOG01667@arNOG	Cytoplasmic	
NAS2_0689	156 CDS	hypothetical protein		Crenarchaeota		0FCH3@creNOG,11XGT@NOG,arCOG00022@arNOG	Cytoplasmic	
NAS2_0690	181 CDS	hypothetical protein		TACK group	N	0FC0K@creNOG,COG5491@NOG,arCOG00452@arNOG	Cytoplasmic	
NAS2_0691	398 CDS	hypothetical protein		cellular organisms		0KST3@eurNOG,COG1470@NOG,arCOG02087@arNOG,arCOG07560@arNOG	Unknown	
NAS2_0692	302 CDS	ABC transporter, ATP-binding protein	K01990	Bacteria	V	0KXSC@eurNOG,COG1131@NOG,arCOG00194@arNOG	multiple	
NAS2_0693	311 CDS	ABC-type transport, permease protein	K01992	Bacteria		0KV3B@eurNOG,0WKYF@methaNOG,COG1277@NOG,arCOG02436@arNOG	Transporter (ABC)	
NAS2_0694	196 CDS	hypothetical protein		Euryarchaeota			CytoplasmicMembrane	
NAS2_0695	165 CDS	no similarity		Euryarchaeota		0KX6Q@eurNOG,1CDGF@theNOG,COG5592@NOG,arCOG06046@arNOG	Cytoplasmic	
NAS2_0696	37 CDS	hypothetical protein		No hits			Unknown	
NAS2_0697	406 CDS	Ammonium transporter	K03320	cellular organisms	T	0KRDI@eurNOG,0WKFI@methaNOG,COG0004@NOG,arCOG04397@arNOG	Cytoplasmic	
NAS2_0698	115 CDS	Nitrogen regulatory protein P-II	K04751	cellular organisms	E	0KTXY@eurNOG,0WMJA@methaNOG,COG0347@NOG,arCOG02305@arNOG	CytoplasmicMembrane	
NAS2_0699	85 CDS	hypothetical protein		Bacteria			Cytoplasmic	
NAS2_0700	373 CDS	Anaerobic glycerol-3-phosphate dehydrogenase subunit A	1.1.5.3	cellular organisms	C	0FBET@creNOG,COG0578@NOG,arCOG00753@arNOG	Unknown	
NAS2_0701	279 CDS	UPF0204 protein	K09716	Crenarchaeota		0FCF0@creNOG,COG1650@NOG,arCOG01616@arNOG	Cytoplasmic	
NAS2_0702	586 CDS	Glutamate synthase [NADPH] large chain	1.4.1.13	Crenarchaeota	E	0FHD8@creNOG,COG0067@NOG,COG0070@NOG,arCOG00095@arNOG,arCOG00097@arNOG	Cytoplasmic	GLT
NAS2_0703	696 CDS	Glutamate synthase [NADPH] large chain II	1.4.1.13	Crenarchaeota	E	0FBEA@creNOG,COG0069@NOG,arCOG00619@arNOG	Cytoplasmic	GLT
NAS2_0704	282 CDS	Permease of the drug/metabolite transporter superfamily		Archaea	E	0FBTK@creNOG,COG0697@NOG,arCOG00271@arNOG	Transporter (Other)	
NAS2_0705	480 CDS	Predicted thiamin transporter ThiT		cellular organisms	G	0FBUS@creNOG,0YRAI@NOG,arCOG02794@arNOG	Transporter (MFS)	
NAS2_0706	366 CDS	hypothetical protein		No hits			CytoplasmicMembrane	
NAS2_0707	219 CDS	Potassium efflux system KefA protein		Archaea	M	0FCEH@creNOG,COG0668@NOG,arCOG01573@arNOG	Cytoplasmic	
NAS2_0708	427 CDS	Predicted thiamin transporter ThiT		Archaea	G	0FBUS@creNOG,0YRAI@NOG,arCOG02794@arNOG	Transporter (Other)	
NAS2_0709	114 CDS	hypothetical protein		Crenarchaeota		COG4818@NOG,arCOG04344@arNOG	Transporter (MFS)	
							CytoplasmicMembrane	

NAS2_0710	290 CDS	Ribokinase	2.7.1.15	K00852	Crenarchaeota	G	0FDZK@creNOG,COG0524@NOG,arCOG00014@arNOG	Cytoplasmic	
NAS2_0711	593 CDS	Anaerobic dehydrogenases, typically selenocysteine-containing			Crenarchaeota	C	0FB28@creNOG,COG0243@NOG,arCOG01491@arNOG	Unknown	MoCo
NAS2_0712	160 CDS	Pyrimidine dimer DNA glycosylase			cellular organisms	L	0FCEX@creNOG,11PIZ@NOG,arCOG05276@arNOG	Cytoplasmic	
NAS2_0713	257 CDS	NAD-dependent protein deacetylase of SIR2 family		K12410	Crenarchaeota	K	0FBW5@creNOG,COG0846@NOG,arCOG04248@arNOG	Unknown	
NAS2_0714	228 CDS	Endonuclease III	4.2.99.18	K07457	Crenarchaeota	L	0FCAD@creNOG,COG2231@NOG,arCOG00481@arNOG	Cytoplasmic	
NAS2_0715	435 CDS	Major facilitator superfamily transport protein			Bacteria		0KTTD@eurNOG,DWSDV@methNOG,DXCKC@NOG,arCOG02682@arNOG	CytoplasmicMembrane	
NAS2_0716	489 CDS	Gamma-glutamyltranspeptidase	2.3.2.2	K00681	Crenarchaeota	E	0FBBD@creNOG,COG04053@arNOG	Extracellular	
NAS2_0717	220 CDS	Sulfite oxidase and related enzymes			Crenarchaeota		0FBZY@creNOG,COG02041@NOG,arCOG00264@arNOG	Cytoplasmic	
NAS2_0718	355 CDS	FIG028593: membrane protein			Crenarchaeota		114FB@NOG,arCOG03704@arNOG	Unknown	
NAS2_0719	69 CDS	hypothetical protein			Not assigned			Unknown	
NAS2_0720	77 CDS	Transcriptional regulator, ArsR family			Archaea	K	0KUJ6@eurNOG,DWSPF@methNOG,COG06040@NOG,arCOG00731@arNOG	Cytoplasmic	
NAS2_0721	95 CDS	hypothetical protein			Archaea			CytoplasmicMembrane	
NAS2_0722	405 CDS	hypothetical protein			Korarchaeota	L	0FBRW@creNOG,COG1106@NOG,arCOG03237@arNOG	Cytoplasmic	
NAS2_0723	218 CDS	167aa long hypothetical protein			Archaea			Cytoplasmic	
NAS2_0724	41 CDS	hypothetical protein			Not assigned			Cytoplasmic	
NAS2_0725	162 CDS	hypothetical protein			Korarchaeota			CytoplasmicMembrane	
NAS2_0726	533 CDS	Fumarate reductase flavoprotein subunit	1.3.99.1		Bacteria	C	02TWY@arNOG,0M09X@eurNOG,0RJG3@halNOG,COG1053@NOG	Cytoplasmic	
NAS2_0727	257 CDS	hypothetical protein			cellular organisms		0KT0I@eurNOG,1CEBD@thermNOG,COG3885@NOG,arCOG01729@arNOG	Transporter ATPase?	
NAS2_0728	239 CDS	ABC transporter, ATP-binding protein		K01990	Crenarchaeota	V	0FBT3@creNOG,COG1131@NOG,arCOG00194@arNOG	Transporter (ABC)	
NAS2_0729	494 CDS	hypothetical protein		K07087	Crenarchaeota		0FFJ0@creNOG,0ZZED@NOG,arCOG10475@arNOG	CytoplasmicMembrane	
NAS2_0730	428 CDS	Acetylornithine deacetylase	3.5.1.16	K01439	TACK group	E	0FAZ1@creNOG,COG0624@NOG,arCOG01107@arNOG	Cytoplasmic	
NAS2_0731	288 CDS	Endonuclease IV	3.1.21.2	K01151	Archaea	L	0KSH1@eurNOG,0WKVB@methaNOG,COG0648@NOG,arCOG01894@arNOG	Cytoplasmic	
NAS2_0732	401 CDS	Glutamyl-tRNA reductase	1.2.1.70	K02492	cellular organisms	H	0KRET@eurNOG,0WRFM@methNOG,COG0373@NOG,arCOG01036@arNOG	Cytoplasmic	
NAS2_0733	285 CDS	Kinase, ptkB family			Euryarchaeota	G		Cytoplasmic	
NAS2_0734	158 CDS	hypothetical protein			Bacteria			Cytoplasmic	
NAS2_0735	256 CDS	Transporter			Crenarchaeota		0YYRN@NOG,arCOG05339@arNOG	CytoplasmicMembrane	
NAS2_0736	402 CDS	hypothetical protein		K07133	Crenarchaeota		0FEJD@creNOG,COG1373@NOG,arCOG03167@arNOG	Cytoplasmic	
NAS2_0737	146 CDS	single-stranded DNA binding protein		K07466	Thaumarchaeota	L	0FCWP@creNOG,COG1599@NOG,arCOG01510@arNOG	Cytoplasmic	
NAS2_0738	361 CDS	Serine--glyoxylate aminotransferase	2.6.1.45		Bacteria	E	0KRE1@eurNOG,COG0075@NOG,arCOG00082@arNOG	Cytoplasmic	
NAS2_0739	339 CDS	Alcohol dehydrogenase	1.1.1.1		Archaea	C	0FAWQ@creNOG,COG0604@NOG,arCOG01458@arNOG	Cytoplasmic	
NAS2_0740	399 CDS	Gluconate dehydratase	4.2.1.39	K01684	Archaea	M	0FBDZ@creNOG,COG4948@NOG,arCOG01168@arNOG	Cytoplasmic	
NAS2_0741	44 CDS	hypothetical protein			No hits			Unknown	
NAS2_0742	311 CDS	Alcohol dehydrogenase	1.1.1.1		Crenarchaeota	C	0FBHD@creNOG,COG1064@NOG,arCOG01455@arNOG	Cytoplasmic	
NAS2_0743	493 CDS	Aldehyde dehydrogenase	1.2.1.3	K07248	Archaea	C	0KRCS@eurNOG,1CCG9@theNOG,COG1012@NOG,arCOG01252@arNOG	Cytoplasmic	
NAS2_0744	291 CDS	Dihydropicolinate synthase family		K01714	DPANN	E	0KRIO@eurNOG,1CD77@theNOG,COG0329@NOG,arCOG04172@arNOG	Cytoplasmic	
NAS2_0745	238 CDS	Ser-tRNA deacylase		K07050	Archaea		0KSPD@eurNOG,1CCNV@theNOG,COG2872@NOG,arCOG01254@arNOG	Cytoplasmic	
NAS2_0746	325 CDS	hypothetical protein			Thaumarchaeota			CytoplasmicMembrane	
NAS2_0747	108 CDS	hypothetical protein			Crenarchaeota		0FDNJ@creNOG,0ZBVC@NOG,arCOG06987@arNOG	Cytoplasmic	
NAS2_0748	39 CDS	hypothetical protein			No hits			Cytoplasmic	
NAS2_0749	387 CDS	Multidrug resistance protein			Euryarchaeota	G	0KSVN@eurNOG,COG0477@NOG,arCOG00132@arNOG	Transporter (MFS)	
NAS2_0750	422 CDS	Diglycerate 2-kinase		K11529	Crenarchaeota	G	0FBFH@creNOG,COG2379@NOG,arCOG04170@arNOG	CytoplasmicMembrane	
NAS2_0751	181 CDS	hypothetical protein		K07034	Thaumarchaeota	G	0FBBS@creNOG,COG1584@NOG,arCOG01793@arNOG	Unknown	
NAS2_0752	650 CDS	Glucoamylase	3.2.1.3		Euryarchaeota	G	0KRZG@eurNOG,1CCJW@theNOG,COG3387@NOG,arCOG03285@arNOG	Extracellular	
NAS2_0753	358 CDS	Glucose 1-dehydrogenase	1.1.1.47		Thaumarchaeota	E	0FBDS@creNOG,COG1063@NOG,arCOG01459@arNOG	Cytoplasmic	
NAS2_0754	244 CDS	Metal-dependent hydrolase			Thaumarchaeota		0FBXQ@creNOG,COG1878@NOG,arCOG02462@arNOG	Cytoplasmic	
NAS2_0755	386 CDS	Threonine synthase	4.2.3.1		Crenarchaeota	E	0FC3P@creNOG,COG0498@NOG,arCOG01434@arNOG	Cytoplasmic	
NAS2_0756	399 CDS	Predicted thiamin transporter ThiT			Crenarchaeota	G	0FDV6@creNOG,0XNTT@NOG,arCOG02793@arNOG	Transporter (MFS)	
NAS2_0757	122 CDS	hypothetical protein			Not assigned			Cytoplasmic	
NAS2_0758	384 CDS	Conserved protein			Euryarchaeota	G	0KV22@eurNOG,11FNQ@NOG,1CD5E@theNOG,arCOG05341@arNOG	Transporter (MFS)	
NAS2_0759	64 CDS	hypothetical protein			Archaea			CytoplasmicMembrane	
NAS2_0760	1032 CDS	Formate dehydrogenase O alpha subunit	1.2.1.2	K00123	Bacteria	C	0FBBX@creNOG,COG0243@NOG,arCOG01491@arNOG,arCOG01493@arNOG	Unknown	FDH
NAS2_0761	275 CDS	Formate dehydrogenase O beta subunit	1.2.1.2	K00124	cellular organisms	C	0FC58@creNOG,COG0437@NOG,arCOG01503@arNOG	CytoplasmicMembrane	FDH
NAS2_0762	237 CDS	Formate dehydrogenase O gamma subunit	1.2.1.2	K00127	cellular organisms	C		CytoplasmicMembrane	FDH
NAS2_0763	227 CDS	formate dehydrogenase formation protein FdhE		K02380	Bacteria	O		Cytoplasmic	FDH
NAS2_0764	148 CDS	hypothetical protein		K07068	Crenarchaeota		0FCAC@creNOG,COG1545@NOG,arCOG01283@arNOG	Cytoplasmic	
NAS2_0765	396 CDS	Acetyl-CoA C-acyltransferase		K00626	Archaea	I	0FB31@creNOG,COG0183@NOG,arCOG01278@arNOG	Cytoplasmic	
NAS2_0766	55 CDS	hypothetical protein			Not assigned			CytoplasmicMembrane	
NAS2_0767	280 CDS	hypothetical protein			Archaea	T		Cytoplasmic	
NAS2_0768	398 CDS	Flavoprotein			cellular organisms	C	0FB7D@creNOG,COG0426@NOG,arCOG00509@arNOG	Cytoplasmic	
NAS2_0769	164 CDS	hypothetical protein			Crenarchaeota			Cytoplasmic	
NAS2_0770	314 CDS	MinD superfamily P-loop ATPase containing an inserted ferredoxin domain			Crenarchaeota	D	0KS0X@eurNOG,1CDQE@thermNOG,COG1149@NOG,arCOG04073@arNOG	Cytoplasmic	
NAS2_0771	322 CDS	MinD superfamily P-loop ATPase containing an inserted ferredoxin domain			Crenarchaeota	D	0FEGX@creNOG,COG1149@NOG,arCOG04073@arNOG	Cytoplasmic	
NAS2_0772	116 CDS	hypothetical protein			Crenarchaeota		0KUQ0@eurNOG,1CEWV@thermNOG,COG1433@NOG,arCOG02734@arNOG	Cytoplasmic	
NAS2_0773	278 CDS	312aa long conserved hypothetical protein			Crenarchaeota			CytoplasmicMembrane	
NAS2_0774	147 CDS	hypothetical protein			Bacteria			Cytoplasmic	
NAS2_0775	732 CDS	Anaerobic dehydrogenases, typically selenocysteine-containing			Crenarchaeota	C	02H6A@arcNOG,0KVQX@eurNOG,COG0243@NOG,arCOG01491@arNOG	Cytoplasmic	MoCo
NAS2_0776	390 CDS	acyl-CoA dehydrogenase		K00249	Crenarchaeota	I	0FB0C@creNOG,COG1960@NOG,arCOG04310@arNOG	Cytoplasmic	
NAS2_0777	131 CDS	Dihydroneopterin aldolase	4.1.2.25	K01633	Bacteria	H	0FE6N@creNOG,COG0801@NOG,arCOG07203@arNOG	Cytoplasmic	
NAS2_0778	155 CDS	hypothetical protein			Crenarchaeota		0FF96@creNOG,COG3193@NOG,arCOG07054@arNOG	Cytoplasmic	
NAS2_0779	288 CDS	Carbon monoxide dehydrogenase medium chain	1.2.99.2	K03519	cellular organisms	C	0FB9S@creNOG,COG1319@NOG,arCOG01926@arNOG	Unknown	Cox/AOR
NAS2_0780	149 CDS	Carbon monoxide dehydrogenase small chain	1.2.99.2	K03518	cellular organisms	C	0FBB5@creNOG,COG2080@NOG,arCOG01925@arNOG	Unknown	Cox/AOR
NAS2_0781	687 CDS	Carbon monoxide dehydrogenase large chain	1.2.99.2		Euryarchaeota	C	0KTQ7@eurNOG,1CD82@theNOG,COG1529@NOG,arCOG01167@arNOG	Unknown	Cox/AOR
NAS2_0782	188 CDS	hypothetical protein			Thaumarchaeota		0FCVQ@creNOG,COG3371@NOG,arCOG02008@arNOG	CytoplasmicMembrane	
NAS2_0783	132 CDS	TVG1210382 protein			Crenarchaeota		0FD46@creNOG,COG4272@NOG,arCOG05396@arNOG	CytoplasmicMembrane	
NAS2_0784	319 CDS	Conserved membrane protein		K07090	Crenarchaeota		0KSMW@eurNOG,1CCN5@theNOG,COG0730@NOG,arCOG02050@arNOG	CytoplasmicMembrane	
NAS2_0785	246 CDS	Aspartate racemase	5.1.1.13	K01779	cellular organisms	E	0KTU0@eurNOG,1CE5P@thermNOG,COG1794@NOG,arCOG02005@arNOG	Cytoplasmic	
NAS2_0786	594 CDS	Amino acid transporter			Crenarchaeota	E	0FB5V@creNOG,COG03531@NOG,arCOG00009@arNOG	CytoplasmicMembrane	AA transporters
NAS2_0787	375 CDS	Cysteine desulfurase	2.8.1.7		Archaea	E	0KRVS@eurNOG,1CDAM@theNOG,COG05020@NOG,arCOG00065@arNOG	Cytoplasmic	
NAS2_0788	378 CDS	Aspartate aminotransferase	2.6.1.1	K00812	Thaumarchaeota	E	0KRFG@eurNOG,COG0436@NOG,arCOG01130@arNOG	Cytoplasmic	AT (Family I)
NAS2_0789	333 CDS	F420-dependent N(5),N(10)-methylenetetrahydromethanopterin reductase	1.5.99.11	K00320	Thaumarchaeota		0KRKG@eurNOG,0WQHX@methNOG,COG2141@NOG,arCOG02410@arNOG	Cytoplasmic	
NAS2_0790	92 CDS	2-oxoglutarate oxidoreductase, delta subunit, putative	1.2.7.3		cellular organisms	C	0KTV0@eurNOG,0WMVP@methaNOG,COG1146@NOG,arCOG00960@arNOG	Cytoplasmic	OFOR
NAS2_0791	359 CDS	2-oxoglutarate oxidoreductase, alpha subunit	1.2.7.3		cellular organisms	C	0KREH@eurNOG,0WKCC@methaNOG,COG0674@NOG,arCOG01607@arNOG	Cytoplasmic	OFOR
NAS2_0792	268 CDS	2-oxoglutarate oxidoreductase, beta subunit	1.2.7.3	K00175	Thaumarchaeota	C	02TE4@arNOG,0KRGW@eurNOG,0WK87@methaNOG,COG1013@NOG,COG1014@NOG,arCOG01600@arNOG	Unknown	OFOR
NAS2_0793	171 CDS	2-oxoglutarate oxidoreductase, gamma subunit	1.2.7.3	K00177	cellular organisms	C		Cytoplasmic	OFOR
NAS2_0794	137 CDS	hypothetical protein			Archaea			Cytoplasmic	
NAS2_0795	227 CDS	DUF124 domain-containing protein			TACK group		0FC1C@creNOG,COG2013@NOG,arCOG01907@arNOG	Cytoplasmic	
NAS2_0796	313 CDS	aldo-keto reductase			Archaea		0FBAS@creNOG,COG0656@NOG,arCOG01618@arNOG	Cytoplasmic	
NAS2_0797	452 CDS	4-aminobutyrate aminotransferase		K00823	Archaea	E	0FAXQ@creNOG,COG0160@NOG,arCOG00915@arNOG	Cytoplasmic	
NAS2_0798	340 CDS	Threonine synthase	4.2.3.1	K01733	Crenarchaeota	E	0FBGD@creNOG,COG0498@NOG,arCOG01434@arNOG	Cytoplasmic	

NAS2_0799	559 CDS	Permease, multidrug efflux		Crenarchaeota	P	0FBVCV@creNOG,0XNN3@NOG,arCOG00144@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_0800	137 CDS	hypothetical protein		Bacteria				CytoplasmicMembrane
NAS2_0801	707 CDS	hypothetical protein		Bacteria				Unknown
NAS2_0802	290 CDS	hypothetical protein		No hits				CytoplasmicMembrane
NAS2_0803	264 CDS	hypothetical protein		Archaea				Unknown
NAS2_0804	337 CDS	Threonine synthase	4.2,3.1	Thaumarchaeota	E	0KPPG@eurNOG,0WKNC@methaNOG,COG0498@NOG,arCOG01434@arNOG		Cytoplasmic
NAS2_0805	576 CDS	Methylmalonyl-CoA mutase	5.4.99.2	Archaea	I	0KRKF@eurNOG,1CCNF@theNOG,COG1884@NOG,arCOG04232@arNOG		Cytoplasmic
NAS2_0806	142 CDS	B12 binding domain of Methylmalonyl-CoA mutase	5.4.99.2	Archaea	I	0KTRG@eurNOG,1CCTR@theNOG,COG2185@NOG,arCOG01710@arNOG		Cytoplasmic
NAS2_0807	299 CDS	putative periplasmic protein kinase ArgK and related GTPases of G3E family		cellular organisms	E	0KXA@eurNOG,1CD9A@theNOG,COG1703@NOG,arCOG01228@arNOG		CytoplasmicMembrane
NAS2_0808	374 CDS	Multidrug-efflux transporter		Crenarchaeota	G	0FBDX@creNOG,COG0477@NOG,arCOG00132@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_0809	43 CDS	hypothetical protein		Not assigned				Unknown
NAS2_0810	423 CDS	Cysteine synthase	2.5.1.47	Bathyarchaeota	E	0FB36@creNOG,COG0031@NOG,arCOG01430@arNOG		Unknown
NAS2_0811	265 CDS	Circadian clock protein KaiC		Crenarchaeota	T	0FB7V@creNOG,COG0467@NOG,arCOG01171@arNOG		Cytoplasmic
NAS2_0812	78 CDS	hypothetical protein		Korarchaeota				Unknown
NAS2_0813	107 CDS	Ferredoxin		Korarchaeota				Cytoplasmic
NAS2_0814	480 CDS	TVG1190485 protein		Crenarchaeota		0KU3U@eurNOG,COG1146@NOG,arCOG02461@arNOG		CytoplasmicMembrane
NAS2_0815	310 CDS	Indole-3-glycerol phosphate synthase		Crenarchaeota	E	0FFBR@creNOG,124F9@NOG,arCOG07388@arNOG		Cytoplasmic
NAS2_0816	171 CDS	redox family protein	4.1.1.48	cellular organisms		0FBC4@creNOG,COG0134@NOG,arCOG01088@arNOG		Cytoplasmic
NAS2_0817	205 CDS	hypothetical protein		Thaumarchaeota		11W24@NOG,arCOG06069@arNOG		CytoplasmicMembrane
NAS2_0818	497 CDS	Drug resistance transporter EmrB/QacA subfamily		Crenarchaeota	P	0FBW0@creNOG,0XNN3@NOG,arCOG00144@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_0819	298 CDS	Single-stranded exonuclease associated with Rad50/Mre11 complex		Archaea		1CBGM@thaNOG,COG1630@NOG,arCOG00367@arNOG		Cytoplasmic
NAS2_0820	495 CDS	Bipolar DNA helicase HerA		Thaumarchaeota		0FBCY@creNOG,COG0433@NOG,arCOG00280@arNOG		Cytoplasmic
NAS2_0821	264 CDS	Thiazole biosynthetic enzyme Thi4		Crenarchaeota	H	0FBLY@creNOG,COG1635@NOG,arCOG00574@arNOG		Unknown
NAS2_0822	425 CDS	NAD-specific glutamate dehydrogenase	1.4.1.4	root;	E	COG0334@NOG,arCOG01352@arNOG		Cytoplasmic
NAS2_0823	155 CDS	Thiol peroxidase, Bcp-type	1.11.1.15	Archaea	O	0FC68@creNOG,COG1225@NOG,arCOG00310@arNOG		Cytoplasmic
NAS2_0824	292 CDS	Translation elongation factor 1 alpha-related protein		Crenarchaeota	J	0FAXT@creNOG,COG3276@NOG,arCOG01564@arNOG		Unknown
NAS2_0825	336 CDS	hypothetical protein		Crenarchaeota		0FC7B@creNOG,COG0491@NOG,arCOG00498@arNOG		Cytoplasmic
NAS2_0826	77 CDS	Transcriptional regulator, AsnC family		Thaumarchaeota	K	0FCVX@creNOG,COG1522@NOG,arCOG01117@arNOG		Cytoplasmic
NAS2_0827	44 CDS	Fumarate hydratase class II	4.2.1.2	Archaea	C	0FB99@creNOG,COG0114@NOG,arCOG01749@arNOG		FUM
NAS2_0828	110 CDS	hypothetical protein		Crenarchaeota				CytoplasmicMembrane
NAS2_0829	39 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic
NAS2_0830	1899 CDS	Predicted cell-wall-anchored protein SasA		Archaea		0FDQB@creNOG,COG3391@NOG,arCOG02560@arNOG,arCOG06052@arNOG		Unknown
NAS2_0831	132 CDS	hypothetical protein		cellular organisms		11WJH@NOG,arCOG03008@arNOG		Unknown
NAS2_0832	718 CDS	ATP-dependent RNA helicase homolog eIF-4A		Bathyarchaeota	L	02HGS@arcNOG,0KRRB@eurNOG,COG1111@NOG,COG1948@NOG,arCOG00872@arNOG		Cytoplasmic
NAS2_0833	109 CDS	hypothetical protein		TACK group		0KV81@eurNOG,0Y5T6@NOG,arCOG08221@arNOG		Unknown
NAS2_0834	158 CDS	hypothetical protein		Crenarchaeota		0FD6E@creNOG,12ADS@NOG,arCOG03871@arNOG		Extracellular
NAS2_0835	90 CDS	hypothetical protein		Not assigned				Cytoplasmic
NAS2_0836	68 CDS	hypothetical protein		Crenarchaeota				Cytoplasmic
NAS2_0837	135 CDS	NADPH:quinone oxidoreductase		cellular organisms		0KTB@eurNOG,1CDAF@theNOG,COG0431@NOG,arCOG04624@arNOG		Cytoplasmic
NAS2_0838	87 CDS	hypothetical protein		cellular organisms				Cytoplasmic
NAS2_0839	48 CDS	hypothetical protein		Not assigned				Cytoplasmic
NAS2_0840	388 CDS	DNA double-strand break repair protein Mre11		Archaea	L	1CB6M@thaNOG,COG0420@NOG,arCOG00397@arNOG		Cytoplasmic
NAS2_0841	829 CDS	DNA double-strand break repair Rad50 ATPase		Archaea	L	0FB4T@creNOG,COG0419@NOG,arCOG00368@arNOG		Cytoplasmic
NAS2_0842	291 CDS	GTP cyclohydrolase I	3.5.4.16	Archaea	L	0KS22@eurNOG,COG1469@NOG,arCOG04301@arNOG		Unknown
NAS2_0843	206 CDS	Site-specific recombinase, resolvase family		root;	L	0KV05@eurNOG,COG1961@NOG,arCOG03162@arNOG		Cytoplasmic
NAS2_0844	439 CDS	Multidrug-efflux transporter		Crenarchaeota	G	0FBP7@creNOG,COG0477@NOG,arCOG00132@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_0845	312 CDS	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	4.1.1.45	Archaea		0KYD3@eurNOG,0WP8E@methaNOG,COG2159@NOG,arCOG01931@arNOG		Cytoplasmic
NAS2_0846	425 CDS	Putative MFS Superfamily sugar transporter		Crenarchaeota	G	0FCD4@creNOG,0XOKC@NOG,arCOG02682@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_0847	289 CDS	putative membrane protein		Archaea		0FB01@creNOG,COG0730@NOG,arCOG02050@arNOG		CytoplasmicMembrane
NAS2_0848	105 CDS	TVG1210382 protein		Korarchaeota		0FD46@creNOG,COG4272@NOG,arCOG05396@arNOG		Cytoplasmic
NAS2_0849	358 CDS	hypothetical protein		Euryarchaeota	L	0KU24@eurNOG,1CDFT@theNOG,COG558@NOG,arCOG07732@arNOG,arCOG07762@arNOG		Cytoplasmic
NAS2_0850	205 CDS	beta-lactamase domain protein		Archaea		0KVBK@eurNOG,1CDD5@theNOG,COG0491@NOG,arCOG00504@arNOG		Cytoplasmic
NAS2_0851	270 CDS	ABC-type multidrug transport system, permease component		Crenarchaeota	V	0FTBT@creNOG,COG0842@NOG,arCOG01465@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0852	306 CDS	ABC transporter, ATP-binding protein		Crenarchaeota	V	0FB09@creNOG,COG1131@NOG,arCOG00194@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0853	46 CDS	hypothetical protein		TACK group				Cytoplasmic
NAS2_0854	281 CDS	Dehydrogenase		cellular organisms		0FBKA@creNOG,COG0656@NOG,arCOG01619@arNOG		Cytoplasmic
NAS2_0855	565 CDS	Permease, multidrug efflux		Crenarchaeota	P	0FBVCV@creNOG,0XNN3@NOG,arCOG00144@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_0856	420 CDS	Na(+)/H(+) antiporter 1		Thaumarchaeota	P	COG0025@NOG,arCOG01961@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_0857	152 CDS	hypothetical protein		Thaumarchaeota				Antiporter
NAS2_0858	46 CDS	hypothetical protein		Thaumarchaeota				Unknown
NAS2_0859	184 CDS	hypothetical protein		Archaea				CytoplasmicMembrane
NAS2_0860	209 CDS	Methyltransferase, UbiE/COQ5 family		cellular organisms		0KTCZ@eurNOG,11NFP@NOG,arCOG01786@arNOG		Cytoplasmic
NAS2_0861	246 CDS	Molybdenum transport ATP-binding protein ModC		Euryarchaeota		0KTHE@eurNOG,0WS16@metNOG,COG2014@NOG,arCOG03216@arNOG	Transporter (ABC)	Cytoplasmic
NAS2_0862	254 CDS	Transmembrane component of general energizing module of ECF transporters		Thaumarchaeota	P	COG0619@NOG,arCOG02250@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0863	256 CDS	Molybdenum transport system protein ModD		Crenarchaeota	H	0FDQG@creNOG,COG0157@NOG,arCOG01483@arNOG	Transporter (ABC)	Cytoplasmic
NAS2_0864	525 CDS	ATPase component NikO of energizing module of nickel ECF transporter		cellular organisms	P	0FB40@creNOG,COG1122@NOG,arCOG00188@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0865	562 CDS	Ferrous iron transport protein B		Archaea	P	0FB9N@creNOG,COG0370@NOG,arCOG00359@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_0866	134 CDS	Universal stress protein UspA and related nucleotide-binding proteins		Thaumarchaeota	T	0FCU0@creNOG,COG0589@NOG,arCOG02053@arNOG		Cytoplasmic
NAS2_0867	242 CDS	hypothetical protein		TACK group		0FC07@creNOG,0XTDK@NOG,arCOG06008@arNOG		CytoplasmicMembrane
NAS2_0868	108 CDS	Twin-arginine translocation protein TatA		Thaumarchaeota	U	0FD48@creNOG,COG1826@NOG,arCOG02694@arNOG		Cytoplasmic
NAS2_0869	344 CDS	Manganese transport protein MntH		Crenarchaeota	P	0FBAV@creNOG,COG1914@NOG,arCOG04531@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_0870	266 CDS	iron(III) dicitrate-binding protein		Thaumarchaeota	P	0FFS2@creNOG,COG0614@NOG,arCOG04233@arNOG		Unknown
NAS2_0871	38 CDS	hypothetical protein		No hits				Cytoplasmic
NAS2_0872	195 CDS	Alkyl hydroperoxide reductase subunit C-like protein		TACK group	O	0KSTQ@eurNOG,1CCXQ@theNOG,COG0450@NOG,arCOG00312@arNOG		Cytoplasmic
NAS2_0873	109 CDS	Transcriptional regulator, ArsR family		Thaumarchaeota	K	COG0640@NOG,arCOG01679@arNOG		Cytoplasmic
NAS2_0874	97 CDS	hypothetical protein		Crenarchaeota				CytoplasmicMembrane
NAS2_0875	277 CDS	hypothetical protein		Thaumarchaeota				Extracellular
NAS2_0876	120 CDS	probable uroporphyrin-III c-methyltransferase	2.1.1.107	cellular organisms		0FCZK@creNOG,COG3189@NOG,arCOG06027@arNOG		Cytoplasmic
NAS2_0877	558 CDS	hypothetical protein		Crenarchaeota				Unknown
NAS2_0878	289 CDS	Beta-lactamase related protein		cellular organisms		0FBKF@creNOG,COG0491@NOG,arCOG00505@arNOG		Cytoplasmic
NAS2_0879	136 CDS	CBS domain protein		Thaumarchaeota	T	02TZE@arNOG,0FFWV@creNOG,0ZX5J@arNOG		Cytoplasmic
NAS2_0880	161 CDS	Probable transmembrane protein		Thaumarchaeota		0FC0N@creNOG,COG1839@NOG,arCOG04298@arNOG		Cytoplasmic
NAS2_0881	85 CDS	hypothetical protein		Thaumarchaeota	K	0FCVX@creNOG,COG1522@NOG,arCOG01117@arNOG		Cytoplasmic
NAS2_0882	133 CDS	hypothetical protein		Thaumarchaeota		0FCBK@creNOG,11NJU@NOG,arCOG05362@arNOG		Cytoplasmic
NAS2_0883	316 CDS	D-3-phosphoglycerate dehydrogenase	1.1.1.95	Thaumarchaeota	C	0FBFQ@creNOG,COG1052@NOG,arCOG01755@arNOG		Cytoplasmic
NAS2_0884	142 CDS	putative exported protein		Crenarchaeota		0FER2@creNOG,COG3439@NOG,arCOG02781@arNOG		Cytoplasmic
NAS2_0885	288 CDS	Permease of the drug/metabolite transporter superfamily		Thaumarchaeota	E	0KY22@eurNOG,1CDEF@theNOG,COG0697@NOG,arCOG00271@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_0886	184 CDS	hypothetical protein		Crenarchaeota		0FC96@creNOG,COG3371@NOG,arCOG02008@arNOG		CytoplasmicMembrane
NAS2_0887	92 CDS	hypothetical protein		cellular organisms				Cytoplasmic

NAS2_0888	384 CDS	Predicted protease of the collagenase family		Crenarchaeota	O	MER0247111	0FB0Y@creNOG,COG0826@NOG,arCOG03202@arNOG		Unknown	Peptidase
NAS2_0889	390 CDS	Transport membrane protein		Thaumarchaeota	G		02U29@arNOG,0FFXA@creNOG,11HDY@arNOG			
NAS2_0890	164 CDS	Alanyl-tRNA synthetase domain protein	K01872	Crenarchaeota	J		0KW8T@eurNOG,1CEU3@thermNOG,COG2872@NOG,arCOG01256@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0891	500 CDS	Acetate permease AcIP	K03307	Crenarchaeota	E		0FBHS@creNOG,COG0591@arNOG,arCOG01316@arNOG	Transporter (Other)	CytoplasmicMembrane	
NAS2_0892	61 CDS	hypothetical membrane protein		cellular organisms			0ZJ86@arNOG,arCOG03694@arNOG		CytoplasmicMembrane	
NAS2_0893	152 CDS	Transcriptional regulator, AsnC family	K03718	Thaumarchaeota	K		1CBWJ@haNOG,COG1522@arNOG,arCOG01580@arNOG		Cytoplasmic	
NAS2_0894	172 CDS	nitroreductase		Thaumarchaeota	C		0FC7T@creNOG,COG0378@arNOG,arCOG00288@arNOG		Cytoplasmic	
NAS2_0895	342 CDS	phosphate regulatory protein homolog		Thaumarchaeota	P		0FBQ0@creNOG,COG0704@arNOG,arCOG00318@arNOG		Unknown	
NAS2_0896	559 CDS	Permease, multidrug efflux		Archaea	P		0FBCV@creNOG,0XNN3@arNOG,arCOG00144@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0897	323 CDS	Sodium/calcium exchanger membrane region	K07301	Crenarchaeota	P		0FC90@creNOG,COG0530@arNOG,arCOG02881@arNOG		CytoplasmicMembrane	
NAS2_0898	185 CDS	Histidine triad nucleotide-binding protein	K02503	Crenarchaeota	F		0KTE6@eurNOG,0WMEF@methaNOG,COG0537@arNOG,arCOG00419@arNOG		Cytoplasmic	
NAS2_0899	541 CDS	Acetyl-CoA:acetoacetyl-CoA transferase, alpha subunit	2.8.3.8	Archaea	I		COG4670@arNOG,arCOG01986@arNOG		Unknown	
NAS2_0900	376 CDS	C4-dicarboxylate transporter		Euryarchaeota	P		0KTNW@eurNOG,1CCYB@theNOG,COG1275@arNOG,arCOG04355@arNOG	Transporter (Other)	CytoplasmicMembrane	
NAS2_0901	395 CDS	Phosphoribosylaminoimidazole carboxylase ATPase subunit	4.1.1.21	Crenarchaeota	F		0FBZ0@creNOG,COG0026@arNOG,arCOG01597@arNOG		CytoplasmicMembrane	
NAS2_0902	163 CDS	Phosphoribosylaminoimidazole carboxylase catalytic subunit	4.1.1.21	cellular organisms	F		0FBVD@creNOG,COG0041@arNOG,arCOG002464@arNOG		Unknown	
NAS2_0903	449 CDS	phosphoribosylaminoimidazole synthetase		Archaea	F		0KR5K@eurNOG,COG0150@arNOG,arCOG00639@arNOG	Transporter (MFS)	Cytoplasmic	
NAS2_0904	472 CDS	Multidrug resistance protein		Crenarchaeota	P		0FB3C@creNOG,0XNN3@arNOG,arCOG00144@arNOG		CytoplasmicMembrane	
NAS2_0905	455 CDS	hypothetical protein		Thaumarchaeota	M		COG1361@arNOG,arCOG02089@arNOG		CytoplasmicMembrane	
NAS2_0906	365 CDS	Chaperone protein DnaJ	K03686	Archaea	O		0KR9S@eurNOG,0WJWJ@methaNOG,COG0484@arNOG,arCOG02846@arNOG		Cytoplasmic	
NAS2_0907	631 CDS	Chaperone protein DnaK	K04043	Archaea	O		0KR98@eurNOG,0WK7W@methaNOG,COG0443@arNOG,arCOG03060@arNOG		Cytoplasmic	
NAS2_0908	158 CDS	Heat shock protein GrpE	K03687	cellular organisms	O		0KTGQ@eurNOG,0WMEG@methaNOG,COG0576@arNOG,arCOG04772@arNOG		Cytoplasmic	
NAS2_0909	250 CDS	Exodeoxyribonuclease III	3.1.1.12	cellular organisms	L		0KRMU@eurNOG,1CCKG@theNOG,COG0708@arNOG,arCOG02207@arNOG		Cytoplasmic	
NAS2_0910	511 CDS	Radical SAM domain heme biosynthesis protein		Thaumarchaeota			0FAZ4@creNOG,COG0535@arNOG,arCOG00949@arNOG		Cytoplasmic	
NAS2_0911	148 CDS	hypothetical protein		Thaumarchaeota			0KUDM@eurNOG,COG0589@arNOG,arCOG02053@arNOG		Cytoplasmic	
NAS2_0912	385 CDS	Arsenical-resistance protein ACR3		Crenarchaeota	P		COG0798@arNOG,arCOG02190@arNOG		CytoplasmicMembrane	
NAS2_0913	465 CDS	hypothetical protein	K07496	root;	L		0FCI7@creNOG,COG0675@arNOG,arCOG00683@arNOG		Cytoplasmic	
NAS2_0914	140 CDS	putative transcription regulator		Thaumarchaeota	K		0KV2Y@eurNOG,COG1522@arNOG,arCOG01580@arNOG		Cytoplasmic	
NAS2_0915	245 CDS	hypothetical protein		Thaumarchaeota				Unknown		
NAS2_0916	521 CDS	Fe-S oxidoreductase		Thaumarchaeota	C		0FBKS@creNOG,COG1032@arNOG,arCOG01357@arNOG		Cytoplasmic	Phs/Psr
NAS2_0917	407 CDS	Sulfite reduction-associated complex DsrMKJOP protein DsrK		Crenarchaeota	C		0FBMZ@creNOG,COG0247@arNOG,arCOG00333@arNOG		CytoplasmicMembrane	Phs/Psr
NAS2_0918	224 CDS	hypothetical protein	K00374	Crenarchaeota	C		0FDA8@creNOG,COG2181@arNOG,arCOG02194@arNOG		CytoplasmicMembrane	Phs/Psr
NAS2_0919	299 CDS	Polysulfide reductase, subunit C, putative		Crenarchaeota	P		0FCM5@creNOG,COG3301@arNOG,arCOG02027@arNOG		CytoplasmicMembrane	Phs/Psr
NAS2_0920	213 CDS	Fe-S-cluster-containing hydrogenase components 1	K04014	Thaumarchaeota	C		0FDTF@creNOG,COG0437@arNOG,arCOG01500@arNOG		Cytoplasmic	Phs/Psr
NAS2_0921	841 CDS	Anaerobic dehydrogenases, typically selenocysteine-containing		Crenarchaeota	C		0FBA2@creNOG,COG0243@arNOG,arCOG01495@arNOG,arCOG01496@arNOG		multples	Phs/Psr
NAS2_0922	250 CDS	Phosphoribosylformylglycinamide synthase, glutamine amidotransfer	6.3.5.3	Thaumarchaeota	F	MER0066352	0K54G@eurNOG,COG0047@arNOG,arCOG00102@arNOG		Cytoplasmic	
NAS2_0923	747 CDS	Phosphoribosylformylglycinamide synthase, synthetase subunit	6.3.5.3	Archaea	F		0KRED@eurNOG,0WJYY@methaNOG,COG0046@arNOG,arCOG00641@arNOG		Cytoplasmic	
NAS2_0924	84 CDS	Phosphoribosylformylglycinamide synthase, PurS subunit	6.3.5.3	cellular organisms	F			Cytoplasmic		
NAS2_0925	458 CDS	Phosphoribosylcyanide formyltransferase 2	K08289	Archaea	F			CytoplasmicMembrane		
NAS2_0926	505 CDS	Phosphoribosylamine-glycine ligase	6.3.4.13	Archaea	F		0FBON@creNOG,COG0027@arNOG,arCOG01598@arNOG		Cytoplasmic	
NAS2_0927	412 CDS	Amidophosphoribosyltransferase	2.4.2.14	Archaea	F	MER0223378	0FBF5@creNOG,COG0151@arNOG,arCOG04415@arNOG		Cytoplasmic	
NAS2_0928	457 CDS	Amidophosphoribosyltransferase	2.4.2.14	TACK group	F	MER0223378	0FBGA@creNOG,COG0034@arNOG,arCOG00094@arNOG		Unknown	
NAS2_0929	392 CDS	Phosphoribosylaminoimidazole-succinocarboxamide synthase	6.3.2.6	cellular organisms	F		0KRNN@eurNOG,COG0034@arNOG,arCOG00093@arNOG		Cytoplasmic	
NAS2_0930	631 CDS	Formate dehydrogenase alpha subunit	1.2.1.2	cellular organisms	C		1CBFT@haNOG,COG0152@arNOG,arCOG00442@arNOG		Cytoplasmic	MoCo
NAS2_0931	145 CDS	Phosphoglycerate mutase	5.4.2.1	Korarchaeota	L		02TVE@arNOG,0M28X@eurNOG,0RJYP@haNOG,COG0243@arNOG		Cytoplasmic	
NAS2_0932	270 CDS	hypothetical protein		Archaea			0KUMU@eurNOG,0WMJL8@methaNOG,COG0328@arNOG,arCOG02942@arNOG		Cytoplasmic	
NAS2_0933	170 CDS	hypothetical protein	K09763	Archaea				Cytoplasmic		
NAS2_0934	112 CDS	hypothetical protein		Crenarchaeota			0FCJH@creNOG,COG3370@arNOG,arCOG01668@arNOG		Cytoplasmic	
NAS2_0935	169 CDS	hypothetical protein		cellular organisms				Cytoplasmic		
NAS2_0936	361 CDS	Permease, major facilitator superfamily		Crenarchaeota	G			Transporter (MFS)	CytoplasmicMembrane	
NAS2_0937	193 CDS	hypothetical protein		Crenarchaeota			02U7U@arNOG,0FFYI@creNOG,0YM60@arNOG		Cytoplasmic	
NAS2_0938	496 CDS	Thermostable carboxypeptidase 1	3.4.17.19	Archaea	E	MER0857689	0FCXS@creNOG,129P2@arNOG,arCOG05401@arNOG		Cytoplasmic	
NAS2_0939	263 CDS	hypothetical protein		Thaumarchaeota		MER0182388	0FBEU@creNOG,COG2317@arNOG,arCOG04247@arNOG		Cytoplasmic	Peptidase
NAS2_0940	290 CDS	nodulin 21-related protein		Thaumarchaeota			0FD2Q@creNOG,COG0121@arNOG,arCOG03639@arNOG		Unknown	
NAS2_0941	276 CDS	Membrane protein	K07090	Crenarchaeota			0FBXD@creNOG,COG1814@arNOG,arCOG01096@arNOG		CytoplasmicMembrane	
NAS2_0942	325 CDS	integral membrane protein	K07027	Thaumarchaeota			0FBD1@creNOG,COG0730@arNOG,arCOG02059@arNOG		CytoplasmicMembrane	
NAS2_0943	384 CDS	putative polysaccharide deacetylase		Thaumarchaeota	M		0FC3S@creNOG,COG1215@arNOG,arCOG01389@arNOG		CytoplasmicMembrane	
NAS2_0944	286 CDS	Radical SAM domain heme biosynthesis protein		Thaumarchaeota			0KRT0@eurNOG,COG0535@arNOG,arCOG00938@arNOG		Cytoplasmic	
NAS2_0945	125 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic		
NAS2_0946	378 CDS	Putative transport protein		Crenarchaeota	G		02U27@arNOG,0FFX9@creNOG,0XS83@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_0947	250 CDS	hypothetical protein		Crenarchaeota			0FC6Y@creNOG,COG4089@arNOG,arCOG02159@arNOG		CytoplasmicMembrane	
NAS2_0948	290 CDS	Phosphomethylpyrimidine kinase	2.5.1.3	Archaea	K		0FBMV@creNOG,COG1992@arNOG,COG2522@arNOG,arCOG00021@arNOG		Unknown	
NAS2_0949	236 CDS	hypothetical protein		Thaumarchaeota	L		0FC7V@creNOG,COG4998@arNOG,arCOG04306@arNOG		Cytoplasmic	
NAS2_0950	678 CDS	Fe-S oxidoreductase		Thaumarchaeota	C		0FB0T@creNOG,COG0247@arNOG,arCOG00332@arNOG		CytoplasmicMembrane	
NAS2_0951	314 CDS	Electron transfer flavoprotein, alpha subunit	K03522	Thaumarchaeota	C		0FC2Q@creNOG,COG2025@arNOG,arCOG00447@arNOG		Cytoplasmic	
NAS2_0952	265 CDS	Electron transfer flavoprotein, beta subunit	K03521	Thaumarchaeota	C		0FBXA@creNOG,COG2066@arNOG,arCOG00446@arNOG		Unknown	
NAS2_0953	764 CDS	Xanthine dehydrogenase, molybdenum binding subunit	1.17.1.4	cellular organisms	C		0FB3T@creNOG,COG1529@arNOG,arCOG01167@arNOG		CytoplasmicMembrane	Cox/AOR
NAS2_0954	167 CDS	Xanthine dehydrogenase iron-sulfur subunit	1.17.1.4	cellular organisms	C		0FBB5@creNOG,COG2080@arNOG,arCOG01925@arNOG		Cytoplasmic	Cox/AOR
NAS2_0955	294 CDS	Xanthine dehydrogenase, FAD binding subunit	1.17.1.4	Thaumarchaeota	C		0FB9S@creNOG,COG1319@arNOG,arCOG01926@arNOG		Unknown	Cox/AOR
NAS2_0956	537 CDS	Long-chain-fatty acid-CoA ligase	6.2.1.3	Bathyarchaeota	I		0KRW5@eurNOG,0WK9Y@methaNOG,COG0318@arNOG,arCOG00856@arNOG		Cytoplasmic	ACSL
NAS2_0957	136 CDS	hypothetical protein	K07068	cellular organisms			0FCCA@creNOG,COG1545@arNOG,arCOG01285@arNOG		Cytoplasmic	
NAS2_0958	394 CDS	Thiolase		Archaea	I		COG0183@arNOG,arCOG01278@arNOG		Cytoplasmic	
NAS2_0959	264 CDS	Enoyl-CoA hydratase	4.2.1.17	Archaea	I	MER1073108	0KU3G@eurNOG,COG1024@arNOG,arCOG000239@arNOG		Cytoplasmic	ECAH
NAS2_0960	148 CDS	Carbon monoxide oxidation accessory protein CoxG	K09386	Thaumarchaeota			0FDJE@creNOG,COG3427@arNOG,arCOG01927@arNOG		Unknown	
NAS2_0961	812 CDS	Carbon monoxide dehydrogenase large chain	1.2.9.9.2	Archaea	C		0FB3T@creNOG,COG1529@arNOG,arCOG01167@arNOG		CytoplasmicMembrane	Cox/AOR
NAS2_0962	167 CDS	Carbon monoxide dehydrogenase small chain	1.2.9.9.2	cellular organisms	C		0FBB5@creNOG,COG2080@arNOG,arCOG01925@arNOG		Cytoplasmic	Cox/AOR
NAS2_0963	294 CDS	Carbon monoxide dehydrogenase medium chain	1.2.9.9.2	cellular organisms	C		0FB9S@creNOG,COG1319@arNOG,arCOG01926@arNOG		Cytoplasmic	Cox/AOR
NAS2_0964	389 CDS	Butyryl-CoA dehydrogenase	1.3.9.9.2	Archaea	I		0KW73@eurNOG,0RGGX@haNOG,COG1960@arNOG,arCOG04350@arNOG		Cytoplasmic	ACADH
NAS2_0965	120 CDS	hypothetical protein	K07107	Archaea						
NAS2_0966	789 CDS	Carbon monoxide dehydrogenase large chain	1.2.9.9.2	Archaea	C		0FB3T@creNOG,COG1529@arNOG,arCOG01167@arNOG		Cytoplasmic	
NAS2_0967	260 CDS	Enoyl-CoA hydratase	4.2.1.17	Thaumarchaeota	I	MER1073108	0FBM3@creNOG,COG1024@arNOG,arCOG000239@arNOG		Cytoplasmic	ECAH
NAS2_0968	280 CDS	3-oxoacyl-[acyl-carrier protein] reductase	1.1.1.100	Thaumarchaeota			0KTBW@eurNOG,0RGZU@haNOG,COG1028@arNOG,arCOG01259@arNOG		Cytoplasmic	
NAS2_0969	280 CDS	Chromosome (plasmid) partitioning protein ParB	K03497	Thaumarchaeota	K					
NAS2_0970	298 CDS	Cyclase family protein		Thaumarchaeota			0KVU8@eurNOG,1CD9N@theNOG,COG1878@arNOG,arCOG02462@arNOG		Cytoplasmic	
NAS2_0971	337 CDS	Fumarylacetoacetate hydrolase family protein		Thaumarchaeota	Q		0KTCQ@eurNOG,COG0179@arNOG,arCOG00235@arNOG		Cytoplasmic	
NAS2_0972	151 CDS	Monamine oxidase regulatory protein		Thaumarchaeota	I		0FCZM@creNOG,COG2030@arNOG,arCOG00774@arNOG		Unknown	
NAS2_0973	158 CDS	UPF0152 protein		Archaea	Q		0FC8V@creNOG,COG2050@arNOG,arCOG00777@arNOG		Cytoplasmic	
NAS2_0974	412 CDS	2-isopropylmalate synthase	2.3.3.13	Archaea	E		0KRDE@eurNOG,0WRRH@metNOG,COG0119@arNOG,arCOG02092@arNOG		Cytoplasmic	
NAS2_0975	185 CDS	hypothetical protein		Thaumarchaeota					CytoplasmicMembrane	
NAS2_0976	440 CDS	Phenylacetate-coenzyme A ligase	6.2.1.30	Thaumarchaeota	Q		0KRHG@eurNOG,0WK8Y@methaNOG,COG1541@arNOG,arCOG02620@arNOG		Cytoplasmic	

NAS2_0977	212 CDS	hypothetical protein		Thaumarchaeota						Cytoplasmic
NAS2_0978	186 CDS	hypothetical protein		Not assigned						CytoplasmicMembrane
NAS2_0979	378 CDS	hypothetical protein		cellular organisms	I					Unknown
NAS2_0980	289 CDS	hypothetical protein		Thaumarchaeota	C					CytoplasmicMembrane
NAS2_0981	832 CDS	Anaerobic dimethyl sulfoxide reductase chain A	1.8.5.3	K07812	Thaumarchaeota	C		COG0437@NOG,arCOG01500@arNOG		Unknown
NAS2_0982	410 CDS	3-ketobacyl-CoA thiolase	2.3.1.16		Thaumarchaeota	I		0KVQX@eurNOG,COG0243@NOG,arCOG01491@arNOG		MoCo
NAS2_0983	145 CDS	hypothetical protein			Thaumarchaeota			0KRB2@eurNOG,COG0183@NOG,arCOG01278@arNOG		ATO
NAS2_0984	404 CDS	CAIB/BAIF family protein			Thaumarchaeota	C		0KT3U@eurNOG,0WQTY@methNOG,COG1545@NOG,arCOG01285@arNOG		Cytoplasmic
NAS2_0985	271 CDS	3-oxoacyl-[acyl-carrier protein] reductase	1.1.1.100	K00046	Thaumarchaeota			0FB8Q@creNOG,COG1804@NOG,arCOG02304@arNOG		Cytoplasmic
NAS2_0986	301 CDS	Kynurenine formamidase, bacterial	3.5.1.9		Thaumarchaeota			02HXP@arcNOG,0KT8W@eurNOG,COG1028@NOG,arCOG01259@arNOG		Cytoplasmic
NAS2_0987	264 CDS	Enoyl-CoA hydratase	4.2.1.17	K01715	Thaumarchaeota	I	MER1073108	0KYHE@eurNOG,COG1878@NOG,arCOG02462@arNOG		Cytoplasmic
NAS2_0988	294 CDS	Fe-S-cluster-containing hydrogenase components 1			Thaumarchaeota	C		COG1024@NOG,arCOG00239@arNOG		ECAH
NAS2_0989	880 CDS	Anaerobic dehydrogenases, typically selenocysteine-containing		K07812	Bacteria	C		COG0437@NOG,arCOG01500@arNOG		Cytoplasmic
NAS2_0990	259 CDS	Zinc ABC transporter, ATP-binding protein ZnuC		K11710	Thaumarchaeota	P		0KVQX@eurNOG,COG0243@NOG,arCOG01491@arNOG		multples
NAS2_0991	290 CDS	Vitamin B12 ABC transporter, permease component BtuC		K02015	Crenarchaeota	P		0FB22@creNOG,COG1120@NOG,arCOG00198@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0992	411 CDS	Vitamin B12 ABC transporter, B12-binding component BtuF		K02016	Thaumarchaeota	P		0FC28@creNOG,COG0609@NOG,arCOG01007@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0993	38 CDS	hypothetical protein			No hits			0FBYJ@creNOG,COG0614@NOG,arCOG04233@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_0994	202 CDS	GTP cyclohydrolase III			Crenarchaeota					Cytoplasmic
NAS2_0995	229 CDS	Cobalt-precorrin-6γ C5-methyltransferase		K03399	Archaea	H		0FE7G@creNOG,COG0457@NOG,arCOG05195@arNOG		Cytoplasmic
NAS2_0996	223 CDS	Cobalt-precorrin-6γ C5-methyltransferase		K03399	Bacteria	H		0KTY@eurNOG,0RFF1@haINOG,COG2241@NOG,arCOG00650@arNOG		Cytoplasmic
NAS2_0997	323 CDS	Asparagine synthase		K01953	Crenarchaeota	E		1CB07@thaNOG,COG2241@NOG,arCOG00650@arNOG		Unknown
NAS2_0998	169 CDS	Conserved protein			cellular organisms	Q		0FCUX@creNOG,COG0367@NOG,arCOG00071@arNOG		Cytoplasmic
NAS2_0999	252 CDS	putative HAD-hydrolase		K20881	Archaea			0KT6W@eurNOG,0WS43@metNOG,COG0500@NOG,arCOG02702@arNOG		ASNS
NAS2_1000	372 CDS	ABC transporter, permease protein		K01992	Thaumarchaeota	V		0KY4F@eurNOG,0WNNM@methaNOG,COG10111@NOG,arCOG02291@arNOG		Cytoplasmic
NAS2_1001	257 CDS	Dauorubicin resistance ATP-binding protein drrA		K01990	Thaumarchaeota	V		0KROR@eurNOG,0WNNM@methaNOG,COG10111@NOG,arCOG02291@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1002	533 CDS	hypothetical protein			Thaumarchaeota			0KRQ5@eurNOG,COG1131@NOG,arCOG00194@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1003	331 CDS	hypothetic protein			Thaumarchaeota			0FBG8@creNOG,COG1361@NOG,arCOG02089@arNOG		CytoplasmicMembrane
NAS2_1004	137 CDS	iron dependent repressor			Archaea			0XTDK@NOG,arCOG06008@arNOG		CytoplasmicMembrane
NAS2_1005	458 CDS	Glycolate dehydrogenase	1.1.99.14		Thaumarchaeota	K		0KUAF@eurNOG,1CCY0@theNOG,COG1321@NOG,arCOG02100@arNOG		Cytoplasmic
NAS2_1006	307 CDS	UDP-glucose 4-epimerase	5.1.3.2		Archaea	C		0KRDB@eurNOG,0WK2S@methaNOG,COG0277@NOG,arCOG00337@arNOG		CytoplasmicMembrane
NAS2_1007	218 CDS	hypothetical protein			Thaumarchaeota	M		0KV0T@eurNOG,0RFF5@haINOG,COG0451@NOG,arCOG00446@arNOG		Cytoplasmic
NAS2_1008	207 CDS	conserved hypothetical protein			Thaumarchaeota			0KUJ1M@eurNOG,COG0491@NOG,arCOG00504@arNOG		Unknown
NAS2_1009	165 CDS	Hydroxycyglutathione hydrolase	3.1.2.6		Thaumarchaeota			0FC97@eurNOG,COG2102@NOG,arCOG0036@arNOG		Cytoplasmic
NAS2_1010	38 CDS	hypothetical protein			No hits			0FCN9@creNOG,COG0491@NOG,arCOG00504@arNOG		Cytoplasmic
NAS2_1011	455 CDS	branched-chain amino acid ABC transporter, periplasmic binding protein		K01999	Thaumarchaeota	E			Transporter (ABC)	CytoplasmicMembrane
NAS2_1012	93 CDS	Ferredoxin			Thaumarchaeota			0FCTG@creNOG,COG2146@NOG,arCOG02854@arNOG		Cytoplasmic
NAS2_1013	230 CDS	hypothetical protein			Thaumarchaeota	C				CytoplasmicMembrane
NAS2_1014	48 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_1015	115 CDS	hypothetical protein			Bacteria					Unknown
NAS2_1016	78 CDS	hypothetical protein			cellular organisms	K				Cytoplasmic
NAS2_1017	86 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1018	199 CDS	hypothetical protein			Archaea					Cytoplasmic
NAS2_1019	200 CDS	hypothetical protein			Not assigned					CytoplasmicMembrane
NAS2_1020	245 CDS	hypothetical protein			Not assigned					Unknown
NAS2_1021	606 CDS	hypothetical protein			Thaumarchaeota					CytoplasmicMembrane
NAS2_1022	216 CDS	hypothetical protein			Not assigned					CytoplasmicMembrane
NAS2_1023	452 CDS	Transposase ISC1476		K07496	root;	L		0FCI7@creNOG,COG0675@NOG,arCOG00683@arNOG		Cytoplasmic
NAS2_1024	95 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1025	114 CDS	hypothetical protein			Crenarchaeota					Cytoplasmic
NAS2_1026	323 CDS	hypothetical protein			Archaea					CytoplasmicMembrane
NAS2_1027	96 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1028	853 CDS	TPR repeat-containing protein 03			Crenarchaeota			0KRJPJ@eurNOG,0WKH5@methaNOG,COG0457@NOG,arCOG03032@arNOG,arCOG03038@arNOG,arCOG03048@arNOG		Unknown
NAS2_1029	1226 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_1030	279 CDS	Short-chain dehydrogenase			Bacteria			0KTZA@eurNOG,0RFAJ@haINOG,COG1028@NOG,arCOG01259@arNOG		Cytoplasmic
NAS2_1031	535 CDS	Flagella-related protein Flal		K07332	Archaea	U		0FBX5@creNOG,COG0630@NOG,arCOG01817@arNOG		CytoplasmicMembrane
NAS2_1032	157 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1033	165 CDS	hypothetical protein			Not assigned					Unknown
NAS2_1034	996 CDS	hypothetical protein			Thaumarchaeota	L				Cytoplasmic
NAS2_1035	197 CDS	hypothetical protein			root;					Cytoplasmic
NAS2_1036	178 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1037	196 CDS	hypothetical protein			Not assigned					Unknown
NAS2_1038	198 CDS	adenylate kinase and related kinases			Bacteria					Cytoplasmic
NAS2_1039	250 CDS	hypothetical protein			Not assigned					Unknown
NAS2_1040	1935 CDS	hypothetical protein			Bathyarchaeota			0FDQB@creNOG,COG3391@NOG,arCOG02560@arNOG,arCOG06052@arNOG		Unknown
NAS2_1041	135 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1042	315 CDS	Molybdopterin biosynthesis protein MoeA			Crenarchaeota	H		0FC5W@creNOG,COG0303@NOG,arCOG00216@arNOG		Cytoplasmic
NAS2_1043	304 CDS	Ferredoxin			Korarchaeota			0KUJU@eurNOG,0WOTH@methNOG,COG1146@NOG,arCOG02461@arNOG		Cytoplasmic
NAS2_1044	141 CDS	Transposase ISC1225			Crenarchaeota	L		02TEF@arNOG,0YA7E@NOG		Cytoplasmic
NAS2_1045	368 CDS	Cytosolic Fe-S cluster assembling factor NBP35		K03593	cellular organisms	D		1CBHE@thaNOG,COG0489@NOG,arCOG000585@arNOG		Unknown
NAS2_1046	394 CDS	hypothetical protein			Euryarchaeota					Cytoplasmic
NAS2_1047	77 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1048	241 CDS	Tsp45I type II restriction enzyme			cellular organisms	V				Cytoplasmic
NAS2_1049	397 CDS	Type III restriction-modification system methylation subunit	2.1.1.72	K07316	cellular organisms			0KS2R@eurNOG,COG2189@NOG,arCOG00108@arNOG		Cytoplasmic
NAS2_1050	719 CDS	Conserved domain protein			Crenarchaeota			0FDGA@creNOG,COG0433@NOG,arCOG04816@arNOG		Cytoplasmic
NAS2_1051	347 CDS	hypothetical protein			Bacteria					Cytoplasmic
NAS2_1052	173 CDS	hypothetical protein			Not assigned					CytoplasmicMembrane
NAS2_1053	38 CDS	hypothetical protein			No hits					Cytoplasmic
NAS2_1054	116 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1055	988 CDS	Predicted ATPase			cellular organisms			0KT9F@eurNOG,0WM9E@methaNOG,COG1483@NOG,arCOG00888@arNOG		Cytoplasmic
NAS2_1056	904 CDS	Adenine-specific DNA methylase containing a Zn-ribbon			Euryarchaeota	L		0KRQW@eurNOG,1CDKB@thermNOG,COG1743@NOG,arCOG00889@arNOG		Unknown
NAS2_1057	1032 CDS	Superfamily II DNA/RNA helicases, SNF2 family			Crenarchaeota	L		0FCG8@creNOG,COG0553@NOG,arCOG00871@arNOG		Cytoplasmic
NAS2_1058	284 CDS	hypothetical protein			Crenarchaeota					Unknown
NAS2_1059	296 CDS	Mrr restriction system protein		K07448	cellular organisms	V		0KSFA@eurNOG,0WK2T@methaNOG,COG1715@NOG,arCOG02781@arNOG		Cytoplasmic
NAS2_1060	722 CDS	Conserved domain protein			Crenarchaeota			0FDGA@creNOG,COG0433@NOG,arCOG04816@arNOG		Cytoplasmic
NAS2_1061	106 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1062	633 CDS	hypothetical protein		K07333	Thaumarchaeota	U		0FD28@creNOG,COG2064@NOG,arCOG01808@arNOG		CytoplasmicMembrane
NAS2_1063	743 CDS	cell surface protein			Crenarchaeota			0M1Y5@eurNOG,0WPK4@methaNOG,0XPQ@NOG,arCOG02498@arNOG,arCOG02508@arNOG		Extracellular
NAS2_1064	298 CDS	hypothetical protein			Not assigned					CytoplasmicMembrane
NAS2_1065	222 CDS	hypothetical protein			Thaumarchaeota					Unknown

NAS2_1066	231 CDS	hypothetical protein		K00571	cellular organisms	L				Unknown
NAS2_1067	490 CDS	hypothetical protein			DPANN					Unknown
NAS2_1068	183 CDS	hypothetical protein			TACK group					Extracellular
NAS2_1069	85 CDS	no similarity			Thaumarchaeota					Cytoplasmic
NAS2_1070	166 CDS	hypothetical protein			Archaea		0KVFD@eurNOG,0Y2I3@NOG,1CD34@theNOG,arCOG05390@arNOG			CytoplasmicMembrane
NAS2_1071	637 CDS	hypothetical protein			Thaumarchaeota	U	0FDAJ@creNOG,128UT@NOG,arCOG05320@arNOG			CytoplasmicMembrane
NAS2_1072	88 CDS	hypothetical protein			Thaumarchaeota		0FD1N@creNOG,126FB@NOG,arCOG04035@arNOG,arCOG07496@arNOG			Cytoplasmic
NAS2_1073	130 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1074	150 CDS	hypothetical protein			Not assigned					CytoplasmicMembrane
NAS2_1075	452 CDS	Transposase ISC1476		K07496	root;	L	0FCI7@creNOG,COG0675@NOG,arCOG00683@arNOG			Cytoplasmic
NAS2_1076	159 CDS	hypothetical protein			Thaumarchaeota					CytoplasmicMembrane
NAS2_1077	400 CDS	Transposase ISC1316		K07496	root;	L	0FDOE@creNOG,COG0675@NOG,arCOG00684@arNOG			Cytoplasmic
NAS2_1078	117 CDS	hypothetical protein			Thaumarchaeota		COG4345@NOG,arCOG03772@arNOG			Cytoplasmic
NAS2_1079	324 CDS	Transcription initiation factor B		K03124	Archaea	K	0KR12@eurNOG,1CCCW@theNOG,COG1405@NOG,arCOG01981@arNOG			Cytoplasmic
NAS2_1080	164 CDS	hypothetical protein			Not assigned					Unknown
NAS2_1081	166 CDS	hypothetical protein			Not assigned					Unknown
NAS2_1082	448 CDS	hypothetical protein			No hits					CytoplasmicMembrane
NAS2_1083	104 CDS	hypothetical protein			Not assigned					CytoplasmicMembrane
NAS2_1084	123 CDS	hypothetical protein			Not assigned					Unknown
NAS2_1085	350 CDS	hypothetical protein			Bacteria					Cytoplasmic
NAS2_1086	224 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1087	131 CDS	hypothetical protein			Archaea		10ZS4@NOG,1CBVP@thaNOG,arCOG08677@arNOG			Cytoplasmic
NAS2_1088	48 CDS	hypothetical protein			No hits					Cytoplasmic
NAS2_1089	266 CDS	hypothetical protein			Thaumarchaeota					Unknown
NAS2_1090	448 CDS	hypothetical protein			cellular organisms	L				Cytoplasmic
NAS2_1091	427 CDS	Cobalt-zinc-cadmium resistance protein			Thaumarchaeota	P	0KVW2@eurNOG,COG0582@NOG,arCOG01241@arNOG			Cytoplasmic
NAS2_1092	485 CDS	NADH-ubiquinone oxidoreductase chain N	1.6.5.3	K00343	Crenarchaeota	C	0KSJ5@eurNOG,0WRPZ@methNOG,COG0053@NOG,arCOG01475@arNOG	Transporter (Other)		CytoplasmicMembrane
NAS2_1093	699 CDS	NADH-ubiquinone oxidoreductase chain L	1.6.5.3	K00341	Crenarchaeota	C	0FBJ4@creNOG,COG1007@NOG,arCOG01540@arNOG	Transporter (Other)		CytoplasmicMembrane Nuo
NAS2_1094	518 CDS	NADH-ubiquinone oxidoreductase chain M	1.6.5.3	K00342	Crenarchaeota	C	02TBG@arNOG,0FFSV@creNOG,COG1009@NOG	Transporter (Other)		CytoplasmicMembrane Nuo
NAS2_1095	103 CDS	NADH dehydrogenase subunit 4L		K00340	Crenarchaeota	C	0FAZ8@creNOG,COG0651@NOG,arCOG01537@arNOG	Transporter (Other)		CytoplasmicMembrane Nuo
NAS2_1096	161 CDS	NADH-ubiquinone oxidoreductase chain J	1.6.5.3	K00339	Crenarchaeota	C				CytoplasmicMembrane Nuo
NAS2_1097	218 CDS	NADH-ubiquinone oxidoreductase chain I	1.6.5.3	K00338	Crenarchaeota	C	0FDH7@creNOG,COG0839@NOG,arCOG04654@arNOG			Unknown
NAS2_1098	357 CDS	NADH-ubiquinone oxidoreductase chain H	1.6.5.3	K00337	Crenarchaeota	C	0FBWP@creNOG,COG1143@NOG,arCOG01543@arNOG		Nuo	
NAS2_1099	414 CDS	NADH-ubiquinone oxidoreductase chain D	1.6.5.3	K00333	Crenarchaeota	C	0FC1P@creNOG,COG1005@NOG,arCOG01546@arNOG			CytoplasmicMembrane Nuo
NAS2_1100	174 CDS	NADH-ubiquinone oxidoreductase chain C	1.6.5.3	K00332	Thaumarchaeota	C	0FAZ5@creNOG,COG0649@NOG,arCOG01548@arNOG		multiples	Nuo
NAS2_1101	211 CDS	NADH-ubiquinone oxidoreductase chain B	1.6.5.3	K00331	TACK group	C	0FCYH@creNOG,COG0852@NOG,arCOG01551@arNOG		multiples	Nuo
NAS2_1102	137 CDS	NADH-ubiquinone oxidoreductase chain A	1.6.5.3	K00330	Thaumarchaeota	C	0FC4Q@creNOG,COG0377@NOG,arCOG01554@arNOG			CytoplasmicMembrane Nuo
NAS2_1103	401 CDS	Threonine synthase	4.2.3.1	K01733	Thaumarchaeota	E	0FFP4@creNOG,COG0838@NOG,arCOG01557@arNOG			CytoplasmicMembrane Nuo
NAS2_1104	331 CDS	Homoserine dehydrogenase	1.1.1.3	K00003	Archaea	E	0KRPG@eurNOG,0WPU3@methNOG,COG0498@NOG,arCOG01434@arNOG			Cytoplasmic
NAS2_1105	464 CDS	Aspartokinase	2.7.2.4	K00928	Archaea	E	1CBJZ@thaNOG,COG0460@NOG,arCOG01351@arNOG			Cytoplasmic
NAS2_1106	404 CDS	Uncharacterized protein			Archaea		0KRS9@eurNOG,0WJZ4@methaNOG,COG0527@NOG,arCOG00861@arNOG			Unknown
NAS2_1107	145 CDS	Diadenosine 55''-P ₁ ,P ₄ -tetraphosphate pyrophosphohydrolase			cellular organisms	L	0KRV8@eurNOG,COG1915@NOG,arCOG04422@arNOG			Cytoplasmic
NAS2_1108	366 CDS	hypothetical protein			cellular organisms	L	0KUXA@eurNOG,COG0494@NOG,arCOG01078@arNOG			Cytoplasmic
NAS2_1109	462 CDS	Cysteinyl-tRNA synthetase	6.1.1.16	K01883	Thaumarchaeota	J	1CB80@thaNOG,COG0446@NOG,arCOG04181@arNOG			Cytoplasmic
NAS2_1110	369 CDS	Glutamate synthase [NADPH] small chain	1.4.1.13	K00266	Crenarchaeota	E	1CBNF@thaNOG,COG0215@NOG,arCOG00486@arNOG			Cytoplasmic
NAS2_1111	333 CDS	Thymidylate synthase thylX		K03465	Thaumarchaeota	F	0FB9G@creNOG,COG0493@NOG,arCOG01292@arNOG			Cytoplasmic
NAS2_1112	404 CDS	RNA methyltransferase, TrmA family			Thaumarchaeota	J	0KUGS@eurNOG,COG1351@NOG,arCOG01883@arNOG			Cytoplasmic
NAS2_1113	124 CDS	Bis(5'-nucleosyl)-tetraphosphate (asymmetrical)	3.6.1.17	K02503	Archaea	F	0M1J6@eurNOG,1CECE@thermNOG,COG285@NOG,arCOG00122@arNOG			Cytoplasmic
NAS2_1114	742 CDS	Archaeal DNA polymerase I	2.7.7.7	K02319	Thaumarchaeota	L	0KTE6@eurNOG,0RHD6@halNOG,COG0537@NOG,arCOG00419@arNOG			Cytoplasmic
NAS2_1115	400 CDS	Single-stranded-DNA-specific exonuclease RecJ		K07463	Thaumarchaeota	L	0FB87@creNOG,COG0417@NOG,arCOG00328@arNOG			Cytoplasmic
NAS2_1116	526 CDS	KH domain-containing protein		K06865	Thaumarchaeota		02H8F@arNOG,0KYJ2@eurNOG,COG0608@NOG,arCOG00427@arNOG			Cytoplasmic
NAS2_1117	152 CDS	Diadenosine 55''-P ₁ ,P ₄ -tetraphosphate pyrophosphohydrolase			Thaumarchaeota		0KRMH@eurNOG,0WQN2@methNOG,COG1855@NOG,arCOG04116@arNOG			Cytoplasmic
NAS2_1118	363 CDS	Inositol-1-phosphate synthase	5.5.1.4	K01858	Archaea	I	0FEJ8@creNOG,COG0494@NOG,arCOG01078@arNOG			Cytoplasmic
NAS2_1119	189 CDS	hypothetical protein			Thaumarchaeota		0KRHH@eurNOG,1CDP1@thermNOG,COG1260@NOG,arCOG04213@arNOG			Cytoplasmic
NAS2_1120	48 CDS	hypothetical protein			Thaumarchaeota		11QY5@NOG,1CBPH@thaNOG,arCOG03142@arNOG			Unknown
NAS2_1121	104 CDS	hypothetical protein			Archaea		0Z38J@NOG,arCOG07440@arNOG			Cytoplasmic
NAS2_1122	187 CDS	Nucleotidase YtbR, HD superfamily		K07023	Thaumarchaeota		0KVJU@eurNOG,COG1896@NOG,arCOG004311@arNOG			Cytoplasmic
NAS2_1123	441 CDS	Histidinol dehydrogenase	1.1.1.23	K00013	Archaea	E	0KRPE@eurNOG,0WRAU@methNOG,COG0141@NOG,arCOG004352@arNOG			Cytoplasmic
NAS2_1124	370 CDS	Multidrug efflux permease			Thaumarchaeota	G	0FBK3@creNOG,COG0477@NOG,arCOG00132@arNOG	Transporter (MFS)		CytoplasmicMembrane
NAS2_1125	407 CDS	Cytochrome d ubiquinol oxidase subunit I		K00425	Thaumarchaeota	C	0FB9Y@creNOG,COG1271@NOG,arCOG002720@arNOG			CytoplasmicMembrane Cyd
NAS2_1126	444 CDS	Cytochrome d ubiquinol oxidase subunit I		K00425	TACK group	C	0FB5H@creNOG,COG1271@NOG,arCOG002721@arNOG			Cytoplasmic
NAS2_1127	261 CDS	3-oxoacyl-[acyl-carrier protein] reductase	1.1.1.100	K00059	Thaumarchaeota		0FBR2@creNOG,COG1028@NOG,arCOG01259@arNOG			Cytoplasmic
NAS2_1128	128 CDS	Methylated-DNA--protein-cysteine methyltransferase	2.1.1.63	K00567	Crenarchaeota	L	0FCY9@creNOG,COG0350@NOG,arCOG02724@arNOG			Cytoplasmic
NAS2_1129	554 CDS	Seryl-tRNA synthetase	6.1.1.11	K01875	Thaumarchaeota	J	0KRKX@eurNOG,0WK8Q@methaNOG,COG01172@NOG,arCOG00403@arNOG			Cytoplasmic
NAS2_1130	223 CDS	Ribose 5-phosphate isomerase A	5.3.1.6	K01807	Thaumarchaeota	G	0FCRE@creNOG,COG0120@NOG,arCOG01122@arNOG			Cytoplasmic
NAS2_1131	165 CDS	hypothetical protein			Thaumarchaeota	P	0FDGR@creNOG,COG4754@NOG,arCOG003579@arNOG			Cytoplasmic
NAS2_1132	223 CDS	hypothetical protein			Thaumarchaeota		0FBZN@creNOG,COG2220@NOG,arCOG00497@arNOG			Cytoplasmic
NAS2_1133	197 CDS	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	2.7.8.5	K17884	Thaumarchaeota	I	1CB5V@thaNOG,COG0558@NOG,arCOG00670@arNOG			CytoplasmicMembrane
NAS2_1134	94 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_1135	289 CDS	Dihydroorotate dehydrogenase	1.3.3.1	K00254	Thaumarchaeota	F	0FDAI@creNOG,COG0167@NOG,arCOG00603@arNOG			Cytoplasmic
NAS2_1136	164 CDS	Molybdopterin-guanine dinucleotide biosynthesis protein MoB		K03753	Thaumarchaeota	H	0KTB7@eurNOG,0WRWD@methNOG,COG1763@NOG,arCOG00532@arNOG			Cytoplasmic
NAS2_1137	251 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_1138	300 CDS	Ribose-phosphate pyrophosphokinase	2.7.6.1	K00948	Thaumarchaeota	F	0KS4B@eurNOG,0WQ5E@methNOG,COG0462@NOG,arCOG00067@arNOG			Cytoplasmic
NAS2_1139	97 CDS	SSU ribosomal protein S26e		K02976	Thaumarchaeota	J	0FCGX@creNOG,COG4830@NOG,arCOG04305@arNOG			Cytoplasmic
NAS2_1140	489 CDS	Prolyl-tRNA synthetase	6.1.1.15	K01881	Thaumarchaeota	J	0FB2A@creNOG,COG0442@NOG,arCOG00402@arNOG			Cytoplasmic
NAS2_1141	258 CDS	Protein-L-isoaspartate methyltransferase	2.1.1.77	K07442	Thaumarchaeota	J	0FBSD@creNOG,COG2519@NOG,arCOG00978@arNOG			Cytoplasmic
NAS2_1142	314 CDS	Homoserine kinase	2.7.1.39	K00872	Thaumarchaeota	E	1CBT3@thaNOG,COG0083@NOG,arCOG01027@arNOG			CytoplasmicMembrane
NAS2_1143	41 CDS	hypothetical protein			No hits					Unknown
NAS2_1144	239 CDS	Branched-chain amino acid transport ATP-binding protein LivG		K01996	cellular organisms	E	COG0410@NOG,COG0411@NOG,arCOG00924@arNOG,arCOG00925@arNOG	Transporter (ABC)	Unknown	AA transporters
NAS2_1145	243 CDS	Branched-chain amino acid transport ATP-binding protein LivM		K01995	cellular organisms	E	0FC4I@creNOG,COG0411@NOG,arCOG00926@arNOG	Transporter (ABC)	multiples	AA transporters
NAS2_1146	344 CDS	Branched-chain amino acid transport system permease protein LivM		K01998	Thaumarchaeota	E	0KWXX@eurNOG,COG4177@NOG,arCOG01274@arNOG	Transporter (ABC)		CytoplasmicMembrane AA transporters
NAS2_1147	296 CDS	High-affinity branched-chain amino acid transport system permease protein LivH		K01997	Thaumarchaeota	E	0KWVI@eurNOG,COG0559@NOG,arCOG01270@arNOG	Transporter (ABC)		CytoplasmicMembrane AA transporters
NAS2_1148	444 CDS	Branched-chain amino acid ABC transporter, amino acid-binding protein		K01999	Thaumarchaeota	E	0KWFJ@eurNOG,COG0683@NOG,arCOG01020@arNOG	Transporter (ABC)	Unknown	AA transporters
NAS2_1149	234 CDS	hypothetical protein			Thaumarchaeota	C	0FDQ5@creNOG,0YJKM@NOG,arCOG05634@arNOG			Cytoplasmic
NAS2_1150	399 CDS	Manganese transport protein MntH			Thaumarchaeota	P	0FBAY@creNOG,COG1914@NOG,arCOG04531@arNOG	Transporter (Other)		CytoplasmicMembrane
NAS2_1151	307 CDS	hypothetical protein			Crenarchaeota	L	0FBM6@creNOG,COG0675@NOG,arCOG00679@arNOG			Cytoplasmic
NAS2_1152	307 CDS	Fumarylacetoacetate hydrolase family protein			Thaumarchaeota	Q	0FB34@creNOG,COG0179@NOG,arCOG00235@arNOG			Cytoplasmic
NAS2_1153	145 CDS	CBS domain protein			Thaumarchaeota		0KTGA@eurNOG,1CCYE@theNOG,COG0517@NOG,arCOG00606@arNOG			Cytoplasmic
NAS2_1154	459 CDS	Phosphate transporter related protein		K08176	TACK group	G	0FB90@creNOG,0XQKC@NOG,arCOG02682@arNOG	Transporter (MFS)		CytoplasmicMembrane

NAS2_1155	317 CDS	Radical SAM domain protein		Thaumarchaeota	C		0KSGU@eurNOG,1CEB4@thermNOG,COG0731@NOG,arCOG00953@arNOG	Cytoplasmic	
NAS2_1156	165 CDS	NADH-FMN oxidoreductase		Crenarchaeota			0FCEY@creNOG,COG1853@NOG,arCOG02017@arNOG	Unknown	
NAS2_1157	323 CDS	Acyl-CoA thioesterase		Crenarchaeota	I		0FD7U@creNOG,COG1607@NOG,arCOG00773@arNOG	Cytoplasmic	
NAS2_1158	204 CDS	Uncharacterized Zn-dependent protease		Thaumarchaeota		MER0223052	0FC7Y@creNOG,COG1994@NOG,arCOG00614@arNOG	CytoplasmicMembrane	Peptidase
NAS2_1159	277 CDS	Queuosine Biosynthesis QueC ATPase	K06920	Thaumarchaeota			0FBB7@creNOG,COG0603@NOG,arCOG00039@arNOG	Cytoplasmic	
NAS2_1160	393 CDS	Alcohol dehydrogenase	1.1.1.1	Crenarchaeota	C		0FBUG@creNOG,COG1454@NOG,arCOG00984@arNOG	Cytoplasmic	
NAS2_1161	238 CDS	Putative preQ0 transporter	K09125	Crenarchaeota			0FCM1@creNOG,COG1738@NOG,arCOG04284@arNOG	CytoplasmicMembrane	
NAS2_1162	251 CDS	Phosphoglycolate phosphatase, archaeal type	3.1.3.18	Crenarchaeota			0FCN1@creNOG,COG0561@NOG,arCOG01213@arNOG	Cytoplasmic	
NAS2_1163	85 CDS	hypothetical protein		Not assigned				multples	
NAS2_1164	80 CDS	hypothetical protein		Archaea				Unknown	
NAS2_1165	106 CDS	hypothetical protein		Korarchaeota			0FDNW@creNOG,COG0011@NOG,arCOG04373@arNOG	Unknown	
NAS2_1166	282 CDS	Molybdenum cofactor biosynthesis protein MoaC		Crenarchaeota	H		0FC7X@creNOG,COG0315@NOG,arCOG01530@arNOG	Unknown	
NAS2_1167	520 CDS	Aldehyde dehydrogenase	1.2.1.3	Archaea	E		0FBCZ@creNOG,COG1012@NOG,arCOG01252@arNOG	Cytoplasmic	
NAS2_1168	402 CDS	Sarcosine oxidase related protein		Crenarchaeota	C		0FBBB@creNOG,COG0665@NOG,arCOG00755@arNOG	Cytoplasmic	
NAS2_1169	325 CDS	hypothetical protein		Crenarchaeota			COG1819@NOG,arCOG01393@arNOG	Cytoplasmic	
NAS2_1170	404 CDS	MgIC family protein		Crenarchaeota			COG3174@NOG,arCOG04203@arNOG	CytoplasmicMembrane	
NAS2_1171	535 CDS	489aa long conserved hypothetical protein		Crenarchaeota	C		COG3174@NOG,COG1032@NOG,arCOG01357@arNOG	Unknown	
NAS2_1172	103 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic	
NAS2_1173	487 CDS	Dihydrolipamide dehydrogenase	1.8.1.4	Archaea	C		0KS32@eurNOG,0WK71@methaNOG,COG1249@NOG,arCOG01068@arNOG	Cytoplasmic	
NAS2_1174	353 CDS	Aminopeptidase Ypdf	K01271	Archaea	E	MER0077643	0FBT9@creNOG,COG0006@NOG,arCOG01000@arNOG	Cytoplasmic	Peptidase
NAS2_1175	140 CDS	molybdenum cofactor carrier protein Mcp1	K06966	Crenarchaeota			0FC9F@creNOG,COG1611@NOG,arCOG02431@arNOG	Cytoplasmic	
NAS2_1176	244 CDS	Flu003003: hypothetical protein		Thaumarchaeota			0FAXP@creNOG,COG1801@NOG,arCOG04291@arNOG	Cytoplasmic	
NAS2_1177	461 CDS	Leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein	K01999	Thaumarchaeota	E		0FBSK@creNOG,COG0683@NOG,arCOG01020@arNOG	Transporter (ABC)	AA transporters
NAS2_1178	302 CDS	Branched-chain amino acid transport system permease protein LivM	K01998	Thaumarchaeota	E		0FDB5@creNOG,COG4177@NOG,arCOG01274@arNOG	Transporter (ABC)	CytoplasmicMembrane AA transporters
NAS2_1179	290 CDS	High-affinity branched-chain amino acid transport system permease protein LivH	K01997	Thaumarchaeota	E		0FCSS@creNOG,COG0559@NOG,arCOG01270@arNOG	Transporter (ABC)	CytoplasmicMembrane AA transporters
NAS2_1180	240 CDS	Branched-chain amino acid transport ATP-binding protein LivF	K01996	Thaumarchaeota	E		COG0410@NOG,COG0411@NOG,arCOG00924@arNOG,arCOG00925@arNOG	Transporter (ABC)	multples AA transporters
NAS2_1181	249 CDS	Branched-chain amino acid transport ATP-binding protein LivG	K01995	cellular organisms	E		0FC4I@creNOG,COG0411@NOG,arCOG00926@arNOG	Transporter (ABC)	multples AA transporters
NAS2_1182	218 CDS	Phosphoglycolate phosphatase	3.1.3.18	Thaumarchaeota			0FD27@creNOG,COG0637@NOG,arCOG02293@arNOG	Cytoplasmic	
NAS2_1183	325 CDS	Thioredoxin reductase	1.8.1.9	Crenarchaeota	O		0FB2G@creNOG,COG0492@NOG,arCOG01296@arNOG	Cytoplasmic	FNR
NAS2_1184	230 CDS	Purine nucleoside phosphorylase	2.4.2.1	Archaea	F		0FB5_@creNOG,COG2820@NOG,arCOG01324@arNOG	Unknown	
NAS2_1185	296 CDS	Adenosylcobinamide amidohydrolase	3.1.3.73	TACK group				Cytoplasmic	
NAS2_1186	180 CDS	Predicted adenosylcobinamide-phosphate guanylyltransferase CobY	2.7.6.2	Thaumarchaeota	H		0FDAG@creNOG,COG2266@NOG,arCOG01871@arNOG	Cytoplasmic	
NAS2_1187	331 CDS	L-threonine 3-O-phosphate decarboxylase	4.1.1.81	Thaumarchaeota	E		0FC81@creNOG,COG0079@NOG,arCOG04273@arNOG	Cytoplasmic	
NAS2_1188	245 CDS	Cobalamin synthase	2.7.8.26	Thaumarchaeota	H		0FD8P@creNOG,COG0368@NOG,arCOG04338@arNOG	CytoplasmicMembrane	
NAS2_1189	317 CDS	Adenosylcobinamide-phosphate synthase	6.3.1.10	Thaumarchaeota	H		0FBVU@creNOG,COG1270@NOG,arCOG04274@arNOG	CytoplasmicMembrane	
NAS2_1190	426 CDS	Probable electron transfer flavoprotein-quinone oxidoreductase FixC	K00313	TACK group	C		0FB1M@creNOG,COG0644@NOG,arCOG00170@arNOG	Unknown	Fix
NAS2_1191	98 CDS	Ferredoxin-like protein	K03855	TACK group	C	MER0499390	0FCXP@creNOG,COG2440@NOG,arCOG01984@arNOG	Cytoplasmic	Fix
NAS2_1192	268 CDS	Electron transfer flavoprotein, beta subunit	K03521	TACK group	C		0FBEH@creNOG,COG2086@NOG,arCOG00446@arNOG	Unknown	Fix
NAS2_1193	368 CDS	Electron transfer flavoprotein, alpha subunit	K03522	TACK group	C		0FBOK@creNOG,COG2025@NOG,arCOG00447@arNOG	Cytoplasmic	Fix
NAS2_1194	527 CDS	Na ⁺ (H ⁺) antiporter		Archaea	P		0KY49@eurNOG,1CD97@theNOG,COG0475@NOG,arCOG01956@arNOG	Transporter (Other)	CytoplasmicMembrane Antiporter
NAS2_1195	347 CDS	Potassium channel protein		Thaumarchaeota	P		0FBUU@creNOG,COG1226@NOG,arCOG01958@arNOG,arCOG07570@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_1196	316 CDS	2-oxoglutarate oxidoreductase, beta subunit	1.2.7.3	Thaumarchaeota	C		0FAXB@creNOG,COG1013@NOG,arCOG0159@arNOG	Cytoplasmic	OFOR
NAS2_1197	633 CDS	2-oxoglutarate oxidoreductase, alpha subunit	1.2.7.3	Crenarchaeota	C		0FB6A@creNOG,COG0674@NOG,COG1014@NOG,arCOG01606@arNOG,arCOG01607@arNOG	Cytoplasmic	OFOR
NAS2_1198	100 CDS	hypothetical protein		Crenarchaeota			0FF7B@creNOG,0ZD6C@NOG,arCOG10177@arNOG	Cytoplasmic	
NAS2_1199	454 CDS	Phosphomethylpyrimidine kinase	2.7.4.7	Crenarchaeota	H		0FAZ2@creNOG,COG0351@NOG,COG1992@NOG,arCOG00020@arNOG	Cytoplasmic	
NAS2_1200	346 CDS	Hydrogenase expression/formation factor related protein		TACK group	O		0FAYX@creNOG,COG0309@NOG,arCOG00636@arNOG	CytoplasmicMembrane	
NAS2_1201	365 CDS	TsaC protein wit YrdC-Sua5 domains	K07566	Crenarchaeota	J		0FBGS@creNOG,COG0009@NOG,arCOG01952@arNOG	Cytoplasmic	
NAS2_1202	139 CDS	Potassium-transporting ATPase C chain	3.6.3.12	Thaumarchaeota	P		0KV06@eurNOG,0WSI0@metNOG,COG2156@NOG,arCOG04805@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1203	713 CDS	Potassium-transporting ATPase B chain	3.6.3.12	TACK group	P		0KSD9@eurNOG,1CCIF@theNOG,COG2216@NOG,arCOG01577@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1204	534 CDS	Potassium-transporting ATPase A chain	3.6.3.12	TACK group	P		COG2060@NOG,arCOG04804@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1205	170 CDS	CBS domain protein		Archaea	T	MER0234341	0KUPC@eurNOG,COG0517@NOG,arCOG00606@arNOG	Cytoplasmic	
NAS2_1206	298 CDS	hypothetical protein		Crenarchaeota			0FBJE@creNOG,COG1831@NOG,arCOG00693@arNOG	Unknown	
NAS2_1207	205 CDS	Superoxide dismutase [Fe]	1.15.1.1	Thaumarchaeota	P		0FAZN@creNOG,COG0905@NOG,arCOG04147@arNOG	Cytoplasmic	SOD
NAS2_1208	174 CDS	Iron-dependent repressor IdeR/DtxR	K03709	Thaumarchaeota	K		0FCIS@creNOG,COG1321@NOG,arCOG002100@arNOG	Cytoplasmic	
NAS2_1209	253 CDS	Iron-sulfur cluster assembly ATPase protein SufC	K09013	Thaumarchaeota	O		0FBM7@creNOG,COG0396@NOG,arCOG04236@arNOG	Transporter (ABC)	Cytoplasmic
NAS2_1210	473 CDS	Iron-sulfur cluster assembly protein SufB	K09014	Archaea	O		0KRZD@eurNOG,1CE01@thermNOG,COG0719@NOG,arCOG01715@arNOG	Transporter (ABC)	Cytoplasmic
NAS2_1211	351 CDS	Iron-sulfur cluster assembly protein SufB	K07033	Crenarchaeota	O		0FCPH@creNOG,COG0719@NOG,arCOG01715@arNOG	Transporter (ABC)	Cytoplasmic
NAS2_1212	88 CDS	hypothetical protein		Not assigned				Cytoplasmic	
NAS2_1213	290 CDS	ATP phosphoribosyltransferase	2.4.2.17	TACK group	E		0FB72@creNOG,COG0040@NOG,arCOG02208@arNOG	Cytoplasmic	
NAS2_1214	234 CDS	Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide ison	5.3.1.16	cellular organisms	E		0FBZ1@creNOG,COG0106@NOG,arCOG00618@arNOG	Cytoplasmic	
NAS2_1215	254 CDS	Imidazole glycerol phosphate synthase cyclase subunit		cellular organisms	E		0FB50@creNOG,COG0107@NOG,arCOG00617@arNOG	Cytoplasmic	
NAS2_1216	107 CDS	Phosphoribosyl-ATP pyrophosphatase	3.6.1.31	cellular organisms	E		0FCZA@creNOG,COG0140@NOG,arCOG02677@arNOG	Cytoplasmic	
NAS2_1217	206 CDS	Imidazole glycerol phosphate synthase amidotransferase subunit		Archaea	E	MER0444269	0FCIA@creNOG,COG0118@NOG,arCOG00089@arNOG	Cytoplasmic	
NAS2_1218	269 CDS	Phosphoribosyl-AMP cyclohydrolase	3.5.4.19	cellular organisms	E		1CBYQ@thaNOG,COG0139@NOG,arCOG02676@arNOG	Cytoplasmic	
NAS2_1219	283 CDS	Aliphatic amidase AmiE	3.5.1.4	Crenarchaeota	E		0FC6P@creNOG,COG0388@NOG,arCOG00682@arNOG	Cytoplasmic	
NAS2_1220	165 CDS	HTH-type transcriptional regulator Ptr2		Crenarchaeota	K		0FCFR@creNOG,COG1522@NOG,arCOG01580@arNOG	Cytoplasmic	
NAS2_1221	292 CDS	282aa long conserved hypothetical protein	K01247	Euryarchaeota	L		0KYDN@eurNOG,COG0122@NOG,arCOG00464@arNOG	Unknown	
NAS2_1222	827 CDS	Aminopeptidase	K01256	Crenarchaeota	E	MER0099881	0FAYY@creNOG,COG0308@NOG,arCOG02969@arNOG	Cytoplasmic	Peptidase
NAS2_1223	153 CDS	Uncharacterized protein		Archaea				Cytoplasmic	
NAS2_1224	205 CDS	Methyltransferase TM1293		Thaumarchaeota	Q		0FCPI@creNOG,COG0500@NOG,arCOG01773@arNOG	Cytoplasmic	
NAS2_1225	78 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic	
NAS2_1226	83 CDS	hypothetical protein		Thaumarchaeota				Unknown	
NAS2_1227	484 CDS	NAD(FAD)-utilizing dehydrogenase	K07137	Crenarchaeota			0FAYZ@creNOG,COG2509@NOG,arCOG02231@arNOG	Unknown	
NAS2_1228	58 CDS	hypothetical protein		TACK group				Cytoplasmic	
NAS2_1229	539 CDS	Chloride channel protein	K03281	TACK group	P	MER0044154	0FBE8@creNOG,COG0038@NOG,arCOG02569@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_1230	413 CDS	TVG2233936 protein		Bathyarchaeota	G		0ZADZ@creNOG,arCOG00131@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_1231	110 CDS	Cysteine synthase	2.5.1.47	Archaea	E		0FB36@creNOG,COG0381@NOG,arCOG001430@arNOG	Cytoplasmic	
NAS2_1232	170 CDS	Pyruvate:ferredoxin oxidoreductase, gamma subunit	K00172	Archaea	C		0FCGW@creNOG,COG1014@NOG,arCOG01603@arNOG	Cytoplasmic	POR
NAS2_1233	106 CDS	Pyruvate:ferredoxin oxidoreductase, delta subunit	1.2.7.1	cellular organisms	C		0FCMZ@creNOG,COG1144@NOG,arCOG01605@arNOG	Cytoplasmic	POR
NAS2_1234	396 CDS	Pyruvate:ferredoxin oxidoreductase, alpha subunit	1.2.7.1	TACK group	C		0FAWM@creNOG,COG0674@NOG,arCOG01608@arNOG	Unknown	POR
NAS2_1235	325 CDS	Pyruvate:ferredoxin oxidoreductase, beta subunit	1.2.7.1	cellular organisms	C		0FB2B@creNOG,COG1013@NOG,arCOG01601@arNOG	Cytoplasmic	POR
NAS2_1236	233 CDS	Endonuclease V	3.1.21.7	Crenarchaeota	L		COG1515@NOG,arCOG00929@arNOG	Cytoplasmic	
NAS2_1237	262 CDS	hypothetical protein	K09134	Crenarchaeota			0FC2N@creNOG,COG1912@NOG,arCOG04309@arNOG	CytoplasmicMembrane	
NAS2_1238	404 CDS	Molybdopterin biosynthesis protein MoeA	K03750	Crenarchaeota	H		0FBSX@creNOG,COG0303@NOG,arCOG00216@arNOG	Cytoplasmic	
NAS2_1239	339 CDS	Molybdopterin biosynthesis protein MoeA		Crenarchaeota	H		0FC5W@creNOG,COG0303@NOG,arCOG00216@arNOG	Unknown	
NAS2_1240	342 CDS	Molybdenum cofactor biosynthesis protein MoaA	K03639	cellular organisms	H		0KRWA@eurNOG,COG2896@NOG,arCOG00930@arNOG	Cytoplasmic	
NAS2_1241	143 CDS	Molybdenum cofactor biosynthesis protein MoaC	K03637	Thaumarchaeota	H		0KTF4@eurNOG,0WM9C@methaNOG,COG0315@NOG,arCOG01530@arNOG	Cytoplasmic	
NAS2_1242	170 CDS	Molybdenum cofactor biosynthesis protein MoaB	K03638	Crenarchaeota	H		0FCAD@creNOG,COG0521@NOG,arCOG00214@arNOG	Cytoplasmic	
NAS2_1243	278 CDS	7,8 dihydropyruvate synthase	K06897	TACK group			0KTXH@eurNOG,1CE32@thermNOG,COG1237@NOG,arCOG00503@arNOG	Cytoplasmic	

NAS2_1244	326 CDS	hypothetical protein		K07022	Crenarchaeota		0FB7T@creNOG,COG2248@NOG,arCOG00969@arNOG	Cytoplasmic
NAS2_1245	144 CDS	Thioredoxin		K03671	Archaea	O	0FC5J@creNOG,COG0526@NOG,arCOG01972@arNOG	Cytoplasmic
NAS2_1246	248 CDS	hypothetical protein			No hits			CytoplasmicMembrane
NAS2_1247	283 CDS	Heme O synthase, protoheme IX farnesyltransferase		K02301	Thaumarchaeota	O	021IH@arCOG,0KSGW@eurNOG,COG0109@NOG,arCOG00479@arNOG	CytoplasmicMembrane
NAS2_1248	211 CDS	Phosphoserine phosphatase	3.1.3.3	K01079	Thaumarchaeota	E	0KS9A@eurNOG,COG0560@NOG,arCOG01158@arNOG	Cytoplasmic
NAS2_1249	330 CDS	hypothetical protein			Not assigned			Cytoplasmic
NAS2_1250	162 CDS	hypothetical protein			Euryarchaeota	J	0KUYT@eurNOG,0WNA3@methaNOG,COG3270@NOG,arCOG02285@arNOG	Cytoplasmic
NAS2_1251	315 CDS	Ribosomal RNA small subunit methyltransferase B		K01741	cellular organisms	J	0KSV1@eurNOG,0WM0M@methaNOG,COG0144@NOG,arCOG00973@arNOG	Cytoplasmic
NAS2_1252	305 CDS	8-oxoguanine DNA glycosylase, archaeal type		K01741	Crenarchaeota	L	0FC9K@creNOG,COG4047@NOG,arCOG04144@arNOG	Cytoplasmic
NAS2_1253	336 CDS	Alcohol dehydrogenase	1.1.1.1	K13953	Archaea	C	0KTBW@eurNOG,COG1064@NOG,arCOG01455@arNOG	Cytoplasmic
NAS2_1254	522 CDS	NAD(P)H epimerase		K17758,K177	Crenarchaeota	G	02T90@arNOG,0FB2U@creNOG,COG0062@NOG,COG0063@NOG,arCOG00018@arNOG	ADH
NAS2_1255	54 CDS	hypothetical protein			Not assigned			Cytoplasmic
NAS2_1256	236 CDS	Putative deoxyribonuclease similar to YcfH, type 3		K03424	Thaumarchaeota	L	0FBTU@creNOG,COG0084@NOG,arCOG00891@arNOG	Cytoplasmic
NAS2_1257	237 CDS	hypothetical protein			Not assigned			Cytoplasmic
NAS2_1258	45 CDS	hypothetical protein			No hits			CytoplasmicMembrane
NAS2_1259	396 CDS	hypothetical protein			Thaumarchaeota	K		Cytoplasmic
NAS2_1260	260 CDS	NAD synthetase	6.3.1.5	K01916	Archaea	H	0FBDK@creNOG,COG0171@NOG,arCOG00069@arNOG	Cytoplasmic
NAS2_1261	160 CDS	hypothetical protein			Not assigned			Cytoplasmic
NAS2_1262	178 CDS	157aa long conserved hypothetical protein			cellular organisms	T	1CB39@thaNOG,COG2453@NOG,arCOG03413@arNOG	Cytoplasmic
NAS2_1263	202 CDS	CTP:molybdopterin cytidyltransferase		K07141	cellular organisms		0FC23@creNOG,COG2068@NOG,arCOG01873@arNOG	Cytoplasmic
NAS2_1264	294 CDS	hypothetical protein			Crenarchaeota			Cytoplasmic
NAS2_1265	767 CDS	Xanthine dehydrogenase, molybdenum binding subunit	1.17.1.4		cellular organisms	C	0FB3T@creNOG,COG1529@NOG,arCOG01167@arNOG	CytoplasmicMembrane
NAS2_1266	288 CDS	Xanthine dehydrogenase, FAD binding subunit	1.17.1.4		cellular organisms	C	0FB9S@creNOG,COG1319@NOG,arCOG01926@arNOG	Cox/AOR
NAS2_1267	164 CDS	Xanthine dehydrogenase iron-sulfur subunit	1.17.1.4	K03518	TACK group	C	0FBB5@creNOG,COG2080@NOG,arCOG01925@arNOG	Cox/AOR
NAS2_1268	426 CDS	Phosphoglycerate kinase	2.7.2.3	K00927	Thaumarchaeota	G	1CBOT@thaNOG,COG0126@NOG,arCOG00496@arNOG	PGK
NAS2_1269	313 CDS	Carboxylesterase		K01066	Archaea	I	0FBR1@creNOG,COG0657@NOG,arCOG02638@arNOG	Cytoplasmic
NAS2_1270	387 CDS	CBS domain protein			Archaea		0KT2B@eurNOG,COG0517@NOG,arCOG00601@arNOG	Cytoplasmic
NAS2_1271	94 CDS	hypothetical protein			Not assigned			Cytoplasmic
NAS2_1272	319 CDS	Ribokinase	2.7.1.15	K00852	cellular organisms	G	0FBDM@creNOG,COG0524@NOG,arCOG00014@arNOG	Cytoplasmic
NAS2_1273	567 CDS	Chromosome partition protein smc		K03529	Archaea		0KRPK@eurNOG,0WQ0C@methaNOG,COG1196@NOG,arCOG00371@arNOG	Cytoplasmic
NAS2_1274	238 CDS	hypothetical protein			Archaea			Cytoplasmic
NAS2_1275	191 CDS	hypothetical protein			Archaea			Cytoplasmic
NAS2_1276	946 CDS	Uncharacterized ATP-dependent helicase		K03724	cellular organisms	L	0FAZF@creNOG,COG1201@NOG,arCOG00557@arNOG	Cytoplasmic
NAS2_1277	172 CDS	carbonic anhydrase, family 3			cellular organisms		0KTE5@eurNOG,0WM6J@methaNOG,COG0663@NOG,arCOG01849@arNOG	Cytoplasmic
NAS2_1278	393 CDS	Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF		K00782	cellular organisms	C	0FAY9@creNOG,COG1139@NOG,arCOG00335@arNOG	Cytoplasmic
NAS2_1279	309 CDS	Heterodisulfide reductase related protein			TACK group	C	0FBE6@creNOG,COG0247@NOG,arCOG00332@arNOG	Unknown
NAS2_1280	406 CDS	GTP-binding and nucleic acid-binding protein YchF		K06942	Archaea	J	1CB9T@thaNOG,COG0012@NOG,arCOG00352@arNOG	Unknown
NAS2_1281	343 CDS	mRNA 3-end processing exonuclease		K07577	Archaea	J	1CBOD@thaNOG,COG1236@NOG,arCOG00545@arNOG	Cytoplasmic
NAS2_1282	855 CDS	FIG003033: Helicase domain protein		K03724	TACK group	L	0KRAB@eurNOG,COG1201@NOG,arCOG00557@arNOG	Cytoplasmic
NAS2_1283	266 CDS	Arogenate dehydrogenase	1.3.1.43	K04517	Thaumarchaeota	E	1CBH1@thaNOG,COG0287@NOG,arCOG00245@arNOG	Unknown
NAS2_1284	349 CDS	NAD(P)-dependent glyceraldehyde 3-phosphate dehydrogenase archi	1.2.1.59	K00150	Crenarchaeota	G	0KRAH@eurNOG,0WR0A@methaNOG,COG0037@NOG,arCOG00493@arNOG	GADPH
NAS2_1285	453 CDS	Pyruvate kinase	2.7.1.40	K00873	Crenarchaeota	G	0FBAW@creNOG,COG0469@NOG,arCOG04120@arNOG	PK
NAS2_1286	1041 CDS	ATP-dependent helicase		K06877	Archaea	L	0FAZY@creNOG,COG1205@NOG,arCOG00555@arNOG	Cytoplasmic
NAS2_1287	165 CDS	Terminal quinol oxidase, subunit II		K16936	TACK group		0FC2K@creNOG,11J7B@NOG,arCOG05342@arNOG	Unknown
NAS2_1288	173 CDS	Terminal quinol oxidase, subunit I		K16937	TACK group		0FBWK@creNOG,0Y2VC@NOG,arCOG02862@arNOG	Tqo
NAS2_1289	464 CDS	Glycolate dehydrogenase	1.1.99.14	K00104	Thaumarchaeota	C	0KRDB@eurNOG,0WK2S@methaNOG,COG0277@NOG,arCOG00337@arNOG	CytoplasmicMembrane
NAS2_1290	412 CDS	Glycolate dehydrogenase	1.1.99.14		Archaea	C	COG0247@NOG,COG0277@NOG,arCOG00337@arNOG	CytoplasmicMembrane
NAS2_1291	152 CDS	hypothetical protein			Thaumarchaeota			Cytoplasmic
NAS2_1292	109 CDS	S-adenosylmethionine decarboxylase proenzyme	4.1.1.50	K01611	Thaumarchaeota	E	0FCQ9@creNOG,COG1586@NOG,arCOG00279@arNOG	Cytoplasmic
NAS2_1293	305 CDS	Spermidine synthase	2.5.1.16	K00797	Crenarchaeota	E	0FAX2@creNOG,COG0421@NOG,arCOG00050@arNOG	Cytoplasmic
NAS2_1294	288 CDS	Isoaspartyl aminopeptidase	3.4.19.5	K13051	cellular organisms	E	0FBKJ@creNOG,COG1446@NOG,arCOG04779@arNOG	Peptidase
NAS2_1295	391 CDS	HtrA protease			TACK group	O	MER0243429	Peptidase
NAS2_1296	250 CDS	COG2047: Uncharacterized protein		K06869	Thaumarchaeota		MER0247168	Unknown
NAS2_1297	113 CDS	hypothetical protein		K13993	Thaumarchaeota	O	0FBQ6@creNOG,COG1938@NOG,arCOG00347@arNOG	Cytoplasmic
NAS2_1298	332 CDS	Glucose-6-phosphate isomerase, archaeal II	5.3.1.9	K15916	Thaumarchaeota	G	0KTOG@eurNOG,0WMBZ@methaNOG,COG0071@NOG,arCOG01832@arNOG	Cytoplasmic
NAS2_1299	232 CDS	Triosephosphate isomerase	5.3.1.1	K01803	Archaea	G	0FBH5@creNOG,COG0166@NOG,arCOG00052@arNOG	PGI
NAS2_1300	349 CDS	Fructose-1,6-bisphosphatase, type V, archaeal	3.1.3.11	K01622	cellular organisms	G	0KRA9@eurNOG,1CE85@thermNOG,COG0149@NOG,arCOG01087@arNOG	TIM
NAS2_1301	189 CDS	hypothetical protein		K06963	Thaumarchaeota		0FB7P@creNOG,COG1980@NOG,arCOG04180@arNOG	Unknown
NAS2_1302	tRNA	tRNA-Val					0FCDX@creNOG,COG1818@NOG,arCOG00084@arNOG	FBAP
NAS2_1303	57 CDS	hypothetical protein		K02927	Thaumarchaeota	J		Cytoplasmic
NAS2_1304	300 CDS	Sulfate adenylyltransferase subunit 2	2.7.7.4	K00390	Crenarchaeota	P	0FDT0@creNOG,COG0175@NOG,arCOG04586@arNOG	Cytoplasmic
NAS2_1305	429 CDS	Choline-sulfatase	3.1.6.6		Crenarchaeota	P	0FCKE@creNOG,COG3119@NOG,arCOG02787@arNOG	Cytoplasmic
NAS2_1306	365 CDS	Transporter			Bacteria			Transporter (MFS)
NAS2_1307	88 CDS	DNA/RNA-binding protein Alba		K03622	Thaumarchaeota	K	0KU0E@eurNOG,COG1581@NOG,arCOG01753@arNOG	CytoplasmicMembrane
NAS2_1308	177 CDS	NusA protein homolog 2, archaeal			Thaumarchaeota	K	1CB8C@thaNOG,COG0195@NOG,arCOG001761@arNOG	Cytoplasmic
NAS2_1309	433 CDS	Aspartyl-tRNA synthetase	6.1.1.23	K01876	Thaumarchaeota	J	1CBQQ@thaNOG,COG0017@NOG,arCOG00406@arNOG	Cytoplasmic
NAS2_1310	395 CDS	369aa long hypothetical cell division control protein			Archaea	O	0FB1Y@creNOG,COG0464@NOG,arCOG01307@arNOG	Cytoplasmic
NAS2_1311	240 CDS	hypothetical protein			Bathymarchaeota			Cytoplasmic
NAS2_1312	220 CDS	hypothetical protein			Archaea	N	0FC0K@creNOG,COG5491@NOG,arCOG00452@arNOG	Cytoplasmic
NAS2_1313	393 CDS	Transcriptional regulator, TmbB family			Thaumarchaeota	K	1CBGH@thaNOG,COG1378@NOG,arCOG02037@arNOG	Cytoplasmic
NAS2_1314	253 CDS	hypothetical protein			Archaea			CytoplasmicMembrane
NAS2_1315	432 CDS	Protein similar to polyadenylation specificity factor, MJ0047 type		K07577	Archaea	J	0FBD2@creNOG,COG1236@NOG,arCOG00541@arNOG	Cytoplasmic
NAS2_1316	232 CDS	COG2047: Uncharacterized protein		K06869	Thaumarchaeota		0FBFB@creNOG,COG1938@NOG,arCOG00347@arNOG	Cytoplasmic
NAS2_1317	505 CDS	archaeosine tRNA-ribosyltransferase		K18779	TACK group	J	0FAY4@creNOG,COG0343@NOG,arCOG00989@arNOG	Unknown
NAS2_1318	148 CDS	Small nuclear ribonucleoprotein homolog			Thaumarchaeota	K	0FCUJZ@creNOG,COG1958@NOG,arCOG00999@arNOG	Cytoplasmic
NAS2_1319	198 CDS	AMP/CMIP kinase AK6		K18532	TACK group	F	0FD94@creNOG,COG1936@NOG,arCOG01039@arNOG	Cytoplasmic
NAS2_1320	304 CDS	putative aldol/keto reductase			Thaumarchaeota		COG0656@NOG,arCOG01619@arNOG	Cytoplasmic
NAS2_1321	425 CDS	Na(+)/H(+) antiporter			Crenarchaeota	P	0FB57@creNOG,COG0475@NOG,arCOG01953@arNOG	CytoplasmicMembrane
NAS2_1322	334 CDS	F420-dependent N(5),N(10)-methylene tetrahydromethanopterin reduct	1.5.99.11		Bacteria	C	0M11Y@eurNOG,0RGMZ@haNOG,COG2141@NOG,arCOG02410@arNOG	Cytoplasmic
NAS2_1323	225 CDS	ATP-dependent RNA helicase, eIF-4A family		K10848	Archaea	L	0FCB7@creNOG,COG1948@NOG,arCOG04206@arNOG	Cytoplasmic
NAS2_1324	315 CDS	3-oxoacyl-[acyl-carrier protein] reductase	1.1.1.100	K00059	Archaea		0KTVJ@eurNOG,1CCIE@thaNOG,COG1028@NOG,arCOG01259@arNOG	Cytoplasmic
NAS2_1325	319 CDS	hypothetical protein			Crenarchaeota	K	0FCXD@creNOG,COG3888@NOG,arCOG01804@arNOG	Cytoplasmic
NAS2_1326	434 CDS	Cytosine/purine/uracil/thiamine/allantoin permease family protein		K03457	Crenarchaeota	F	0FEJY@creNOG,COG1457@NOG,arCOG03447@arNOG	Transporter (Other)
NAS2_1327	447 CDS	Dihydroorotase	3.5.2.3	K01465	Crenarchaeota	F	0FC47@creNOG,COG0044@NOG,arCOG00689@arNOG	CytoplasmicMembrane
NAS2_1328	328 CDS	amidohydrolase 2		K07045	Crenarchaeota		0FFNC@creNOG,COG2159@NOG,arCOG01931@arNOG	Cytoplasmic
NAS2_1329	653 CDS	Acetyl-coenzyme A synthetase	6.2.1.1	K01895	Crenarchaeota	I	0FBBY@creNOG,COG0365@NOG,arCOG04201@arNOG	Cytoplasmic
NAS2_1330	181 CDS	Putative regulatory protein		K07034	Thaumarchaeota		0FBBS@creNOG,COG1584@NOG,arCOG03176@arNOG	ACS
NAS2_1331	194 CDS	hypothetical protein			Thaumarchaeota	K	02TP7@arNOG,0FFUT@creNOG,COG0454@NOG	CytoplasmicMembrane
NAS2_1332	288 CDS	ABC transporter, permease protein		K01992	Thaumarchaeota	V	0FBMQ@creNOG,COG0842@NOG,arCOG01467@arNOG	Cytoplasmic

NAS2_1333	334 CDS	Methionine ABC transporter ATP-binding protein	K01990	Thaumarchaeota	V	0FAYQ@creNOG,COG1131@NOG,arCOG00194@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1334	140 CDS	Transcriptional regulator, PadR family		Archaea	K	0FCYP@creNOG,COG1695@NOG,arCOG00002@arNOG		Cytoplasmic
NAS2_1335	189 CDS	hypothetical protein		Crenarchaeota		0FC0V@creNOG,11IRK@NOG,arCOG05631@arNOG		Cytoplasmic
NAS2_1336	132 CDS	hypothetical protein	K07006	Bacteria				Cytoplasmic
NAS2_1337	100 CDS	hypothetical membrane protein		Euryarchaeota				CytoplasmicMembrane
NAS2_1338	126 CDS	Small heat shock protein hsp20 family		Archaea	O	0FCR0@creNOG,COG0071@NOG,arCOG01832@arNOG		Cytoplasmic
NAS2_1339	77 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic
NAS2_1340	518 CDS	ABC1 family protein ## group 1		Thaumarchaeota		1CBMW@thaNOG,COG0661@NOG,arCOG01189@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1341	113 CDS	hypothetical protein		Not assigned				CytoplasmicMembrane
NAS2_1342	423 CDS	Predicted thiamin transporter ThiT		Crenarchaeota	G	0FBQ1@creNOG,0Y72W@NOG,arCOG02792@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_1343	419 CDS	hypothetical protein	K07496	Archaea	L	0FBM6@creNOG,COG0675@NOG,arCOG00679@arNOG		Cytoplasmic
NAS2_1344	215 CDS	First ORF in transposon ISC1913		Archaea	L	0FBSM@creNOG,COG2452@NOG,arCOG03164@arNOG		Cytoplasmic
NAS2_1345	293 CDS	Small-conductance mechanosensitive channel protein		Archaea	M	0KY6S@eurNOG,1CDFC@theNOG,COG0668@NOG,arCOG01568@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_1346	602 CDS	Glucosylase	3.2.1.3	Crenarchaeota	G	COG3387@NOG,arCOG03286@arNOG		Extracellular
NAS2_1347	441 CDS	Glycosyltransferase		Crenarchaeota	M	0FBEJ@creNOG,COG0438@NOG,arCOG01408@arNOG		Unknown
NAS2_1348	429 CDS	motif-4Fe-4S ferredoxins, iron-sulfur binding region signature		Archaea	C	0KS03@eurNOG,1CCH2@theNOG,COG0247@NOG,arCOG00333@arNOG		Cytoplasmic
NAS2_1349	468 CDS	D-lactate dehydrogenase (cytochrome)		Archaea	C	0KRDB@eurNOG,1CCBU@theNOG,COG0277@NOG,arCOG00337@arNOG		CytoplasmicMembrane
NAS2_1350	1037 CDS	Helicase, SNF2/RAD54 family	K00104	cellular organisms	L	0KSH9@eurNOG,0WNB8@methaNOG,COG30553@NOG,arCOG00889@arNOG		CytoplasmicMembrane
NAS2_1351	298 CDS	SWF/SNF family helicase		cellular organisms		0KTD6@eurNOG,COG4279@NOG,arCOG03431@arNOG		Cytoplasmic
NAS2_1352	408 CDS	L-Proline:Glycine betaine transporter ProP		Crenarchaeota	G	0FE3A@creNOG,0XP71@NOG,arCOG02691@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_1353	324 CDS	Thiamine-monophosphate kinase	2.7.4.16	Euryarchaeota	O	0FBJF@creNOG,COG0309@NOG,arCOG00636@arNOG		Unknown
NAS2_1354	413 CDS	hypothetical protein		Crenarchaeota		0FCRB@creNOG,COG4342@NOG,arCOG01244@arNOG,arCOG05989@arNOG		Cytoplasmic
NAS2_1355	75 CDS	Conserved protein		Crenarchaeota		02U8M@arNOG,0FFYQ@creNOG,12CTF@NOG		Cytoplasmic
NAS2_1356	134 CDS	Conserved Archaeal protein		Crenarchaeota		0FD45@creNOG,COG4113@NOG,arCOG00729@arNOG		Cytoplasmic
NAS2_1357	49 CDS	hypothetical protein		Crenarchaeota				Cytoplasmic
NAS2_1358	256 CDS	hypothetical protein	K06921	Crenarchaeota		0FB33@creNOG,COG1672@NOG,arCOG03169@arNOG		Cytoplasmic
NAS2_1359	435 CDS	Conserved protein	K07133	Crenarchaeota		0FC7Q@creNOG,COG1373@NOG,arCOG03167@arNOG		Unknown
NAS2_1360	217 CDS	hypothetical protein		Archaea		0FEHQ@creNOG,11KYG@NOG,arCOG01426@arNOG		Cytoplasmic
NAS2_1361		rRNA						
NAS2_1362	168 CDS	Transposase		Thaumarchaeota	L	0KUJ1@eurNOG,COG3547@NOG,arCOG03585@arNOG		Cytoplasmic
NAS2_1363	157 CDS	Mobile element protein		Archaea	L	0KUJ1@eurNOG,COG3547@NOG,arCOG03585@arNOG		Cytoplasmic
NAS2_1364	344 CDS	transposase		Thaumarchaeota	L	0KU0I@eurNOG,COG2801@NOG,arCOG02125@arNOG		Cytoplasmic
NAS2_1365	388 CDS	398aa long conserved hypothetical protein		Crenarchaeota	M	0FBW6@creNOG,COG0438@NOG,arCOG01417@arNOG		Cytoplasmic
NAS2_1366	284 CDS	hypothetical protein		Crenarchaeota		0 added@creNOG,0XVCD@NOG,arCOG06064@arNOG		Cytoplasmic
NAS2_1367	394 CDS	Glycosyltransferase		Crenarchaeota	M	0FB8E@creNOG,COG0438@NOG,arCOG01403@arNOG		Cytoplasmic
NAS2_1368	340 CDS	Nucleotidyl transferase possibly involved in theonylecarbamoyladenosine formation		Archaea	M	0KRDF@eurNOG,0WRH3@meNOG,COG0662@NOG,COG1208@NOG,arCOG00663@arNOG		Cytoplasmic
NAS2_1369	515 CDS	Membrane protein involved in the export of O-antigen and teichoic acid		Archaea	M			CytoplasmicMembrane
NAS2_1370	100 CDS	hypothetical protein		Not assigned				Cytoplasmic
NAS2_1371	90 CDS	hypothetical protein		Archaea	L			Unknown
NAS2_1372	146 CDS	hypothetical protein		Korarchaeota				CytoplasmicMembrane
NAS2_1373	43 CDS	hypothetical protein		Not assigned				Cytoplasmic
NAS2_1374	56 CDS	hypothetical protein		Archaea				Cytoplasmic
NAS2_1375	56 CDS	hypothetical protein		No hits				Extracellular
NAS2_1376	403 CDS	hypothetical protein		Euryarchaeota				Cytoplasmic
NAS2_1377	312 CDS	hypothetical protein		DPANN				Cytoplasmic
NAS2_1378	147 CDS	hypothetical protein		Not assigned				Cytoplasmic
NAS2_1379	37 CDS	hypothetical protein		Euryarchaeota				Cytoplasmic
NAS2_1380	205 CDS	Transposase ISC1058		Archaea	L	0FFH4@creNOG,0XPNN@NOG,arCOG02754@arNOG		Cytoplasmic
NAS2_1381	445 CDS	Cell Envelope, Surface polysaccharides and lipopolysaccharides		Crenarchaeota	M	0FBW6@creNOG,COG0438@NOG,arCOG01417@arNOG		Cytoplasmic
NAS2_1382	254 CDS	hypothetical protein		Crenarchaeota		COG3463@NOG,arCOG03812@arNOG		CytoplasmicMembrane
NAS2_1383	122 CDS	ABC-type phosphate transport system, permease component		Crenarchaeota				Extracellular
NAS2_1384	250 CDS	ABC-type phosphate transport system, permease component		Crenarchaeota				Extracellular
NAS2_1385	339 CDS	ADP-heptose synthase		cellular organisms	M	02TPF@arNOG,0M26B@eurNOG,COG2870@NOG		Cytoplasmic
NAS2_1386	72 CDS	hypothetical protein		Not assigned				Cytoplasmic
NAS2_1387	221 CDS	Ribulose-phosphate 3-epimerase	5.1.3.1	Bacteria	G	0KT7M@eurNOG,0WQ86@methNOG,COG0036@NOG,arCOG05046@arNOG		Cytoplasmic
NAS2_1388	44 CDS	hypothetical protein		Not assigned				Unknown
NAS2_1389	279 CDS	Transketolase, N-terminal section	2.2.1.1	cellular organisms	G	0KS0F@eurNOG,0WQ7Y@methNOG,COG3959@NOG,arCOG01053@arNOG		Cytoplasmic
NAS2_1390	309 CDS	Transketolase, C-terminal section	2.2.1.1	cellular organisms	G	0KRYZ@eurNOG,COG3958@NOG,arCOG01051@arNOG		Cytoplasmic
NAS2_1391	229 CDS	Nucleotidyl transferase possibly involved in theonylecarbamoyladenosine formation	K00966	Bacteria	M	0KSSC@eurNOG,0WKRT@methaNOG,COG1208@NOG,arCOG00666@arNOG		Cytoplasmic
NAS2_1392	348 CDS	D,D-heptose 7-phosphate kinase	K07031	cellular organisms		COG2605@NOG,arCOG01030@arNOG		Cytoplasmic
NAS2_1393	201 CDS	Phosphoheptose isomerase 1	K03271	cellular organisms	G	0KTHS@eurNOG,COG0279@NOG,arCOG05355@arNOG		Cytoplasmic
NAS2_1394	180 CDS	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase	K03273	cellular organisms		0KU8C@eurNOG,COG0241@NOG,arCOG07384@arNOG		Cytoplasmic
NAS2_1395	281 CDS	Transaldolase	2.2.1.2	cellular organisms	G	0KBS5@eurNOG,COG0176@NOG,arCOG05061@arNOG		Cytoplasmic
NAS2_1396	332 CDS	Glycosyltransferase		Euryarchaeota	M	0FBFE@creNOG,COG0438@NOG,arCOG01403@arNOG		Cytoplasmic
NAS2_1397	171 CDS	hypothetical protein		Thaumarchaeota	L			Cytoplasmic
NAS2_1398	85 CDS	hypothetical protein		Thaumarchaeota	L			Cytoplasmic
NAS2_1399	128 CDS	Transposase ISC1058		Thaumarchaeota	L	0XPNN@NOG,arCOG02754@arNOG		Cytoplasmic
NAS2_1400	163 CDS	hypothetical protein		Not assigned				Cytoplasmic
NAS2_1401	269 CDS	methyltransferase, FkbM family domain protein		Crenarchaeota	Q	0 added@creNOG,COG0500@NOG,arCOG01400@arNOG		Cytoplasmic
NAS2_1402	268 CDS	periplasmic serine protease		cellular organisms	O	0KSGG@eurNOG,COG0616@NOG,arCOG01911@arNOG		Cytoplasmic
NAS2_1403	51 CDS	hypothetical protein		No hits				Unknown
NAS2_1404	50 CDS	hypothetical protein		Not assigned				Unknown
NAS2_1405	316 CDS	hypothetical protein	K06921	Thaumarchaeota		0FBZB@creNOG,COG1672@NOG,arCOG03169@arNOG		Cytoplasmic
NAS2_1406	52 CDS	hypothetical protein		Not assigned				Extracellular
NAS2_1407	46 CDS	hypothetical protein		Not assigned				Unknown
NAS2_1408	49 CDS	hypothetical protein		Thaumarchaeota				Unknown
NAS2_1409	287 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic
NAS2_1410	280 CDS	hypothetical protein		Crenarchaeota				Cytoplasmic
NAS2_1411	336 CDS	hypothetical protein	K06921	Thaumarchaeota		0FEHQ@creNOG,11KYG@NOG,arCOG01426@arNOG		Cytoplasmic
NAS2_1412	188 CDS	hypothetical protein		Korarchaeota		0FBPK@creNOG,COG1672@NOG,arCOG03169@arNOG		Unknown
NAS2_1413	218 CDS	hypothetical protein		Korarchaeota	K	COG2253@NOG,arCOG03839@arNOG		Cytoplasmic
NAS2_1414	121 CDS	115aa long conserved hypothetical protein	K07064	Crenarchaeota		0FEPK@creNOG,COG1848@NOG,arCOG02730@arNOG		Cytoplasmic
NAS2_1415	74 CDS	Prevent host death protein, Phd antitoxin like		Crenarchaeota	K	0 added@creNOG,COG2002@NOG,arCOG00816@arNOG		Cytoplasmic
NAS2_1416	263 CDS	7,8 dihydropterolate synthase	K06897	Thaumarchaeota		0FCPM@creNOG,COG1237@NOG,arCOG05033@arNOG		Unknown
NAS2_1417	158 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic
NAS2_1418	367 CDS	hypothetical protein	K06921	Crenarchaeota		0FBZB@creNOG,COG1672@NOG,arCOG03169@arNOG		Cytoplasmic
NAS2_1419	47 CDS	hypothetical protein		Not assigned				Cytoplasmic
NAS2_1420	354 CDS	hypothetical protein	K06921	Crenarchaeota		0FBPK@creNOG,COG1672@NOG,arCOG03169@arNOG		Unknown
NAS2_1421	390 CDS	hypothetical protein	K08368	Crenarchaeota	G	0 added@creNOG,0XGKC@NOG,arCOG02682@arNOG	Transporter (MFS)	CytoplasmicMembrane

NAS2_1422	435 CDS	Chloride channel protein		K03281	cellular organisms	P	MER0044154	0FBEB@creNOG,COG0038@NOG,arCOG02569@arNOG	Transporter (Other)	CytoplasmicMembrane
NAS2_1423	1056 CDS	Isoleucyl-tRNA synthetase	6.1.1.5	K01870	Archaea	J		1CB3E@thaNOG,COG0060@NOG,arCOG00807@arNOG		Cytoplasmic
NAS2_1424	290 CDS	Inositol-1-monophosphatase	3.1.3.25	K01092	Archaea	G		0KSUF@eurNOG,0WRBU@metNOG,COG0483@NOG,arCOG01349@arNOG		Cytoplasmic
NAS2_1425	128 CDS	hypothetical protein			Crenarchaeota			0FCR6@creNOG,COG2835@NOG,arCOG04124@arNOG		Cytoplasmic
NAS2_1426	188 CDS	3-polyphenyl-4-hydroxybenzoate carboxy-lyase Ubix		K03186	cellular organisms	H		0FCQA@creNOG,COG0163@NOG,arCOG01703@arNOG		Cytoplasmic
NAS2_1427	242 CDS	Chromosome partitioning protein ParB			Archaea	K		0FD15@creNOG,COG1475@NOG,arCOG01875@arNOG		Cytoplasmic
NAS2_1428	74 CDS	SSU ribosomal protein S17e		K02962	Archaea	J		0FDUJ@creNOG,COG1383@NOG,arCOG01885@arNOG		Cytoplasmic
NAS2_1429	73 CDS	Archaeal histone			Thaumarchaeota			0KUCD@eurNOG,COG2036@NOG,arCOG02144@arNOG		Cytoplasmic
NAS2_1430	136 CDS	CBS domain protein			Thaumarchaeota	T		02TZE@arNOG,0FFWW@creNOG,0ZXJ5@NOG		Cytoplasmic
NAS2_1431	267 CDS	hypothetical protein			Bacteria					Cytoplasmic
NAS2_1432	397 CDS	Archaeal S-adenosylmethionine synthetase	2.5.1.6	K00789	cellular organisms	E		0FAWG@creNOG,COG1812@NOG,arCOG01678@arNOG		Unknown
NAS2_1433	238 CDS	hypothetical protein			Not assigned					Cytoplasmic
NAS2_1434	91 CDS	hypothetical protein		K03622	Archaea					Cytoplasmic
NAS2_1435	93 CDS	DNA-directed RNA polymerase subunit K	2.7.7.6		TACK group	K		1CBNG@thaNOG,COG1758@NOG,arCOG01268@arNOG		Cytoplasmic
NAS2_1436	199 CDS	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases		K01628	cellular organisms	G		0KT2U@eurNOG,1CEQX@thermNOG,COG0235@NOG,arCOG04226@arNOG		Cytoplasmic
NAS2_1437	273 CDS	Prephenate dehydratase	4.2.1.51		cellular organisms	E		0FC7W@creNOG,COG0077@NOG,arCOG00255@arNOG		Cytoplasmic
NAS2_1438	319 CDS	Branched-chain amino acid aminotransferase	2.6.1.42	K00826	Thaumarchaeota	E		0FBIR@creNOG,COG0115@NOG,arCOG02297@arNOG		Cytoplasmic
NAS2_1439	tRNA	tRNA-Ala								AT (Family III)
NAS2_1440	tRNA	tRNA-Cys								
NAS2_1441	433 CDS	Transport protein			Archaea	G	MER0011529	0XP7I@NOG,arCOG02691@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_1442	308 CDS	Pantoate kinase, archaeal		K06982	Crenarchaeota	H		0FFSB@creNOG,COG1829@NOG,arCOG04263@arNOG		CytoplasmicMembrane
NAS2_1443	291 CDS	putative dehydrogenase			cellular organisms	I		0FBJK@creNOG,COG2084@NOG,arCOG00247@arNOG		Unknown
NAS2_1444	142 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_1445	130 CDS	hypothetical protein		K03892	Thaumarchaeota	K				Cytoplasmic
NAS2_1446	489 CDS	Glutamine synthetase type I	6.3.1.2	K01915	Thaumarchaeota	E		0FB8X@creNOG,COG0174@NOG,arCOG01909@arNOG		Cytoplasmic
NAS2_1447	147 CDS	Transcriptional regulator, AsnC family			Thaumarchaeota	K		0KTPD@eurNOG,1CEYX@thermNOG,COG1522@NOG,arCOG01580@arNOG		Cytoplasmic
NAS2_1448	91 CDS	hypothetical protein			Not assigned					Unknown
NAS2_1449	351 CDS	COG1180: Radical SAM, Pyruvate-formate lyase-activating enzyme like		K04069	Archaea	O		0FBAQ@creNOG,COG1180@NOG,arCOG00946@arNOG		Cytoplasmic
NAS2_1450	205 CDS	hypothetical protein			Thaumarchaeota			0Y6R8@creNOG,1CBVJ@thaNOG,arCOG05463@arNOG		Cytoplasmic
NAS2_1451	558 CDS	Heat shock protein 60 family chaperone GroEL, Thermosome subunit			Archaea	O		0FB1U@creNOG,COG0459@NOG,arCOG01257@arNOG		Cytoplasmic
NAS2_1452	433 CDS	TidE protein		K03592	Thaumarchaeota		MER0152002	0KRUP@eurNOG,COG0312@NOG,arCOG00322@arNOG		Cytoplasmic
NAS2_1453	476 CDS	TidD protein		K03568	Archaea		MER0016255	0FB1I@creNOG,COG0312@NOG,arCOG00321@arNOG		Cytoplasmic
NAS2_1454	829 CDS	hypothetical protein			Thaumarchaeota					CytoplasmicMembrane
NAS2_1455	251 CDS	Mobile element protein		K07496	root;	L		0FDQE@creNOG,COG0675@NOG,arCOG00684@arNOG		Unknown
NAS2_1456	77 CDS	ISA1214-2, putative transposase			Euryarchaeota	L		0KUZ4@eurNOG,1CDFT@thaNOG,COG5558@NOG,arCOG07732@arNOG,arCOG07762@arNOG		Unknown
NAS2_1457	59 CDS	hypothetical protein			cellular organisms	L				Cytoplasmic
NAS2_1458	114 CDS	hypothetical protein			Thaumarchaeota					Cytoplasmic
NAS2_1459	602 CDS	DNA topoisomerase I	5.99.1.2	K03168	Archaea	L		02TD2@arNOG,0KRV0@eurNOG,0WKF4@methaNOG,COG0550@NOG,COG0551@NOG,arCOG01527@arNOG		Cytoplasmic
NAS2_1460	tRNA	tRNA-Leu								
NAS2_1461	tRNA	tRNA-Met								
NAS2_1462	179 CDS	2-oxoglutarate oxidoreductase, gamma subunit	1.2.7.3	K00177	Thaumarchaeota	C		0FDBF@creNOG,COG1014@NOG,arCOG01602@arNOG		Unknown
NAS2_1463	286 CDS	2-oxoglutarate oxidoreductase, beta subunit	1.2.7.3	K00175	TACK group	C		0KR9G@eurNOG,COG1013@NOG,arCOG01599@arNOG		Unknown
NAS2_1464	386 CDS	2-oxoglutarate oxidoreductase, alpha subunit	1.2.7.3	K00174	Crenarchaeota	C		0FB6A@creNOG,COG0674@NOG,arCOG01607@arNOG		Unknown
NAS2_1465	108 CDS	2-oxoglutarate oxidoreductase, delta subunit, putative	1.2.7.3	K00176	Archaea	C		0FDDT@creNOG,COG1146@NOG,arCOG00959@arNOG		Cytoplasmic
NAS2_1466	407 CDS	ABC transporter, permease protein		K02004	TACK group	V		0FB1G@creNOG,COG0577@NOG,arCOG02312@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1467	536 CDS	hypothetical protein			Thaumarchaeota	M		0FDRT@creNOG,COG1361@NOG,arCOG02079@arNOG,arCOG04400@arNOG	Transporter (ABC)	Unknown
NAS2_1468	238 CDS	Lipoprotein releasing system ATP-binding protein LolD		K02003	Archaea	V		0FBB9@creNOG,COG1136@NOG,arCOG00922@arNOG	Transporter (ABC)	CytoplasmicMembrane
NAS2_1469	tRNA	tRNA-Gly								
NAS2_1470	167 CDS	hypothetical protein			Bacteria	H				Unknown
NAS2_1471	430 CDS	Hydroxymethylglutaryl-CoA reductase	1.1.1.34	K00054	cellular organisms	I		0KYEA@eurNOG,COG1257@NOG,arCOG04260@arNOG		Unknown
NAS2_1472	tRNA	tRNA-Val								
NAS2_1473	873 CDS	Ribonucleotide reductase of class II	1.17.4.1	K00525	Thaumarchaeota			02H8Z@arNOG,0KRJW@eurNOG,COG0209@NOG,arCOG04276@arNOG		Unknown
NAS2_1474	tRNA	tRNA-Ala								
NAS2_1475	48 CDS	hypothetical protein			No hits					Unknown
NAS2_1476	172 CDS	UPF0129 protein		K07060	Archaea			0KUF9@eurNOG,1CEQI@thermNOG,COG1439@NOG,arCOG00721@arNOG		Cytoplasmic
NAS2_1477	266 CDS	NAD kinase	2.7.1.23	K00858	cellular organisms	G		0KS11@eurNOG,COG0061@NOG,arCOG01348@arNOG		Cytoplasmic
NAS2_1478	230 CDS	conserved hypothetical protein			Archaea			0FAZV@creNOG,COG2102@NOG,arCOG00035@arNOG	Transporter (ABC)	Cytoplasmic
NAS2_1479	441 CDS	Signal recognition particle, subunit Fth SRP54		K03106	Archaea	U		0KR9C@eurNOG,1CDXW@thermNOG,COG0541@NOG,arCOG01228@arNOG		Cytoplasmic
NAS2_1480	376 CDS	tRNA pseudouridine 55 synthase Archaea		K07583	Thaumarchaeota	J		0FB0I@creNOG,COG1258@NOG,arCOG01015@arNOG		Cytoplasmic
NAS2_1481	94 CDS	LSU ribosomal protein L21e		K02889	Thaumarchaeota	J		0FCPY@creNOG,COG2139@NOG,arCOG04129@arNOG		Cytoplasmic
NAS2_1482	116 CDS	DNA-directed RNA polymerase subunit F	2.7.7.6	K03051	Thaumarchaeota	K		1CC0S@thaNOG,COG1460@NOG,arCOG01016@arNOG		Cytoplasmic
NAS2_1483	193 CDS	Predicted RNA-binding protein			Thaumarchaeota	J		1CB66@thaNOG,COG1491@NOG,arCOG04130@arNOG		Cytoplasmic
NAS2_1484	247 CDS	S-adenosylmethionine-6-N,N'-adenosyl-rRNA dimethyltransferase	2.1.1.182	K02528	cellular organisms	J		1CBHK@thaNOG,COG0030@NOG,arCOG04131@arNOG		Cytoplasmic
NAS2_1485	188 CDS	Protein-N(5)-glutamine methyltransferase PmC		K02493	Crenarchaeota	J		0KTK6@eurNOG,0RH3F@halNOG,COG2890@NOG,arCOG00109@arNOG		Cytoplasmic
NAS2_1486	350 CDS	GTP-binding protein RBG1/RBG2		K06944	Archaea			0FB0W@creNOG,COG1163@NOG,arCOG00358@arNOG		Unknown
NAS2_1487	143 CDS	Citrate synthase	2.3.3.1	K01647	Euryarchaeota	C		0FAX7@creNOG,COG0372@NOG,arCOG04237@arNOG		Cytoplasmic
NAS2_1488	255 CDS	Citrate synthase	2.3.3.1	K01647	Thaumarchaeota	C		0KRNU@eurNOG,COG00372@NOG,arCOG04237@arNOG		Cytoplasmic
NAS2_1489	413 CDS	tRNA S(4U) 4-thiouridine synthase		K03151	cellular organisms	H		02HSQ@arNOG,0KRTE@eurNOG,COG0301@NOG,arCOG00038@arNOG		Cytoplasmic
NAS2_1490	168 CDS	3-isopropylmalate dehydratase small subunit	4.2.1.33	K01704	cellular organisms	E		0KT17@eurNOG,COG0066@NOG,arCOG02230@arNOG		Cytoplasmic
NAS2_1491	454 CDS	3-isopropylmalate dehydratase large subunit	4.2.1.33	K01703	Archaea	E		1CB3V@thaNOG,COG0065@NOG,arCOG01698@arNOG		Cytoplasmic
NAS2_1492	175 CDS	hypothetical protein			Thaumarchaeota	K				Cytoplasmic
NAS2_1493	326 CDS	Ribose-1,5-bisphosphate isomerase		K18237	Thaumarchaeota	J		0FB6J@creNOG,COG1184@NOG,arCOG01124@arNOG		Cytoplasmic
NAS2_1494	317 CDS	Ribose-1,5-bisphosphate isomerase		K18237	Crenarchaeota	J		0FBLJ@creNOG,COG1184@NOG,arCOG01124@arNOG		Cytoplasmic
NAS2_1495	499 CDS	hypothetical protein			Crenarchaeota			0FC6X@creNOG,11N0I@NOG,arCOG02216@arNOG		CytoplasmicMembrane
NAS2_1496	370 CDS	hypothetical protein			Crenarchaeota			0YJHY@eurNOG,arCOG05971@arNOG		CytoplasmicMembrane
NAS2_1497	432 CDS	Niacin transporter NiaP			Thaumarchaeota	G		0Y7ZW@creNOG,arCOG02792@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_1498	102 CDS	thioredoxin		K03671	Thaumarchaeota	O		0KTYB@eurNOG,1CB38@thaNOG,COG0526@NOG,arCOG01972@arNOG		Cytoplasmic
NAS2_1499	188 CDS	hypothetical protein			Thaumarchaeota			0FBVM@creNOG,11H41@NOG,arCOG05323@arNOG		Unknown
NAS2_1500	486 CDS	Multidrug resistance protein			Thaumarchaeota	P		0FB61@creNOG,0XNN3@NOG,arCOG00144@arNOG	Transporter (MFS)	CytoplasmicMembrane
NAS2_1501	111 CDS	TVG010389 protein			Thaumarchaeota			0FCWQ@creNOG,11THJ@NOG,arCOG05388@arNOG		Cytoplasmic
NAS2_1502	716 CDS	Oligosaccharyl transferase, STT3 subunit		K07151	Thaumarchaeota			0FB55@creNOG,COG1287@NOG,arCOG02044@arNOG		CytoplasmicMembrane
NAS2_1503	123 CDS	hypothetical protein			Not assigned					CytoplasmicMembrane
NAS2_1504	221 CDS	hypothetical protein			Archaea	F				Cytoplasmic
NAS2_1505	330 CDS	Phosphoribosylaminoimidazolecarboxamide formyltransferase		K06863	Crenarchaeota	F		0FB10@creNOG,COG1759@NOG,arCOG04346@arNOG		Cytoplasmic
NAS2_1506	352 CDS	putative phosphoribosylaminoimidazolecarboxamide formyltransferase		K06863	Crenarchaeota	F		0FBEQ@creNOG,COG1759@NOG,arCOG04346@arNOG		Cytoplasmic
NAS2_1507	202 CDS	hypothetical protein			Archaea			0FCVA@creNOG,0ZXD4@NOG,arCOG01806@arNOG		Cytoplasmic
NAS2_1508	367 CDS	Carbamoyl-phosphate synthase small chain	6.3.5.5	K01956	Archaea	F	MER0244767	0FB56@creNOG,COG0505@NOG,arCOG00064@arNOG		Cytoplasmic
NAS2_1509	1070 CDS	Carbamoyl-phosphate synthase large chain	6.3.5.5	K01955	Archaea	F		0FB91@creNOG,COG0458@NOG,arCOG01594@arNOG		Cytoplasmic
NAS2_1510	514 CDS	GMP synthase [glutamine-hydrolyzing]	6.3.5.2	K01951	Archaea	F	MER0442866	0FBAJ@creNOG,COG0518@NOG,COG0519@NOG,arCOG00085@arNOG		CytoplasmicMembrane

NAS2_1511	238 CDS	Adenine phosphoribosyltransferase, fused to N-terminal DNA-binding domain	K00759	Korarchaeota	F	COG0503@NOG,arCOG00031@arNOG		Cytoplasmic	
NAS2_1512	95 CDS	hypothetical protein		Crenarchaeota				Cytoplasmic	
NAS2_1513	226 CDS	hypothetical protein		Crenarchaeota				CytoplasmicMembrane	
NAS2_1514	325 CDS	Oligopeptide transport ATP-binding protein OppF		cellular organisms	E	0KS6U@eurNOG,0RFG3@halNOG,COG0444@NOG,COG4608@NOG,arCOG00181@arNOG,arCOG00184@arNOG	Transporter (ABC)	CytoplasmicMembrane	Pep transporter
NAS2_1515	318 CDS	Oligopeptide transport ATP-binding protein OppD	K02031	cellular organisms	E	0M21B@eurNOG,COG1123@metNOG,arCOG00181@arNOG,arCOG00184@arNOG	Transporter (ABC)	CytoplasmicMembrane	Pep transporter
NAS2_1516	212 CDS	hypothetical protein		Thaumarchaeota				Unknown	Pep transporter
NAS2_1517	493 CDS	putative peptide transport permease	K02034	Thaumarchaeota	P	0FBUI@creNOG,COG1173@NOG,arCOG00749@arNOG	Transporter (ABC)	CytoplasmicMembrane	Pep transporter
NAS2_1518	434 CDS	Dipeptide transport system permease protein DppB	K02033	Thaumarchaeota	P	0FBMI@creNOG,COG0601@NOG,arCOG00751@arNOG	Transporter (ABC)	CytoplasmicMembrane	Pep transporter
NAS2_1519	912 CDS	oligopeptide binding protein, putative		Thaumarchaeota	E	MERO469033 COG0747@NOG,arCOG01673@arNOG	Transporter (ABC)	CytoplasmicMembrane	Pep transporter
NAS2_1520	399 CDS	Fosmidomycin resistance protein		Crenarchaeota	G	02U25@arNOG,0FFX8@creNOG,0ZVRB@NOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_1521	384 CDS	MFS permease protein		Archaea	M	COG0477@NOG,arCOG00130@arNOG	Transporter (MFS)	CytoplasmicMembrane	
NAS2_1522	314 CDS	Putative enzyme of poly-gamma-glutamate biosynthesis	K07282	Bacteria	G	0KSRA@eurNOG,0WRV7@metNOG,COG2843@NOG,arCOG07503@arNOG		CytoplasmicMembrane	
NAS2_1523	554 CDS	MoaA/NiB/PqQ family protein	K06937	Thaumarchaeota		1CBF3@thaNOG,COG1964@NOG,arCOG00933@arNOG		Cytoplasmic	
NAS2_1524	305 CDS	Aspartate carbamoyltransferase	2.1.3.2 K00609	TACK group	F	0FBFD@creNOG,COG0540@NOG,arCOG000911@arNOG		Cytoplasmic	
NAS2_1525	180 CDS	hypothetical protein		Thaumarchaeota		1117Q@NOG,1CBPZ@thaNOG,arCOG08749@arNOG		Cytoplasmic	
NAS2_1526	252 CDS	Transcriptional regulator, TrmB family		Thaumarchaeota	K	1CB9R@thaNOG,COG1378@NOG,arCOG02038@arNOG		Cytoplasmic	
NAS2_1527	162 CDS	Signal peptidase I	3.4.21.89 K13280	Thaumarchaeota	U	COG0681@NOG,arCOG01739@arNOG		CytoplasmicMembrane	
NAS2_1528	184 CDS	TATA-box binding protein		Thaumarchaeota		1CBAZ@thaNOG,COG2101@NOG,arCOG01764@arNOG		Cytoplasmic	
NAS2_1529	356 CDS	Isocitrate dehydrogenase [NAD]	1.1.1.41 K00031	Archaea	E	0KRWT@eurNOG,0WK9S@methaNOG,COG0473@NOG,arCOG01163@arNOG	IDH		
NAS2_1530	390 CDS	Conserved protein		Archaea	L	COG1468@NOG,arCOG00790@arNOG		Cytoplasmic	
NAS2_1531	117 CDS	hypothetical protein		Not assigned				CytoplasmicMembrane	
NAS2_1532	130 CDS	hypothetical protein		Archaea				Cytoplasmic	
NAS2_1533	182 CDS	hypothetical protein		Not assigned				Cytoplasmic	
NAS2_1534	287 CDS	rRNA (Guanine37'-N1) -methyltransferase	2.1.1.31 K15429	Archaea		0FBR9@creNOG,COG2520@NOG,arCOG00033@arNOG		Cytoplasmic	
NAS2_1535	603 CDS	RNAse L inhibitor		Archaea		02GVR@arcNOG,0KRBC@eurNOG,COG1245@NOG,arCOG00187@arNOG	Transporter (ABC)	multispecies	
NAS2_1536	431 CDS	hypothetical protein		Thaumarchaeota		0FBD9@creNOG,COG1602@NOG,arCOG04269@arNOG		Cytoplasmic	
NAS2_1537	294 CDS	Twin-arginine translocation protein TatC	K03118	Crenarchaeota	U	0FBPR@creNOG,COG0805@NOG,arCOG01919@arNOG		CytoplasmicMembrane	Sre
NAS2_1538	166 CDS	Twin-arginine translocation protein TatA		Crenarchaeota	U	0FEXC@creNOG,COG1826@NOG,arCOG05911@arNOG		Cytoplasmic	Sre
NAS2_1539	103 CDS	Twin-arginine translocation protein TatA	K03116	Thaumarchaeota	U	0FD48@creNOG,COG1826@NOG,arCOG02694@arNOG		Cytoplasmic	Sre
NAS2_1540	434 CDS	myoiodoprotein oxidoreductase, membrane subunit		Thaumarchaeota	C	0FDS@creNOG,0ZV09@arcNOG,arCOG02026@arNOG		CytoplasmicMembrane	Sre
NAS2_1541	230 CDS	Polysulfide reductase, subunit B, putative		Thaumarchaeota	C	0FCRV@creNOG,COG0437@NOG,arCOG01500@arNOG		CytoplasmicMembrane	Sre
NAS2_1542	1032 CDS	Polysulfide reductase, subunit A, putative		Crenarchaeota	C	0FBA2@creNOG,COG0243@NOG,arCOG01495@arNOG		Unknown	Sre
NAS2_1543	179 CDS	cytoplasmic chaperone TorD family protein		TACK group	C	COG3381@NOG,arCOG01506@arNOG		Unknown	Sre
NAS2_1544	466 CDS	Iron-sulfur cluster-binding protein		Thaumarchaeota	C	0FFT1@creNOG,COG1145@NOG,arCOG02181@arNOG		Cytoplasmic	Sre
NAS2_1545	729 CDS	Cell division protein FtsH	K13525	Archaea	O	MERO269263 0KRDG@eurNOG,COG0464@NOG,arCOG01308@arNOG		Cytoplasmic	
NAS2_1546		rRNA-Arg							
NAS2_1547	82 CDS	hypothetical protein		Thaumarchaeota				Unknown	
NAS2_1548		rRNA-Gln							
NAS2_1549	105 CDS	LSU ribosomal protein L12a							
NAS2_1550	901 CDS	Alanyl-tRNA synthetase	6.1.1.7 K02869	Archaea	J	0FD04@creNOG,COG2058@NOG,arCOG04287@arNOG		Cytoplasmic	
NAS2_1551	434 CDS	asparagine synthetase B	K01872	Thaumarchaeota	J	1CBHD@thaNOG,COG00113@NOG,arCOG01255@arNOG		Cytoplasmic	
NAS2_1552	256 CDS	Molybdopterin binding motif, ClnA N-terminal domain	K01953	Thaumarchaeota	E	0KRA8@eurNOG,1CDD3@methaNOG,COG0387@NOG,arCOG00071@arNOG	ASNS		
NAS2_1553	386 CDS	hypothetical protein		Thaumarchaeota	H	0FBUI@creNOG,COG1058@NOG,arCOG00215@arNOG		Cytoplasmic	
NAS2_1554		rRNA-His				1CB90@thaNOG,COG04046@NOG,arCOG04181@arNOG		CytoplasmicMembrane	
NAS2_1555	114 CDS	Eukaryotic translation initiation factor 5A	K03263	Archaea	J	0FC51@creNOG,COG0231@NOG,arCOG04277@arNOG		Cytoplasmic	
NAS2_1556	345 CDS	hypothetical protein		cellular organisms	H			Cytoplasmic	
NAS2_1557	373 CDS	glycosyltransferase		Thaumarchaeota		0KTRZ@eurNOG,0WK54@methaNOG,COG1819@NOG,arCOG01393@arNOG		CytoplasmicMembrane	
NAS2_1558	207 CDS	COG2078: Uncharacterized ACR	K09141	Archaea		0KT45@eurNOG,0W06D@methNOG,COG2078@NOG,arCOG01336@arNOG		Cytoplasmic	
NAS2_1559	177 CDS	FIG046540: CBS domain protein		Archaea		02TZJ@arNOG,0M2AF@eurNOG,0WPQY@methaNOG,11SM0@NOG		Cytoplasmic	
NAS2_1560	654 CDS	COG1293, Predicted RNA-binding protein homologous to eukaryotic snRNP		Archaea	K	1CBEX@thaNOG,COG1293@NOG,arCOG01695@arNOG		Cytoplasmic	
NAS2_1561	56 CDS	hypothetical protein		Thaumarchaeota				CytoplasmicMembrane	
NAS2_1562	159 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic	
NAS2_1563	384 CDS	DNA repair and recombination protein RadA	K04483	Archaea	L	1CBFB@thaNOG,COG0468@NOG,arCOG00415@arNOG		Unknown	
NAS2_1564	229 CDS	Fibrillarin	K04795	Archaea	J	0FB4E@creNOG,COG1889@NOG,arCOG00078@arNOG		Cytoplasmic	
NAS2_1565	405 CDS	rRNA biogenesis protein Nop5/Nop56	K14564	Thaumarchaeota	J	0FB3X@creNOG,COG1498@NOG,arCOG01923@arNOG		Cytoplasmic	
NAS2_1566	56 CDS	hypothetical protein	K02983	Thaumarchaeota	J			Cytoplasmic	
NAS2_1567	175 CDS	Inosine/xanthosine triphosphatase		Thaumarchaeota		0FCN0@creNOG,COG1986@NOG,arCOG01221@arNOG		Cytoplasmic	
NAS2_1568	532 CDS	histone acetyltransferase, ELP3 family	K07739	Archaea	B	0KR9Y@eurNOG,COG1243@NOG,arCOG01361@arNOG		Cytoplasmic	
NAS2_1569	443 CDS	Glutamyl-tRNA(Gln) amidotransferase asparaginase subunit	6.3.5.7 K09482	TACK group	E	0FB8H@creNOG,COG0252@NOG,arCOG01924@arNOG		Cytoplasmic	
NAS2_1570	640 CDS	Glutamyl-tRNA(Gln) amidotransferase transferase subunit	6.3.5.7 K03330	Archaea	J	0FBSN@creNOG,COG2511@NOG,arCOG01719@arNOG		Cytoplasmic	
NAS2_1571	150 CDS	hypothetical protein		Thaumarchaeota				Unknown	
NAS2_1572	166 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic	
NAS2_1573	122 CDS	hypothetical protein		Archaea				Cytoplasmic	
NAS2_1574	285 CDS	hypothetical protein		Thaumarchaeota				Cytoplasmic	
NAS2_1575	492 CDS	Bipolar DNA helicase HerA	K06915	Thaumarchaeota				Unknown	
NAS2_1576	238 CDS	hypothetical protein	K07731	Thaumarchaeota	K	0KSYC@eurNOG,0WOMB@methNOG,COG1709@NOG,arCOG04060@arNOG		Cytoplasmic	
NAS2_1577	252 CDS	COG1836		cellular organisms		COG1836@NOG,arCOG02245@arNOG		CytoplasmicMembrane	
NAS2_1578	567 CDS	Glycyl-tRNA synthetase	6.1.1.14 K01880	Archaea	J	0FB51@creNOG,COG0423@NOG,arCOG00405@arNOG		Cytoplasmic	
NAS2_1579	391 CDS	hypothetical protein		Crenarchaeota		0FB4Z@creNOG,COG2403@NOG,arCOG01229@arNOG		Cytoplasmic	
NAS2_1580	308 CDS	Alanyl-tRNA synthetase	6.1.1.7 K01872	Archaea	J			Cytoplasmic	
NAS2_1581	289 CDS	LSU ribosomal protein P0	K02864	Archaea	J	0FAYK@creNOG,COG0244@NOG,arCOG04288@arNOG		Cytoplasmic	
NAS2_1582	217 CDS	LSU ribosomal protein L10Ae	K02863	Thaumarchaeota	J	1CB4M@thaNOG,COG0081@NOG,arCOG04289@arNOG		Cytoplasmic	
NAS2_1583	164 CDS	LSU ribosomal protein L12e	K02867	Thaumarchaeota	J	0FC00@creNOG,COG0080@NOG,arCOG04372@arNOG		Cytoplasmic	
NAS2_1584	292 CDS	hypothetical protein		Archaea	O	0FB3I@creNOG,COG0616@NOG,arCOG01911@arNOG		Unknown	Peptidase
NAS2_1585	156 CDS	Putative transcription antitermination protein NusG	K02601	Thaumarchaeota	K	0FCKF@creNOG,COG0250@NOG,arCOG01920@arNOG		Cytoplasmic	
NAS2_1586	82 CDS	hypothetical protein	K07342	Thaumarchaeota				CytoplasmicMembrane	
NAS2_1587	41 CDS	hypothetical protein		Thaumarchaeota				Unknown	
NAS2_1588	311 CDS	Ornithine carbamoyltransferase	2.1.3.3 K00611	Thaumarchaeota	E	02H00@arcNOG,0KRNR@eurNOG,COG0078@NOG,arCOG00912@arNOG		Cytoplasmic	
NAS2_1589	298 CDS	Signal recognition particle receptor protein FtsY	K03110	Archaea	U	0FB1D@creNOG,COG0552@NOG,arCOG01227@arNOG		multispecies	
NAS2_1590	142 CDS	Prefoldin alpha subunit	K04797	Thaumarchaeota	O	1CC0E@thaNOG,COG1730@NOG,arCOG01341@arNOG		Cytoplasmic	
NAS2_1591	224 CDS	Eukaryotic translation initiation factor 6	K03264	Thaumarchaeota	J	1CBSW@thaNOG,COG1976@NOG,arCOG04176@arNOG		Unknown	
NAS2_1592	76 CDS	hypothetical protein	K02910	Thaumarchaeota	J	0FDS@creNOG,COG2097@NOG,arCOG04473@arNOG		Cytoplasmic	
NAS2_1593	51 CDS	hypothetical protein	K02924	Archaea	J			Cytoplasmic	
NAS2_1594	98 CDS	DNA-binding protein MTH1615	K06875	Thaumarchaeota		0FD0G@creNOG,COG2118@NOG,arCOG04179@arNOG		Cytoplasmic	
NAS2_1595	161 CDS	SSU ribosomal protein S19e	K02966	Thaumarchaeota	J	0FC1I@creNOG,COG2238@NOG,arCOG01344@arNOG		Cytoplasmic	
NAS2_1596	112 CDS	hypothetical protein	K03540	Thaumarchaeota				Cytoplasmic	
NAS2_1597	233 CDS	N1-specific pseudouridine methyltransferase NEP1	K14568	Thaumarchaeota	J	0KT42@eurNOG,COG1756@NOG,arCOG04122@arNOG		Cytoplasmic	
NAS2_1598		rRNA-Gly							
NAS2_1599	402 CDS	hypothetical protein	K01999	Thaumarchaeota	E			Unknown	

NAS2_1600	48 CDS	hypothetical protein		No hits				Unknown
NAS2_1601	61 CDS	hypothetical protein		No hits				Cytoplasmic
NAS2_1602	445 CDS	Putative membrane-bound ClpP-class protease associated with aq_911	K07403	Thaumarchaeota	O	MER1072474	0KSE1@eurNOG,1CCGS@theNOG,COG1030@NOG,arCOG01910@arNOG	CytoplasmicMembrane Peptidase
NAS2_1603	290 CDS	Putative stomatin/prohibitin-family membrane protease subunit aq_911		Thaumarchaeota	O	MER0796921	0KS9Y@eurNOG,1CCHN@theNOG,COG0330@NOG,arCOG01915@arNOG	Unknown
NAS2_1604	135 CDS	hypothetical protein		Euryarchaeota				Cytoplasmic
NAS2_1605	tRNA	tRNA-Leu						
NAS2_1606	tRNA	tRNA-Ser						
NAS2_1607	61 CDS	hypothetical protein		Archaea			0KX3U@eurNOG,0XU82@NOG,1CDGP@theNOG,arCOG05360@arNOG	Unknown
NAS2_1608	217 CDS	Orotate phosphoribosyltransferase	2.4.2.10	K00762	Thaumarchaeota	F	0FCJl@creNOG,COG0461@NOG,arCOG00029@arNOG	Cytoplasmic
NAS2_1609	183 CDS	Orotate phosphoribosyltransferase	2.4.2.10	K00762	Thaumarchaeota	F	0FCJl@creNOG,COG0461@NOG,arCOG00029@arNOG	Cytoplasmic
NAS2_1610	236 CDS	Orotidine 5'-phosphate decarboxylase	4.1.1.23	K01591	Euryarchaeota	F	0KS2C@eurNOG,0WKRPQ@methaNOG,COG0284@NOG,arCOG00081@arNOG	Unknown
NAS2_1611	88 CDS	hypothetical protein		K09721	Thaumarchaeota		0FCGM@creNOG,COG1698@NOG,arCOG04308@arNOG	Cytoplasmic
NAS2_1612	120 CDS	hypothetical protein		K07143	Thaumarchaeota			Cytoplasmic
NAS2_1613	272 CDS	hypothetical protein		K00943	Thaumarchaeota	F		Cytoplasmic
NAS2_1614	129 CDS	Aconitate hydratase X, predicted		K09128	Thaumarchaeota		0FD5Y@creNOG,COG1786@NOG,arCOG04279@arNOG	Cytoplasmic
NAS2_1615	449 CDS	UbiD family decarboxylase			Thaumarchaeota	H	1CB91@thaNOG,COG0043@NOG,arCOG01671@arNOG	Cytoplasmic
NAS2_1616	141 CDS	hypothetical protein			Thaumarchaeota			Unknown
NAS2_1617	248 CDS	DNA polymerase sliding clamp protein PCNA		K04802	Thaumarchaeota	L	1CBPU@thaNOG,COG0592@NOG,arCOG00488@arNOG	Cytoplasmic
NAS2_1618	371 CDS	DNA primase large subunit		K18882	Archaea	L	0FBXU@creNOG,COG2219@NOG,arCOG03013@arNOG	Cytoplasmic
NAS2_1619	342 CDS	DNA primase small subunit		K02683	Thaumarchaeota	L	1CBSH@thaNOG,COG1467@NOG,arCOG04110@arNOG	Cytoplasmic
NAS2_1620	186 CDS	hypothetical protein			Thaumarchaeota			Unknown
NAS2_1621	99 CDS	LSU ribosomal protein L44e		K02929	Archaea	J	0FCHP@creNOG,COG1631@NOG,arCOG04109@arNOG	Cytoplasmic
NAS2_1622	65 CDS	SSU ribosomal protein S27e		K02978	Archaea	J	0FCXC@creNOG,COG2051@NOG,arCOG04108@arNOG	Cytoplasmic
NAS2_1623	251 CDS	Eukaryotic translation initiation factor 2 alpha subunit		K03237	Archaea	J	0KRUR@eurNOG,COG1093@NOG,arCOG04107@arNOG	Cytoplasmic
NAS2_1624	252 CDS	Coenzyme F420-0-L-glutamate ligase			Thaumarchaeota		0KSS3@eurNOG,0WKN1@methaNOG,COG1478@NOG,arCOG02714@arNOG	Cytoplasmic
NAS2_1625	538 CDS	Methionyl-tRNA synthetase	6.1.1.10	K01874	Thaumarchaeota	J	0FB2H@creNOG,COG0143@NOG,arCOG00810@arNOG	Cytoplasmic
NAS2_1626	104 CDS	SSU ribosomal protein S20e		K02946	Thaumarchaeota	J	0KTDt@eurNOG,1CEW3@thermNOG,COG0051@NOG,arCOG01758@arNOG	Cytoplasmic
NAS2_1627	103 CDS	hypothetical protein		K07466	Thaumarchaeota	L	0KS23@eurNOG,0WKHB@methaNOG,COG1599@NOG,arCOG01510@arNOG	Cytoplasmic
NAS2_1628	299 CDS	Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase		K01001	Thaumarchaeota	M	1CBD3@thaNOG,COG0472@NOG,arCOG03199@arNOG	CytoplasmicMembrane
NAS2_1629	166 CDS	Acetylacyl transferase related protein			TACK group		1CBPY@thaNOG,COG0110@NOG,arCOG01848@arNOG	Cytoplasmic
NAS2_1630	310 CDS	Myo-inositol 2-dehydrogenase	1.1.1.18	K18855	Archaea		1CBEK@thaNOG,COG0673@NOG,arCOG01622@arNOG	Cytoplasmic
NAS2_1631	292 CDS	hypothetical protein			Thaumarchaeota	I		Cytoplasmic
NAS2_1632	tRNA	tRNA-Glu						
NAS2_1633	108 CDS	hypothetical protein		K07108	Archaea	K		Cytoplasmic
NAS2_1634	309 CDS	Octaprenyl diphosphate synthase	2.5.1.1	K02523	Thaumarchaeota	H	1CBMT@thaNOG,COG0142@NOG,arCOG01727@arNOG	Cytoplasmic
NAS2_1635	tRNA	tRNA-Gln						
NAS2_1636	331 CDS	hypothetical protein		K09726	Thaumarchaeota		1CBKK@thaNOG,COG1817@NOG,arCOG01395@arNOG	Cytoplasmic
NAS2_1637	543 CDS	Heat shock protein 60 family chaperone GroEL, Thermosome subunit			cellular organisms	O	0FB1U@creNOG,COG0459@NOG,arCOG01257@arNOG	Cytoplasmic
NAS2_1638	tRNA	tRNA-Ser						
NAS2_1639	314 CDS	Tiis and Tlca-like n-type ATP pyrophosphatase superfamily			Thaumarchaeota	D	1CBHC@thaNOG,COG00037@NOG,arCOG00042@arNOG	Cytoplasmic
NAS2_1640	699 CDS	Archaeal DNA polymerase II large subunit	2.7.7.7	K02322	Thaumarchaeota	L	0KRHY@eurNOG,0WUJY@methaNOG,COG1933@NOG,arCOG04447@arNOG	Cytoplasmic
NAS2_1641	245 CDS	(S)-3-O-geranylgeranylglycerol phosphate synthase		K17104	Archaea		0FCOM@creNOG,COG1846@NOG,arCOG01085@arNOG	Unknown
NAS2_1642	87 CDS	hypothetical protein			Thaumarchaeota		0FCX9@creNOG,COG4888@NOG,arCOG04136@arNOG	Cytoplasmic
NAS2_1643	234 CDS	glutaredoxin-like protein			Thaumarchaeota	O	0KS9D@eurNOG,COG0526@NOG,arCOG01218@arNOG	CytoplasmicMembrane
NAS2_1644	89 CDS	DNA/RNA-binding protein Alba		K03622	Thaumarchaeota	K	0KU0E@eurNOG,COG1581@NOG,arCOG01753@arNOG	Cytoplasmic
NAS2_1645	544 CDS	hypothetical protein		K08979	Thaumarchaeota		1CB4N@thaNOG,COG3356@NOG,arCOG04351@arNOG	CytoplasmicMembrane
NAS2_1646	43 CDS	hypothetical protein			Archaea			CytoplasmicMembrane
NAS2_1647	453 CDS	Serine hydroxymethyltransferase	2.1.2.1	K00600	Archaea	E	1CBDW@thaNOG,COG0112@NOG,arCOG00070@arNOG	Cytoplasmic
NAS2_1648	373 CDS	Conserved protein			Thaumarchaeota	M	0FCNK@creNOG,COG0750@NOG,arCOG04064@arNOG	CytoplasmicMembrane Peptidase
NAS2_1649	391 CDS	DNA primase			Thaumarchaeota	L	0FAY2@creNOG,COG0358@NOG,arCOG04281@arNOG	Cytoplasmic
NAS2_1650	110 CDS	hypothetical protein			Thaumarchaeota	L		Cytoplasmic
NAS2_1651	94 CDS	hypothetical protein		K02917	Thaumarchaeota	J		Cytoplasmic
NAS2_1652	tRNA	tRNA-Leu						
NAS2_1653	659 CDS	Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative			Thaumarchaeota	C	0KRK4@eurNOG,1CCHH@theNOG,COG1042@NOG,arCOG01338@arNOG,arCOG01340@arNOG	Cytoplasmic
NAS2_1654	76 CDS	Transcriptional regulator, AsnC family			Thaumarchaeota	K	0FCVX@creNOG,COG1522@NOG,arCOG01117@arNOG	Cytoplasmic
NAS2_1655	237 CDS	transposase			Thaumarchaeota	L	0KUY3@eurNOG,COG3316@NOG,arCOG02134@arNOG	Unknown
NAS2_1656	116 CDS	hypothetical protein			Thaumarchaeota			Cytoplasmic