Supplementary Table 6. Classification of the unique genes based on the arCOG classification.

									Number of genes				
		arCOG clasification	gene	product	COG classification	pFAM domain	cdc	TIGR classification	EPIPELAGIC MGIII	BATHY1	BATHY2	Thalassoarchaea	MG2-GG3
INFORMATION STORAGE AND PROCESSING													
arCOG00415	L	Replication, recombination and repair	RecA	RecA/RadA recombinase	COG00468	pfam14520,pfa	cd01123	TIGR02236	1				
arCOG00439	L	Replication, recombination and repair	MCM2	Predicted ATPase involved in replication control, Cdc46/Mcm family	COG01241	pfam14551,pfa	cd00009		1				
arCOG04110	L	Replication, recombination and repair	PRI1	Eukaryotic-type DNA primase, catalytic (small) subunit	COG01467	pfam01896	cd04860	TIGR00335	1			1	1
arCOG00787	L	Replication, recombination and repair	-	UvrD/Rep family helicase fused to exonuclease family domain	COG02887	pfam12705	cd09637	TIGR01249,TIGR00372	1				
arCOG05109	L	Replication, recombination and repair	DnaQ	DNA polymerase III, epsilon subunit or related 3'-5' exonuclease	COG00847	pfam00929	cd06127	TIGR00573	1				1
arCOG01898	L	Replication, recombination and repair	Uve	UV damage repair endonuclease	COG04294	pfam03851		TIGR00629	1				
arCOG00469	L	Replication, recombination and repair	HolB	ATPase involved in DNA replication HolB, small subunit	COG00470	pfam13177,pfa	cd00009	TIGR02397	2				1
arCOG01894	L	Replication, recombination and repair	Nfo	Endonuclease IV	COG00648	pfam01261	cd00019	TIGR00587	2				
arCOG01073	L	Replication, recombination and repair	-	NUDIX family hydrolase	COG00494	pfam00293	cd03424	TIGR00052	2				
arCOG01347	L	Replication, recombination and repair	CDC9	ATP-dependent DNA ligase	COG01793	pfam04675,pfa	cd07901,cd079	TIGR00574	2				
arCOG02840	L	Replication, recombination and repair	PhrB	Deoxyribodipyrimidine photolyase	COG00415	pfam00875,pfam03441		TIGR03556	2				1
arCOG01078	L	Replication, recombination and repair	-	NUDIX family hydrolase	COG00494	pfam00293	cd03428		3	1		1	1
arCOG00464	L	Replication, recombination and repair	AlkA	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase	COG00122	pfam07934,pfa	cd00056	TIGR00588	3		1		1
arCOG03142	L	Replication, recombination and repair	-	Nuclease of RNase H fold, RuvC/YqgF family					3		1	1	1
arCOG01486	L	Replication, recombination and repair	RnmV	5S rRNA maturation endonuclease (Ribonuclease M5), contains TOPRIM dom	COG01658	pfam01751	cd01027		4	1		1	1
arCOG08649	L	Replication, recombination and repair	-	Topoisomerase IB	COG03569	pfam02919,pfa	cd00660,cd00659		4				1
arCOG00417	L	Replication, recombination and repair	RecA	RecA/RadA recombinase	COG00468		cd01394	TIGR02237	5				
arCOG04367	L	Replication, recombination and repair	GyrA	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	COG00188	pfam00521,pfa	cd00187	TIGR01063				2	
arCOG00872	L	Replication, recombination and repair	MPH1	ERCC4-like helicase	COG01111	pfam00270,pfa	cd00046,cd120	TIGR00643,TIGR00580,TIGR00596			1	2	1
arCOG00551	L	Replication, recombination and repair	-	DNA replication initiation complex subunit, GINS15 family	COG01711		cd11714			1			
arCOG00427	L	Replication, recombination and repair	RecJ/CdcS	Single-stranded DNA-specific exonuclease RecJ	COG00608					1	1		
arCOG02258	L	Replication, recombination and repair	-	RPA family protein, a subunit of RPA complex in P.furiosus	COG03390					1		2	
arCOG01166	L	Replication, recombination and repair	MutL	DNA mismatch repair enzyme (predicted ATPase)	COG00323	pfam13589,pfa	cd00075,cd007	TIGR00585				1	
arCOG04121	L	Replication, recombination and repair	RnhB	Ribonuclease HII	COG00164	pfam01351	cd07180	TIGR00729				2	
arCOG00470	L	Replication, recombination and repair	HolB	ATPase involved in DNA replication HolB, large subunit	COG00470	pfam00004	cd00009	TIGR02397				1	1
arCOG04371	L	Replication, recombination and repair	GyrB	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	COG00187	pfam02518,pfa	cd00075,cd008	TIGR01059				1	1
arCOG00488	L	Replication, recombination and repair	DnaN	DNA polymerase sliding clamp subunit (PCNA homolog)	COG00592	pfam00705,pfa	cd00577	TIGR00590				2	1
arCOG01527	L	Replication, recombination and repair	TopA	Topoisomerase IA	COG00550	pfam01751,pfa	cd03362,cd001	TIGR01057		1		1	
arCOG04050	L	Replication, recombination and repair	FEN1	5'-3' exonuclease	COG00258	pfam00752,pfa	cd09867	TIGR03674		1			
arCOG00558	L	Replication, recombination and repair	SrmB	Superfamily II DNA and RNA helicase	COG00513	pfam00270,pfa	cd00268,cd000	TIGR01389				1	2
arCOG00328	L	Replication, recombination and repair	PolB3	DNA polymerase PolB3	COG00417	pfam03104,pfa	cd05781,cd055	TIGR00592				4	1
arCOG01510	L	Replication, recombination and repair	RPA1	Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subun	COG01599		cd04491,cd04491			2		2	1
arCOG01072	L	Replication, recombination and repair	-	NUDIX family hydrolase	COG00494	pfam00293	cd03426			1			
arCOG03013	L	Replication, recombination and repair	PRI2	Eukaryotic-type DNA primase, large subunit	COG02219	pfam04104	cd06560			1			1
arCOG00553	L	Replication, recombination and repair	BRR2	Replicative superfamily II helicase	COG01204	pfam00270,pfa	cd00046,cd000	TIGR04121				3	1
arCOG01526	L	Replication, recombination and repair	TopG2	Reverse gyrase	COG01110	pfam00270,pfa	cd00046,cd033	TIGR01054				2	
arCOG00368	L	Replication, recombination and repair	SbcC	ATPase involved in DNA repair, SbcC	COG00419	pfam13476,pfa	cd03240,cd001	TIGR00611,TIGR02168			1		
arCOG02724	L	Replication, recombination and repair	Ada	Methylated DNA-protein cysteine methyltransferase	COG00350	pfam01035	cd06445	TIGR00589			1	1	
arCOG00397	L	Replication, recombination and repair	SbcD	DNA repair exonuclease, SbcD	COG00420	pfam00149	cd00840				1		
arCOG00329	L	Replication, recombination and repair	PolB2	DNA polymerase PolB2, inactivated	COG00417	pfam00136	cd05531	TIGR00592				1	1
arCOG00802	L	Replication, recombination and repair	RecB	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase a	COG01074	pfam00580,pfam13361		TIGR02785					1
arCOG02895	L	Replication, recombination and repair	MutS2	DNA structure-specific ATPase involved in suppression of recombination, Mu	COG01193	pfam00488	cd03243	TIGR01069				1	1
arCOG04694	L	Replication, recombination and repair	UvrA	Excinuclease ABC subunit A, ATPase	COG00178		cd03271,cd032	TIGR00630				3	
arCOG00462	L	Replication, recombination and repair	MutY	A/G-specific DNA glycosylase	COG01194	pfam00730	cd00056	TIGR01084					1
arCOG03646	L	Replication, recombination and repair	XseB	Exonuclease VII small subunit	COG01722	pfam02609		TIGR01280					1
arCOG04513	L	Replication, recombination and repair	XseA	Exonuclease VII, large subunit	COG01570	pfam13742,pfa	cd04489	TIGR00237					1
arCOG04754	L	Replication, recombination and repair	Lig	NAD-dependent DNA ligase	COG00272	pfam01653,pfa	cd00114,cd000	TIGR00575					1
arCOG07300	L	Replication, recombination and repair	-	Uncharacterized protein associated with inactivated PolB-like polymerase									1
arCOG01082	L	Replication, recombination and repair	-	NUDIX family hydrolase	COG00494	pfam00293	cd02885					1	
arCOG01305	L	Replication, recombination and repair	-	Topoisomerase DNA binding C4 zinc finger fused to uncharacterized N-termi	COG01637							1	
arCOG02896	L	Replication, recombination and repair	MutS	Mismatch repair ATPase (MutS family)	COG00249	pfam01624,pfa	cd03284	TIGR01070				1	
arCOG01981	K	Transcription	SUA7	Transcription initiation factor TFIIB, Brf1 subunit/Transcription initiation fact	COG01405	pfam08271,pfa	cd00043		5	1		1	
arCOG01863	K	Transcription	-	Predicted transcription factor, homolog of eukaryotic MBF1	COG01813	pfam01381	cd00093	TIGR00270	3	1	1	1	
arCOG02611	K	Transcription	-	Predicted transcriptional regulator, containd two HTH domains	COG03398	pfam13412,pfa	cd00090,cd00090		3	1	1	2	1
arCOG07561	K	Transcription	-	Predicted membrane-associated trancriptional regulator	COG02512				3	1	1	2	4
arCOG00770	K	Transcription	DinG	Rad3-related DNA helicase	COG01199	pfam06733,pfam13307		TIGR00604	2		1	2	1
arCOG05671	K	Transcription	CsgD	Transcriptional regulator LuxR family	COG02771				2				
arCOG01680	K	Transcription	ArsR	Transcriptional regulator containing HTH domain, ArsR family	COG00640	pfam01022	cd00090		1		1		
arCOG04280	K	Transcription	NagC	Transcriptional regulator/sugar kinase	COG01940	pfam00480	cd00012	TIGR00744			1		
arCOG01753	K	Transcription	Ssh10b	Archaeal DNA-binding protein	COG01581	pfam01918		TIGR00285		1	1		
arCOG00579	K	Transcription	RPB9	DNA-directed RNA polymerase, subunit M/Transcription elongation factor TF	COG01594			TIGR01384				1	
arCOG01684	K	Transcription	-	Transcriptional regulator, ArsR family	COG01777	pfam01022	cd00090,cd00090					3	1
arCOG00675	K	Transcription	RPB7	DNA-directed RNA polymerase, subunit E'/Rpb7	COG01095	pfam03876,pfa	cd04331,cd044	TIGR00448					1
arCOG04258	K	Transcription	RPB5	DNA-directed RNA polymerase, subunit H, RpoH/RPB5	COG02012	pfam01191						1	1
arCOG01580	K	Transcription	-	DNA-binding transcriptional regulator, Lrp family	COG01522	pfam13412,pfa	cd00090			1		1	
arCOG05161	K	Transcription	WecD	Acetyltransferase (GNAT) family	COG00454					1			
arCOG04111	K	Transcription	RPB11	DNA-directed RNA polymerase, subunit L	COG01761	pfam13656	cd06927						1
arCOG01764	K	Transcription	SPT15	TATA-box binding protein (TBP), component of TFIID and TFIIIB	COG02101	pfam00352,pfa	cd04518			1			
arCOG02099	K	Transcription	TroR	Mn-dependent transcriptional regulator (DtxR family)	COG01321	pfam01325,pfam02742,pfam04023						1	1
arCOG04241	K	Transcription	RpoA/Rpc	DNA-directed RNA polymerase subunit D	COG00202	pfam01193	cd07030					1	1
arCOG02038	K	Transcription	-	Sugar-specific transcriptional regulator TrmB	COG01378						1		
arCOG02037	K	Transcription	-	Sugar-specific transcriptional regulator TrmB	COG01378	pfam01978						1	1
arCOG01057	K	Transcription	HxlR	DNA-binding transcriptional regulator, HxlR family	COG01733	pfam01638	cd00090						3
arCOG00608	K	Transcription	-	Predicted transcriptional regulator with C-terminal CBS domains	COG03620	pfam01381,pfa	cd00093,cd046	TIGR03070,TIGR01137					1
arCOG04248	K	Transcription	SIR2	NAD-dependent protein deacetylase, SIR2 family	COG00846	pfam02146	cd01413						1
arCOG04377	K	Transcription	-	Transcriptional regulator MarR family, contains HTH domain	COG04738								1
arCOG00826	K	Transcription	WecD	Acetyltransferase (GNAT) family	COG00454	pfam00583	cd04301	TIGR01575				1	
arCOG02644	K	Transcription	AcrR	Transcriptional regulator, TetR/AcrR family	COG01309	pfam00440		TIGR03613					1
arCOG05152	K	Transcription	-	Transcriptional regulator, contains HTH domain									1
arCOG02271	K	Transcription	-	Transcriptional regulator, contains HTH domain	COG03413	pfam04967						4	2
arCOG02274	K	Transcription	-	Transcriptional regulator, contains HTH domain	COG03413	pfam04967							3
arCOG02280	K	Transcription	-	Transcriptional regulator, contains HTH domain	COG03413	pfam04967						1	
arCOG04818	K	Transcription	HepA	Superfamily II DNA/RNA helicase, SNF2 family	COG00553	pfam13091,pfa	cd09178,cd000	TIGR01587				1	
arCOG02197	J	Translation, ribosomal structure and biogenesis	Cgi121	Subunit of KEOPS complex (Cgi121BUD32KAE1)	COG01617	pfam08617			5	1			
arCOG04107	J	Translation, ribosomal structure and biogenesis	SUI2	Translation initiation factor 2, alpha subunit (eIF-2alpha)	COG01093	pfam00575,pfa	cd04452	TIGR00717	5	1			
arCOG02466	J	Translation, ribosomal structure and biogenesis	GAR1	RNA-binding protein involved in rRNA processing	COG03277				4	1			
arCOG02286	J	Translation, ribosomal structure and biogenesis	Ncl1	Ribosome biogenesis protein, NOL1/NOP2/fmu family	COG03270	pfam13636			4	1			
arCOG04108	J	Translation, ribosomal structure and biogenesis	RPS27A	Ribosomal protein S27E	COG02051	pfam01667			4			1	
arCOG00973	J	Translation, ribosomal structure and biogenesis	RsmB	16S rRNA C967 or C1407 C5-methylase, RsmB/RsmF family	COG00144	pfam01189		TIGR00446	4	1		1	
arCOG00042	J	Translation, ribosomal structure and biogenesis	TilS	tRNA(Ile)-lysidine synthase TilS/MesJ	COG00037	pfam01171	cd01993	TIGR02432	4			1	
arCOG00033	J	Translation, ribosomal structure and biogenesis	Trm5	Wybutosine (yW) biosynthesis enzyme, Trm5 methyltransferase	COG02520	pfam02475			4		1	2	1
arCOG04449	J	Translation, ribosomal structure and biogenesis	TruA	Pseudouridylate synthase	COG00101	pfam01416,pfa	cd02866	TIGR00071	4			1	
arCOG01179	J	Translation, ribosomal structure and biogenesis	InfA	Translation initiation factor 1 (IF-1)	COG00361	pfam01176	cd05793	TIGR00523	3				
arCOG04150	J	Translation, ribosomal structure and biogenesis	Krr1	rRNA processing protein Krr1/Pno1, contains KH domain	COG01094			TIGR03665	3				
arCOG04149	J	Translation, ribosomal structure and biogenesis	NMD3	NMD protein affecting ribosome stability and mRNA decay	COG01499	pfam04981			3	1		1	1
arCOG00078	J	Translation, ribosomal structure and biogenesis	NOP1	Fibrillarin-like rRNA methylase	COG01889	pfam01269			3			1	1
arCOG00784	J	Translation, ribosomal structure and biogenesis	POP4	RNase P/RNase MRP subunit p29	COG01588	pfam01868			3		1	2	
arCOG00501	J	Translation, ribosomal structure and biogenesis	Rnz	Ribonuclease Z, beta-lactamase superfamily hydrolase	COG01234	pfam12706		TIGR02651	3			2	1
arCOG04070	J	Translation, ribosomal structure and biogenesis	RplC	Ribosomal protein L3	COG00087	pfam00297		TIGR03626	3				
arCOG00985	J	Translation, ribosomal structure and biogenesis	Tma20	Predicted RNA-binding protein, contains PUA domain	COG02016	pfam09183,pfam01472		TIGR03684	3	1	1	2	1
arCOG00047	J	Translation, ribosomal structure and biogenesis	Trm11	tRNA G10 N-methylase Trm11	COG01041	pfam01170		TIGR01177	3		1		
arCOG04156	J	Translation, ribosomal structure and biogenesis	TYW3	Wybutosine (yW) biosynthesis enzyme	COG01590	pfam02676			3				
arCOG00910	J	Translation, ribosomal structure and biogenesis	-	Predicted RNA methylase	COG02263	pfam13659			2	1	1	1	1
arCOG01695	J	Translation, ribosomal structure and biogenesis	-	Predicted component of the ribosome quality control (RQC) complex, YloA/Tl	COG01293	pfam05833,pfam05670			2	1	1	1	1
arCOG00676	J	Translation, ribosomal structure and biogenesis	Csl4	Exosome complex RNA-binding protein Csl4, contains S1 and Zn-ribbon doma	COG01096	pfam14382,pfa	cd05692		2	1	1	1	1
arCOG00809	J	Translation, ribosomal structure and biogenesis	LeuS	Leucyl-tRNA synthetase	COG00495	pfam00133,pfa	cd00812,cd008	TIGR00395	2				
arCOG00842	J	Translation, ribosomal structure and biogenesis	RimL	Acetyltransferase, RimL family	COG01670	pfam13302			2		1		
arCOG04345	J	Translation, ribosomal structure and biogenesis	RPR2	RNase P subunit RPR2	COG02023	pfam04032			2		1	1	
arCOG01701	J	Translation, ribosomal structure and biogenesis	SEN2	tRNA splicing endonuclease	COG01676	pfam02778,pfam01974		TIGR00324	2	1	1		
arCOG10124	J	Translation, ribosomal structure and biogenesis	TYW2	Wybutosine (yW) biosynthesis enzyme, TYW2 transferase	COG02520	pfam02475	cd02440	TIGR01444	2			2	1
arCOG01358	J	Translation, ribosomal structure and biogenesis	MiaB	2-methylthioadenine synthetase	COG00621	pfam00919,pfa	cd01335	TIGR00089	1				
arCOG00721	J	Translation, ribosomal structure and biogenesis	Nob1	Endonuclease Nob1, consists of a PIN domain and a Zn-ribbon module	COG01439		cd09876		1	1		1	1
arCOG00038	J	Translation, ribosomal structure and biogenesis	ThiI	tRNA S(4)U 4-thiouridine synthase	COG00301	pfam02926,pfa	cd11716,cd017	TIGR00342,TIGR04271	1		1	1	1
arCOG00990	J	Translation, ribosomal structure and biogenesis	-	Queuine tRNA-ribosyltransferase, contain PUA domain	COG01549	pfam14810,pfam01472		TIGR00432		1		2	1
arCOG01346	J	Translation, ribosomal structure and biogenesis	-	RNA-binding protein containing KH domain, possibly ribosomal protein	COG01534	pfam01985						2	1
arCOG04130	J	Translation, ribosomal structure and biogenesis	-	Predicted RNA-binding protein	COG01491	pfam04919						1	1
arCOG01254	J	Translation, ribosomal structure and biogenesis	AlaX	Ser-tRNA(Ala) deacylase AlaX (editing enzyme)	COG02872	pfam01411,pfam07973		TIGR03683				2	1
arCOG00487	J	Translation, ribosomal structure and biogenesis	ArgS	Arginyl-tRNA synthetase	COG00018	pfam00750,pfa	cd00671,cd079	TIGR00456				1	1
arCOG01185	J	Translation, ribosomal structure and biogenesis	Bud32	tRNA A-37 threonylcarbamoyl transferase component Bud32	COG03642	pfam00069	cd05151	TIGR03724				3	
arCOG04249	J	Translation, ribosomal structure and biogenesis	CCA1	tRNA nucleotidyltransferase (CCA-adding enzyme)	COG01746	pfam01909,pfa	cd05400	TIGR03671		1	1		
arCOG00486	J	Translation, ribosomal structure and biogenesis	CysS	Cysteinyl-tRNA synthetase	COG00215	pfam01406,pfa	cd00672,cd079	TIGR00435		1			
arCOG04161	J	Translation, ribosomal structure and biogenesis	DPH5	Diphthamide biosynthesis methyltransferase	COG01798	pfam00590	cd11647	TIGR00522					1
arCOG00035	J	Translation, ribosomal structure and biogenesis	Dph6	Diphthamide synthase (EF-2-diphthine--ammonia ligase)	COG02102	pfam01902	cd01994	TIGR03679				1	
arCOG04332	J	Translation, ribosomal structure and biogenesis	EbsC	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase, ybaK family	COG02606	pfam04073	cd04333	TIGR00011				2	
arCOG01988	J	Translation, ribosomal structure and biogenesis	EFB1	Translation elongation factor EF-1beta	COG02092	pfam00736	cd00292	TIGR00489					1
arCOG04277	J	Translation, ribosomal structure and biogenesis	Efp	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)	COG00231	pfam08207,pfa	cd04467	TIGR00037					1
arCOG04312	J	Translation, ribosomal structure and biogenesis	Fcf1	rRNA-processing protein FCF1, contains PIN domain	COG01412		cd09879					2	1
arCOG01559	J	Translation, ribosomal structure and biogenesis	FusA	Translation elongation factor G, EF-G (GTPase)	COG00480	pfam00009,pfa	cd01885,cd037	TIGR00490				1	
arCOG00978	J	Translation, ribosomal structure and biogenesis	GCD14	tRNA(1-methyladenosine) methyltransferase	COG02519	pfam08704	cd02440	TIGR03534		1	1	1	1
arCOG01616	J	Translation, ribosomal structure and biogenesis	GEK1	D-aminoacyl-tRNA deacylase, involved in ethanol tolerance	COG01650	pfam04414							1
arCOG00109	J	Translation, ribosomal structure and biogenesis	HemK	Methylase of polypeptide chain release factors	COG02890	pfam13659	cd02440	TIGR00537			1		
arCOG00404	J	Translation, ribosomal structure and biogenesis	HisS	Histidyl-tRNA synthetase	COG00124	pfam13393,pfa	cd00773,cd008	TIGR00442		1			1
arCOG00807	J	Translation, ribosomal structure and biogenesis	IleS	Isoleucyl-tRNA synthetase	COG00060	pfam00133,pfa	cd00818,cd008	TIGR00392				1	
arCOG01560	J	Translation, ribosomal structure and biogenesis	InfB	Translation initiation factor 2 (IF-2; GTPase)	COG00532	pfam00009,pfa	cd01887,cd037	TIGR00491					1
arCOG01736	J	Translation, ribosomal structure and biogenesis	LigT	2'-5' RNA ligase	COG01514	pfam13563		TIGR02258			1		
arCOG00810	J	Translation, ribosomal structure and biogenesis	MetG	Methionyl-tRNA synthetase	COG00143	pfam09334,pfa	cd00814,cd079	TIGR00398				1	
arCOG00906	J	Translation, ribosomal structure and biogenesis	Nop10	rRNA maturation protein Nop10, contains Zn-ribbon domain	COG02260	pfam04135						1	

arCOG01741	J	Translation, ribosomal structure and biogenesis	PelA	Release factor eRF1	COG01537	pfam03463,pfam03464,pfam03		TIGR00111		1		2	1
arCOG00412	J	Translation, ribosomal structure and biogenesis	PheT	Phenylalanyl-tRNA synthetase beta subunit	COG00072	pfam03483,pfa	cd00769	TIGR00471				2	1
arCOG00402	J	Translation, ribosomal structure and biogenesis	ProS	Prolyl-tRNA synthetase	COG00442	pfam00587,pfa	cd00778,cd008	TIGR00408				1	
arCOG04228	J	Translation, ribosomal structure and biogenesis	Pth2	Peptidyl-tRNA hydrolase	COG01990	pfam01981	cd02430	TIGR00283				2	2
arCOG01015	J	Translation, ribosomal structure and biogenesis	Pus10	tRNA U54 and U55 pseudouridine synthase Pus10	COG01258			TIGR01213				1	1
arCOG00039	J	Translation, ribosomal structure and biogenesis	QueC	7-cyano-7-deazaguanine synthase (queuosine biosynthesis)	COG00603	pfam06508	cd01995	TIGR00364			1		
arCOG05111	J	Translation, ribosomal structure and biogenesis	RlmH	23S rRNA pseudoU1915 N3-methylase RlmH	COG01576	pfam02590		TIGR00246					1
arCOG06660	J	Translation, ribosomal structure and biogenesis	RluA	Pseudouridylate synthase, 23S RNA-specific	COG00564	pfam00849	cd02869	TIGR00005				1	1
arCOG00780	J	Translation, ribosomal structure and biogenesis	RPL18A	Ribosomal protein L18E	COG01727	pfam00828		TIGR01071			1		1
arCOG04175	J	Translation, ribosomal structure and biogenesis	RPL20A	Ribosomal protein L20A (L18A)	COG02157	pfam01775							1
arCOG01950	J	Translation, ribosomal structure and biogenesis	RPL24A	Ribosomal protein L24E	COG02075	pfam01246	cd00472				1		
arCOG01752	J	Translation, ribosomal structure and biogenesis	RPL30	Ribosomal protein L30E	COG01911	pfam01248				1			
arCOG04049	J	Translation, ribosomal structure and biogenesis	RPL40A	Ribosomal protein L40E	COG01552							1	
arCOG04208	J	Translation, ribosomal structure and biogenesis	RPL43A	Ribosomal protein L37AE/L43A	COG01997	pfam01780		TIGR00280				1	
arCOG04288	J	Translation, ribosomal structure and biogenesis	RplJ	Ribosomal protein L10	COG00244	pfam00466	cd05795					1	
arCOG04372	J	Translation, ribosomal structure and biogenesis	RplK	Ribosomal protein L11	COG00080	pfam03946,pfa	cd00349	TIGR01632				2	1
arCOG04094	J	Translation, ribosomal structure and biogenesis	RplX	Ribosomal protein L24	COG00198		cd06089	TIGR01080				2	
arCOG04186	J	Translation, ribosomal structure and biogenesis	RPS1A	Ribosomal protein S3AE	COG01890	pfam01015				1		1	
arCOG04182	J	Translation, ribosomal structure and biogenesis	RPS24A	Ribosomal protein S24E	COG02004	pfam01282				1			1
arCOG04239	J	Translation, ribosomal structure and biogenesis	RpsD	Ribosomal protein S4 or related protein	COG00522	pfam00163,pfa	cd00165	TIGR01018				1	1
arCOG00678	J	Translation, ribosomal structure and biogenesis	Rrp4	Exosome complex RNA-binding protein Rrp4, contains S1 and KH domains	COG01097		cd05789			1			1
arCOG04131	J	Translation, ribosomal structure and biogenesis	RsmA	16S rRNA A1518 and A1519 N6-dimethyltransferase RsmA/KsgA/DIM1	COG00030	pfam00398		TIGR00755				1	1
arCOG04246	J	Translation, ribosomal structure and biogenesis	RtcB	RNA 3'-P ligase, RtcB family protein	COG01690	pfam01139		TIGR03073		1			
arCOG01564	J	Translation, ribosomal structure and biogenesis	SelB	Selenocysteine-specific translation elongation factor or SelB-II domain	COG03276		cd03696	TIGR00475		1			
arCOG01923	J	Translation, ribosomal structure and biogenesis	SIK1	RNA processing factor Prp31, contains Nop domain	COG01498	pfam01798					1	1	1
arCOG01952	J	Translation, ribosomal structure and biogenesis	SUA5	tRNA A37 threonylcarbamoyladenosine synthetase subunit TsaC/SUA5/YrdC	COG00009	pfam01300		TIGR00057		1		1	1
arCOG04223	J	Translation, ribosomal structure and biogenesis	SUI1	Translation initiation factor 1 (eIF-1/SUI1)	COG00023	pfam01253	cd11567	TIGR01158				1	
arCOG00056	J	Translation, ribosomal structure and biogenesis	Tan1	tRNA(Ser,Leu) C12 N-acetylase TAN1, contains THUMP domain	COG01818	pfam02926,pfa	cd11718,cd061	TIGR00342		1			
arCOG01630	J	Translation, ribosomal structure and biogenesis	TdcF	Translation initiation inhibitor, yjgF family	COG00251	pfam01042	cd00448	TIGR00004			1	2	1
arCOG01561	J	Translation, ribosomal structure and biogenesis	TEF1	Translation elongation factor EF-1 alpha, GTPase	COG05256	pfam00009,pfa	cd01883,cd036	TIGR00483				3	
arCOG00401	J	Translation, ribosomal structure and biogenesis	ThrS	Threonyl-tRNA synthetase	COG00441	pfam00587,pfa	cd00771,cd008	TIGR00418		1			
arCOG01115	J	Translation, ribosomal structure and biogenesis	TiaS	tRNA(Ile2) 2-agmatinylcytidine synthetase; containing Zn-ribbon domain and	COG01571	pfam08489,pfa	cd04482	TIGR03280					1
arCOG04176	J	Translation, ribosomal structure and biogenesis	TIF6	Translation initiation factor 6 (eIF-6)	COG01976	pfam01912	cd00527	TIGR00323		1			
arCOG01219	J	Translation, ribosomal structure and biogenesis	TRM1	N2,N2-dimethylguanosine tRNA methyltransferase	COG01867	pfam02005		TIGR00308				1	1
arCOG01018	J	Translation, ribosomal structure and biogenesis	TrmJ	tRNA C32,U32 (ribose-2'-O)-methylase TrmJ or a related methyltransferase	COG00565	pfam00588		TIGR00050				1	2
arCOG00987	J	Translation, ribosomal structure and biogenesis	TruB	Pseudouridine synthase	COG00130	pfam08068,pfa	cd02572	TIGR00425		1		1	1
arCOG04252	J	Translation, ribosomal structure and biogenesis	TruD	tRNA(Glu) U13 pseudouridine synthase TruD	COG00585	pfam01142	cd02577	TIGR00094		1		1	1
arCOG04733	J	Translation, ribosomal structure and biogenesis	Tsr3	Ribosome biogenesis protein Tsr3, contains Fer4-like metal-binding domain c	COG02042	pfam04034						1	
arCOG00541	J	Translation, ribosomal structure and biogenesis	YSH1	Predicted exonuclease of the beta-lactamase fold involved in RNA processing	COG01236	pfam00753,pfam10996,pfam01		TIGR03675				4	
CELLULAR PROCESSES AND SIGNALING													
arCOG11012	D	Cell cycle control, cell division, chromosome partitioning	ATS1	Alpha-tubulin suppressor and related RCC1 domain-containing proteins	COG05184	pfam13540,pfam00415,pfam00415,pfam00415,pfam00415,pfam00415						1	2
arCOG02201	D	Cell cycle control, cell division, chromosome partitioning	FtsZ	Cell division GTPase	COG00206	pfam00091,pfa	cd02201	TIGR00065	5				1
arCOG05007	D	Cell cycle control, cell division, chromosome partitioning	Maf	Nucleotide-binding protein implicated in inhibition of septum formation	COG00424	pfam02545	cd00555	TIGR00172				1	1
arCOG03061	D	Cell cycle control, cell division, chromosome partitioning	MreB	Actin-like ATPase involved in cell morphogenesis	COG01077	pfam06723	cd10227	TIGR00904					3
arCOG00586	D	Cell cycle control, cell division, chromosome partitioning	Soj	ATPase involved in chromosome partitioning, ParA family	COG01192	pfam01656	cd02042	TIGR03453				2	
arCOG02416	N	Cell motility	-	Pilin/Flagellin, FlaG/FlaF family	COG03430	pfam07790							2
arCOG02079	N	Cell motility	-	S-layer protein, possibly associated with type IV pili like system	COG01361				4				
arCOG01829	N	Cell motility	FlaB	Archaeal flagellins	COG01681							1	
arCOG01822	N	Cell motility	FlaG	Archaellum protein G, flagellin of FlaG/FlaF family	COG03354								1
arCOG04148	N	Cell motility	FlaH	ATPase involved in biogenesis of archaellum	COG02874	pfam06745	cd01394	TIGR03881					1
arCOG01809	N	Cell motility	FlaJ	Archaellum assembly protein J, TadC family	COG01955								1
arCOG02298	N	Cell motility	FlaK/PulO	Peptidase A24A, prepilin type IV	COG01989	pfam01478,pfam06847				1			1
arCOG01817	N	Cell motility	VirB11	ATPase involved in archaellum/pili biosynthesis	COG00630	pfam00437	cd01130	TIGR03819					1
arCOG01410	M	Cell wall/membrane/envelope biogenesis	AglA	Glycosyltransferase	COG00438	pfam13579,pfa	cd03794	TIGR02149	9	2			1
arCOG00118	M	Cell wall/membrane/envelope biogenesis	WecE	Predicted pyridoxal phosphate-dependent enzyme apparently involved in reg	COG00399	pfam01041	cd00616	TIGR03588	7				1
arCOG00894	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG00463	pfam00535	cd04179	TIGR04182	5			1	
arCOG00666	M	Cell wall/membrane/envelope biogenesis	GCD1	N-acetylglucosamine-1-phosphate uridyltransferase	COG01208	pfam00483,pfa	cd04181,cd056	TIGR03992	4		1	1	1
arCOG01568	M	Cell wall/membrane/envelope biogenesis	MscS	Small-conductance mechanosensitive channel	COG00668	pfam00924			4			5	2
arCOG01411	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438	pfam13439,pfa	cd03801	TIGR03999	4			3	1
arCOG00252	M	Cell wall/membrane/envelope biogenesis	WecC	UDP-N-acetyl-D-mannosaminuronate dehydrogenase	COG00677	pfam03721,pfa	cd05266	TIGR03026	4				
arCOG03336	M	Cell wall/membrane/envelope biogenesis	-	Surface protein containing fasciclin-like repeats	COG02335	pfam02469			3				1
arCOG01403	M	Cell wall/membrane/envelope biogenesis	AglL	Glycosyltransferase	COG00438	pfam13439,pfa	cd03804		3			5	2
arCOG02209	M	Cell wall/membrane/envelope biogenesis	AglR	MATE family membrane protein, Rfbx family	COG02244		cd13128		3	1			
arCOG00899	M	Cell wall/membrane/envelope biogenesis	AglD2	Predicted flippase	COG00392	pfam03706		TIGR00374	2				
arCOG00668	M	Cell wall/membrane/envelope biogenesis	GCD1	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccha	COG01208	pfam00483,pfa	cd04181,cd056	TIGR03992	2				
arCOG06759	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438				2				
arCOG01222	M	Cell wall/membrane/envelope biogenesis	TagD	Cytidylyltransferase fused to conserved domain of DUF357 family	COG00615	pfam01467	cd02170	TIGR02199	2				
arCOG03335	M	Cell wall/membrane/envelope biogenesis	-	Surface protein containing fasciclin-like repeats	COG02335	pfam02469			1				
arCOG03199	M	Cell wall/membrane/envelope biogenesis	AglH/Rfe	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylgluco	COG00472	pfam00953	cd06856	TIGR00445	1				
arCOG02820	M	Cell wall/membrane/envelope biogenesis	MurE	UDP-N-acetylmuramyl tripeptide synthase	COG00769	pfam08245,pfam02875		TIGR01082	1				
arCOG04827	M	Cell wall/membrane/envelope biogenesis	TagB	Glycosyl/glycerophosphate transferase involved in teichoic acid biosynthesis	COG01887	pfam04464			1				
arCOG01369	M	Cell wall/membrane/envelope biogenesis	WcaG	Nucleoside-diphosphate-sugar epimerase	COG00451	pfam01370	cd05234	TIGR01179	1	1		2	4
arCOG01392	M	Cell wall/membrane/envelope biogenesis	WecB	UDP-N-acetylglucosamine 2-epimerase	COG00381	pfam02350	cd03786	TIGR00236	1				
arCOG02488	M	Cell wall/membrane/envelope biogenesis	-	Cell surface protein, a component of a putative secretion system	SC.00293					1			
arCOG01385	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG00463	pfam00535	cd02522	TIGR04283			1	1	2
arCOG02532	M	Cell wall/membrane/envelope biogenesis	-	Secreted Beta-propeller repeat protein fused to CARDB-like adhesion module	COG03291	pfam07705		TIGR04213		1	2		2
arCOG07560	M	Cell wall/membrane/envelope biogenesis	-	Cell surface protein							1	1	
arCOG00895	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG00463	pfam00535	cd06442	TIGR04182					1
arCOG02487	M	Cell wall/membrane/envelope biogenesis	-	Cell surface protein, a component of a putative secretion system		pfam02369							1
arCOG02538	M	Cell wall/membrane/envelope biogenesis	-	Secreted protein, with PKD repeat domain	COG03291			TIGR04213					1
arCOG00896	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG00463	pfam00535	cd04179	TIGR04182					1
arCOG05365	M	Cell wall/membrane/envelope biogenesis	AglB	Oligosaccharyltransferase membrane subunit	COG01287	pfam02516,pfam13620,pfam13		TIGR04154		1	1	1	2
arCOG00664	M	Cell wall/membrane/envelope biogenesis	AglF/RfbA	Glucose-1-phosphate uridylyltransferase	COG01209	pfam00483	cd04181	TIGR03992					1
arCOG00253	M	Cell wall/membrane/envelope biogenesis	AglM/Ugd	UDP-glucose 6-dehydrogenase	COG01004	pfam03721,pfam00984,pfam03		TIGR03026					1
arCOG01381	M	Cell wall/membrane/envelope biogenesis	AglO	Glycosyl transferase family 2	COG00463	pfam00535	cd00761	TIGR04283				1	1
arCOG00663	M	Cell wall/membrane/envelope biogenesis	GCD1	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccha	COG01208	pfam00483	cd04181	TIGR03992		1			
arCOG00057	M	Cell wall/membrane/envelope biogenesis	GlmS	Glucosamine 6-phosphate synthetase	COG00449	pfam00310,pfa	cd00714,cd050	TIGR01135		1		1	1
arCOG01373	M	Cell wall/membrane/envelope biogenesis	Gmd	GDP-D-mannose dehydratase	COG01089	pfam01370,pfa	cd05260	TIGR01472					1
arCOG02313	M	Cell wall/membrane/envelope biogenesis	LolE	ABC-type transport system, involved in lipoprotein release, permease compo	COG04591	pfam12704,pfam02687		TIGR02212					1
arCOG02821	M	Cell wall/membrane/envelope biogenesis	MurD	UDP-N-acetylmuramoylalanine-D-glutamate ligase	COG00771	pfam08245,pfam02875		TIGR01082		1			
arCOG07536	M	Cell wall/membrane/envelope biogenesis	NanM	N-acetylneuraminic acid mutarotase	COG03055								1
arCOG01405	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438	pfam13439,pfa	cd03794	TIGR04063				1	
arCOG01409	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438	pfam13692	cd03794	TIGR03087				1	
arCOG00194	V	Defense mechanisms	CcmA	ABC-type multidrug transport system, ATPase component	COG01131	pfam00005	cd03230	TIGR01188	9	2			1
arCOG00786	V	Defense mechanisms	Cas4	CRISPR-associated protein Cas4, RecB family exonuclease	COG01468	pfam01930	cd09637	TIGR00372	5	1			1
arCOG01731	V	Defense mechanisms	NorM	Na+-driven multidrug efflux pump	COG00534	pfam01554,pfa	cd13137	TIGR00797	5				
arCOG01463	V	Defense mechanisms	-	ABC-type multidrug transport system, permease component	COG00842	pfam01061		TIGR01247	4				
arCOG02312	V	Defense mechanisms	SalY	ABC-type antimicrobial peptide transport system, permease component	COG00577	pfam02687		TIGR02212	4			1	1
arCOG03787	V	Defense mechanisms	-	LEA14-like dessication related protein	COG05608	pfam03168,pfam03168			3	1			
arCOG00922	V	Defense mechanisms	SalX	ABC-type antimicrobial peptide transport system, ATPase component	COG01136	pfam00005	cd03255	TIGR02673	3				1
arCOG00196	V	Defense mechanisms	CcmA	ABC-type multidrug transport system, ATPase component	COG01131	pfam00005	cd03230	TIGR03740	2		1		
arCOG03779	V	Defense mechanisms	McrB	GTPase subunit of restriction endonuclease	COG01401	pfam07728	cd00009		2				
arCOG00516	V	Defense mechanisms	NimA	Nitroimidazol reductase NimA or a related FMN-containing flavoprotein, pyri	COG03467	pfam01243		TIGR04023	2				
arCOG00525	V	Defense mechanisms	NimA	Nitroimidazol reductase NimA or a related FMN-containing flavoprotein, pyri	COG03467	pfam12724,pfam01243			2				
arCOG03966	V	Defense mechanisms	-	CopG family DNA-binding protein							1		
arCOG03166	V	Defense mechanisms	-	AAA+ superfamily ATPase fused to HTH and RecB nuclease domains	COG01672							1	1
arCOG03521	V	Defense mechanisms	-	Type II restriction enzyme, methylase subunit	COG01002	pfam12950							1
arCOG02632	V	Defense mechanisms	HsdM	Type I restriction-modification system methyltransferase subunit	COG00286	pfam12161,pfam02384		TIGR00497				2	
arCOG02777	V	Defense mechanisms	Mrr	Restriction endonuclease	COG01715	pfam04471							1
arCOG01663	V	Defense mechanisms	RelE	Cytotoxic translational repressor of toxin-antitoxin stability system	COG02026	pfam05016					1		
arCOG02204	U	Intracellular trafficking, secretion, and vesicular transport	Sss1	Preprotein translocase subunit Sss1	COG02443				4	1			
arCOG01919	U	Intracellular trafficking, secretion, and vesicular transport	TatC	Sec-independent protein secretion pathway component TatC	COG00805	pfam00902		TIGR00945	3	1		3	1
arCOG01217	U	Intracellular trafficking, secretion, and vesicular transport	SEC65	Signal recognition particle 19 kDa protein	COG01400				2	1	1	2	1
arCOG02694	U	Intracellular trafficking, secretion, and vesicular transport	TatA	Sec-independent protein secretion pathway component	COG01826			TIGR01411	2			1	
arCOG02673	U	Intracellular trafficking, secretion, and vesicular transport	-	OxaA/SpoJ/YidC translocase/secretase, sec-independent itegration of nascen	COG01422	pfam01956						1	1
arCOG04471	U	Intracellular trafficking, secretion, and vesicular transport	-	Exosortase	COG04083	pfam09721		TIGR04125					1
arCOG01227	U	Intracellular trafficking, secretion, and vesicular transport	FtsY	Signal recognition particle GTPase	COG00552	pfam02881,pfa	cd03115	TIGR00064				4	1
arCOG03383	U	Intracellular trafficking, secretion, and vesicular transport	TolB	Periplasmic component of the Tol biopolymer transport system	COG00823	pfam00930,pfam08308		TIGR02800					1
arCOG01241	X	Mobilome: prophages, transposons	XerC	XerD/XerC family integrase	COG00582	pfam13495,pfa	cd00796	TIGR02224				2	1
arCOG03473	X	Mobilome: prophages, transposons	-	Transposase	COG05421				2				
arCOG03669	O	Posttranslational modification, protein turnover, chaperones	-	Subtilase family protease	COG04934	pfam09286	cd11377,cd04056		12	2	3	3	
arCOG01912	O	Posttranslational modification, protein turnover, chaperones	-	Membrane protein implicated in regulation of membrane protease activity	COG01585	pfam01957			3				
arCOG02815	O	Posttranslational modification, protein turnover, chaperones	-	Conserved domain frequently associated with peptide methionine sulfoxide r	COG00229	pfam01641		TIGR00357	3				
arCOG03607	O	Posttranslational modification, protein turnover, chaperones	-	Cysteine protease, C1A family	COG04870	pfam00112	cd02619		2	1			
arCOG02007	O	Posttranslational modification, protein turnover, chaperones	-	Prenyltransferase family protein containing thioredoxin domain	COG01331	pfam03190	cd02955		2		1		
arCOG03614	O	Posttranslational modification, protein turnover, chaperones	-	Cysteine protease, C1A family	COG04870	pfam00112	cd02619			1			
arCOG03202	O	Posttranslational modification, protein turnover, chaperones	-	Collagenase family protease	COG00826	pfam01297,pfam01136					1		
arCOG10598	O	Posttranslational modification, protein turnover, chaperones	-	ATP-dependent protease La PUA-like domain		pfam02190						1	1
arCOG03685	O	Posttranslational modification, protein turnover, chaperones	-	Predicted redox protein, regulator of disulfide bond formation	COG01765	pfam02566							1
arCOG00312	O	Posttranslational modification, protein turnover, chaperones	AhpC	AhpC/TSA family peroxiredoxin	COG00450	pfam00578,pfa	cd03016	TIGR03137	5				1
arCOG01297	O	Posttranslational modification, protein turnover, chaperones	AhpF	Alkyl hydroperoxide reductase, large subunit	COG03634	pfam07992		TIGR03140	1				
arCOG00702	O	Posttranslational modification, protein turnover, chaperones	AprE	Subtilisin-like serine protease	COG01404	pfam00082	cd07477	TIGR03921	6	1	1	2	1
arCOG02553	O	Posttranslational modification, protein turnover, chaperones	AprE	Subtilisin-like serine protease	COG01404	pfam05048			2	1	1		
arCOG06823	O	Posttranslational modification, protein turnover, chaperones	AprE	Subtilisin-like serine protease	COG01404	pfam00082	cd05562	TIGR03921	1			1	
arCOG03610	O	Posttranslational modification, protein turnover, chaperones	AprE	Subtilisin-like serine protease	COG01404		cd02619				2	1	
arCOG01226	O	Posttranslational modification, protein turnover, chaperones	ArgK	Putative periplasmic protein kinase ArgK or related GTPase of G3E family	COG01703	pfam03308	cd03114	TIGR00750		1		2	1
arCOG00310	O	Posttranslational modification, protein turnover, chaperones	Bcp	Peroxiredoxin	COG01225	pfam00578	cd03018	TIGR03137	2			7	
arCOG01328	O	Posttranslational modification, protein turnover, chaperones	CcmB	ABC-type transport system involved in cytochrome c biogenesis, permease co	COG02386				2				
arCOG00267	O	Posttranslational modification, protein turnover, chaperones	CcmC	ABC-type transport system involved in cytochrome c biogenesis, permease co	COG00755	pfam01578		TIGR01191		1			
arCOG04957	O	Posttranslational modification, protein turnover, chaperones	CcmE	Cytochrome c-type biogenesis protein CcmE	COG02332					1		2	1
arCOG00270	O	Posttranslational modification, protein turnover, chaperones	CcmF	Cytochrome c biogenesis factor	COG01138	pfam01578		TIGR00353				1	1

arCOG01308	O	Posttranslational modification, protein turnover, chaperones	Cdc48	ATPase of the AAA+ class , CDC48 family	COG0464	pfam00004,pfa	cd00009,cd000	TIGR01243				3	1
arCOG00065	O	Posttranslational modification, protein turnover, chaperones	csdA	Selenocysteine lyase/Cysteine desulfurase	COG0520	pfam00266	cd06453	TIGR01979					1
arCOG03103	O	Posttranslational modification, protein turnover, chaperones	CtaA	Uncharacterized protein required for cytochrome oxidase assembly	COG01612	pfam02628				1			1
arCOG06880	O	Posttranslational modification, protein turnover, chaperones	DnaJ	DnaJ type Zn finger domain	COG00484			TIGR02349				3	
arCOG02846	O	Posttranslational modification, protein turnover, chaperones	DnaJ	DnaJ-class molecular chaperone	COG00484	pfam00226	cd06257	TIGR02349					1
arCOG04142	O	Posttranslational modification, protein turnover, chaperones	DYS1	Deoxyhypusine synthase	COG01899	pfam01916		TIGR00321		1			
arCOG04712	O	Posttranslational modification, protein turnover, chaperones	ECM4	Predicted glutathione S-transferase	COG00435	pfam13409,pfa	cd03190						1
arCOG01341	O	Posttranslational modification, protein turnover, chaperones	GIM5	Predicted prefoldin, molecular chaperone implicated in de novo protein folding	COG1730	pfam02996	cd00584	TIGR00293		1	1		
arCOG05154	O	Posttranslational modification, protein turnover, chaperones	GroEL	Chaperonin GroEL (HSP60 family)	COG00459	pfam00118	cd03344	TIGR02348	5				
arCOG01257	O	Posttranslational modification, protein turnover, chaperones	GroEL	Chaperonin GroEL, HSP60 family	COG00459	pfam00118	cd03343	TIGR02339				7	2
arCOG04772	O	Posttranslational modification, protein turnover, chaperones	GrpE	Molecular chaperone GrpE (heat shock protein)	COG00576	pfam01025	cd00446			1		2	1
arCOG02606	O	Posttranslational modification, protein turnover, chaperones	GrxC	Glutaredoxin	COG00695	pfam00462	cd02976	TIGR02196	1				
arCOG02607	O	Posttranslational modification, protein turnover, chaperones	GrxC	Glutaredoxin	COG00695	pfam00462	cd02976	TIGR02196		1			1
arCOG01915	O	Posttranslational modification, protein turnover, chaperones	HflC	Membrane protease subunit, stomatin/prohibitin homolog	COG00330	pfam01145	cd08826	TIGR01933				1	
arCOG02959	O	Posttranslational modification, protein turnover, chaperones	Iap	Zn-dependent amino- or carboxypeptidase, M28 family	COG02234	pfam04389	cd05643						3
arCOG04560	O	Posttranslational modification, protein turnover, chaperones	IscA	Fe-S cluster assembly iron-binding protein IscA	COG00316	pfam01521		TIGR00049				2	
arCOG02443	O	Posttranslational modification, protein turnover, chaperones	NosY	ABC-type transport system involved in multi-copper enzyme maturation, per	COG01277	pfam12679			1				
arCOG02438	O	Posttranslational modification, protein turnover, chaperones	NosY	ABC-type transport system involved in multi-copper enzyme maturation, per	COG01277	pfam12679				1			
arCOG01846	O	Posttranslational modification, protein turnover, chaperones	PaaD	Metal-sulfur cluster biosynthetic enzyme	COG02151	pfam01883,pfa	cd02037	TIGR02945,TIGR01969	2				
arCOG00976	O	Posttranslational modification, protein turnover, chaperones	Pcm	Protein-L-isoaspartate carboxylmethyltransferase	COG02518	pfam01135	cd02440	TIGR00080			1	1	
arCOG05850	O	Posttranslational modification, protein turnover, chaperones	Pcp	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)	COG02039	pfam01470	cd00501	TIGR00504					1
arCOG04767	O	Posttranslational modification, protein turnover, chaperones	PpiB	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	COG00652							1	1
arCOG01306	O	Posttranslational modification, protein turnover, chaperones	RPT1	ATP-dependent 26S proteasome regulatory subunit	COG01222	pfam00004	cd00009	TIGR01242				1	
arCOG00609	O	Posttranslational modification, protein turnover, chaperones	RseP	Membrane-associated protease RseP, regulator of RpoE activity in bacteria	COG00750	pfam02163	cd06160			1			
arCOG04064	O	Posttranslational modification, protein turnover, chaperones	RseP	Membrane-associated protease RseP, regulator of RpoE activity in bacteria	COG00750	pfam02163	cd06159	TIGR00054				1	
arCOG00981	O	Posttranslational modification, protein turnover, chaperones	SlpA	FKBP-type peptidyl-prolyl cis-trans isomerase 2	COG01047	pfam00254		TIGR00115	2				
arCOG00980	O	Posttranslational modification, protein turnover, chaperones	SlpA	FKBP-type peptidyl-prolyl cis-trans isomerase 2	COG01047	pfam00254				1	1		
arCOG02784	O	Posttranslational modification, protein turnover, chaperones	SRAP	Putative SOS response-associated peptidase YedK	COG02135	pfam02586							1
arCOG03580	O	Posttranslational modification, protein turnover, chaperones	STE14	Putative protein-S-isoprenylcysteine methyltransferase	COG02020	pfam04191			2				
arCOG01715	O	Posttranslational modification, protein turnover, chaperones	SufB	Cysteine desulfurase activator SufB	COG00719	pfam01458		TIGR01981	3	1		1	1
arCOG07441	O	Posttranslational modification, protein turnover, chaperones	SurA	Parvulin-like peptidyl-prolyl isomerase	COG00760	pfam00639		TIGR02933				1	1
arCOG00321	O	Posttranslational modification, protein turnover, chaperones	TldD	Zn-dependent protease, component of TldD/TldE system	COG00312	pfam01523							1
arCOG00322	O	Posttranslational modification, protein turnover, chaperones	TldE	Inactivated Zn-dependent protease, component of TldD/TldE system	COG00312	pfam01523						1	1
arCOG06181	O	Posttranslational modification, protein turnover, chaperones	TrxA	Thiol-disulfide isomerase or thioredoxin	COG00526	pfam00578	cd02966		3	1	1		
arCOG01972	O	Posttranslational modification, protein turnover, chaperones	TrxA	Thiol-disulfide isomerase or thioredoxin	COG00526	pfam00085	cd02947	TIGR01068	1				
arCOG01929	O	Posttranslational modification, protein turnover, chaperones	XdhC	Xanthine and CO dehydrogenase maturation factor, XdhC/CoxF family	COG01975	pfam13478						1	
arCOG02985	T	Signal transduction mechanisms	-	Membrane proteinase of CAAX superfamily, regulator of anti-sigma factor	COG02339	pfam13367			3	1	1	1	1
arCOG02967	T	Signal transduction mechanisms	-	NACHT family NTPase fused to HEAT repeats domain	COG5635	pfam13646,pfam13646			3		1		1
arCOG01180	T	Signal transduction mechanisms	RIO1	Serine/threonine protein kinase involved in cell cycle control	COG01718	pfam01163	cd05145	TIGR03724	3				
arCOG04820	T	Signal transduction mechanisms	-	SOUL heme-binding protein		pfam04832			3			1	
arCOG06193	T	Signal transduction mechanisms	-	Signal transduction histidine kinase and PAS domains	COG00642	pfam13426,pfa	cd00130,cd001	TIGR00229,TIGR00229,TIGR01386	2				
arCOG04425	T	Signal transduction mechanisms	Wzb	Protein-tyrosine-phosphatase	COG00394	pfam01451	cd00115	TIGR02689	1				
arCOG05374	T	Signal transduction mechanisms	-	GAF domain-containing protein	COG01956	pfam13185			1		1		
arCOG01171	T	Signal transduction mechanisms	RAD55	RecA-superfamily ATPase implicated in signal transduction	COG00467	pfam06745	cd01124	TIGR03877					2
arCOG04453	T	Signal transduction mechanisms	DisA_N	Diadenylate cyclase (c-di-AMP synthetase), DisA_N domain	COG01624	pfam02457							1
arCOG03799	T	Signal transduction mechanisms	AtoS	GAF, PAS/PAC domains containing signal transduction protein	COG02202	pfam05763						1	2
arCOG01143	T	Signal transduction mechanisms	ApaH	Serine/threonine protein phosphatase PP2A family	COG00639	pfam00149	cd00144						2
arCOG02391	T	Signal transduction mechanisms	CheY	Rec domain	COG00784	pfam00072	cd00156	TIGR02154				3	1
arCOG03413	T	Signal transduction mechanisms	CDC14	Protein-tyrosine phosphatase	COG02453	pfam00782	cd00047						1
arCOG03517	T	Signal transduction mechanisms	-	Formylglycine-generating sulfatase enzyme	COG01262	pfam12867,pfam03781		TIGR03440					1
arCOG01992	T	Signal transduction mechanisms	SixA	Phosphohistidine phosphatase SixA	COG02062	pfam00300	cd07067	TIGR00249				1	
arCOG06801	T	Signal transduction mechanisms	SrkA	Ser/Thr protein kinase RdoA involved in Cpx stress response, MazF antagonis	COG02334	pfam01636	cd05153					3	
METABOLISM													
arCOG02767	E	Amino acid transport and metabolism	-	Metal-dependent membrane protease, CAAX family	COG01266	pfam02517			3				
arCOG03600	E	Amino acid transport and metabolism	-	Transglutaminase-like cysteine protease	COG01305				2				
arCOG14875	E	Amino acid transport and metabolism	-	Aspartyl protease		pfam05618			2			1	
arCOG03611	E	Amino acid transport and metabolism	-	Peptidase C1A subfamily			cd08546,cd14254		2				2
arCOG07760	E	Amino acid transport and metabolism	-	Peptidase family C25		pfam01364	cd02258		1				
arCOG04333	E	Amino acid transport and metabolism	-	Aspartate/tyrosine/aromatic aminotransferase	COG00436	pfam00155	cd00609	TIGR03947		1			
arCOG01130	E	Amino acid transport and metabolism	-	Aspartate/tyrosine/aromatic aminotransferase	COG00436	pfam00155	cd00609	TIGR03540				2	
arCOG02165	E	Amino acid transport and metabolism	-	Transglutaminase-like cysteine protease	COG01305	pfam01841							1
arCOG01131	E	Amino acid transport and metabolism	-	Aspartate/tyrosine/aromatic aminotransferase	COG00436	pfam00155	cd00609	TIGR01265				1	
arCOG04044	E	Amino acid transport and metabolism	-	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonic acid synthase, DhnA-aldolase f	COG01830	pfam01791	cd00958	TIGR01949				2	1
arCOG01888	E	Amino acid transport and metabolism	AmpS	Leucyl aminopeptidase (aminopeptidase T)	COG02309	pfam02073						2	
arCOG01890	E	Amino acid transport and metabolism	AmpS	Leucyl aminopeptidase (aminopeptidase T)	COG02309	pfam02073						2	
arCOG01924	E	Amino acid transport and metabolism	AnsB	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D	COG00252	pfam00710	cd08962	TIGR02153				1	
arCOG00863	E	Amino acid transport and metabolism	ArcC	Carbamate kinase	COG00549	pfam00696	cd04235	TIGR00746		1		2	
arCOG01107	E	Amino acid transport and metabolism	ArgE	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase or relat	COG00624	pfam01546	cd05650	TIGR01910		1	1		
arCOG00912	E	Amino acid transport and metabolism	ArgF	Ornithine carbamoyltransferase	COG00078	pfam02729,pfam00185		TIGR00658	3				1
arCOG04134	E	Amino acid transport and metabolism	AroA	5-enolpyruvylshikimate-3-phosphate synthase	COG00128	pfam00275	cd01556	TIGR01356				1	1
arCOG01033	E	Amino acid transport and metabolism	AroE	Shikimate 5-dehydrogenase	COG00169	pfam08501,pfa	cd01065	TIGR00507				1	
arCOG01025	E	Amino acid transport and metabolism	AroK2	Archaeal shikimate kinase	COG01685	pfam00288		TIGR01920				2	1
arCOG00494	E	Amino acid transport and metabolism	Asd	Aspartate-semialdehyde dehydrogenase	COG00136	pfam01118,pfam02774		TIGR00978				1	1
arCOG00121	E	Amino acid transport and metabolism	AsnB	Asparagine synthase (glutamine-hydrolyzing)	COG00367	pfam00733			1				
arCOG00071	E	Amino acid transport and metabolism	AsnB	Asparagine synthase (glutamine-hydrolyzing)	COG00367	pfam00733	cd01991	TIGR01536		1		2	1
arCOG01594	E	Amino acid transport and metabolism	CarB	Carbamoylphosphate synthase large subunit	COG00458	pfam00289,pfam02786,pfam02		TIGR01369	1				
arCOG00073	E	Amino acid transport and metabolism	CysH	PAPS reductase related enzyme fused to RNA-binding PUA domain and ferre	COG00175	pfam01507	cd01713	TIGR00434				2	
arCOG01430	E	Amino acid transport and metabolism	CysK	Cysteine synthase	COG00031	pfam00291	cd01561	TIGR01136		1	1		1
arCOG00755	E	Amino acid transport and metabolism	DadA	Glycine/D-amino acid oxidase (deaminating)	COG00665	pfam01266			2			2	
arCOG01646	E	Amino acid transport and metabolism	DAP2	Dipeptidyl aminopeptidase/acylaminoacyl-peptidase	COG01506	pfam07859	cd00312		8	1		2	
arCOG03109	E	Amino acid transport and metabolism	DdaH	N-Dimethylarginine dimethylaminohydrolase	COG01834	pfam02274		TIGR01078		1		3	
arCOG05395	E	Amino acid transport and metabolism	FtcD	Formiminotetrahydrofolate cyclodeaminase	COG03404							2	
arCOG00915	E	Amino acid transport and metabolism	GabT	4-aminobutyrate aminotransferase or related aminotransferase	COG00160	pfam00202	cd00610	TIGR00707		1			
arCOG01303	E	Amino acid transport and metabolism	GcvH	Glycine cleavage system H protein (lipoate-binding)	COG00509	pfam01597	cd06848	TIGR00527				1	
arCOG00756	E	Amino acid transport and metabolism	GcvT	Glycine cleavage system T protein (aminomethyltransferase)	COG00404	pfam01571,pfam08669		TIGR00528					1
arCOG00757	E	Amino acid transport and metabolism	GcvT	Glycine cleavage system T protein (aminomethyltransferase)	COG00404	pfam01571,pfam08669		TIGR00528				2	
arCOG02706	E	Amino acid transport and metabolism	GloA	Lactoylglutathione lyase or related enzyme	COG00346	pfam13669	cd07249	TIGR03081	1				
arCOG00095	E	Amino acid transport and metabolism	GltB	Glutamate synthase domain 1	COG00067	pfam00310	cd01907	TIGR01134					1
arCOG00096	E	Amino acid transport and metabolism	GltB	Glutamate synthase domain 3	COG00070	pfam01493	cd00981	TIGR03122		1		1	
arCOG00619	E	Amino acid transport and metabolism	GltB	Glutamate synthase domain 2 and ferredoxin domain	COG00069	pfam01645	cd02808					1	
arCOG07384	E	Amino acid transport and metabolism	HisB	Histidinol phosphatase or related phosphatase	COG00241	pfam13242	cd01427	TIGR01656					1
arCOG04273	E	Amino acid transport and metabolism	HisC	Histidinol-phosphate/aromatic aminotransferase or cobyric acid decarboxyla	COG00079	pfam00155	cd00609	TIGR01140				1	
arCOG01799	E	Amino acid transport and metabolism	HisJ	ABC-type amino acid transport/signal transduction system, periplasmic comp	COG00834	pfam00497	cd13624	TIGR01096				1	
arCOG01798	E	Amino acid transport and metabolism	HisM	ABC-type amino acid transport system, permease component	COG00765	pfam00528	cd06261	TIGR03003				1	
arCOG04671	E	Amino acid transport and metabolism	HutH	Histidine ammonia-lyase	COG02986	pfam00221	cd00332	TIGR01225				2	
arCOG04670	E	Amino acid transport and metabolism	HutU	Urocanate hydratase	COG02987	pfam01175		TIGR01228	5				
arCOG01512	E	Amino acid transport and metabolism	HyuB	N-methylhydantoinase B/acetone carboxylase, alpha subunit	COG00146	pfam02538			1				
arCOG04779	E	Amino acid transport and metabolism	IaaA	Isoaspartyl peptidase or L-asparaginase, Ntn-hydrolase superfamily	COG01446	pfam01112	cd14950					1	
arCOG02297	E	Amino acid transport and metabolism	IlvE	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate ly	COG00115	pfam01063	cd01558	TIGR01122	3				1
arCOG01698	E	Amino acid transport and metabolism	LeuC	Homoaconitate hydratase/3-isopropylmalate dehydratase large subunit fami	COG00065	pfam00330	cd01583	TIGR02086				1	
arCOG01021	E	Amino acid transport and metabolism	LivK	ABC-type branched-chain amino acid transport system, periplasmic compone	COG00683	pfam13458	cd06268					1	
arCOG00243	E	Amino acid transport and metabolism	LYS9	Saccharopine dehydrogenase or related enzyme	COG01748	pfam03435			5	1			
arCOG00861	E	Amino acid transport and metabolism	LysC	Aspartokinase	COG00527								1
arCOG00060	E	Amino acid transport and metabolism	MetC	Cystathionine beta-lyase/cystathionine gamma-synthase	COG00626	pfam01053	cd00614	TIGR02080			1		1
arCOG00027	E	Amino acid transport and metabolism	MfnA	L-tyrosine decarboxylase, PLP-dependent protein	COG00076	pfam00282	cd06450	TIGR03812	1				1
arCOG04322	E	Amino acid transport and metabolism	PepB	Leucyl aminopeptidase	COG00260	pfam02789,pfa	cd00433					2	
arCOG04758	E	Amino acid transport and metabolism	PepF	Oligoendopeptidase F	COG01164	pfam08439,pfa	cd09608	TIGR00181				1	
arCOG01000	E	Amino acid transport and metabolism	PepP	Xaa-Pro aminopeptidase	COG00006	pfam01321,pfa	cd01092	TIGR00500			1		
arCOG00177	E	Amino acid transport and metabolism	PotA	ABC-type spermidine/putrescine transport system, ATPase component	COG03842	pfam00005	cd03301	TIGR03265				1	
arCOG06322	E	Amino acid transport and metabolism	PutA	Proline dehydrogenase	COG00506	pfam01619			3				1
arCOG01316	E	Amino acid transport and metabolism	PutP	Na+/proline symporter	COG00591	pfam00474	cd10322	TIGR00813	1				
arCOG00088	E	Amino acid transport and metabolism	PuuD	Gamma-glutamyl-gamma-aminobutyrate hydrolase PuuD (putrescine degrad	COG02071	pfam07722	cd01745	TIGR00888				4	
arCOG01947	E	Amino acid transport and metabolism	RhtB	Threonine efflux protein	COG01280	pfam01810			3				
arCOG01948	E	Amino acid transport and metabolism	RhtB	Threonine efflux protein	COG01280	pfam01810		TIGR00949					1
arCOG01158	E	Amino acid transport and metabolism	SerB	Phosphoserine phosphatase	COG00560	pfam00702		TIGR01491	5	1		1	2
arCOG01459	E	Amino acid transport and metabolism	Tdh	Threonine dehydrogenase or related Zn-dependent dehydrogenase	COG01063	pfam08240,pfa	cd08235	TIGR00692					1
arCOG05121	E	Amino acid transport and metabolism	TesA	Lysophospholipase L1 or related esterase	COG02755				1				
arCOG01434	E	Amino acid transport and metabolism	ThrC	Threonine synthase and cysteate synthase	COG00498	pfam01155,pfa	cd01563	TIGR02605,TIGR00260				1	1
arCOG02014	E	Amino acid transport and metabolism	TrpE	Anthranilate/para-aminobenzoate synthase component I	COG00147	pfam04715,pfam00425		TIGR01820				1	1
arCOG07581	G	Carbohydrate transport and metabolism	-	Glycosyl hydrolase family 18, contains cellulose binding domain	COG03325	pfam02839,pfa	cd12215,cd00146,cd06548		7		1	3	3
arCOG00138	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477				5				
arCOG03641	G	Carbohydrate transport and metabolism	PfkA	6-phosphofructokinase	COG00205	pfam00365	cd00363	TIGR02483	5				
arCOG04431	G	Carbohydrate transport and metabolism	GlpF	Glycerol uptake facilitator or related permease (Major Intrinsic Protein Famil	COG00580	pfam00230	cd00333	TIGR00861	4	1		1	
arCOG00130	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174		3	1			
arCOG01349	G	Carbohydrate transport and metabolism	SuhB	Archaeal fructose-1,6-bisphosphatase or related enzyme of inositol monoph	COG00483	pfam00459	cd01642	TIGR01331	2	1	1	1	
arCOG00271	G	Carbohydrate transport and metabolism	RhaT	Permease of the drug/metabolite transporter (DMT) superfamily	COG00697	pfam00892,pfam00892		TIGR00950	2				1
arCOG02876	G	Carbohydrate transport and metabolism	CDA1	Peptidoglycan/xylan/chitin deacetylase, PgdA/CDA1 family	COG00726	pfam01522	cd10941	TIGR03006	2				
arCOG01122	G	Carbohydrate transport and metabolism	RpiA	Ribose 5-phosphate isomerase	COG00120	pfam06026	cd01398	TIGR00021	1				
arCOG00052	G	Carbohydrate transport and metabolism	Pgi	Glucose-6-phosphate isomerase	COG00166	pfam01380,pfa	cd05017,cd056	TIGR02128	1	1		1	1
arCOG01111	G	Carbohydrate transport and metabolism	PpsA	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	COG00574	pfam01326,pfam00391,pfam02		TIGR01418	1	1			
arCOG04934	G	Carbohydrate transport and metabolism	-	Peptidoglycan/xylan/chitin deacetylase, PgdA/CDA1 family	COG00726				1				
arCOG07840	G	Carbohydrate transport and metabolism	-	Glycosyl hydrolase family 18, contains cellulose binding domain	COG03325	pfam02839,pfa	cd12215,cd00146,cd06543		1			2	
arCOG00767	G	Carbohydrate transport and metabolism	(ManB)	Phosphomannomutase	COG01109	pfam02878,pfa	cd03087	TIGR03990					1
arCOG00274	G	Carbohydrate transport and metabolism	RhaT	Permease of the drug/metabolite transporter (DMT) superfamily	COG00697	pfam00892,pfam00892		TIGR00950		1	1	2	
arCOG00014	G	Carbohydrate transport and metabolism	RbsK	Sugar kinase, ribokinase family	COG00524	pfam00294	cd01174	TIGR02152		1		5	
arCOG05046	G	Carbohydrate transport and metabolism	Rpe	Pentose-5-phosphate-3-epimerase	COG00036	pfam00834	cd00429	TIGR01163				1	
arCOG00496	G	Carbohydrate transport and metabolism	Pgk	3-phosphoglycerate kinase	COG00126	pfam00162	cd00318					1	1
arCOG02796	G	Carbohydrate transport and metabolism	-	Glucose/sorbosone dehydrogenase	COG02133	pfam07995		TIGR03606			1	1	1
arCOG00135	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam05977	cd06174	TIGR00900				2	
arCOG01029	G	Carbohydrate transport and metabolism	GalK	Galactokinase	COG00153	pfam10509,pfam08544		TIGR00131					1
arCOG01393	G	Carbohydrate transport and metabolism	-	Glycosyl transferase, related to UDP-glucuronosyltransferase	COG01819								1

arCOG04120	G	Carbohydrate transport and metabolism	PykF	Pyruvate kinase	COG00469	pfam00224,pfa	cd00288	TIGR01064					1
arCOG05061	G	Carbohydrate transport and metabolism	TalA	Transaldolase	COG00176	pfam00923	cd00956	TIGR00875					1
arCOG05412	G	Carbohydrate transport and metabolism	BglB	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase	COG02723	pfam00232		TIGR03356					1
arCOG04339	G	Carbohydrate transport and metabolism	TagG	ABC-type polysaccharide/polyol phosphate export systems, permease compc	COG01682	pfam01061						1	1
arCOG04263	H	Coenzyme transport and metabolism	-	Pantoate kinase	COG01829	pfam00288			4			1	
arCOG00021	H	Coenzyme transport and metabolism	-	Predicted transcriptional regulator fused phosphomethylpyrimidine kinase, i	COG01992	pfam10120			4				1
arCOG01484	H	Coenzyme transport and metabolism	RibD	Pyrimidine reductase, riboflavin biosynthesis	COG01985	pfam01872		TIGR01508	3	1	1		
arCOG01940	H	Coenzyme transport and metabolism	BirA	Biotin-(acetyl-CoA carboxylase) ligase	COG00340	pfam03099		TIGR00121	3	1	1	2	
arCOG00040	H	Coenzyme transport and metabolism	Hpt1	Hypoxanthine phosphoribosyltransferase	COG02236	pfam00156	cd06223	TIGR01251	3	1			
arCOG02172	H	Coenzyme transport and metabolism	QueD	6-pyruvoyl-tetrahydropterin synthase	COG00720	pfam01242	cd00470	TIGR03367	3		1		
arCOG01045	H	Coenzyme transport and metabolism	CoaE	Dephospho-CoA kinase	COG00237		cd02022		3		1	1	
arCOG00226	H	Coenzyme transport and metabolism	TbpA	ABC-type thiamine transport system, periplasmic component	COG04143	pfam13343	cd13545	TIGR01254	2				1
arCOG01589	H	Coenzyme transport and metabolism	RimK	Glutathione synthase/glutaminyl transferase/alpha-L-glutamate ligase	COG00189	pfam08443		TIGR02144	2				
arCOG03402	H	Coenzyme transport and metabolism	MtbC1	Methanogenic corrinoid protein MtbC1	COG05012	pfam02607,pfa	cd02065	TIGR02370	2				
arCOG00476	H	Coenzyme transport and metabolism	UbiA	4-hydroxybenzoate polyprenyltransferase or related prenyltransferase	COG00382	pfam01040	cd13961	TIGR01476	1				1
arCOG00972	H	Coenzyme transport and metabolism	NadR	Nicotinamide mononucleotide adenylyltransferase	COG01056	pfam01467	cd02166	TIGR01527	1	1	1	1	1
arCOG04139	H	Coenzyme transport and metabolism	ApbA	Ketopantoate reductase	COG01893	pfam02558,pfam08546		TIGR00745	1	1	1		
arCOG01522	H	Coenzyme transport and metabolism	HemY	Protoporphyrinogen oxidase	COG01232	pfam01593		TIGR00562	1				
arCOG01490	H	Coenzyme transport and metabolism	FolA	Dihydrofolate reductase	COG00262	pfam00186	cd00209					1	
arCOG01223	H	Coenzyme transport and metabolism	CAB4	Phosphopantetheine adenylyltransferase	COG01019	pfam01467	cd02164	TIGR00125		1	1	1	
arCOG01320	H	Coenzyme transport and metabolism	RibB	3,4-dihydroxy-2-butanone 4-phosphate synthase	COG00108	pfam00926		TIGR00506		1			
arCOG01671	H	Coenzyme transport and metabolism	UbiD	3-polyprenyl-4-hydroxybenzoate decarboxylase or related decarboxylase	COG00043	pfam01977		TIGR03701		1			
arCOG02939	H	Coenzyme transport and metabolism	PhhB	Pterin-4a-carbinolamine dehydratase	COG02154	pfam01329	cd00488			1		1	
arCOG01482	H	Coenzyme transport and metabolism	NadC	Nicotinate-nucleotide pyrophosphorylase	COG00157	pfam02749,pfa	cd01572	TIGR00078				1	
arCOG04137	H	Coenzyme transport and metabolism	SAM1	S-adenosylhomocysteine hydrolase	COG00499	pfam05221	cd00401	TIGR00936		1			
arCOG03838	H	Coenzyme transport and metabolism	PqqD	Coenzyme PQQ synthesis protein D		pfam05402				1	1		1
arCOG00069	H	Coenzyme transport and metabolism	NadE	NH3-dependent NAD+ synthetase	COG00171	pfam02540	cd00553	TIGR00552				3	1
arCOG01942	H	Coenzyme transport and metabolism	LipB	Lipoate-protein ligase B	COG00321	pfam03099		TIGR00214		1			
arCOG00480	H	Coenzyme transport and metabolism	MenA	1,4-dihydroxy-2-naphthoate octaprenyltransferase	COG01575	pfam01040	cd13962	TIGR02235			1		
arCOG00489	H	Coenzyme transport and metabolism	PduO	Cob(I)alamin adenosyltransferase	COG02096	pfam01923		TIGR00636					1
arCOG02817	H	Coenzyme transport and metabolism	FolC	Folylpolyglutamate synthase and Dihydropteroate synthase	COG00285	pfam08245,pfa	cd00739	TIGR01499,TIGR01496				1	1
arCOG01704	H	Coenzyme transport and metabolism	Dfp	Phosphopantothenoylcysteine synthetase/decarboxylase	COG00452	pfam02441,pfam04127		TIGR00521				2	1
arCOG00214	H	Coenzyme transport and metabolism	MoaB	Molybdopterin biosynthesis enzyme	COG00521	pfam00994	cd00886	TIGR02667			1		
arCOG00534	H	Coenzyme transport and metabolism	MoaE	Molybdopterin converting factor, large subunit	COG00314	pfam02391	cd00756				1		
arCOG00930	H	Coenzyme transport and metabolism	MoaA	Molybdenum cofactor biosynthesis enzyme	COG02896	pfam04055,pfa	cd01335	TIGR02668			1	1	
arCOG01530	H	Coenzyme transport and metabolism	MoaC	Molybdenum cofactor biosynthesis enzyme	COG00315	pfam01967	cd01419	TIGR00581			1		
arCOG01872	H	Coenzyme transport and metabolism	MobA	Molybdopterin-guanine dinucleotide biosynthesis protein A	COG00746	pfam12804	cd02503				1	2	
arCOG00217	H	Coenzyme transport and metabolism	MoeA	Molybdopterin biosynthesis enzyme	COG00303	pfam03453,pfa	cd00887	TIGR00177			1	3	
arCOG02199	H	Coenzyme transport and metabolism	Mcr1	NAD(P)H-flavin reductase	COG00543						1		
arCOG01676	H	Coenzyme transport and metabolism	ThiF	Dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosyr	COG00476	pfam00899,pfa	cd00757	TIGR02356				2	1
arCOG01873	H	Coenzyme transport and metabolism	MobA	GT-A family glycosyltransferase involved in molybdopterin guanine dinucleot	COG02068	pfam12804	cd04182	TIGR03310				1	1
arCOG04348	H	Coenzyme transport and metabolism	UbiE	Ubiquinone/menaquinone biosynthesis C-methylase UbiE	COG02226	pfam08241		TIGR01934				1	1
arCOG00572	H	Coenzyme transport and metabolism	NadB	Aspartate oxidase	COG00029	pfam00890,pfam02910		TIGR00551				1	
arCOG02624	H	Coenzyme transport and metabolism	PaaK	Coenzyme F390 synthetase	COG01541			TIGR02304					1
arCOG00570	C	Energy production and conversion	FixC	Dehydrogenase (flavoprotein)	COG00644	pfam13450		TIGR02032	6	2		2	1
arCOG02921	C	Energy production and conversion	PetE	Plastocyanin	COG03794	pfam00127	cd04220	TIGR03102	4				
arCOG00701	C	Energy production and conversion	UgpQ	Glycerophosphoryl diester phosphodiesterase	COG00584	pfam03009	cd08568		4				
arCOG00519	C	Energy production and conversion	FldA	Flavodoxin	COG00716	pfam12682			3			1	
arCOG02017	C	Energy production and conversion	RutF	NADH-FMN oxidoreductase RutF, flavin reductase (DIM6/NTAB) family	COG01853	pfam01613		TIGR03615	2			1	1
arCOG02929	C	Energy production and conversion	PetE	Plastocyanin	COG03794	pfam00127	cd13921	TIGR02657	1				
arCOG02398	C	Energy production and conversion	CcdA	Cytochrome c biogenesis protein	COG00785	pfam02683			1		1		
arCOG01599	C	Energy production and conversion	PorB	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidores	COG01013	pfam02775,pfa	cd03375	TIGR02177	1				
arCOG00571	C	Energy production and conversion	SdhA	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	COG01053	pfam00890,pfam02910		TIGR03378,TIGR01812	1			4	1
arCOG01551	C	Energy production and conversion	NuoC	NADH dehydrogenase subunit C	COG00852	pfam00329		TIGR01961				3	1
arCOG01539	C	Energy production and conversion	NuoL	NADH dehydrogenase subunit L	COG01009	pfam00662,pfam00361		TIGR01974					1
arCOG01540	C	Energy production and conversion	NuoN	NADH dehydrogenase subunit N	COG01007	pfam00361		TIGR01770		1			
arCOG02095	C	Energy production and conversion	OadA1	Pyruvate/oxaloacetate carboxyltransferase	COG05016	pfam00682,pfa	cd07937	TIGR01108			1	1	1
arCOG04138	C	Energy production and conversion	NtpI	Archaeal/vacuolar-type H+-ATPase subunit I	COG01269	pfam01496						1	
arCOG00869	C	Energy production and conversion	NtpE	Archaeal/vacuolar-type H+-ATPase subunit E	COG01390					1	1		
arCOG01054	C	Energy production and conversion	AcoA	Pyruvate/2-oxoglutarate/acetoin dehydrogenase complex, dehydrogenase (E	COG01071	pfam00676	cd02000	TIGR03181				1	
arCOG04279	C	Energy production and conversion	-	Swiveling domain associated with predicted aconitase	COG01786	pfam01989	cd01356			1			
arCOG00573	C	Energy production and conversion	SdhA	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	COG01053	pfam00890,pfam02910		TIGR02061		1			
arCOG02618	C	Energy production and conversion	-	Ferredoxin	COG01146	pfam13187,pfam12139		TIGR02060		1			
arCOG01235	C	Energy production and conversion	CyoA	Heme/copper-type cytochrome/quinol oxidase, subunit 2	COG01622	pfam00116	cd13918	TIGR02866		1	1	1	
arCOG00446	C	Energy production and conversion	FixA	Electron transfer flavoprotein, beta subunit	COG02086	pfam01012	cd01714					1	
arCOG01252	C	Energy production and conversion	PutA	Lactaldehyde dehydrogenase, Succinate semialdehyde dehydrogenase or oth	COG01012	pfam00171	cd07088	TIGR01780		1		3	
arCOG00288	C	Energy production and conversion	NfnB	Nitroreductase	COG00778	pfam00881	cd02150	TIGR02476				1	
arCOG01458	C	Energy production and conversion	Qor	NADPH:quinone reductase or related Zn-dependent oxidoreductase	COG00604	pfam08240,pfa	cd08264	TIGR02824				1	1
arCOG00963	C	Energy production and conversion	GlpC	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	COG00479	pfam13085,pfam13183,pfam02		TIGR00384,TIGR03288				2	
arCOG04650	C	Energy production and conversion	CyoC	Heme/copper-type cytochrome/quinol oxidase, subunit 3	COG01845	pfam00510	cd00386	TIGR02842					2
arCOG00338	C	Energy production and conversion	SdhC	Succinate dehydrogenase subunit C	COG02048	pfam02754,pfam02754		TIGR03288				2	1
arCOG03363	C	Energy production and conversion	NtpF	Archaeal/vacuolar-type H+-ATPase subunit H	COG02811							1	
arCOG00962	C	Energy production and conversion	FrdB	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	COG00479	pfam13085,pfam13183		TIGR00384				2	1
arCOG01617	C	Energy production and conversion	Tas	Aryl-alcohol dehydrogenase related enzyme	COG00667	pfam00248	cd06660	TIGR01293				3	1
arCOG04358	C	Energy production and conversion	FdhD	Uncharacterized protein required for formate dehydrogenase activity	COG01526	pfam02634		TIGR00129				2	
arCOG01236	C	Energy production and conversion	CyoA	Heme/copper-type cytochrome/quinol oxidase, subunit 2	COG01622	pfam00116	cd13842	TIGR02866					1
arCOG02304	C	Energy production and conversion	Mct/CaiB	Succinyl-CoA:mesaconate CoA-transferase or predicted acyl-CoA transferase,	COG01804	pfam02515		TIGR03253					1
arCOG02476	C	Energy production and conversion	HdrA	Heterodisulfide reductase, subunit A; ferredoxin domain	COG01148	pfam07992,pfam13237,pfam1		TIGR03140,TIGR04105,TIGR03385,TIGR04105					1
arCOG02842	C	Energy production and conversion	Fdx	Ferredoxin	COG00633	pfam00111	cd00207	TIGR02008				1	
arCOG09746	P	Inorganic ion transport and metabolism	-	Sulfotransferase related protein		pfam00685			4		1		
arCOG04750	P	Inorganic ion transport and metabolism	-	Sirohydrochlorin iron chelatase fused to [2Fe-2S] Ferredoxin	COG02138	pfam01903,pfa	cd03416,cd03414,cd02980		4			1	
arCOG02881	P	Inorganic ion transport and metabolism	ECM27	Ca2+/Na+ antiporter	COG00530	pfam01699,pfam01699		TIGR00367	3	1		1	
arCOG00206	P	Inorganic ion transport and metabolism	PhnC	ABC-type phosphate/phosphonate transport system, ATPase component	COG03638	pfam00005	cd03256	TIGR02315	3				
arCOG02021	P	Inorganic ion transport and metabolism	PspE	Rhodanese-related sulfurtransferase	COG00607	pfam00581	cd00158	TIGR02981	2	1	1		3
arCOG04233	P	Inorganic ion transport and metabolism	FepB	ABC-type Fe3+-hydroxamate transport system, periplasmic component	COG00614	pfam01497	cd01143	TIGR04281	2				1
arCOG00163	P	Inorganic ion transport and metabolism	ThiP	ABC-type Fe3+ transport system, permease component	COG01178	pfam00528,pfa	cd06261,cd062	TIGR03262	2				1
arCOG02763	P	Inorganic ion transport and metabolism	-	Heavy-metal-associated domain (HMA)	COG02608	pfam00403	cd00371	TIGR02052	1			1	
arCOG00238	P	Inorganic ion transport and metabolism	ArsB	Na+/H+ antiporter NhaD or related arsenite permease	COG01055	pfam03600	cd01117	TIGR00785	1				
arCOG01005	P	Inorganic ion transport and metabolism	LraI	ABC-type metal ion transport system, periplasmic component/surface adhes	COG00803	pfam01297	cd01018	TIGR03772,TIGR03772	1				
arCOG02851	P	Inorganic ion transport and metabolism	(NirD)	Ferredoxin subunit of nitrite reductase or ring-hydroxylating dioxygenase	COG02146	pfam00355	cd03467		1				
arCOG08934	P	Inorganic ion transport and metabolism	-	Alkylhydroperoxidase family enzyme	COG02128	pfam02627			1				
arCOG04487	P	Inorganic ion transport and metabolism	KatG	Catalase (peroxidase I)	COG00376	pfam00141,pfa	cd00649,cd006	TIGR00198	1				
arCOG02497	P	Inorganic ion transport and metabolism	-	Lipoprotein NosD family, contains CASH domains	COG03420	pfam12708		TIGR04247	1				
arCOG00318	P	Inorganic ion transport and metabolism	PhoU	Phosphate uptake regulator	COG00704	pfam04014,pfam01895,pfam0		TIGR02135	1			1	1
arCOG06837	P	Inorganic ion transport and metabolism	-	Lipoprotein NosD family, contains CASH domains	COG03420	pfam05048		TIGR04247,TIGR03024	1				2
arCOG01959	P	Inorganic ion transport and metabolism	TrkA	TrkA, K+ transport system, NAD-binding component	COG00569	pfam02254,pfam02080,pfam02254,pfam02080						1	1
arCOG04231	P	Inorganic ion transport and metabolism	CutA	Uncharacterized protein involved in tolerance to divalent cations	COG01324	pfam03091						3	1
arCOG02499	P	Inorganic ion transport and metabolism	-	Lipoprotein NosD family, contains CASH domains	COG03420	pfam13229,pfam13229		TIGR04247			1		
arCOG02265	P	Inorganic ion transport and metabolism	CorA	Mg2+ and Co2+ transporter	COG00598	pfam01544	cd12828	TIGR00383			1		
arCOG04397	P	Inorganic ion transport and metabolism	AmtB	Ammonia permease	COG00004	pfam00909		TIGR00836			1		
arCOG02764	P	Inorganic ion transport and metabolism	CopZ	Copper-ion-binding protein	COG02608	pfam00403	cd00371	TIGR02052					1
arCOG01805	P	Inorganic ion transport and metabolism	PhnD	ABC-type phosphate/phosphonate transport system, periplasmic component	COG03221	pfam12974	cd01071	TIGR01098				1	
arCOG02050	P	Inorganic ion transport and metabolism	-	Sulfite exporter, TauE/SafE family	COG00730	pfam01925						2	1
arCOG00202	P	Inorganic ion transport and metabolism	EcfA2	Energy-coupling factor transporter ATP-binding protein EcfA2	COG01122	pfam00005	cd03225	TIGR01166					1
arCOG01040	P	Inorganic ion transport and metabolism	CysC	Adenylylsulfate kinase or related kinase	COG00529	pfam01583	cd02027	TIGR00455				1	
arCOG01096	P	Inorganic ion transport and metabolism	CCC1	Predicted Fe2+/Mn2+ transporter, VIT1/CCC1 family	COG01814	pfam02915,pfa	cd01044,cd02431					1	
arCOG01576	P	Inorganic ion transport and metabolism	ZntA	Cation transport ATPase	COG02217	pfam00403,pfa	cd00371,cd014	TIGR00003,TIGR01511				1	1
arCOG02062	P	Inorganic ion transport and metabolism	TusA	TusA-related sulfurtransferase	COG00425	pfam01206	cd00291					1	1
arCOG05356	P	Inorganic ion transport and metabolism	Fes	Enterochelin esterase or related enzyme	COG02382	pfam00756						1	1
arCOG11907	P	Inorganic ion transport and metabolism	-	Fe-S metabolizm associated domain		pfam02657		TIGR03391				1	1
arCOG00230	P	Inorganic ion transport and metabolism	-	Periplasmic molybdate-binding protein/domain	COG01910	pfam00126,pfam12727		TIGR00637					1
arCOG02849	P	Inorganic ion transport and metabolism	ArsA	Oxyanion-translocating ATPase	COG00003	pfam02374	cd02035	TIGR00345					1
arCOG04559	P	Inorganic ion transport and metabolism	EmrE	Membrane transporter of cations and cationic drugs	COG02076	pfam00893							1
arCOG01964	P	Inorganic ion transport and metabolism	Kch	Kef-type K+ transport system, predicted NAD-binding component	COG01226	pfam07885							2
arCOG00167	P	Inorganic ion transport and metabolism	PstC	ABC-type phosphate transport system, permease component	COG00573		cd06261	TIGR02138				1	
arCOG00168	P	Inorganic ion transport and metabolism	PstA	ABC-type phosphate transport system, permease component	COG00581		cd06261	TIGR00974				1	
arCOG00213	P	Inorganic ion transport and metabolism	PstS	ABC-type phosphate transport system, periplasmic component	COG00226	pfam12849	cd13565	TIGR00975				1	
arCOG00231	P	Inorganic ion transport and metabolism	PstB	ABC-type phosphate transport system, ATPase component	COG01117	pfam00005	cd03260	TIGR00972				1	
arCOG00232	P	Inorganic ion transport and metabolism	PhoU	Phosphate uptake regulator	COG00704			TIGR02135				1	
arCOG02555	P	Inorganic ion transport and metabolism	-	Lipoprotein NosD family, contains CASH domains	COG03420							1	
arCOG02852	P	Inorganic ion transport and metabolism	(NirD)	Ferredoxin subunit of nitrite reductase or ring-hydroxylating dioxygenase	COG02146	pfam00355	cd03528	TIGR02377				1	
arCOG03797	P	Inorganic ion transport and metabolism	-	Ferritin-like domain	COG01633	pfam05763						1	
arCOG01259	I	Lipid transport and metabolism	FabG	Short-chain alcohol dehydrogenase	COG01028		cd05233	TIGR01830	5			3	5
arCOG00670	I	Lipid transport and metabolism	PgsA	Phosphatidylglycerophosphate synthase	COG00558	pfam01066			5	1			2
arCOG01767	I	Lipid transport and metabolism	PksG	3-hydroxy-3-methylglutaryl CoA synthase	COG03425	pfam08545,pfa	cd00827	TIGR00748	5			1	2
arCOG00671	I	Lipid transport and metabolism	PssA	Phosphatidylserine synthase	COG01183	pfam01066		TIGR04217	5				
arCOG13950	I	Lipid transport and metabolism	-	Phosphatidylglycerophosphatase A		pfam04608	cd06971		4				
arCOG04199	I	Lipid transport and metabolism	FAA1	Long-chain acyl-CoA synthetase (AMP-forming)	COG01022	pfam00501	cd05907	TIGR01923	4				1
arCOG01278	I	Lipid transport and metabolism	PaaJ	Acetyl-CoA acetyltransferase	COG00183		cd00829	TIGR01930	4				1
arCOG08932	I	Lipid transport and metabolism	LCB5	Diacylglycerol kinase family enzyme	COG01597	pfam00781		TIGR03702	3	1	1	2	1
arCOG00860	I	Lipid transport and metabolism	-	Isopentenyl phosphate kinase, enzyme of modified mevalonate pathway	COG01608	pfam00696	cd04241	TIGR02075	3	1		1	1
arCOG01028	I	Lipid transport and metabolism	ERG12	Mevalonate kinase	COG01577	pfam00288		TIGR00549	3	1		3	1
arCOG02936	I	Lipid transport and metabolism	ERG9	Phytoene/squalene synthetase	COG01562	pfam00494	cd00683	TIGR03465	3				
arCOG01137	I	Lipid transport and metabolism	FadM	Acyl-CoA thioesterase FadM	COG00824	pfam13279	cd00586	TIGR00051	3		1		
arCOG01879	I	Lipid transport and metabolism	-	Dolichol kinase family protein	COG00170				3				1
arCOG02245	I	Lipid transport and metabolism	-	Cytidylyltransferase family enzyme	COG01836	pfam01940		TIGR00297	2			2	1
arCOG04351	I	Lipid transport and metabolism	-	Predicted membrane associated lipid hydrolase, neutral ceramidase superfar	COG03356	pfam09843			2	1			
arCOG00249	I	Lipid transport and metabolism	FadB	3-hydroxyacyl-CoA dehydrogenase, some fused to Enoyl-CoA hydratase	COG01250	pfam02737,pfa	cd06558	TIGR02437,TIGR02437	1			1	
arCOG00239	I	Lipid transport and metabolism	CaiD	Enoyl-CoA hydratase/carnithine racemase	COG01024	pfam00378	cd06558	TIGR03210	1			3	
arCOG01880	I	Lipid transport and metabolism	SEC59	Dolichol kinase	COG00170				1				
arCOG00856	I	Lipid transport and metabolism	CaiC	Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II	COG00318	pfam00501	cd12119	TIGR01923	1				
arCOG09737	I	Lipid transport and metabolism	LicD	Phosphorylcholine metabolism protein LicD	COG03475	pfam04991			1				

arCOG04106	I	Lipid transport and metabolism	CdsA	CDP-diglyceride synthetase	COG00575	pfam01864						1		
arCOG01532	I	Lipid transport and metabolism	UppS	Undecaprenyl pyrophosphate synthase	COG00020	pfam01255	cd00475	TIGR00055				1		
arCOG01843	I	Lipid transport and metabolism	-	Sterol carrier protein	COG03255	pfam02036				1				
arCOG01085	I	Lipid transport and metabolism	PcrB	(S)-3-O-geranylgeranylglyceryl phosphate synthase, TIM-barrel fold	COG01646	pfam01884	cd02812	TIGR01768				2	1	
arCOG04260	I	Lipid transport and metabolism	HMG1	Hydroxymethylglutaryl-CoA reductase	COG01257	pfam00368	cd00643	TIGR00533					1	
arCOG01710	I	Lipid transport and metabolism	Sbm	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-binding)	COG02185	pfam02310	cd02071	TIGR00640				2		
arCOG02705	I	Lipid transport and metabolism	-	Acetyl-CoA carboxylase, carboxyltransferase component	COG04799	pfam01039		TIGR01117					1	
arCOG01707	I	Lipid transport and metabolism	CaiA	Acyl-CoA dehydrogenase	COG01960	pfam02771,pfa	cd00567	TIGR03207				1		
arCOG01282	I	Lipid transport and metabolism	PaaJ	Acetyl-CoA acetyltransferase	COG00183	pfam00108,pfa	cd00751	TIGR01930					1	
arCOG04470	I	Lipid transport and metabolism	Psd	Phosphatidylserine decarboxylase	COG00688	pfam02666		TIGR00164					1	
arCOG01650	I	Lipid transport and metabolism	PldB	Lysophospholipase, alpha-beta hydrolase superfamily	COG02267	pfam12697		TIGR03695				1		
arCOG02039	I	Lipid transport and metabolism	Cls	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthase or re	COG01502	pfam13091,pfa	cd07493,cd09127,cd09128						1	
arCOG00241	I	Lipid transport and metabolism	CaiD	Enoyl-CoA hydratase/carnithine racemase	COG01024	pfam00378	cd06558	TIGR02280				2		
arCOG01261	I	Lipid transport and metabolism	FabG	Short-chain alcohol dehydrogenase	COG01028	pfam00106	cd05233	TIGR01830				1	2	
arCOG03951	I	Lipid transport and metabolism	PgpB	Membrane-associated phospholipid phosphatase	COG00671	pfam01569	cd03386					3		
arCOG00674	I	Lipid transport and metabolism	PgsA	Phosphatidylglycerophosphate synthase	COG00558	pfam01066						1		
arCOG06122	I	Lipid transport and metabolism	Acs	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	COG00365	pfam00501	cd05959	TIGR02262				1		
arCOG00911	F	Nucleotide transport and metabolism	PyrB	Aspartate carbamoyltransferase, catalytic chain	COG00540	pfam02729,pfam00185		TIGR00670	3					
arCOG04415	F	Nucleotide transport and metabolism	PurD	Phosphoribosylamine-glycine ligase	COG00151	pfam02844,pfam01071,pfam02		TIGR00877	3	1				
arCOG01038	F	Nucleotide transport and metabolism	Fap7	Broad-specificity NMP kinase	COG01936	pfam13238			3			1	1	
arCOG00018	F	Nucleotide transport and metabolism	Nnr2	NAD(P)H-hydrate repair enzyme Nnr, NAD(P)H-hydrate dehydratase domain	COG00063	pfam03853,pfa	cd01171	TIGR00197,TIGR00196	3	1				
arCOG01891	F	Nucleotide transport and metabolism	Tmk	Thymidylate kinase	COG00125	pfam02223	cd01672	TIGR00041	3	1		1		
arCOG00081	F	Nucleotide transport and metabolism	PyrF	Orotidine-5'-phosphate decarboxylase	COG00284	pfam00215	cd04725	TIGR01740	3					
arCOG03575	F	Nucleotide transport and metabolism	-	Polyphosphate kinase 2	COG02326	pfam03976,pfa	cd01672	TIGR03708	3					
arCOG00087	F	Nucleotide transport and metabolism	GuaA	GMP synthase - Glutamine amidotransferase domain	COG00518	pfam00117	cd01742	TIGR00888	2					
arCOG00093	F	Nucleotide transport and metabolism	PurF	Glutamine phosphoribosylpyrophosphate amidotransferase	COG00034	pfam00310,pfa	cd00715,cd062	TIGR01134	2					
arCOG04276	F	Nucleotide transport and metabolism	NrdA	Ribonucleotide reductase, alpha subunit	COG00209	pfam03477,pfa	cd02888	TIGR02504	1					
arCOG00090	F	Nucleotide transport and metabolism	GuaA	GMP synthase - Glutamine amidotransferase domain	COG00518	pfam00117	cd01741	TIGR00888	1	1		3		
arCOG02825	F	Nucleotide transport and metabolism	PurN	Folate-dependent phosphoribosylglycinamide formyltransferase PurN	COG00299				1				2	
arCOG04184	F	Nucleotide transport and metabolism	RdgB	Inosine/xanthosine triphosphate pyrophosphatase, all-alpha NTP-PPase fami	COG00127	pfam01725	cd00515	TIGR00042			1	2		
arCOG00028	F	Nucleotide transport and metabolism	-	Orotate phosphoribosyltransferase homolog	COG00856	pfam00156	cd06223	TIGR02985,TIGR00336				1	1	
arCOG00029	F	Nucleotide transport and metabolism	PyrE	Orotate phosphoribosyltransferase	COG00461	pfam00156	cd06223	TIGR00336		1				
arCOG00419	F	Nucleotide transport and metabolism	Hit	HIT family hydrolase	COG00537	pfam01230	cd01275					3	1	
arCOG04462	F	Nucleotide transport and metabolism	PurS	Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component	COG01828	pfam02700		TIGR00302				1		
arCOG04421	F	Nucleotide transport and metabolism	PurC	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	COG00152	pfam01259	cd01415	TIGR00081					1	
arCOG00641	F	Nucleotide transport and metabolism	PurL	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain	COG00046	pfam00586,pfa	cd02203,cd022	TIGR01736				1		
arCOG01565	F	Nucleotide transport and metabolism	NrnA	nanoRNase/pAp phosphatase, hydrolyzes c-di-AMP and oligoRNAs	COG00618	pfam01368				1			1	
arCOG04346	F	Nucleotide transport and metabolism	-	5-formaminoimidazole-4-carboxamide-1-beta-D-ribofuranosyl 5'-monophosp	COG01759	pfam06849,pfam06973		TIGR00877		1			2	
arCOG00603	F	Nucleotide transport and metabolism	PyrD	Dihydroorotate dehydrogenase	COG00167	pfam01180	cd04740	TIGR01037			1	2		
arCOG01037	F	Nucleotide transport and metabolism	Cmk	Cytidylate kinase	COG01102	pfam13189	cd02020	TIGR02173		1		1	1	
arCOG00612	F	Nucleotide transport and metabolism	GuaB	IMP dehydrogenase/GMP reductase	COG00516	pfam00478	cd00381	TIGR01302				2		
arCOG05252	F	Nucleotide transport and metabolism	-	Predicted secreted endonuclease distantly related to archaeal Holliday junct	COG04741	pfam10107					1			
arCOG00030	F	Nucleotide transport and metabolism	Apt	Adenine/guanine phosphoribosyltransferase or related PRPP-binding protein	COG00503	pfam00156	cd06223	TIGR01090				1		
arCOG00858	F	Nucleotide transport and metabolism	PyrH	Uridylate kinase	COG00528	pfam00696	cd04253	TIGR02076				1	1	
arCOG02013	F	Nucleotide transport and metabolism	DeoA	Thymidine phosphorylase	COG00213	pfam01568,pfam02885,pfam0		TIGR03327					1	
arCOG04311	F	Nucleotide transport and metabolism	-	5'-deoxynucleotidase, HD superfamily hydrolase	COG01896	pfam13023							1	
arCOG01075	F	Nucleotide transport and metabolism	-	NUDIX family hydrolase	COG01051	pfam00293	cd04673					7	3	
arCOG04320	F	Nucleotide transport and metabolism	DeoC	Deoxyribose-phosphate aldolase	COG00274	pfam01791	cd00959	TIGR00126				1		
arCOG01327	F	Nucleotide transport and metabolism	Pnp	Purine nucleoside phosphorylase	COG00005	pfam01048		TIGR01694				1		
arCOG00695	F	Nucleotide transport and metabolism	SsnA	Cytosine deaminase or related metal-dependent hydrolase	COG00402	pfam01979	cd01298	TIGR03314				2	2	
arCOG01566	F	Nucleotide transport and metabolism	NrnA	nanoRNase/pAp phosphatase, hydrolyzes c-di-AMP and oligoRNAs	COG00618	pfam02254,pfam01368,pfam02272							1	
arCOG00777	Q	Secondary metabolites biosynthesis, transport and catabolism	PaaI	HGG motif-containing thioesterase, possibly involved in aromatic compound	COG02050	pfam03061	cd03443	TIGR00369	6			1		
arCOG03570	Q	Secondary metabolites biosynthesis, transport and catabolism	-	SAM-dependent methyltransferase	COG00500	pfam12847	cd02440	TIGR02021	4			1		
arCOG01792	Q	Secondary metabolites biosynthesis, transport and catabolism	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR01934	4					
arCOG01521	Q	Secondary metabolites biosynthesis, transport and catabolism	-	Phytoene dehydrogenase or related enzyme	COG01233	pfam13450			4					
arCOG04347	Q	Secondary metabolites biosynthesis, transport and catabolism	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR01934	3					
arCOG03914	Q	Secondary metabolites biosynthesis, transport and catabolism	SufI	Multicopper oxidase	COG02132	pfam07732	cd11024	TIGR02376	3					
arCOG01523	Q	Secondary metabolites biosynthesis, transport and catabolism	-	Phytoene dehydrogenase or related enzyme	COG01233	pfam01593		TIGR03467	3			1	1	
arCOG01778	Q	Secondary metabolites biosynthesis, transport and catabolism	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR02072	3					
arCOG01781	Q	Secondary metabolites biosynthesis, transport and catabolism	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR02072	2					
arCOG00235	Q	Secondary metabolites biosynthesis, transport and catabolism	MhpD	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (	COG00179	pfam01557		TIGR02303	1			1	1	
arCOG00696	Q	Secondary metabolites biosynthesis, transport and catabolism	HutI	Imidazolonepropionase or related amidohydrolase	COG01228	pfam13147	cd01296	TIGR01224				2	1	
arCOG06106	Q	Secondary metabolites biosynthesis, transport and catabolism	-	Predicted ring-cleavage extradiol dioxygenase	COG02514	pfam12681,pfa	cd07255,cd072	TIGR03211			1			
arCOG05015	Q	Secondary metabolites biosynthesis, transport and catabolism	-	SAM-dependent methyltransferase	COG00500	pfam12847	cd02440	TIGR03534				1		
arCOG01943	Q	Secondary metabolites biosynthesis, transport and catabolism	PncA	Amidase related to nicotinamidase	COG01335	pfam00857	cd00431	TIGR03614					1	
arCOG04786	Q	Secondary metabolites biosynthesis, transport and catabolism	-	1,2-phenylacetyl-CoA epoxidase, catalytic subunit	COG03396	pfam05138		TIGR02158				1		
arCOG06169	Q	Secondary metabolites biosynthesis, transport and catabolism	-	Arylsulfotransferase family protein		pfam05935							1	
arCOG01402	Q	Secondary metabolites biosynthesis, transport and catabolism	AglP	SAM-dependent methyltransferase	COG00500	pfam05050		TIGR01444					2	
POORLY CHARACTERIZED														
arCOG04364	S	Function unknown	-	Uncharacterized protein	COG01772	pfam04407			8					
arCOG05839	S	Function unknown	-	Uncharacterized protein				TIGR04292	6					
arCOG02142	S	Function unknown	-	Pheromone shutdown protein TraB, contains GTxH motif	COG01916	pfam01963		TIGR00261	5	1		1	1	
arCOG02884	S	Function unknown	-	Membrane associated protein with extracellular Ig-like domain, a componen	COG04743				5					
arCOG10153	S	Function unknown	-	Uncharacterized membrane protein, DUF4112 family		pfam13430			5					
arCOG04596	S	Function unknown	-	Uncharacterized membrane protein					4					
arCOG03124	S	Function unknown	-	Pentapeptide repeats containing protein	COG01357	pfam00805,pfam00805			4	1		3	2	
arCOG02087	S	Function unknown	-	Predicted membrane protein	COG01470	pfam10633,pfam13620,pfam10633			4		1	2		
arCOG10338	S	Function unknown	-	Uncharacterized protein	SC.00914	pfam13517,pfam13517,pfam13517,pfam13517			4		1			
arCOG10444	S	Function unknown	-	Uncharacterized protein					4			4		
arCOG06533	S	Function unknown	-	Uncharacterized membrane protein					4					
arCOG04579	S	Function unknown	-	Uncharacterized protein, DUF2071 family	COG03361	pfam09844			4					
arCOG05495	S	Function unknown	-	Uncharacterized protein, contains N-terminal coiled-coil domain	COG04911	pfam09969			3	1				
arCOG04412	S	Function unknown	-	Uncharacterized protein	COG04004				3	1				
arCOG03232	S	Function unknown	-	VanZ like family protein	COG05652	pfam04892			3		1			
arCOG02508	S	Function unknown	-	Secreted protein, with PKD repeat domain	COG03291	pfam00801,pfa	cd00146,cd001	TIGR00864	3		2		1	
arCOG02491	S	Function unknown	-	WD40 repeats containing protein	COG02319	pfam13360			3				1	
arCOG07412	S	Function unknown	-	Uncharacterized protein					2	1				
arCOG05338	S	Function unknown	-	Uncharacterized protein					2		1	2	1	
arCOG03888	S	Function unknown	-	Uncharacterized membrane protein					2					
arCOG01119	S	Function unknown	-	GYD domain, alpha/beta barrel superfamily	COG04274	pfam08734			2					
arCOG08211	S	Function unknown	-	Uncharacterized membrane protein	SC.00448				2					
arCOG08977	S	Function unknown	-	Uncharacterized membrane protein	COG04270				2			2	1	
arCOG11014	S	Function unknown	-	HTH-domain containing transcriptional regulator	SC.00234	pfam06224			1					
arCOG03633	S	Function unknown	-	Uncharacterized membrane protein YckC, RDD family	COG01714	pfam06271			1	1				
arCOG08231	S	Function unknown	-	Periplasmic protein with immunoglobin-like fold		pfam00932			1	1			1	
arCOG05330	S	Function unknown	-	Uncharacterized protein					1	1				
arCOG02081	S	Function unknown	-	Predicted membrane protein	COG01470	pfam10633			1			1	2	
arCOG02206	S	Function unknown	-	Uncharacterized membrane protein					1		1	1		
arCOG05022	S	Function unknown	-	Uncharacterized protein, contains PQ loop repeat	COG04095				1			1	1	
arCOG06958	S	Function unknown	-	Uncharacterized protein					1			2		
arCOG06742	S	Function unknown	-	NosD-like cell surface protein					1					
arCOG08643	S	Function unknown	-	Secreted protein with C-terminal PEFG domain					1					
arCOG02527	S	Function unknown	-	Secreted protein, with PKD repeat domain	COG03291				1					
arCOG02177	S	Function unknown	-	Uncharacterized membrane protein	COG01967	pfam01889					1	2	1	
arCOG04565	S	Function unknown	-	Predicted membrane protein, DUF368 family	COG02035	pfam04018					1			
arCOG05517	S	Function unknown	-	Uncharacterized protein						1	1			
arCOG04619	S	Function unknown	-	Uncharacterized membrane protein, contains bPH2 (bacterial pleckstrin hom	COG03428	pfam03703,pfam03703,pfam03703				1		1		
arCOG10198	S	Function unknown	-	Uncharacterized membrane protein, DUF2899 family		pfam11449						1		
arCOG04076	S	Function unknown	-	Uncharacterized protein, DUF359 family	COG01909	pfam04019				1		1		
arCOG07813	S	Function unknown	-	LamG-like jellyroll fold domain	SC.00184	pfam13385							1	
arCOG02546	S	Function unknown	-	Secreted protein, contains PKD repeats and vWA domain	COG03291	pfam05048,pfa	cd00146,cd001	TIGR04247,TIGR04247,TIGR00864,TIGR04213		1		2		
arCOG03606	S	Function unknown	-	Uncharacterized protein	SC.00401					1				
arCOG01917	S	Function unknown	-	Zn-ribbon domain containing protein						1		1		
arCOG02761	S	Function unknown	-	Uncharacterized protein, DUF302 family	COG03439	pfam03625	cd14797			1				
arCOG04321	S	Function unknown	-	Uncharacterized protein DUF711 family, similar to ribonucleotide reductase	COG02848	pfam05167	cd08025			1				
arCOG05852	S	Function unknown	-	HEAT repeats containing protein	COG01413					1				
arCOG01159	S	Function unknown	-	Uncharacterized archaeal coiled-coil protein	COG01340			TIGR02168		1		4		
arCOG08673	S	Function unknown	-	Uncharacterized protein						1			1	
arCOG05351	S	Function unknown	-	Uncharacterized membrane protein		pfam11433				1				
arCOG01907	S	Function unknown	AIM24	Uncharacterized protein, AIM24 family	COG02013	pfam01987		TIGR00266				1		
arCOG04214	S	Function unknown	-	Uncharacterized protein	COG00432	pfam01894		TIGR00149					1	
arCOG01330	S	Function unknown	-	Uncharacterized membrane protein	COG02426	pfam06695					1	2		
arCOG04269	S	Function unknown	-	Protein, predicted to be involved in DNA repair	COG01602	pfam04894,pfam04895					1			
arCOG02565	S	Function unknown	-	Secreted uncharacterized protein	COG05276						1			
arCOG06429	S	Function unknown	-	Uncharacterized protein, contains NRDE domain	COG03332	pfam05742					1			
arCOG04693	S	Function unknown	-	Uncharacterized protein								1		
arCOG03949	S	Function unknown	-	Uncharacterized membrane protein	COG03815	pfam09858						2		
arCOG07680	S	Function unknown	-	Uncharacterized membrane protein	COG02832	pfam04304							1	
arCOG11882	S	Function unknown	-	Uncharacterized membrane protein								2		
arCOG04662	S	Function unknown	-	Uncharacterized membrane protein	SC.00128								1	
arCOG05345	S	Function unknown	-	Uncharacterized protein									1	
arCOG04500	S	Function unknown	-	Uncharacterized protein with Ig-like domain								1	1	
arCOG02170	S	Function unknown	-	Uncharacterized protein	SC.00300	pfam13559						1		
arCOG09426	S	Function unknown	-	Uncharacterized membrane protein								2		
arCOG03118	S	Function unknown	-	Membrane protein DegA family	COG01238	pfam09335						1	1	
arCOG02561	S	Function unknown	-	WD40 repeats containing protein	COG02319	pfam13191,pfa	cd00200,cd002	TIGR02794,TIGR02800,TIGR02800				1		
arCOG00620	S	Function unknown	-	Uncharacterized conserved DUF39 domain fused to CBS domain	COG01900	pfam01837,pfa	cd04605	TIGR03287,TIGR01302					1	
arCOG04574	S	Function unknown	LemA	Uncharacterized protein	COG01704	pfam04011							1	
arCOG04811	S	Function unknown	-	Uncharacterized membrane protein, Fun14 family	COG02383								1	
arCOG04848	S	Function unknown	-	Uncharacterized protein, DUF1722 family	COG03272	pfam04463,pfam08349							1	
arCOG06436	S	Function unknown	-	Uncharacterized protein, YdiU/UPF0061 family	COG00397	pfam02696							1	

arCOG06646	S	Function unknown	-	Uncharacterized membrane protein, YccA/Bax inhibitor family	COG04760	pfam12811							1
arCOG14289	S	Function unknown	-	Uncharacterized protein									1
arCOG10710	S	Function unknown	-	Uncharacterized protein									2
arCOG01908	S	Function unknown	AIM24	Uncharacterized protein, AIM24 family	COG02013	pfam01987						1	
arCOG03873	S	Function unknown	-	Uncharacterized membrane protein	COG02855	pfam03601		TIGR00698				1	
arCOG05340	S	Function unknown	-	Uncharacterized membrane protein								1	
arCOG05874	S	Function unknown	-	Uncharacterized protein								1	
arCOG06493	S	Function unknown	-	HEAT repeats containing protein	COG01413	pfam13646,pfam03130						1	
arCOG10568	S	Function unknown	-	Uncharacterized membrane protein								1	
arCOG02539	S	Function unknown	-	Secreted protein, with PKD repeat domain	COG03291							2	
arCOG10301	S	Function unknown	-	Uncharacterized protein	COG03011	pfam04134						2	
arCOG03682	R	General function prediction only	SPS1	Membrane associated serine/threonine protein kinase	COG00515	pfam00069	cd14014		6	4	2		1
arCOG06897	R	General function prediction only	-	Predicted ATP-grasp enzyme	COG03919	pfam15632		TIGR01369	6		1		
arCOG00347	R	General function prediction only	-	Archaeal enzyme of ATP-grasp superfamily	COG01938	pfam09754		TIGR00161	5	1			1
arCOG04444	R	General function prediction only	-	ACT domain containing protein	COG04747	pfam01842,pfa	cd04908,cd04908		5	2	1		
arCOG02293	R	General function prediction only	-	HAD superfamily hydrolase	COG00637	pfam13419	cd01427	TIGR02009	5		1		
arCOG04303	R	General function prediction only	-	Uncharacterized Rossmann fold enzyme	COG01634	pfam01973	cd07995		4	1			1
arCOG02174	R	General function prediction only	-	Predicted exporter of the RND superfamily	COG01033	pfam03176,pfam03176		TIGR00921	4			7	2
arCOG01285	R	General function prediction only	-	OB-fold domain and Zn-ribbon containing protein, possible acyl-CoA-binding	COG01545	pfam12172,pfam01796			4				
arCOG00517	R	General function prediction only	-	Rhodanese Homology Domain fused to Zn-dependent hydrolase of beta-lacta	COG00491	pfam00753		TIGR03413	3			1	2
arCOG00313	R	General function prediction only	Sco1	Cytochrome oxidase Cu insertion factor, SCO1/SenC/PrrC family	COG01999	pfam02630	cd02968		3	1			2
arCOG03096	R	General function prediction only	-	NAD dependent epimerase/dehydratase family enzyme	COG01090	pfam01370,pfa	cd05242	TIGR01777	3	1			
arCOG02812	R	General function prediction only	-	Bacteriorhodopsin	COG05524	pfam01036			3				
arCOG00352	R	General function prediction only	Nog1	GTP-binding protein, GTP1/Obg family	COG01084	pfam01926	cd01897	TIGR02729	3				
arCOG02259	R	General function prediction only	-	Zn-finger domain containing protein	SC.00304				3				
arCOG03439	R	General function prediction only	-	vWFa domain containing protein					2		1	3	2
arCOG07416	R	General function prediction only	MhpC	Alpha/beta superfamily hydrolase	COG00596	pfam12695		TIGR03695	2			1	1
arCOG02889	R	General function prediction only	-	Predicted deacylase	COG03608	pfam04952	cd06252	TIGR02994	2				
arCOG01622	R	General function prediction only	MviM	Predicted dehydrogenase	COG00673	pfam01408,pfam02894			2				1
arCOG03991	R	General function prediction only	-	PKD repeats containing protein	COG03291	pfam00801	cd00146	TIGR00864,TIGR04213	1	1		1	
arCOG01651	R	General function prediction only	-	Alpha/beta superfamily hydrolase	COG01073	pfam08538			1				
arCOG01425	R	General function prediction only	-	RecB family nuclease with coiled-coil N-terminal domain	SC.00001				1	1		1	
arCOG01141	R	General function prediction only	-	ICC-like phosphoesterase	COG00622	pfam12850	cd00841	TIGR00040	1				
arCOG01395	R	General function prediction only	-	Lipid-A-disaccharide synthase related glycosyltransferase	COG01817	pfam04007			1				
arCOG01648	R	General function prediction only	MhpC	Alpha/beta superfamily hydrolase	COG00596	pfam12697		TIGR02427	1				
arCOG02164	R	General function prediction only	-	Predicted transglutaminase-like protease	COG01800	pfam04473			1				
arCOG00614	R	General function prediction only	SpoIVFB	Zn-dependent protease	COG01994		cd06158		1				
arCOG03015	R	General function prediction only	-	Uncharacterized protein YbjT, contains NAD(P)-binding and DUF2867 domair	COG00702	pfam13460	cd05271	TIGR03466	1			1	
arCOG02625	R	General function prediction only	-	Predicted metal-dependent hydrolase	COG01451	pfam01863			1				
arCOG06095	R	General function prediction only	-	ABC-2 family transporter protein	COG01277	pfam12679			1				
arCOG01136	R	General function prediction only	ARC1	EMAP domain RNA-binding protein	COG00073	pfam01588	cd02800	TIGR00399	1			1	
arCOG01213	R	General function prediction only	Cof	HAD superfamily hydrolase	COG00561	pfam08282	cd01427	TIGR01487	1			2	1
arCOG00833	R	General function prediction only	RimI	Acetyltransferase (GNAT) family	COG00456	pfam00583	cd04301	TIGR01575		1			1
arCOG02452	R	General function prediction only	-	KaiC-like protein ATPase	COG00467					1			1
arCOG04430	R	General function prediction only	-	HD superfamily phosphohydrolase	COG01078	pfam01966	cd00077					2	1
arCOG02680	R	General function prediction only	-	Uncharacterized archaeal Zn-finger protein	COG01326					1	1		1
arCOG09205	R	General function prediction only	-	Predicted metal-dependent hydrolase	COG01547	pfam03745					1		
arCOG09415	R	General function prediction only	-	Membrane associated metal-binding domain fused to Reeler domain		pfam02014	cd08544				1	2	2
arCOG00626	R	General function prediction only	TlyC	Hemolysins or related protein containing CBS domains	COG01253	pfam01595,pfa	cd04590	TIGR03520				1	
arCOG02291	R	General function prediction only	-	HAD superfamily hydrolase	COG01011	pfam13419	cd01427	TIGR02252		1	1		
arCOG00979	R	General function prediction only	-	Predicted O-methyltransferase YrrM	COG04122	pfam13578	cd02440			1	1		
arCOG01619	R	General function prediction only	ARA1	Aldo/keto reductase, related to diketogulonate reductase	COG00656	pfam00248	cd06660	TIGR01293			1		
arCOG01641	R	General function prediction only	-	Predicted RNA-binding protein, contains TRAM domain	COG03269							1	
arCOG00504	R	General function prediction only	-	Metal-dependent hydrolase of the beta-lactamase superfamily II	COG00491	pfam00753		TIGR03413					1
arCOG00348	R	General function prediction only	-	Archaeal enzyme of ATP-grasp superfamily	COG02047	pfam09754		TIGR00162				1	
arCOG04055	R	General function prediction only	-	SHS2 domain protein implicated in nucleic acid metabolism	COG01371	pfam01951						1	1
arCOG00893	R	General function prediction only	-	Predicted metal-dependent hydrolase (urease superfamily)	COG01831	pfam01026						2	1
arCOG02579	R	General function prediction only	-	Fe-S-cluster containining protein	COG00727								1
arCOG04212	R	General function prediction only	-	Predicted DNA-binding protein with PD1-like DNA-binding motif	COG01661	pfam03479	cd11378			1			
arCOG06747	R	General function prediction only	-	SIR2 superfamily protein	COG00846	pfam02146,pfa	cd01406			1			
arCOG06769	R	General function prediction only	-	GTPase SAR1 family domain fused to Leucine-rich repeats domain	COG01100	pfam13855,pfa	cd00116,cd099	TIGR00231		1			
arCOG00499	R	General function prediction only		Metal-dependent hydrolase of the beta-lactamase superfamily	COG01235	pfam12706		TIGR02651		1		1	
arCOG01225	R	General function prediction only	-	GTPase SAR1 or related small G protein	COG01100	pfam03029	cd02027,cd00880						1
arCOG03450	R	General function prediction only	-	Predicted surface protease of transglutaminase family						1			
arCOG04624	R	General function prediction only	-	Multimeric flavodoxin WrbA	COG00431							1	1
arCOG02155	R	General function prediction only	-	Protein implicated in RNA metabolism, contains PRC-barrel domain	COG01873	pfam05239				1			
arCOG01848	R	General function prediction only	WbbJ	Acetyltransferase (isoleucine patch superfamily)	COG00110	pfam00132,pfa	cd03358	TIGR03570					1
arCOG06534	R	General function prediction only	-	Cohesin domain containing secreted protein		pfam00963	cd08547				1		
arCOG04179	R	General function prediction only	PDCD5	DNA-binding TFAR19-related protein, PDSD5 family	COG02118	pfam01984					1		1
arCOG00601	R	General function prediction only	-	Protein containing two CBS domains (some fused to C-terminal double-strand	COG00517	pfam00571,pfa	cd04633,cd046	TIGR01302,TIGR01302			1		
arCOG02289	R	General function prediction only	-	Uncharacterized protein, DUF169 family	COG02043	pfam02596					1		
arCOG03994	R	General function prediction only	-	PKD domain containing protein	COG03291	pfam05048,pfa	cd14251,cd001	TIGR04247,TIGR04275,TIGR04275,TIGR04275,TIGR04275,TIGR042			1		
arCOG03038	R	General function prediction only	-	TPR repeats containing protein	COG00457						1	1	1
arCOG05195	R	General function prediction only	-	TPR repeats containing protein	COG00457	pfam13414	cd00189	TIGR02521				2	
arCOG00353	R	General function prediction only	HflX	GTP-binding protein protease modulator	COG02262	pfam13167,pfa	cd01878	TIGR03156				1	1
arCOG01043	R	General function prediction only	-	Predicted RNA binding protein with dsRBD fold	COG01931	pfam01877						1	1
arCOG04589	R	General function prediction only	CinA	Uncharacterized protein (competence- and mitomycin-induced)	COG01546	pfam02464		TIGR00199				1	1
arCOG05137	R	General function prediction only	-	TPR repeats containing protein	COG00457	pfam13414,pfa	cd00189,cd001	TIGR02917				1	
arCOG01084	R	General function prediction only	MazG	Predicted pyrophosphatase	COG01694	pfam03819	cd11535						1
arCOG00497	R	General function prediction only	-	Zn-dependent hydrolase of the beta-lactamase fold	COG02220	pfam13483							1
arCOG00606	R	General function prediction only	-	CBS domain	COG00517	pfam00478	cd04623	TIGR01302					1
arCOG04469	R	General function prediction only	-	Tripartite tricarboxylate transporter (TTT) class transporter	COG01784	pfam01970							1
arCOG03032	R	General function prediction only	-	TPR repeats containing protein	COG00457	pfam13414,pfa	cd00189	TIGR02917				1	
arCOG10597	R	General function prediction only	-	Hemocyanin family protein, binds copper ions		pfam00264						1	
arCOG00498	R	General function prediction only	-	Metal-dependent hydrolase of the beta-lactamase superfamily II	COG00491	pfam00753		TIGR03413				1	1
arCOG00500	R	General function prediction only	ElaC	Metal-dependent hydrolase of the beta-lactamase superfamily	COG01234	pfam12706		TIGR02651				1	
arCOG02642	R	General function prediction only	PerM	Predicted PurR-regulated permease PerM	COG00628	pfam01594		TIGR02872				2	1
arCOG01030	R	General function prediction only	-	Predicted kinase related to galactokinase and mevalonate kinase	COG02605							5	
arCOG01850	R	General function prediction only	WbbJ	Acetyltransferase (isoleucine patch superfamily)	COG00110	pfam00132	cd04647	TIGR03532					1
arCOG02303	R	General function prediction only	SurE	Predicted acid phosphatase	COG00496	pfam01975,pfam14423		TIGR00087					1
arCOG02839	R	General function prediction only	-	Uncharacterized protein related to deoxyribodipyrimidine photolyase	COG03046	pfam04244,pfam03441							1
arCOG02986	R	General function prediction only	BioY	Uncharacterized protein	COG01268	pfam02632							1
arCOG03047	R	General function prediction only	-	TPR repeats containing protein	COG00457								1
arCOG03271	R	General function prediction only	YtfP	Uncharacterized protein YtfP, gamma-glutamylcyclotransferase (GGCT)/AIG2	COG02105	pfam06094	cd06661						1
arCOG05099	R	General function prediction only	YtfP	Uncharacterized protein YtfP, gamma-glutamylcyclotransferase (GGCT)/AIG2	COG02105	pfam06094	cd06661						1
arCOG08119	R	General function prediction only	PhoX	Secreted phosphatase, PhoX family	COG03211	pfam05787							1
arCOG03561	R	General function prediction only	-	Secreted protein with beta-propeller repeat domain	COG03391	pfam01436,pfa	cd14955						2
arCOG07781	R	General function prediction only	-	Cell surface protein									2
arCOG02562	R	General function prediction only	-	Beta-propeller repeat containing protein	COG03391							1	3
arCOG03169	R	General function prediction only	-	AAA+ superfamily ATPase	COG01672	pfam01637,pfam01978						1	
arCOG07790	R	General function prediction only	-	D-glucuronyl C5-epimerase C-terminal domain related protein		pfam06662						1	
arCOG02560	R	General function prediction only	-	Secreted protein with beta-propeller repeat domain	COG03391		cd05819	TIGR03866				1	
arCOG06256	R	General function prediction only	-	Predicted esterase	COG00400	pfam02230						2	
arCOG00082	EF		PucG	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase	COG00075	pfam00266	cd06451	TIGR03301	1			1	1