Supplementary Table 5. Protein categories based on arCOG database.

									Epipelagic CG-MGIII bins						Pelagic CG-MGIII bins		Other Euryarchaea		
		arCOG clasification	gene	product	COG classification	pFAM domain	cdc	TIGR classification	Epi1	Epi2	Epi3	Epi4	Epi5	Epi6	Bathy1	Bathy-2	A.boneii T469	MG2-GG3	Thalassoarchaea
INFORMATION STORAGE AND PROCESSING																			
arCOG00415	L	Replication, recombination and repair	RecA	RecA/RadA recombinase	COG00468	pfam14520,pfam0842	cd01123	TIGR02236	1	1	1	1	1	1	1	1	1	1	1
arCOG04143	L	Replication, recombination and repair	-	DNA topoisomerase VI, subunit A	COG01697	pfam04406	cd00223		1	1	1	1	1	1	1	1	1	1	5
arCOG04455	L	Replication, recombination and repair	HYS2	Archaeal DNA polymerase II, small subunit/DNA polymerase delta, subunit B	COG01311	pfam01336,pfam0404	cd04490,cd07386		1	1	1	1		1	1	1	1	1	1
arCOG00459	L	Replication, recombination and repair	Nth	EndoIII-related endonuclease	COG00177	pfam00730,pfam1057	cd00056	TIGR01083	1	1	1	1			1	1	2	1	1
arCOG00417	L	Replication, recombination and repair	RecA	RecA/RadA recombinase	COG00468		cd01394	TIGR02237	1	1	1		1	2	1	1	1		
arCOG04367	L	Replication, recombination and repair	GyrA	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	COG00188	pfam00521,pfam0398	cd00187	TIGR01063	1	2	1	1	1	1	1	1	1	1	3
arCOG00872	L	Replication, recombination and repair	MPH1	ERCC4-like helicase	COG01111	pfam00270,pfam0027	cd00046,cd120	TIGR00643,TIGR	1	2	1	1		1	1	1	1	1	2
arCOG04447	L	Replication, recombination and repair	-	Archaeal DNA polymerase II, large subunit	COG01933	pfam03833,pfam09845		TIGR00354	1	2		1			1	1	1	1	1
arCOG00551	L	Replication, recombination and repair	-	DNA replication initiation complex subunit, GINS15 family	COG01711		cd11714		1		1				1	1	1		
arCOG04990	L	Replication, recombination and repair	-	Predicted endonuclease, contains HTH and PD-DExK nuclease domains		pfam14811			1			1			1	1		1	2
arCOG00467	L	Replication, recombination and repair	CDC6	Cdc6-related protein, AAA superfamily ATPase	COG01474	pfam13401,pfam0907	cd00009,cd087	TIGR02928	2	1	1	1		1	1	1	1	2	6
arCOG02610	L	Replication, recombination and repair	ScpA	Chromatin segregation and condensation protein Rec8/ScpA/Scc1, kleisin fam	COG01354	pfam02616				1				1	1	1	1	1	2
arCOG00439	L	Replication, recombination and repair	MCM2	Predicted ATPase involved in replication control, Cdc46/Mcm family	COG01241	pfam14551,pfam0049	cd00009				1	1	1	1	1	1	1	1	2
arCOG00427	L	Replication, recombination and repair	RecJ/Cdc45	Single-stranded DNA-specific exonuclease RecJ	COG00608										1	1	2		
arCOG02258	L	Replication, recombination and repair	-	RPA family protein, a subunit of RPA complex in P.furiosus	COG03390				1	1	1	1	1	1	1		1	1	3
arCOG04582	L	Replication, recombination and repair	Dpo4/DinP	Family Y DNA polymerase	COG00389	pfam00817,pfam1179	cd03586		1	1	1	1	1		1			1	1
arCOG01166	L	Replication, recombination and repair	MutL	DNA mismatch repair enzyme (predicted ATPase)	COG00323	pfam13589,pfam0111	cd00075,cd007	TIGR00585	1	1	1	1		1	1		1	1	2
arCOG01165	L	Replication, recombination and repair	-	DNA topoisomerase VI, subunit B	COG01389	pfam02518,pfam0348	cd00075,cd008	TIGR01052	1	1	1	1			1		1	1	4
arCOG01486	L	Replication, recombination and repair	RnmV	5S rRNA maturation endonuclease (Ribonuclease M5), contains TOPRIM doma	COG01658	pfam01751	cd01027		1	1	1		1		1		1	1	1
arCOG04121	L	Replication, recombination and repair	RnhB	Ribonuclease HII	COG00164	pfam01351	cd07180	TIGR00729	1	1	1				1		1	1	2
arCOG00470	L	Replication, recombination and repair	HolB	ATPase involved in DNA replication HolB, large subunit	COG00470	pfam00004	cd00009	TIGR02397	1	2	1	1	1		1		1	1	1
arCOG04371	L	Replication, recombination and repair	GyrB	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit	COG00187	pfam02518,pfam0020	cd00075,cd008	TIGR01059	1	2	1	1			1		1	1	3
arCOG04110	L	Replication, recombination and repair	PRI1	Eukaryotic-type DNA primase, catalytic (small) subunit	COG01467	pfam01896	cd04860	TIGR00335	1	2	2			1	1		1	2	5
arCOG00488	L	Replication, recombination and repair	DnaN	DNA polymerase sliding clamp subunit (PCNA homolog)	COG00592	pfam00705,pfam0274	cd00577	TIGR00590	1		1	1	1	1	1		1	1	2
arCOG01078	L	Replication, recombination and repair	-	NUDIX family hydrolase	COG00494	pfam00293	cd03428			1	1				1		2	1	1
arCOG00787	L	Replication, recombination and repair	-	UvrD/Rep family helicase fused to exonuclease family domain	COG02887	pfam12705	cd09637	TIGR01249,TIGR00372		1		1			1		1		
arCOG01527	L	Replication, recombination and repair	TopA	Topoisomerase IA	COG00550	pfam01751,pfam0113	cd03362,cd001	TIGR01057							1		1	1	2
arCOG04050	L	Replication, recombination and repair	FEN1	5'-3' exonuclease	COG00258	pfam00752,pfam0086	cd09867	TIGR03674							1		1	1	2
arCOG00558	L	Replication, recombination and repair	SrmB	Superfamily II DNA and RNA helicase	COG00513	pfam00270,pfam0027	cd00268,cd000	TIGR01389							1		1	3	3
arCOG00129	L	Replication, recombination and repair	-	DNA modification methylase	COG00863	pfam01555,pfam01555		TIGR01177							1		1		
arCOG00328	L	Replication, recombination and repair	PolB3	DNA polymerase PolB3	COG00417	pfam03104,pfam0013	cd05781,cd055	TIGR00592	1	1					2	1	2	1	4
arCOG00905	L	Replication, recombination and repair	-	Uracil-DNA glycosylase	COG01573	pfam03167	cd10031	TIGR00758		1					2	1	2		
arCOG01510	L	Replication, recombination and repair	RPA1	Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subuni	COG01599		cd04491,cd04491		2	3	2	2	1	2	2	2	3	2	3
arCOG01072	L	Replication, recombination and repair	-	NUDIX family hydrolase	COG00494	pfam00293	cd03426		1	1	1	1		1	2				
arCOG03013	L	Replication, recombination and repair	PRI2	Eukaryotic-type DNA primase, large subunit	COG02219	pfam04104	cd06560		1	1	1				2		1	1	1
arCOG00469	L	Replication, recombination and repair	HolB	ATPase involved in DNA replication HolB, small subunit	COG00470	pfam13177,pfam0854	cd00009	TIGR02397	1	1	1				2		1	2	2
arCOG00553	L	Replication, recombination and repair	BRR2	Replicative superfamily II helicase	COG01204	pfam00270,pfam0027	cd00046,cd000	TIGR04121	2	3	1	2	1		3		1	1	4
arCOG01894	L	Replication, recombination and repair	Nfo	Endonuclease IV	COG00648	pfam01261	cd00019	TIGR00587	1	1	1		1			1	1	1	4
arCOG01526	L	Replication, recombination and repair	TopG2	Reverse gyrase	COG01110	pfam00270,pfam0175	cd00046,cd033	TIGR01054	1	2	1	1				1	1		2
arCOG00464	L	Replication, recombination and repair	AlkA	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase	COG00122	pfam07934,pfam0073	cd00056	TIGR00588	1		1			1		1	1	1	
arCOG03142	L	Replication, recombination and repair	-	Nuclease of RNase H fold, RuvC/YqgF family					1		1					1	1	1	1
arCOG00368	L	Replication, recombination and repair	SbcC	ATPase involved in DNA repair, SbcC	COG00419	pfam13476,pfam1351	cd03240,cd001	TIGR00611,TIGR02168		1				1		1	3		
arCOG02897	L	Replication, recombination and repair	MutS	Mismatch repair ATPase (MutS family)	COG00249	pfam01624,pfam0518	cd03284	TIGR01070		1				2		1	1	1	1
arCOG02724	L	Replication, recombination and repair	Ada	Methylated DNA-protein cysteine methyltransferase	COG00350	pfam01035	cd06445	TIGR00589		1						1	1	1	1
arCOG00397	L	Replication, recombination and repair	SbcD	DNA repair exonuclease, SbcD	COG00420	pfam00149	cd00840									1	2		
arCOG02257	L	Replication, recombination and repair	-	RPA family protein, a subunit of RPA complex in P.furiosus	COG03390											1			
arCOG08649	L	Replication, recombination and repair	-	Topoisomerase IB	COG03569	pfam02919,pfam0102	cd00660,cd00659		1	1		1						1	
arCOG04281	L	Replication, recombination and repair	DnaG	DNA primase (bacterial type)	COG00358	pfam13662	cd01029	TIGR01391	1	2							1	1	2
arCOG01073	L	Replication, recombination and repair	-	NUDIX family hydrolase	COG00494	pfam00293	cd03424	TIGR00052	1			1					1		
arCOG01347	L	Replication, recombination and repair	CDC9	ATP-dependent DNA ligase	COG01793	pfam04675,pfam0106	cd07901,cd079	TIGR00574	1								1		
arCOG02840	L	Replication, recombination and repair	PhrB	Deoxyribodipyrimidine photolyase	COG00415	pfam00875,pfam03441		TIGR03556	2	3	1							2	7
arCOG05109	L	Replication, recombination and repair	DnaQ	DNA polymerase III, epsilon subunit or related 3'-5' exonuclease	COG00847	pfam00929	cd06127	TIGR00573		1								1	
arCOG00890	L	Replication, recombination and repair	-	DNA modification methylase	COG00863	pfam01555				1									
arCOG01898	L	Replication, recombination and repair	Uve	UV damage repair endonuclease	COG04294	pfam03851		TIGR00629		1									
arCOG00115	L	Replication, recombination and repair	-	DNA modification methylase	COG00863	pfam01555											1	1	1
arCOG00792	L	Replication, recombination and repair	-	Superfamily I DNA/RNA helicase	COG01112	pfam13086,pfam13087		TIGR00376									1	1	1
arCOG00919	L	Replication, recombination and repair	-	Holliday junction resolvase, archaeal type	COG01591	pfam01870	cd00523										1	1	2
arCOG02207	L	Replication, recombination and repair	XthA	Exonuclease III	COG00708	pfam03372	cd09073	TIGR00633									1	1	2
arCOG00048	L	Replication, recombination and repair	RlmL	23S rRNA G2445 N2-methylase RlmL	COG00116	pfam02926,pfam0117	cd11715	TIGR01177									1		
arCOG00426	L	Replication, recombination and repair	RecJ	DHH superfamily phosphohydrolase/exonuclease	COG00608	pfam01368											1		
arCOG00463	L	Replication, recombination and repair	-	Uri superfamily endonuclease	COG01833	pfam01986	cd10441										1		
arCOG00928	L	Replication, recombination and repair	-	Endonuclease V homolog	COG01628	pfam01949											1		
arCOG01074	L	Replication, recombination and repair	-	NUDIX family hydrolase	COG00494	pfam00293	cd03427	TIGR02705									1		
arCOG04206	L	Replication, recombination and repair	MUS81	ERCC4-type nuclease	COG01948	pfam02732,pfam12826		TIGR00596									1		
arCOG04295	L	Replication, recombination and repair	Mpg	3-methyladenine DNA glycosylase	COG02094	pfam02245	cd00540	TIGR00567									1		
arCOG04357	L	Replication, recombination and repair	ENDO3c	Thermostable 8-oxoguanine DNA glycosylase	COG01059	pfam00730	cd00056										1		
arCOG04926	L	Replication, recombination and repair	PolB	DNA polymerase elongation subunit (family B)	COG00417												1		
arCOG05336	L	Replication, recombination and repair	HimA	Bacterial nucleoid DNA-binding protein	COG00776	pfam00216	cd13831	TIGR00987									1		
arCOG06233	L	Replication, recombination and repair	-	Toprim domain and Zn-finger domain		pfam01751,pfam0113	cd03362,cd001	TIGR01057									1		
arCOG06670	L	Replication, recombination and repair	-	Nuclease-related protein, NERD family		pfam08378											1		
arCOG14866	L	Replication, recombination and repair	-	HhH domain containing DNA-binding domain		pfam12836											1		
arCOG00280	L	Replication, recombination and repair	-	HerA helicase	COG00433	pfam01935											2		
arCOG01290	L	Replication, recombination and repair	SplB	DNA repair photolyase	COG01533	pfam04055	cd01335										2		
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 an	COG01074	pfam00580,pfam13361		TIGR02785										1	1

arCOG02895	L	Replication, recombination and repair	MutS2	DNA structure-specific ATPase involved in suppression of recombination, Mut	COG01193	pfam00488	cd03243	TIGR01069										1	1
arCOG04748	L	Replication, recombination and repair	UvrB	Excinuclease ABC subunit B, helicase	COG00556	pfam04851,pfam1481	cd00046,cd000	TIGR00631										1	1
arCOG00305	L	Replication, recombination and repair	POL4	DNA polymerase IV (family X)	COG01796													1	3
arCOG04694	L	Replication, recombination and repair	UvrA	Excinuclease ABC subunit A, ATPase	COG00178		cd03271,cd032	TIGR00630										1	7
arCOG00462	L	Replication, recombination and repair	MutY	A/G-specific DNA glycosylase	COG01194	pfam00730	cd00056	TIGR01084										1	
arCOG00873	L	Replication, recombination and repair	-	Excinuclease-associated helix-hairpin-helix domain	COG00322	pfam01541,pfam0215	cd10434,cd065	TIGR00194										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,pfam0260	cd04489	TIGR00237										1	
arCOG04754	L	Replication, recombination and repair	Lig	NAD-dependent DNA ligase	COG00272	pfam01653,pfam0312	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-termin	COG01637														1
arCOG02896	L	Replication, recombination and repair	MutS	Mismatch repair ATPase (MutS family)	COG00249	pfam01624,pfam0518	cd03284	TIGR01070											1
arCOG02942	L	Replication, recombination and repair	RnhA	Ribonuclease HI	COG00328	pfam13456	cd09279												1
arCOG04753	L	Replication, recombination and repair	UvrC	Excinuclease ABC subunit C	COG00322	pfam01541,pfam0215	cd10434,cd098	TIGR00194											4
arCOG04244	K	Transcription	RPB10	DNA-directed RNA polymerase, subunit N (RpoN/RPB10)	COG01644	pfam01194			1	1		1		1	1	1	1	1	
arCOG04280	K	Transcription	NagC	Transcriptional regulator/sugar kinase	COG01940	pfam00480	cd00012	TIGR00744	1	1		1		1	1	1	1		
arCOG01863	K	Transcription	-	Predicted transcription factor, homolog of eukaryotic MBF1	COG01813	pfam01381	cd00093	TIGR00270	1	1		1			1	1	1	1	2
arCOG04061	K	Transcription	EGD2	Transcription factor homologous to NACalpha-BTF3	COG01308		cd14359	TIGR00264	1	2	1	1	1	1	1	1	1		
arCOG01753	K	Transcription	Ssh10b	Archaeal DNA-binding protein	COG01581	pfam01918		TIGR00285	1		1	1		1	1	1	1		2
arCOG01762	K	Transcription	RpoB/Rpo2	DNA-directed RNA polymerase subunit B	COG00085	pfam04563,pfam0456	cd00653	TIGR03670		1	1	1		1	1	1	1	1	1
arCOG04257	K	Transcription	RpoC/Rpo3	DNA-directed RNA polymerase subunit A'	COG00086	pfam04997,pfam0062	cd02582	TIGR02390		1	1	1		1	1	1	1	1	3
arCOG02613	K	Transcription	-	Chromosome segregation and condensation protein B	COG01386	pfam04079		TIGR00281		1				1	1	1	1	1	
arCOG03112	K	Transcription	-	Fic family protein	COG03177	pfam02661		TIGR02613		1				1	1	1			
arCOG04256	K	Transcription	RpoC/Rpo11	DNA-directed RNA polymerase subunit A''	COG00086	pfam04998	cd06528	TIGR02389		2	1	1		1	1	1	1	1	2
arCOG01128	K	Transcription	TenA	Transcriptional activator TenA	COG00819	pfam03070		TIGR04306							1	1			
arCOG00579	K	Transcription	RPB9	DNA-directed RNA polymerase, subunit M/Transcription elongation factor TFI	COG01594			TIGR01384	1	1	1	1		1	1		1	1	2
arCOG04366	K	Transcription	-	ArsR family transcriptional regulator	COG04860	pfam09824			1	1	1	1		1	1		1		
arCOG01684	K	Transcription	-	Transcriptional regulator, ArsR family	COG01777	pfam01022	cd00090,cd00090		1	1	1		1	2	1		1	1	4
arCOG01361	K	Transcription	ELP3	Histone acetyltransferase	COG01243	pfam04055		TIGR01211	1	1					1		1		
arCOG01016	K	Transcription	Rpo4	DNA-directed RNA polymerase, subunit Rpo4/RpoF	COG01460	pfam03874			1	2	1	1	1	1	1		1	1	1
arCOG01920	K	Transcription	NusG	Transcription antiterminator NusG	COG00250	pfam03439	cd09887,cd060	TIGR00405	1	2	1	1		1	1		1	1	2
arCOG00675	K	Transcription	RPB7	DNA-directed RNA polymerase, subunit E'/Rpb7	COG01095	pfam03876,pfam0057	cd04331,cd044	TIGR00448	1						1		1	1	
arCOG04077	K	Transcription	Spt4	Transcription elongation factor Spt4/RpoE2, zinc finger protein	COG02093	pfam06093			1						1		1		
arCOG04258	K	Transcription	RPB5	DNA-directed RNA polymerase, subunit H, RpoH/RPB5	COG02012	pfam01191				1	1	1		1	1		1	1	1
arCOG01268	K	Transcription	Rpo6/RpoZ	DNA-directed RNA polymerase subunit K/omega	COG01758	pfam01192				1		1	1	1	1		1	1	1
arCOG02611	K	Transcription	-	Predicted transcriptional regulator, containd two HTH domains	COG03398	pfam13412,pfam1341	cd00090,cd00090		1	1		1			2	2	1	3	6
arCOG07561	K	Transcription	-	Predicted membrane-associated trancriptional regulator	COG02512				2	1		1			2	2	2	7	7
arCOG01580	K	Transcription	-	DNA-binding transcriptional regulator, Lrp family	COG01522	pfam13412,pfam0103	cd00090		1	1	1	1			2		5	2	6
arCOG05161	K	Transcription	WecD	Acetyltransferase (GNAT) family	COG00454				1	1		1		1	2				
arCOG04111	K	Transcription	RPB11	DNA-directed RNA polymerase, subunit L	COG01761	pfam13656	cd06927		1	2	1	1		1	2		1	1	
arCOG01764	K	Transcription	SPT15	TATA-box binding protein (TBP), component of TFIID and TFIIIB	COG02101	pfam00352,pfam0035	cd04518		2	1	2	1	1	2	3	1	1	1	1
arCOG01981	K	Transcription	SUA7	Transcription initiation factor TFIIB, Brf1 subunit/Transcription initiation facto	COG01405	pfam08271,pfam0038	cd00043		3	4	3	2	1	1	3	1	2	2	6
arCOG02099	K	Transcription	TroR	Mn-dependent transcriptional regulator (DtxR family)	COG01321	pfam01325,pfam02742,pfam04023			2	2	1	1		1	3			2	3
arCOG04060	K	Transcription	-	Predicted transcriptional regulator	COG01709	pfam01381	cd00093		1	1	1	1	1			1	1		
arCOG00770	K	Transcription	DinG	Rad3-related DNA helicase	COG01199	pfam06733,pfam13307		TIGR00604	1		1					1	1	1	2
arCOG04241	K	Transcription	RpoA/Rpo1	DNA-directed RNA polymerase subunit D	COG00202	pfam01193	cd07030		1			1				1	1	1	1
arCOG05349	K	Transcription	ArsR	Transcriptional regulator containing HTH domain, ArsR family	COG00640	pfam12840	cd00090			1						1	1		
arCOG01680	K	Transcription	ArsR	Transcriptional regulator containing HTH domain, ArsR family	COG00640	pfam01022	cd00090			2						1	1		
arCOG02038	K	Transcription	-	Sugar-specific transcriptional regulator TrmB	COG01378											1	1	1	
arCOG02037	K	Transcription	-	Sugar-specific transcriptional regulator TrmB	COG01378	pfam01978			1	1	1	1						1	2
arCOG04686	K	Transcription	VacB	Exoribonuclease R	COG00557	pfam00773		TIGR02063	1		1	1	1					1	
arCOG04341	K	Transcription	RPC12	DNA-directed RNA polymerase, subunit RPC12/RpoP (contains C4-type Zn-fing	COG01996				1										
arCOG03182	K	Transcription	MarR	Transcriptional regulator, MarR family	COG01846	pfam01047	cd00090			1							1		2
arCOG01057	K	Transcription	HxlR	DNA-binding transcriptional regulator, HxlR family	COG01733	pfam01638	cd00090			1							2	5	3
arCOG05671	K	Transcription	CsgD	Transcriptional regulator LuxR family	COG02771					1									
arCOG00839	K	Transcription	WecD	Acetyltransferase (GNAT) family	COG00454	pfam13508	cd04301	TIGR01575				1							1
arCOG00608	K	Transcription	-	Predicted transcriptional regulator with C-terminal CBS domains	COG03620	pfam01381,pfam0057	cd00093,cd046	TIGR03070,TIGR01137									1	1	
arCOG04248	K	Transcription	SIR2	NAD-dependent protein deacetylase, SIR2 family	COG00846	pfam02146	cd01413										1	1	
arCOG04377	K	Transcription	-	Transcriptional regulator MarR family, contains HTH domain	COG04738												1	1	
arCOG00002	K	Transcription	-	Transcriptional regulator, PadR family	COG01695	pfam03551		TIGR03433									1		
arCOG00492	K	Transcription	ARO8	Transcriptional regulators containing a DNA-binding HTH domain and an amin	COG01167	pfam00155	cd00609	TIGR03947									1		
arCOG00610	K	Transcription	-	Predicted transcriptional regulator, contains C-terminal CBS domains	COG02524	pfam03444,pfam0047	cd04588	TIGR00331,TIGR01302									1		
arCOG00732	K	Transcription	MarR	Transcriptional regulator, MarR family	COG01846	pfam13601	cd00090										1		
arCOG00743	K	Transcription	-	Predicted transcriptional regulator													1		
arCOG00845	K	Transcription	WecD	Acetyltransferase (GNAT) family	COG00454	pfam00583	cd04301	TIGR01575									1		
arCOG01055	K	Transcription	-	Transcriptional regulator, contains HTH domain	COG03432	pfam14947											1		
arCOG01586	K	Transcription	-	DNA-binding transcriptional regulator, Lrp family	COG01522	pfam13404,pfam1340	cd00090,cd00090										1		
arCOG01683	K	Transcription	ArsR	Transcriptional regulator containing HTH domain, ArsR family	COG00640	pfam01978	cd00090										1		
arCOG01685	K	Transcription	ArsR	Transcriptional regulator containing HTH domain, ArsR family	COG00640	pfam12840	cd00090										1		
arCOG01760	K	Transcription	NusA	Transcription elongation factor	COG00195		cd02134,cd021	TIGR01952									1		
arCOG01804	K	Transcription	-	Transcriptional regulator, contains HTH domain	COG03888	pfam13412	cd00090,cd13553										1		
arCOG02808	K	Transcription	-	Transcriptional regulator, contains HTH domain	COG04742												1		
arCOG03698	K	Transcription	-	Transciptional regulator, contains HTH domain	COG04344	pfam10007											1		
arCOG04081	K	Transcription	TIP49	DNA helicase TIP49, TBP-interacting protein	COG01224	pfam06068	cd00009	TIGR01241,TIGR02397									1		
arCOG04152	K	Transcription	-	Predicted transcriptional regulator	COG01395	pfam01381	cd00093										1		
arCOG04399	K	Transcription	-	Predicted transcriptional regulator	COG01497												1		
arCOG04479	K	Transcription	-	Transcriptional regulator containing an HTH domain fused to a Zn-ribbon	COG03357												1		
arCOG04939	K	Transcription	-	Transcriptional regulator, contains wHTH domain	SC.00517												1		
arCOG07764	K	Transcription	-	Predicted transcriptional regulator	COG01318												1		
arCOG13514	K	Transcription	-	Transcriptional regulator, contains N-terminal RHH domain													1		

arCOG01117	K	Transcription	-	Lrp/AsnC family C-terminal domain	COG01522	pfam01037											2	3	6
arCOG00826	K	Transcription	WecD	Acetyltransferase (GNAT) family	COG00454	pfam00583	cd04301	TIGR01575									2		1
arCOG00001	K	Transcription	-	Transcriptional regulator, PadR family	COG01695	pfam03551											2		
arCOG00998	K	Transcription	LSM1	Small nuclear ribonucleoprotein (snRNP) homolog	COG01958	pfam01423	cd01726										2		
arCOG01345	K	Transcription	-	Predicted transcriptional regulator	COG03388												2		
arCOG02100	K	Transcription	TroR	Mn-dependent transcriptional regulator (DtxR family)	COG01321	pfam01325,pfam02742											2		
arCOG02394	K	Transcription	CheF	Component of chemotaxis system associated with archaellum, contains CheF-	COG02469												2		
arCOG02795	K	Transcription	GbsR	DNA-binding transcriptional regulator GbsR, MarR family	COG01510												2		
arCOG03067	K	Transcription	ArsR	Transcriptional regulator containing HTH domain, ArsR family	COG00640	pfam12840											3		
arCOG02983	K	Transcription	CspC	Cold shock protein, CspA family	COG01278	pfam00313	cd04458	TIGR02381										1	2
arCOG01875	K	Transcription	-	ParB-like nuclease domain	COG01475	pfam02195												1	3
arCOG02644	K	Transcription	AcrR	Transcriptional regulator, TetR/AcrR family	COG01309	pfam00440		TIGR03613										1	
arCOG05152	K	Transcription	-	Transcriptional regulator, contains HTH domain														1	
arCOG03748	K	Transcription	MarR	Transcriptional regulator, MarR family	COG01846													2	1
arCOG02271	K	Transcription	-	Transcriptional regulator, contains HTH domain	COG03413	pfam04967												2	4
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,pfam0765	cd09178,cd000	TIGR01587											1
arCOG00398	J	Translation, ribosomal structure and biogenesis	-	ASCH domain, predicted RNA-binding domain	COG02411	pfam04266	cd06552										1		
arCOG00423	J	Translation, ribosomal structure and biogenesis	-	Oligoribonuclease NrnB or cAMP/cGMP phosphodiesterase, DHH superfamily	COG02404	pfam01368,pfam02272											1		
arCOG00910	J	Translation, ribosomal structure and biogenesis	-	Predicted RNA methylase	COG02263	pfam13659						1	1	1	1	1	1	1	1
arCOG00953	J	Translation, ribosomal structure and biogenesis	-	Homolog of Wybutosine (yW) biosynthesis enzyme, Fe-S oxidoreductase	COG00731	pfam04055											1		
arCOG00990	J	Translation, ribosomal structure and biogenesis	-	Queuine tRNA-ribosyltransferase, contain PUA domain	COG01549	pfam14810,pfam01472		TIGR00432	1	1	1	1			1		1	1	2
arCOG00991	J	Translation, ribosomal structure and biogenesis	-	tRNA modification protein, contains pre-PUA and PUA domains	COG01370	pfam14810,pfam01472		TIGR00432	1	1					1	1	1	1	2
arCOG01042	J	Translation, ribosomal structure and biogenesis	-	Exosome subunit, RNA binding protein with dsRBD fold	COG01325	pfam01877											1	1	1
arCOG01346	J	Translation, ribosomal structure and biogenesis	-	RNA-binding protein containing KH domain, possibly ribosomal protein	COG01534	pfam01985											1	1	2
arCOG01695	J	Translation, ribosomal structure and biogenesis	-	Predicted component of the ribosome quality control (RQC) complex, YloA/Ta	COG01293	pfam05833,pfam05670			1						1	1	1	2	2
arCOG01861	J	Translation, ribosomal structure and biogenesis	-	3'-5' exoribonuclease YhaM, can participate in 23S rRNA maturation, HD supe	COG03481	pfam01966		TIGR00277									2		
arCOG04130	J	Translation, ribosomal structure and biogenesis	-	Predicted RNA-binding protein	COG01491	pfam04919			1	2	1	1	1	1	1		1	1	1
arCOG04318	J	Translation, ribosomal structure and biogenesis	-	Predicted RNA-binding protein of the translin family	COG02178	pfam01997	cd14820										1		
arCOG01255	J	Translation, ribosomal structure and biogenesis	AlaS	Alanyl-tRNA synthetase	COG00013	pfam01411,pfam0797	cd00673,cd077	TIGR03683	1	2	1	1			1	1	2	1	1
arCOG01254	J	Translation, ribosomal structure and biogenesis	AlaX	Ser-tRNA(Ala) deacylase AlaX (editing enzyme)	COG02872	pfam01411,pfam07973		TIGR03683			1	1			1		1	1	2
arCOG01256	J	Translation, ribosomal structure and biogenesis	AlaX	Ser-tRNA(Ala) deacylase AlaX (editing enzyme)	COG02872			TIGR03683									1		
arCOG00487	J	Translation, ribosomal structure and biogenesis	ArgS	Arginyl-tRNA synthetase	COG00018	pfam00750,pfam0574	cd00671,cd079	TIGR00456	1		1	1	1	1	1		1	1	1
arCOG00406	J	Translation, ribosomal structure and biogenesis	AsnS	Aspartyl/asparaginyl-tRNA synthetase	COG00017	pfam01336,pfam0015	cd04316,cd007	TIGR00458			1		1			1	1	1	1
arCOG00407	J	Translation, ribosomal structure and biogenesis	AsnS	Aspartyl/asparaginyl-tRNA synthetase	COG00017	pfam01336,pfam0015	cd04319,cd007	TIGR00457	1	2	1	1	1	1	1		1	1	2
arCOG01185	J	Translation, ribosomal structure and biogenesis	Bud32	tRNA A-37 threonylcarbamoyl transferase component Bud32	COG03642	pfam00069	cd05151	TIGR03724	2	2	1	1		1	2		1	2	4
arCOG04249	J	Translation, ribosomal structure and biogenesis	CCA1	tRNA nucleotidyltransferase (CCA-adding enzyme)	COG01746	pfam01909,pfam0924	cd05400	TIGR03671	1	1	1		1	2	1	1	1		
arCOG02197	J	Translation, ribosomal structure and biogenesis	Cgi121	Subunit of KEOPS complex (Cgi121BUD32KAE1)	COG01617	pfam08617			1	1		1			1		1		
arCOG00676	J	Translation, ribosomal structure and biogenesis	Csl4	Exosome complex RNA-binding protein Csl4, contains S1 and Zn-ribbon domai	COG01096	pfam14382,pfam0057	cd05692					1	1	1	1	1	1	1	1
arCOG00486	J	Translation, ribosomal structure and biogenesis	CysS	Cysteinyl-tRNA synthetase	COG00215	pfam01406,pfam0919	cd00672,cd079	TIGR00435	1	1		2		2	3	2	1	1	2
arCOG04112	J	Translation, ribosomal structure and biogenesis	DPH2	Diphthamide synthase subunit DPH2	COG01736	pfam01866		TIGR00322	1	1	1	1	1	1	2		1	1	2
arCOG04161	J	Translation, ribosomal structure and biogenesis	DPH5	Diphthamide biosynthesis methyltransferase	COG01798	pfam00590	cd11647	TIGR00522	1		1		1			1	1	1	2
arCOG00035	J	Translation, ribosomal structure and biogenesis	Dph6	Diphthamide synthase (EF-2-diphthine--ammonia ligase)	COG02102	pfam01902	cd01994	TIGR03679	1	1		1			1		1	1	1
arCOG00358	J	Translation, ribosomal structure and biogenesis	DRG	Ribosome-interacting GTPase 1	COG01163	pfam02824	cd01896,cd01666		1	2	1	1	1		2		1	1	1
arCOG00604	J	Translation, ribosomal structure and biogenesis	DusA	tRNA-dihydrouridine synthase	COG00042	pfam01207	cd02801	TIGR00737										1	3
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	1	1	1		1	1		1	1	
arCOG04277	J	Translation, ribosomal structure and biogenesis	Efp	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)	COG00231	pfam08207,pfam0128	cd04467	TIGR00037	1		1			1	1	1	1	1	
arCOG04122	J	Translation, ribosomal structure and biogenesis	Emg1	rRNA pseudouridine-1189 N-methylase Emg1, Nep1/Mra1 family	COG01756	pfam03587											1		
arCOG01742	J	Translation, ribosomal structure and biogenesis	eRF1	Peptide chain release factor eRF1	COG01503	pfam03463,pfam03464,pfam03465		TIGR03676					1			1	1	1	1
arCOG04312	J	Translation, ribosomal structure and biogenesis	Fcf1	rRNA-processing protein FCF1, contains PIN domain	COG01412		cd09879		1		1	1		1	1	1	1	1	2
arCOG00079	J	Translation, ribosomal structure and biogenesis	FtsJ	23S rRNA U2552 (ribose-2'-O)-methylase RlmE/FtsJ	COG00293	pfam01728	cd02440	TIGR00438	1	1		1			1		1	1	1
arCOG01559	J	Translation, ribosomal structure and biogenesis	FusA	Translation elongation factor G, EF-G (GTPase)	COG00480	pfam00009,pfam0314	cd01885,cd037	TIGR00490	1	1	1	1		1	1		1	1	2
arCOG02466	J	Translation, ribosomal structure and biogenesis	GAR1	RNA-binding protein involved in rRNA processing	COG03277				1	1	1	1			1		1		
arCOG01719	J	Translation, ribosomal structure and biogenesis	GatE	Archaeal Glu-tRNAGln amidotransferase subunit E (contains GAD domain)	COG02511	pfam02934,pfam02637		TIGR00134	1	1	1	1	1		1	1	1	1	3
arCOG01563	J	Translation, ribosomal structure and biogenesis	GCD11	Translation initiation factor 2, gamma subunit eIF-2 gamma, GTPase	COG05257	pfam00009,pfam0917	cd01888,cd036	TIGR03680	1		1	1		1	1	1	1	1	4
arCOG00978	J	Translation, ribosomal structure and biogenesis	GCD14	tRNA(1-methyladenosine) methyltransferase	COG02519	pfam08704	cd02440	TIGR03534	1	1	1		1	2	1	1	1	1	1
arCOG01124	J	Translation, ribosomal structure and biogenesis	GCD2	Translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family	COG01184	pfam01008		TIGR00511									1		
arCOG01640	J	Translation, ribosomal structure and biogenesis	GCD7	Translation initiation factor 2, beta subunit (eIF-2beta)/eIF-5 N-terminal doma	COG01601	pfam01873		TIGR00311								1			
arCOG01616	J	Translation, ribosomal structure and biogenesis	GEK1	D-aminoacyl-tRNA deacylase, involved in ethanol tolerance	COG01650	pfam04414			1	1	1	1			1		1	1	
arCOG04302	J	Translation, ribosomal structure and biogenesis	GlnS	Glutamyl- or glutaminyl-tRNA synthetase	COG00008	pfam00749,pfam0395	cd09287	TIGR00463	2	2	1	1	1	1	1		1	1	2
arCOG00405	J	Translation, ribosomal structure and biogenesis	GRS1	Glycyl-tRNA synthetase (class II)	COG00423	pfam00587,pfam0312	cd00774,cd008	TIGR00389		1	1				1	1	1	1	1
arCOG00357	J	Translation, ribosomal structure and biogenesis	GTP1	Ribosome-binding ATPase YchF, GTP1/OBG family	COG00012	pfam01926,pfam0843	cd01899,cd016	TIGR02729	1						2		1	1	2
arCOG00109	J	Translation, ribosomal structure and biogenesis	HemK	Methylase of polypeptide chain release factors	COG02890	pfam13659	cd02440	TIGR00537	1	2					1	1	1		
arCOG00404	J	Translation, ribosomal structure and biogenesis	HisS	Histidyl-tRNA synthetase	COG00124	pfam13393,pfam0312	cd00773,cd008	TIGR00442	1	1					1		1	1	2
arCOG00807	J	Translation, ribosomal structure and biogenesis	IleS	Isoleucyl-tRNA synthetase	COG00060	pfam00133,pfam0826	cd00818,cd008	TIGR00392		1				1			1	1	4
arCOG01179	J	Translation, ribosomal structure and biogenesis	InfA	Translation initiation factor 1 (IF-1)	COG00361	pfam01176	cd05793	TIGR00523	1	1		1					1	1	2
arCOG01560	J	Translation, ribosomal structure and biogenesis	InfB	Translation initiation factor 2 (IF-2; GTPase)	COG00532	pfam00009,pfam0314	cd01887,cd037	TIGR00491	1	2	1	1		1	1	1	1	1	
arCOG01183	J	Translation, ribosomal structure and biogenesis	Kae1p/TsaD	Subunit of KEOPS complex, tRNA A37 threonylcarbamoyltransferase, contains	COG00533	pfam00814		TIGR03722			1	1		1					2
arCOG04063	J	Translation, ribosomal structure and biogenesis	KptA	RNA:NAD 2'-phosphotransferase	COG01859	pfam01885			1	2	1	1		1	1	1	1	1	2
arCOG04150	J	Translation, ribosomal structure and biogenesis	Krr1	rRNA processing protein Krr1/Pno1, contains KH domain	COG01094			TIGR03665	1	1		1					1	1	2
arCOG00809	J	Translation, ribosomal structure and biogenesis	LeuS	Leucyl-tRNA synthetase	COG00495	pfam00133,pfam0826	cd00812,cd008	TIGR00395	1	1							1		
arCOG01736	J	Translation, ribosomal structure and biogenesis	LigT	2'-5' RNA ligase	COG01514	pfam13563		TIGR02258								1	1		
arCOG00485	J	Translation, ribosomal structure and biogenesis	LysS	Lysyl-tRNA synthetase, class I	COG01384	pfam01921	cd00674	TIGR00467	1		1				1	1		1	1
arCOG00408	J	Translation, ribosomal structure and biogenesis	LysU	Lysyl-tRNA synthetase (class II)	COG01190	pfam01336,pfam0015	cd04322,cd007	TIGR00499									1		
arCOG01001	J	Translation, ribosomal structure and biogenesis	Map	Methionine aminopeptidase	COG00024	pfam00557	cd01088	TIGR00501	1	2	1	1	1	1	2		1	1	2
arCOG00810	J	Translation, ribosomal structure and biogenesis	MetG	Methionyl-tRNA synthetase	COG00143	pfam09334,pfam0826	cd00814,cd079	TIGR00398	1		1			1		1	1	1	2
arCOG01358	J	Translation, ribosomal structure and biogenesis	MiaB	2-methylthioadenine synthetase	COG00621	pfam00919,pfam0405	cd01335	TIGR00089	1								1		
arCOG02286	J	Translation, ribosomal structure and biogenesis	Ncl1	Ribosome biogenesis protein, NOL1/NOP2/fmu family	COG03270	pfam13636			1	1	1	1			1		1		
arCOG04149	J	Translation, ribosomal structure and biogenesis	NMD3	NMD protein affecting ribosome stability and mRNA decay	COG01499	pfam04981			1	1				1	1	2	1	1	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	1
arCOG00078	J	Translation, ribosomal structure and biogenesis	NOP1	Fibrillarin-like rRNA methylase	COG01889	pfam01269			1	1	1						1	1	1
arCOG00906	J	Translation, ribosomal structure and biogenesis	Nop10	rRNA maturation protein Nop10, contains Zn-ribbon domain	COG02260	pfam04135			1	1		1	1	1	1		1	1	2
arCOG04414	J	Translation, ribosomal structure and biogenesis	Pcc1	Subunit of KEOPS complex (Cgi121BUD32KAE1)	COG02892				1		1		1		1		1		
arCOG01741	J	Translation, ribosomal structure and biogenesis	PelA	Release factor eRF1	COG01537	pfam03463,pfam03464,pfam03465		TIGR00111	1	2	1	1	1	1	1	1	1	1	2
arCOG00410	J	Translation, ribosomal structure and biogenesis	PheS	Phenylalanyl-tRNA synthetase alpha subunit	COG00016	pfam01409	cd00496	TIGR00468	1	2	1				1	1	1	1	1
arCOG00412	J	Translation, ribosomal structure and biogenesis	PheT	Phenylalanyl-tRNA synthetase beta subunit	COG00072	pfam03483,pfam0348	cd00769	TIGR00471	1	2	1		1	1	1		1	1	2
arCOG00784	J	Translation, ribosomal structure and biogenesis	POP4	RNase P/RNase MRP subunit p29	COG01588	pfam01868			1	2	1					1	1		2
arCOG01365	J	Translation, ribosomal structure and biogenesis	POP5	RNase P/RNase MRP subunit POP5	COG01369	pfam01900											1		
arCOG00402	J	Translation, ribosomal structure and biogenesis	ProS	Prolyl-tRNA synthetase	COG00442	pfam00587,pfam0312	cd00778,cd008	TIGR00408	1	1	1	1	1	1	1		1	1	3
arCOG04228	J	Translation, ribosomal structure and biogenesis	Pth2	Peptidyl-tRNA hydrolase	COG01990	pfam01981	cd02430	TIGR00283	1	1	1	1		1	1		1	2	2
arCOG01015	J	Translation, ribosomal structure and biogenesis	Pus10	tRNA U54 and U55 pseudouridine synthase Pus10	COG01258			TIGR01213	1	3	1	1	1	1	1		1	1	1
arCOG13558	J	Translation, ribosomal structure and biogenesis	QueA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase		pfam02547		TIGR00113									1		
arCOG00039	J	Translation, ribosomal structure and biogenesis	QueC	7-cyano-7-deazaguanine synthase (queuosine biosynthesis)	COG00603	pfam06508	cd01995	TIGR00364		1						1	1	1	1
arCOG04210	J	Translation, ribosomal structure and biogenesis	QueFC	NADPH-dependent 7-cyano-7-deazaguanine reductase QueF, C-terminal dom	COG00780	pfam14489		TIGR03139									1		
arCOG04125	J	Translation, ribosomal structure and biogenesis	RCL1	RNA 3'-terminal phosphate cyclase	COG00430	pfam01137	cd00874	TIGR03399									1		
arCOG00842	J	Translation, ribosomal structure and biogenesis	RimL	Acetyltransferase, RimL family	COG01670	pfam13302			1	1						1	1		
arCOG00187	J	Translation, ribosomal structure and biogenesis	Rli1	Translation initiation factor RLI1, contains Fe-S and AAA+ ATPase domains	COG01245	pfam00005,pfam0000	cd03237,cd032	TIGR03269	1	2	1	1		1	1	1	1	1	6
arCOG05111	J	Translation, ribosomal structure and biogenesis	RlmH	23S rRNA pseudoU1915 N3-methylase RlmH	COG01576	pfam02590		TIGR00246									1	1	
arCOG06660	J	Translation, ribosomal structure and biogenesis	RluA	Pseudouridylate synthase, 23S RNA-specific	COG00564	pfam00849	cd02869	TIGR00005										1	2
arCOG00547	J	Translation, ribosomal structure and biogenesis	RnjA	mRNA degradation ribonuclease J1/J2	COG00595	pfam12706		TIGR03675,TIGR02651									1		
arCOG00501	J	Translation, ribosomal structure and biogenesis	Rnz	Ribonuclease Z, beta-lactamase superfamily hydrolase	COG01234	pfam12706		TIGR02651	1	1		1					1	1	2
arCOG01575	J	Translation, ribosomal structure and biogenesis	Rph	Ribonuclease PH	COG00689	pfam01138,pfam0372	cd11366	TIGR02065	1	1	1		1		1		2	2	4
arCOG04209	J	Translation, ribosomal structure and biogenesis	RPL15A	Ribosomal protein L15E	COG01632	pfam00827					1	1			1	1	1	1	3
arCOG00780	J	Translation, ribosomal structure and biogenesis	RPL18A	Ribosomal protein L18E	COG01727	pfam00828		TIGR01071	1	1		1		1	1	1	1	1	
arCOG04089	J	Translation, ribosomal structure and biogenesis	RPL19A	Ribosomal protein L19E	COG02147	pfam01280	cd01418		1	2	1			1	1	1	1	1	1
arCOG04175	J	Translation, ribosomal structure and biogenesis	RPL20A	Ribosomal protein L20A (L18A)	COG02157	pfam01775											1	1	
arCOG04129	J	Translation, ribosomal structure and biogenesis	RPL21A	Ribosomal protein L21E	COG02139	pfam01157			1	2	1	1	1	1	1		1	1	1
arCOG01950	J	Translation, ribosomal structure and biogenesis	RPL24A	Ribosomal protein L24E	COG02075	pfam01246	cd00472		1	1				1	1	1	1		
arCOG01752	J	Translation, ribosomal structure and biogenesis	RPL30	Ribosomal protein L30E	COG01911	pfam01248				1	1	1		1	1	1	1	1	2
arCOG04473	J	Translation, ribosomal structure and biogenesis	RPL31A	Ribosomal protein L31E	COG02097	pfam01198	cd00463		1	2	1	1	1	1	1	1	1	1	1
arCOG00781	J	Translation, ribosomal structure and biogenesis	RPL32	Ribosomal protein L32E	COG01717	pfam01655	cd00513		1	2	1			1	1	1	1	1	1
arCOG04177	J	Translation, ribosomal structure and biogenesis	RPL39	Ribosomal protein L39E	COG02167	pfam00832											1		1
arCOG04049	J	Translation, ribosomal structure and biogenesis	RPL40A	Ribosomal protein L40E	COG01552							1							1
arCOG04109	J	Translation, ribosomal structure and biogenesis	RPL42A	Ribosomal protein L44E	COG01631	pfam00935			1	1		1	1	1	1		1		2
arCOG04208	J	Translation, ribosomal structure and biogenesis	RPL43A	Ribosomal protein L37AE/L43A	COG01997	pfam01780		TIGR00280	1	1	1				1		1		2
arCOG01751	J	Translation, ribosomal structure and biogenesis	Rpl7Ae	Ribosomal protein L7AE	COG01358	pfam01248		TIGR03677	1	1				1	1	1	1	1	1
arCOG04289	J	Translation, ribosomal structure and biogenesis	RplA	Ribosomal protein L1	COG00081	pfam00687	cd00403	TIGR01169	1	1	1				1	1	1	1	2
arCOG04067	J	Translation, ribosomal structure and biogenesis	RplB	Ribosomal protein L2	COG00090	pfam00181,pfam03947		TIGR01171	1	1	1			1		1	1	1	2
arCOG04070	J	Translation, ribosomal structure and biogenesis	RplC	Ribosomal protein L3	COG00087	pfam00297		TIGR03626	1	1	1					1	1	1	2
arCOG04071	J	Translation, ribosomal structure and biogenesis	RplD	Ribosomal protein L4	COG00088	pfam00573		TIGR03672	1	1	1					1	1	1	2
arCOG04092	J	Translation, ribosomal structure and biogenesis	RplE	Ribosomal protein L5	COG00094	pfam00281,pfam00673			1	2	1			1	1	1	1	1	1
arCOG04090	J	Translation, ribosomal structure and biogenesis	RplF	Ribosomal protein L6P	COG00097	pfam00347,pfam00347		TIGR03653	1	2	1			1	1	1	1	1	1
arCOG04288	J	Translation, ribosomal structure and biogenesis	RplJ	Ribosomal protein L10	COG00244	pfam00466	cd05795		1	1	1				1	1	1	1	2
arCOG04372	J	Translation, ribosomal structure and biogenesis	RplK	Ribosomal protein L11	COG00080	pfam03946,pfam0029	cd00349	TIGR01632	1	2	1	1		1	1		1	1	2
arCOG04242	J	Translation, ribosomal structure and biogenesis	RplM	Ribosomal protein L13	COG00102	pfam00572	cd00392	TIGR01077	1	1		1		1	1	1	1	1	
arCOG04095	J	Translation, ribosomal structure and biogenesis	RplN	Ribosomal protein L14	COG00093	pfam00238		TIGR03673	1	2	1			1		1	1	1	2
arCOG00779	J	Translation, ribosomal structure and biogenesis	RplO	Ribosomal protein L15	COG00200	pfam00828			1	2	1			1	1	1	1	1	1
arCOG04113	J	Translation, ribosomal structure and biogenesis	RplP	Ribosomal protein L10AE/L16	COG00197	pfam00252	cd01433	TIGR00279	1	1	1	1			1		1	1	1
arCOG04088	J	Translation, ribosomal structure and biogenesis	RplR	Ribosomal protein L18	COG00256	pfam00861,pfam1420	cd00432		1	2	1			1	1	1	1	1	1
arCOG04098	J	Translation, ribosomal structure and biogenesis	RplV	Ribosomal protein L22	COG00091	pfam00237	cd00336	TIGR01038	1	1	1			1		1	1	1	3
arCOG04072	J	Translation, ribosomal structure and biogenesis	RplW	Ribosomal protein L23	COG00089	pfam00276		TIGR03636	1	1	1			1		1	1	1	2
arCOG04094	J	Translation, ribosomal structure and biogenesis	RplX	Ribosomal protein L24	COG00198		cd06089	TIGR01080	1	2	1			1		1	1		2
arCOG00785	J	Translation, ribosomal structure and biogenesis	RpmC	Ribosomal protein L29	COG00255	pfam00831	cd00427	TIGR00012	1	2	1			1		1	1		
arCOG04086	J	Translation, ribosomal structure and biogenesis	RpmD	Ribosomal protein L30	COG01841		cd01657	TIGR01309	1	2	1			1	1	1	1	1	1
arCOG04287	J	Translation, ribosomal structure and biogenesis	RPP1A	Ribosomal protein L12E/L44/L45/RPP1/RPP2	COG02058	pfam00428	cd05832	TIGR03685	1	1	1				1	1	1	1	2
arCOG04345	J	Translation, ribosomal structure and biogenesis	RPR2	RNase P subunit RPR2	COG02023	pfam04032				1		1				1	1		1
arCOG01885	J	Translation, ribosomal structure and biogenesis	RPS17A	Ribosomal protein S17E	COG01383	pfam00833			1	1	1	1	1	1	2	1	1	1	1
arCOG01344	J	Translation, ribosomal structure and biogenesis	RPS19A	Ribosomal protein S19E (S16A)	COG02238	pfam01090			1	2	1	1	1	1	1	1	1	1	1
arCOG04186	J	Translation, ribosomal structure and biogenesis	RPS1A	Ribosomal protein S3AE	COG01890	pfam01015			1						1	1	1	1	3
arCOG04182	J	Translation, ribosomal structure and biogenesis	RPS24A	Ribosomal protein S24E	COG02004	pfam01282			1						1		1	1	
arCOG04108	J	Translation, ribosomal structure and biogenesis	RPS27A	Ribosomal protein S27E	COG02051	pfam01667			1	1		1	1	1			1		1
arCOG04183	J	Translation, ribosomal structure and biogenesis	RPS27AE	Ribosomal protein S27AE	COG01998				1								1		
arCOG04314	J	Translation, ribosomal structure and biogenesis	RPS28A	Ribosomal protein S28E/S33	COG02053	pfam01200	cd04457		1	1				1	1	1	1	1	1
arCOG04093	J	Translation, ribosomal structure and biogenesis	RPS4A	Ribosomal protein S4E	COG01471	pfam08071,pfam0147	cd00165,cd06087		1	2	1			1	1	1	1	1	2
arCOG01946	J	Translation, ribosomal structure and biogenesis	RPS6A	Ribosomal protein S6E/S10	COG02125	pfam01092			1		1	1		1	1	1	1	1	3
arCOG04154	J	Translation, ribosomal structure and biogenesis	RPS8A	Ribosomal protein S8E	COG02007	pfam01201	cd11382	TIGR00307	1		1				1	1	1	1	2
arCOG04245	J	Translation, ribosomal structure and biogenesis	RpsB	Ribosomal protein S2	COG00052	pfam00318	cd01425	TIGR01012		1		1	1		1		1	1	2
arCOG04097	J	Translation, ribosomal structure and biogenesis	RpsC	Ribosomal protein S3	COG00092	pfam07650,pfam0018	cd02411	TIGR01008	1	2	1			1		1	1	1	2
arCOG04239	J	Translation, ribosomal structure and biogenesis	RpsD	Ribosomal protein S4 or related protein	COG00522	pfam00163,pfam0147	cd00165	TIGR01018	1			1				1	1	1	1
arCOG04087	J	Translation, ribosomal structure and biogenesis	RpsE	Ribosomal protein S5	COG00098	pfam00333,pfam03719		TIGR01020	1	2	1			2	1	1	1	1	1
arCOG04254	J	Translation, ribosomal structure and biogenesis	RpsG	Ribosomal protein S7	COG00049	pfam00177	cd14867	TIGR01028	1	1	1	1		1	1		1	1	1
arCOG04091	J	Translation, ribosomal structure and biogenesis	RpsH	Ribosomal protein S8	COG00096	pfam00410			1	2	1			1	1	1	1	1	1
arCOG04243	J	Translation, ribosomal structure and biogenesis	RpsI	Ribosomal protein S9	COG00103	pfam00380		TIGR03627	1	1		1		1	1	1	1	1	
arCOG01758	J	Translation, ribosomal structure and biogenesis	RpsJ	Ribosomal protein S10	COG00051	pfam00338		TIGR01046	1	1		1		1	1		1	1	2
arCOG04240	J	Translation, ribosomal structure and biogenesis	RpsK	Ribosomal protein S11	COG00100	pfam00411		TIGR03628	1			1				1	1	1	1
arCOG04255	J	Translation, ribosomal structure and biogenesis	RpsL	Ribosomal protein S12	COG00048	pfam00164	cd03367	TIGR00982	1	1	1	1		1	1		1	1	1
arCOG01722	J	Translation, ribosomal structure and biogenesis	RpsM	Ribosomal protein S13	COG00099	pfam00416		TIGR03629	1			1				1	1	1	1
arCOG00782	J	Translation, ribosomal structure and biogenesis	RpsN	Ribosomal protein S14	COG00199	pfam00253			1	1	1			1			1		
arCOG04185	J	Translation, ribosomal structure and biogenesis	RpsO	Ribosomal protein S15P	COG00184	pfam08069,pfam0031	cd00353		1	1			1	2	1	1	1	1	2
arCOG04096	J	Translation, ribosomal structure and biogenesis	RpsQ	Ribosomal protein S17	COG00186	pfam00366		TIGR03630	1	2	1			1		1	1	1	2

arCOG04099	J	Translation, ribosomal structure and biogenesis	RpsS	Ribosomal protein S19	COG00185	pfam00203		TIGR01025	1	1	1			1		1	1	1	2
arCOG00678	J	Translation, ribosomal structure and biogenesis	Rrp4	Exosome complex RNA-binding protein Rrp4, contains S1 and KH domains	COG01097		cd05789		1	1	1		1		1		1	1	1
arCOG01574	J	Translation, ribosomal structure and biogenesis	Rrp42	Exosome complex RNA-binding protein Rrp42, RNase PH superfamily	COG02123	pfam01138,pfam0372	cd11365	TIGR01966	1	1	1		1		1		1	1	2
arCOG04131	J	Translation, ribosomal structure and biogenesis	RsmA	16S rRNA A1518 and A1519 N6-dimethyltransferase RsmA/KsgA/DIM1	COG00030	pfam00398		TIGR00755	1	1	1				1		1	1	1
arCOG00973	J	Translation, ribosomal structure and biogenesis	RsmB	16S rRNA C967 or C1407 C5-methylase, RsmB/RsmF family	COG00144	pfam01189		TIGR00446	1	1	1	1			1		1	1	3
arCOG00975	J	Translation, ribosomal structure and biogenesis	RsmB	16S rRNA C967 or C1407 C5-methylase, RsmB/RsmF family	COG00144	pfam01189	cd02440	TIGR00446									1		
arCOG01239	J	Translation, ribosomal structure and biogenesis	RsmE	RNA base methyltransferase family enzyme	COG01901	pfam04013			1	2	1	1			1	1	1	1	1
arCOG04246	J	Translation, ribosomal structure and biogenesis	RtcB	RNA 3'-P ligase, RtcB family protein	COG01690	pfam01139		TIGR03073							1		1	1	1
arCOG04187	J	Translation, ribosomal structure and biogenesis	Sdo1	Ribosome maturation protein Sdo1	COG01500	pfam01172,pfam09377		TIGR00291	1	1	1		1		1		1	1	1
arCOG01564	J	Translation, ribosomal structure and biogenesis	SelB	Selenocysteine-specific translation elongation factor or SelB-II domain	COG03276		cd03696	TIGR00475	1	1					1			1	3
arCOG01701	J	Translation, ribosomal structure and biogenesis	SEN2	tRNA splicing endonuclease	COG01676	pfam02778,pfam01974		TIGR00324	1		1				1	1	1	1	5
arCOG00403	J	Translation, ribosomal structure and biogenesis	SerS	Seryl-tRNA synthetase	COG00172	pfam02403,pfam0058	cd00770	TIGR00414	1			1		1	1	1	1	1	1
arCOG01923	J	Translation, ribosomal structure and biogenesis	SIK1	RNA processing factor Prp31, contains Nop domain	COG01498	pfam01798			1	1	1	1		1		1	1	1	2
arCOG01952	J	Translation, ribosomal structure and biogenesis	SUA5	tRNA A37 threonylcarbamoyladenosine synthetase subunit TsaC/SUA5/YrdC	COG00009	pfam01300		TIGR00057	1	2	1	1	1	1	2		1	1	1
arCOG04223	J	Translation, ribosomal structure and biogenesis	SUI1	Translation initiation factor 1 (eIF-1/SUI1)	COG00023	pfam01253	cd11567	TIGR01158	1	2	1			1		1	1	1	2
arCOG04107	J	Translation, ribosomal structure and biogenesis	SUI2	Translation initiation factor 2, alpha subunit (eIF-2alpha)	COG01093	pfam00575,pfam0754	cd04452	TIGR00717	1	1		1	1	1	1		1	1	2
arCOG00056	J	Translation, ribosomal structure and biogenesis	Tan1	tRNA(Ser,Leu) C12 N-acetylase TAN1, contains THUMP domain	COG01818	pfam02926,pfam1441	cd11718,cd061	TIGR00342							1				
arCOG01630	J	Translation, ribosomal structure and biogenesis	TdcF	Translation initiation inhibitor, yjgF family	COG00251	pfam01042	cd00448	TIGR00004	2	2	2			1	3	2		2	4
arCOG01561	J	Translation, ribosomal structure and biogenesis	TEF1	Translation elongation factor EF-1 alpha, GTPase	COG05256	pfam00009,pfam0314	cd01883,cd036	TIGR00483	1	1	1	1		1	1		1	1	5
arCOG00989	J	Translation, ribosomal structure and biogenesis	Tgt	Queuine/archaeosine tRNA-ribosyltransferase	COG00343	pfam01702		TIGR00432									1		
arCOG00038	J	Translation, ribosomal structure and biogenesis	ThiI	tRNA S(4)U 4-thiouridine synthase	COG00301	pfam02926,pfam0256	cd11716,cd017	TIGR00342,TIGR04271			1					1	2	2	2
arCOG00401	J	Translation, ribosomal structure and biogenesis	ThrS	Threonyl-tRNA synthetase	COG00441	pfam00587,pfam0312	cd00771,cd008	TIGR00418	1	1				1	1		1	1	4
arCOG01115	J	Translation, ribosomal structure and biogenesis	TiaS	tRNA(Ile2) 2-agmatinylcytidine synthetase; containing Zn-ribbon domain and	COG01571	pfam08489,pfam0728	cd04482	TIGR03280	1	1		1			1	1	1	1	1
arCOG04176	J	Translation, ribosomal structure and biogenesis	TIF6	Translation initiation factor 6 (eIF-6)	COG01976	pfam01912	cd00527	TIGR00323	1	2	1	1	1	1	1	1	1	1	1
arCOG00042	J	Translation, ribosomal structure and biogenesis	TilS	tRNA(Ile)-lysidine synthase TilS/MesJ	COG00037	pfam01171	cd01993	TIGR02432	1	1		1					2	1	3
arCOG00985	J	Translation, ribosomal structure and biogenesis	Tma20	Predicted RNA-binding protein, contains PUA domain	COG02016	pfam09183,pfam01472		TIGR03684	1	1				1	1	1	1	1	2
arCOG01951	J	Translation, ribosomal structure and biogenesis	TmcA	tRNA(Met) C34 N-acetyltransferase TmcA	COG01444	pfam08351,pfam05127,pfam13718											1		
arCOG01219	J	Translation, ribosomal structure and biogenesis	TRM1	N2,N2-dimethylguanosine tRNA methyltransferase	COG01867	pfam02005		TIGR00308	1	2	1	1		1	2		1	1	1
arCOG00047	J	Translation, ribosomal structure and biogenesis	Trm11	tRNA G10 N-methylase Trm11	COG01041	pfam01170		TIGR01177	1			1				1	1	1	2
arCOG00033	J	Translation, ribosomal structure and biogenesis	Trm5	Wybutosine (yW) biosynthesis enzyme, Trm5 methyltransferase	COG02520	pfam02475			2	1	1	2		1		1	2	1	2
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	1	1	1	2	1	1	1	2	2
arCOG01887	J	Translation, ribosomal structure and biogenesis	TrpS	Tryptophanyl-tRNA synthetase	COG00180	pfam00579	cd00806	TIGR00233	1	1	1	1	1		1		1	1	3
arCOG04449	J	Translation, ribosomal structure and biogenesis	TruA	Pseudouridylate synthase	COG00101	pfam01416,pfam0141	cd02866	TIGR00071	1	1	1	1					1	1	2
arCOG00987	J	Translation, ribosomal structure and biogenesis	TruB	Pseudouridine synthase	COG00130	pfam08068,pfam0150	cd02572	TIGR00425							1		1	1	1
arCOG04252	J	Translation, ribosomal structure and biogenesis	TruD	tRNA(Glu) U13 pseudouridine synthase TruD	COG00585	pfam01142	cd02577	TIGR00094	1	2	1	1		1	2		1	1	1
arCOG00761	J	Translation, ribosomal structure and biogenesis	TsaA	tRNA (Thr-GGU) A37 N-methylase	COG01720	pfam01980	cd09281	TIGR00104									1		
arCOG04733	J	Translation, ribosomal structure and biogenesis	Tsr3	Ribosome biogenesis protein Tsr3, contains Fer4-like metal-binding domain o	COG02042	pfam04034				1		1	1	1	1		1	1	2
arCOG01886	J	Translation, ribosomal structure and biogenesis	TyrS	Tyrosyl-tRNA synthetase	COG00162	pfam00579	cd00805	TIGR00234	1		1	1	1	1	1		1	1	2
arCOG04174	J	Translation, ribosomal structure and biogenesis	TYW1	Wybutosine (yW) biosynthesis enzyme, Fe-S oxidoreductase	COG00731	pfam04055,pfam0860	cd01335	TIGR03972	1	2	1				1	1	1	1	3
arCOG10124	J	Translation, ribosomal structure and biogenesis	TYW2	Wybutosine (yW) biosynthesis enzyme, TYW2 transferase	COG02520	pfam02475	cd02440	TIGR01444			1		1					1	2
arCOG04156	J	Translation, ribosomal structure and biogenesis	TYW3	Wybutosine (yW) biosynthesis enzyme	COG01590	pfam02676			1		1		1				1		
arCOG00808	J	Translation, ribosomal structure and biogenesis	ValS	Valyl-tRNA synthetase	COG00525	pfam00133,pfam0826	cd00817,cd079	TIGR00422	1	1	1					1	1	2	6
arCOG04225	J	Translation, ribosomal structure and biogenesis	YmdB	O-acetyl-ADP-ribose deacetylase (regulator of RNase III), contains Macro dom	COG02110	pfam01661	cd02907										1	1	1
arCOG00541	J	Translation, ribosomal structure and biogenesis	YSH1	Predicted exonuclease of the beta-lactamase fold involved in RNA processing	COG01236	pfam00753,pfam10996,pfam07521		TIGR03675	1			1			1	1	1	1	6
arCOG00545	J	Translation, ribosomal structure and biogenesis	YSH1	Predicted exonuclease of the beta-lactamase fold involved in RNA processing	COG01236			TIGR04122	1	1	1		1	2					
CELLULAR PROCESSES AND SIGNALING																			
arCOG02263	D	Cell cycle control, cell division, chromosome partit	-	Predicted cell division protein, SepF homolog	COG02450	pfam04472			1	1	1	1			1		1		
arCOG11012	D	Cell cycle control, cell division, chromosome partit	ATS1	Alpha-tubulin suppressor and related RCC1 domain-containing proteins	COG05184	pfam13540,pfam00415,pfam00415,pfam00415,pfam00415,pfa				1	2						7	3	6
arCOG04701	D	Cell cycle control, cell division, chromosome partit	CrcB/FEX	Integral membrane protein possibly involved in fluoride export and chromoso	COG00239	pfam02537		TIGR00494											3
arCOG02201	D	Cell cycle control, cell division, chromosome partit	FtsZ	Cell division GTPase	COG00206	pfam00091,pfam1232	cd02201	TIGR00065	2	3	1	2		1	1			2	1
arCOG05007	D	Cell cycle control, cell division, chromosome partit	Maf	Nucleotide-binding protein implicated in inhibition of septum formation	COG00424	pfam02545	cd00555	TIGR00172									2	1	3
arCOG03061	D	Cell cycle control, cell division, chromosome partit	MreB	Actin-like ATPase involved in cell morphogenesis	COG01077	pfam06723	cd10227	TIGR00904										1	1
arCOG00585	D	Cell cycle control, cell division, chromosome partit	Mrp	Mrp family protein, ATPase, contains iron-sulfur cluster	COG00489	pfam10609	cd02037	TIGR01969										1	3
arCOG00371	D	Cell cycle control, cell division, chromosome partit	Smc	Chromosome segregation ATPase	COG01196	pfam02463	cd03278,cd032	TIGR02169							1			3	
arCOG00586	D	Cell cycle control, cell division, chromosome partit	Soj	ATPase involved in chromosome partitioning, ParA family	COG01192	pfam01656	cd02042	TIGR03453											1
arCOG02416	N	Cell motility	-	Pilin/Flagellin, FlaG/FlaF family	COG03430	pfam07790				1					1			3	1
arCOG00434	N	Cell motility	-	AAA+ ATPase of MoxR-like family, a component of a putative secretion systen	COG00714	pfam07726	cd00009	TIGR02031	2	1	1	2			2	2	2	2	3
arCOG02079	N	Cell motility	-	S-layer protein, possibly associated with type IV pili like system	COG01361				1	1	1	1		1			1		
arCOG02423	N	Cell motility	-	Pilin/Flagellin, FlaG/FlaF family	COG03430	pfam07790			1	1	1		1	2			2		
arCOG02911	N	Cell motility	-	Predicted pilin/flagellin	SC.00343												1		
arCOG02382	N	Cell motility	CheB	Chemotaxis response regulator containing a CheY-like receiver domain and a	COG02201	pfam00072,pfam0133	cd00156	TIGR02875										1	
arCOG01819	N	Cell motility	CpaF	Pilus assembly protein, ATPase of CpaF family	COG04962	pfam00437	cd01130	TIGR03819	1	2	1	1	1	1		1		1	1
arCOG01829	N	Cell motility	FlaB	Archaeal flagellins	COG01681												3		1
arCOG02964	N	Cell motility	FlaD	Archaellum protein D/E	COG03351	pfam05377,pfam04659											2		
arCOG01824	N	Cell motility	FlaF	Archaellum protein F, flagellin of FlaG/FlaF family	COG03353												1		
arCOG01822	N	Cell motility	FlaG	Archaellum protein G, flagellin of FlaG/FlaF family	COG03354												1	1	
arCOG04148	N	Cell motility	FlaH	ATPase involved in biogenesis of archaellum	COG02874	pfam06745	cd01394	TIGR03881									1	1	
arCOG01809	N	Cell motility	FlaJ	Archaellum assembly protein J, TadC family	COG01955												1	1	
arCOG02298	N	Cell motility	FlaK/PulO	Peptidase A24A, prepilin type IV	COG01989	pfam01478,pfam06847			1	1	1	1		1	2		1	1	
arCOG01808	N	Cell motility	TadC	Pilus assembly protein TadC	COG02064	pfam00482,pfam00482			2	2	2	2	2	2	2		2	2	4
arCOG01811	N	Cell motility	TadC	Pilus assembly protein TadC	COG02064				1	1	1	1	1	1		1			
arCOG01812	N	Cell motility	TadC	Pilus assembly protein TadC	COG02064				1	3	1	1	1	1		1		1	1
arCOG01817	N	Cell motility	VirB11	ATPase involved in archaellum/pili biosynthesis	COG00630	pfam00437	cd01130	TIGR03819	1	1	1	1	1	1	1	1	3	2	2
arCOG02488	M	Cell wall/membrane/envelope biogenesis	-	Cell surface protein, a component of a putative secretion system	SC.00293				1	1	1	1			1	1	1		
arCOG01385	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG00463	pfam00535	cd02522	TIGR04283	1	1	1	1			1	1	2	2	3
arCOG05978	M	Cell wall/membrane/envelope biogenesis	-	Extracellular protein containing Kelch and FN3 domains		pfam07081				2					1	1	8		
arCOG00894	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG00463	pfam00535	cd04179	TIGR04182	2	1	2	2	2	1	2	1	1	2	3
arCOG02532	M	Cell wall/membrane/envelope biogenesis	-	Secreted Beta-propeller repeat protein fused to CARDB-like adhesion module	COG03291	pfam07705		TIGR04213	1			2	1	1	2	2	1	2	
arCOG07560	M	Cell wall/membrane/envelope biogenesis	-	Cell surface protein							1					1			1

arCOG03336	M	Cell wall/membrane/envelope biogenesis	-	Surface protein containing fasciclin-like repeats	COG02335	pfam02469			1		1		1					3	1
arCOG09173	M	Cell wall/membrane/envelope biogenesis	-	Cell surface protein		pfam07790,pfam0770	cd00146,cd001	TIGR00864,TIGR	1				1						
arCOG02086	M	Cell wall/membrane/envelope biogenesis	-	S-layer domain	COG01361				2										
arCOG03335	M	Cell wall/membrane/envelope biogenesis	-	Surface protein containing fasciclin-like repeats	COG02335	pfam02469				1									1
arCOG08795	M	Cell wall/membrane/envelope biogenesis	-	Predicted S-layer protein with Ig-like domain	SC.00192	pfam00127	cd13921	TIGR02657		1									
arCOG02482	M	Cell wall/membrane/envelope biogenesis	-	WD40/PQQ-like beta propeller repeat containing protein	COG01520	pfam13570,pfam1357	cd10276	TIGR03300			1								
arCOG01383	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG01216	pfam00535	cd04186	TIGR04017,TIGR01556						1			1	1	2
arCOG00568	M	Cell wall/membrane/envelope biogenesis	-	Oligosaccharyl transferase STT3 or related protein	COG01287												1		
arCOG01391	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG01215	pfam13641	cd06421	TIGR03030									1		
arCOG02080	M	Cell wall/membrane/envelope biogenesis	-	S-layer domain	COG01361												1		
arCOG02559	M	Cell wall/membrane/envelope biogenesis	-	Cell surface protein	SC.00325												1		
arCOG03553	M	Cell wall/membrane/envelope biogenesis	-	Cell surface protein	COG01572	pfam11824,pfam07705											1		
arCOG12808	M	Cell wall/membrane/envelope biogenesis	-	Glycosyltransferase, GT1 family	COG00438		cd03822										1		
arCOG01389	M	Cell wall/membrane/envelope biogenesis	-	Glycosyl transferase family 2	COG01215	pfam13641	cd06423	TIGR03937										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										2	1
arCOG01410	M	Cell wall/membrane/envelope biogenesis	AglA	Glycosyltransferase	COG00438	pfam13579,pfam0053	cd03794	TIGR02149	5	5	3	3	1	1	2	4	1	1	
arCOG05365	M	Cell wall/membrane/envelope biogenesis	AglB	Oligosaccharyltransferase membrane subunit	COG01287	pfam02516,pfam13620,pfam13620,pf		TIGR04154	1	1	1	1	1	1	1	1	1	2	1
arCOG00899	M	Cell wall/membrane/envelope biogenesis	AglD2	Predicted flippase	COG00392	pfam03706		TIGR00374	1		1						1		
arCOG00664	M	Cell wall/membrane/envelope biogenesis	AglF/RfbA	Glucose-1-phosphate uridyltransferase	COG01209	pfam00483	cd04181	TIGR03992									1	1	
arCOG03199	M	Cell wall/membrane/envelope biogenesis	AglH/Rfe	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucos	COG00472	pfam00953	cd06856	TIGR00445	1								1		
arCOG01403	M	Cell wall/membrane/envelope biogenesis	AglL	Glycosyltransferase	COG00438	pfam13439,pfam0053	cd03804		3	2	1	2	1	1	1	3	6	5	9
arCOG00253	M	Cell wall/membrane/envelope biogenesis	AglM/Ugd	UDP-glucose 6-dehydrogenase	COG01004	pfam03721,pfam00984,pfam03720		TIGR03026	1	1				1	1	2		1	
arCOG01381	M	Cell wall/membrane/envelope biogenesis	AglO	Glycosyl transferase family 2	COG00463	pfam00535	cd00761	TIGR04283										1	1
arCOG02209	M	Cell wall/membrane/envelope biogenesis	AglR	MATE family membrane protein, Rfbx family	COG02244		cd13128		3	2	1	1	1	1	1	3	2		
arCOG10648	M	Cell wall/membrane/envelope biogenesis	BglC	Aryl-phospho-beta-D-glucosidase BglC, GH1 family	COG02730	pfam00150											1		
arCOG01375	M	Cell wall/membrane/envelope biogenesis	FlaA1	NDP-sugar epimerase, includes UDP-GlcNAc-inverting 4,6-dehydratase FlaA1 a	COG01086	pfam02719	cd05237	TIGR03589						1					
arCOG00665	M	Cell wall/membrane/envelope biogenesis	GalU	UDP-glucose pyrophosphorylase	COG01210	pfam00483	cd02541	TIGR01099	1					1	1			1	1
arCOG00666	M	Cell wall/membrane/envelope biogenesis	GCD1	N-acetylglucosamine-1-phosphate uridyltransferase	COG01208	pfam00483,pfam0013	cd04181,cd056	TIGR03992	3	3	3	3	2		1	1	3	3	3
arCOG00663	M	Cell wall/membrane/envelope biogenesis	GCD1	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysacchar	COG01208	pfam00483	cd04181	TIGR03992							1				
arCOG00668	M	Cell wall/membrane/envelope biogenesis	GCD1	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysacchar	COG01208	pfam00483,pfam0013	cd04181,cd056	TIGR03992	1	1									
arCOG00057	M	Cell wall/membrane/envelope biogenesis	GlmS	Glucosamine 6-phosphate synthetase	COG00449	pfam00310,pfam0138	cd00714,cd050	TIGR01135	1	1		1			1	1	1	1	1
arCOG01373	M	Cell wall/membrane/envelope biogenesis	Gmd	GDP-D-mannose dehydratase	COG01089	pfam01370,pfam1395	cd05260	TIGR01472										1	
arCOG00068	M	Cell wall/membrane/envelope biogenesis	GutQ	Predicted sugar phosphate isomerase involved in capsule formation	COG00794	pfam01380	cd05005	TIGR03127									1		
arCOG02313	M	Cell wall/membrane/envelope biogenesis	LolE	ABC-type transport system, involved in lipoprotein release, permease compor	COG04591	pfam12704,pfam02687		TIGR02212										1	
arCOG06815	M	Cell wall/membrane/envelope biogenesis	MpaA	Murein tripeptide amidase MpaA	COG02866	pfam00246	cd06228											1	1
arCOG01568	M	Cell wall/membrane/envelope biogenesis	MscS	Small-conductance mechanosensitive channel	COG00668	pfam00924			2	2	1	1	1		1	1	1	2	5
arCOG02821	M	Cell wall/membrane/envelope biogenesis	MurD	UDP-N-acetylmuramoylalanine-D-glutamate ligase	COG00771	pfam08245,pfam02875		TIGR01082					1	1	1				
arCOG02820	M	Cell wall/membrane/envelope biogenesis	MurE	UDP-N-acetylmuramyl tripeptide synthase	COG00769	pfam08245,pfam02875		TIGR01082	1	2								1	
arCOG07536	M	Cell wall/membrane/envelope biogenesis	NanM	N-acetylneuraminic acid mutarotase	COG03055													1	
arCOG02005	M	Cell wall/membrane/envelope biogenesis	RacX	Aspartate racemase	COG01794	pfam01177		TIGR00035									1		
arCOG01411	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438	pfam13439,pfam0053	cd03801	TIGR03999	2				1			1	1	1	3
arCOG06759	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438					2									
arCOG01417	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438	pfam00534	cd01635										1		
arCOG01405	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438	pfam13439,pfam1369	cd03794	TIGR04063											1
arCOG01409	M	Cell wall/membrane/envelope biogenesis	RfaG	Glycosyltransferase	COG00438	pfam13692	cd03794	TIGR03087											1
arCOG01371	M	Cell wall/membrane/envelope biogenesis	RfbB	dTDP-D-glucose 4,6-dehydratase	COG01088	pfam01370	cd05246	TIGR01181									1		
arCOG04188	M	Cell wall/membrane/envelope biogenesis	RfbC	dTDP-4-dehydrorhamnose 3,5-epimerase or related enzyme	COG01898	pfam00908		TIGR01221									1		
arCOG01367	M	Cell wall/membrane/envelope biogenesis	RfbD	dTDP-4-dehydrorhamnose reductase	COG01091	pfam04321	cd05254	TIGR01214									1		
arCOG01168	M	Cell wall/membrane/envelope biogenesis	RspA	L-alanine-DL-glutamate epimerase or related enzyme of enolase superfamily	COG04948	pfam02746,pfam0118	cd03316	TIGR02534									1		
arCOG04827	M	Cell wall/membrane/envelope biogenesis	TagB	Glycosyl/glycerophosphate transferase involved in teichoic acid biosynthesis T	COG01887	pfam04464						1					1		
arCOG01222	M	Cell wall/membrane/envelope biogenesis	TagD	Cytidylyltransferase fused to conserved domain of DUF357 family	COG00615	pfam01467	cd02170	TIGR02199	2	1	1	2		1	1		1	1	3
arCOG04468	M	Cell wall/membrane/envelope biogenesis	WcaG	Nucleoside-diphosphate-sugar epimerase	COG00451	pfam01370,pfam1395	cd05272	TIGR01179	1	2					1		1		3
arCOG01369	M	Cell wall/membrane/envelope biogenesis	WcaG	Nucleoside-diphosphate-sugar epimerase	COG00451	pfam01370	cd05234	TIGR01179	4	4	1			2	3	1	2	6	4
arCOG04826	M	Cell wall/membrane/envelope biogenesis	WcaK	Polysaccharide pyruvyl transferase family protein	COG02327	pfam04230		TIGR03609									1		
arCOG01392	M	Cell wall/membrane/envelope biogenesis	WecB	UDP-N-acetylglucosamine 2-epimerase	COG00381	pfam02350	cd03786	TIGR00236				1			1				1
arCOG00252	M	Cell wall/membrane/envelope biogenesis	WecC	UDP-N-acetyl-D-mannosaminuronate dehydrogenase	COG00677	pfam03721,pfam0098	cd05266	TIGR03026	1	1	1	1					1	1	1
arCOG00118	M	Cell wall/membrane/envelope biogenesis	WecE	Predicted pyridoxal phosphate-dependent enzyme apparently involved in reg	COG00399	pfam01041	cd00616	TIGR03588	3	1	1	1		2				2	1
arCOG03634	M	Cell wall/membrane/envelope biogenesis	WecH	Surface polysaccharide O-acyltransferase, integral membrane enzyme	COG03274	pfam01757			1	1	1								
arCOG03787	V	Defense mechanisms	-	LEA14-like dessication related protein	COG05608	pfam03168,pfam03168			1	1		2			1				
arCOG08906	V	Defense mechanisms	-	Predicted antitoxins containing the HTH domain	COG02886	pfam03683									1				
arCOG01467	V	Defense mechanisms	-	ABC-type multidrug transport system, permease component	COG00842	pfam01061		TIGR01247	2	1	1				2	1			
arCOG03966	V	Defense mechanisms	-	CopG family DNA-binding protein												1			
arCOG01463	V	Defense mechanisms	-	ABC-type multidrug transport system, permease component	COG00842	pfam01061		TIGR01247	1	1	1	1		1					
arCOG00722	V	Defense mechanisms	-	Predicted antitoxins containing the HTH domain	COG02886	pfam03683			1	2	1	1	1	1					
arCOG04735	V	Defense mechanisms	-	CopG/MetJ, RHH domain containing DNA-binding protein, often an antitoxin i	COG03609					1								1	1
arCOG00713	V	Defense mechanisms	-	PIN domain containing protein	COG01848	pfam01850	cd09861										1		
arCOG01009	V	Defense mechanisms	-	CopG/MetJ, RHH domain containing DNA-binding protein, often an antitoxin i	COG03609												1		
arCOG01469	V	Defense mechanisms	-	ABC-type multidrug transport system, permease component	COG00842												1		
arCOG02123	V	Defense mechanisms	-	HEPN domain containing protein	COG01895	pfam05168											1		
arCOG02780	V	Defense mechanisms	-	Endonuclease, HJR/Mrr/RecB family													1		
arCOG05724	V	Defense mechanisms	-	RecB family restriction endonuclease, SeqA-like protein	COG02810	pfam04313,pfam03925											1		
arCOG06522	V	Defense mechanisms	-	HNH nuclease domain containing protein	COG03183												1		
arCOG06948	V	Defense mechanisms	-	PIN domain	SC.00610												1		
arCOG06971	V	Defense mechanisms	-	CopG/RHH family DNA binding protein	COG03609												1		
arCOG09828	V	Defense mechanisms	-	RelB family antitoxin	SC.00879												1		
arCOG06966	V	Defense mechanisms	-	CopG/RHH family DNA binding protein	COG03609												2		
arCOG03166	V	Defense mechanisms	-	AAA+ superfamily ATPase fused to HTH and RecB nuclease domains	COG01672												4	1	5
arCOG03521	V	Defense mechanisms	-	Type II restriction enzyme, methylase subunit	COG01002	pfam12950												1	

arCOG00815	V	Defense mechanisms	AbrB	AbrB family transcriptional regulator	COG02002	pfam04014		TIGR01439									1		
arCOG01452	V	Defense mechanisms	Cas1	CRISPR-associated protein Cas1	COG01518	pfam01867	cd09636	TIGR00287									2		
arCOG02666	V	Defense mechanisms	Cas10	CRISPR associated protein Cas10, large subunit of Type III system effector com	COG01353	pfam01966											1		
arCOG04194	V	Defense mechanisms	Cas2	CRISPR-associated protein Cas2	COG01343	pfam09827	cd09725	TIGR01573									1		
arCOG00786	V	Defense mechanisms	Cas4	CRISPR-associated protein Cas4, RecB family exonuclease	COG01468	pfam01930	cd09637	TIGR00372	1	2	1	1		1	1		1	1	
arCOG00790	V	Defense mechanisms	Cas4	CRISPR-associated protein Cas4, RecB family exonuclease	COG01468		cd09637	TIGR00372									1		
arCOG00794	V	Defense mechanisms	Cas4	CRISPR-associated protein Cas4, RecB family nuclease	COG01468	pfam01930	cd09637	TIGR00372									1		
arCOG04342	V	Defense mechanisms	Cas6	CRISPR-Cas system related protein Cas6, RAMP superfamily	COG01583	pfam01881	cd09652	TIGR01877									1		
arCOG00196	V	Defense mechanisms	CcmA	ABC-type multidrug transport system, ATPase component	COG01131	pfam00005	cd03230	TIGR03740	2	1	1			1	1	1		1	2
arCOG00194	V	Defense mechanisms	CcmA	ABC-type multidrug transport system, ATPase component	COG01131	pfam00005	cd03230	TIGR01188	7	7	6	2	1	1	6	3	5	4	6
arCOG02665	V	Defense mechanisms	Cmr3g5	CRISPR-Cas system related protein, RAMP superfamily Cas5 group	COG01769	pfam09700											1		
arCOG06487	V	Defense mechanisms	Csm2SS	CRISPR/Cas system CSM-associated protein Csm2, small subunit	COG01421	pfam03750	cd09647	TIGR01870									1		
arCOG02658	V	Defense mechanisms	Csm3g7	CRISPR-Cas system related protein, RAMP superfamily Cas7 group	COG01337	pfam03787	cd09683	TIGR02581									1		
arCOG03222	V	Defense mechanisms	Csm4g5	CRISPR-Cas system related protein, RAMP superfamily Cas5 group	COG01567		cd09663	TIGR01903									1		
arCOG03718	V	Defense mechanisms	Csm5g7	CRISPR/Cas system CSM-associated protein Csm5, group 7 of RAMP superfam	COG01332		cd09662	TIGR01899									1		
arCOG01449	V	Defense mechanisms	Csx1	CARF domain containing protein	COG01517			TIGR01884									1		
arCOG07641	V	Defense mechanisms	Csx1	CARF domain containing protein, contains HTH and HEPN domains	COG01517	pfam09455	cd09732	TIGR02221									1		
arCOG03847	V	Defense mechanisms	Csx1	CARF domain containing protein	COG01517												2		
arCOG00373	V	Defense mechanisms	DndD	DNA sulfur modification protein DndD, ATPase	COG01196	pfam13514		TIGR02169								1	1		
arCOG02632	V	Defense mechanisms	HsdM	Type I restriction-modification system methyltransferase subunit	COG00286	pfam12161,pfam02384		TIGR00497									1		2
arCOG03779	V	Defense mechanisms	McrB	GTPase subunit of restriction endonuclease	COG01401	pfam07728	cd00009		2	1	1					2	1		
arCOG05102	V	Defense mechanisms	McrC	McrBC 5-methylcytosine restriction system component	COG04268	pfam10117											1		
arCOG02841	V	Defense mechanisms	MdlB	ABC-type multidrug transport system, ATPase and permease component	COG01132	pfam00664,pfam0000	cd03253	TIGR02203	1	1		1	1				2	2	3
arCOG02777	V	Defense mechanisms	Mrr	Restriction endonuclease	COG01715	pfam04471												1	
arCOG01008	V	Defense mechanisms	NikR	Transcriptional regulator, CopG/Arc/MetJ family (DNA-binding and a metal-bi	COG00864	pfam08753		TIGR02793									1	1	1
arCOG02836	V	Defense mechanisms	NikR	Transcriptional regulator, CopG/Arc/MetJ family (DNA-binding and a metal-bi	COG00864												1		
arCOG00516	V	Defense mechanisms	NimA	Nitroimidazol reductase NimA or a related FMN-containing flavoprotein, pyri	COG03467	pfam01243		TIGR04023	1			1							
arCOG00525	V	Defense mechanisms	NimA	Nitroimidazol reductase NimA or a related FMN-containing flavoprotein, pyri	COG03467	pfam12724,pfam01243				2	1			1					
arCOG01731	V	Defense mechanisms	NorM	Na+-driven multidrug efflux pump	COG00534	pfam01554,pfam0155	cd13137	TIGR00797	1	1	1	1	1				3		
arCOG01663	V	Defense mechanisms	RelE	Cytotoxic translational repressor of toxin-antitoxin stability system	COG02026	pfam05016										1			
arCOG01665	V	Defense mechanisms	RelE	Cytotoxic translational repressor of toxin-antitoxin stability system	COG02026	pfam05016											3		
arCOG00922	V	Defense mechanisms	SalX	ABC-type antimicrobial peptide transport system, ATPase component	COG01136	pfam00005	cd03255	TIGR02673	3	2	3	1			2	2	2	4	7
arCOG02312	V	Defense mechanisms	SalY	ABC-type antimicrobial peptide transport system, permease component	COG00577	pfam02687		TIGR02212	1	1	1	1					2	2	3
arCOG02957	U	Intracellular trafficking, secretion, and vesicular tr	SBH1	Preprotein translocase subunit Sec61beta	COG04023	pfam03911			1	1					1	1	1		2
arCOG02673	U	Intracellular trafficking, secretion, and vesicular tr	-	OxaA/SpoJ/YidC translocase/secretase, sec-independent itegration of nascent	COG01422	pfam01956			1	2				1	1	1	1	1	1
arCOG04169	U	Intracellular trafficking, secretion, and vesicular tr	SecY	Preprotein translocase subunit SecY	COG00201	pfam10559,pfam00344		TIGR00967	1	2				1	1	1	1	1	2
arCOG01217	U	Intracellular trafficking, secretion, and vesicular tr	SEC65	Signal recognition particle 19 kDa protein	COG01400				1		1				1	1	1	1	2
arCOG04736	U	Intracellular trafficking, secretion, and vesicular tr	TatC	Sec-independent protein secretion pathway component TatC	COG00805	pfam00902,pfam00902		TIGR01912,TIGR01912						1	1	1			1
arCOG01739	U	Intracellular trafficking, secretion, and vesicular tr	LepB	Signal peptidase I	COG00681	pfam00717	cd06530	TIGR02228	1	1	1	1	1	1	1		1	1	2
arCOG02204	U	Intracellular trafficking, secretion, and vesicular tr	Sss1	Preprotein translocase subunit Sss1	COG02443				1	2	1	1		1	1		1	1	2
arCOG01919	U	Intracellular trafficking, secretion, and vesicular tr	TatC	Sec-independent protein secretion pathway component TatC	COG00805	pfam00902		TIGR00945	1	2		1			1			2	3
arCOG01228	U	Intracellular trafficking, secretion, and vesicular tr	Ffh	Signal recognition particle GTPase	COG00541	pfam02881,pfam0044	cd03115	TIGR00959		1	1	1			1		1	1	1
arCOG02694	U	Intracellular trafficking, secretion, and vesicular tr	TatA	Sec-independent protein secretion pathway component	COG01826			TIGR01411		2	1			1	1				1
arCOG04471	U	Intracellular trafficking, secretion, and vesicular tr	-	Exosortase	COG04083	pfam09721		TIGR04125							1		1	1	1
arCOG01227	U	Intracellular trafficking, secretion, and vesicular tr	FtsY	Signal recognition particle GTPase	COG00552	pfam02881,pfam0044	cd03115	TIGR00064	1								1	1	5
arCOG01997	U	Intracellular trafficking, secretion, and vesicular tr	MarC	Multiple antibiotic transporter	COG02095	pfam01914		TIGR00427									1		
arCOG03382	U	Intracellular trafficking, secretion, and vesicular tr	TolB	Periplasmic component of the Tol biopolymer transport system	COG00823	pfam00930		TIGR02800									1		
arCOG04816	U	Intracellular trafficking, secretion, and vesicular tr	-	TraG/TraD/VirD4 family enzyme, ATPase	COG03505	pfam12846											1		
arCOG07496	U	Intracellular trafficking, secretion, and vesicular tr	VirB4	Type IV secretory pathway, VirB4 component	COG03451												1		
arCOG03383	U	Intracellular trafficking, secretion, and vesicular tr	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,pfam0058	cd00796	TIGR02224								1	4	1	2
arCOG03473	X	Mobilome: prophages, transposons	-	Transposase	COG05421					2									
arCOG03989	X	Mobilome: prophages, transposons	XerC	XerD/XerC family integrase	COG00582	pfam00589	cd00397										1		
arCOG10214	X	Mobilome: prophages, transposons	-	Relaxase/mobilization nuclease domain-containing protein													1		
arCOG10424	X	Mobilome: prophages, transposons	GepA	Uncharacterized phage-associated protein	COG03600												1		
arCOG02751	X	Mobilome: prophages, transposons	-	Transposase, IS5 family	COG03039	pfam01609											10		
arCOG01915	O	Posttranslational modification, protein turnover, c	HflC	Membrane protease subunit, stomatin/prohibitin homolog	COG00330	pfam01145	cd08826	TIGR01933	1	1	1				1	1	1		1
arCOG01912	O	Posttranslational modification, protein turnover, c	-	Membrane protein implicated in regulation of membrane protease activity	COG01585	pfam01957			1	1	1				1	1	1		
arCOG01306	O	Posttranslational modification, protein turnover, c	RPT1	ATP-dependent 26S proteasome regulatory subunit	COG01222	pfam00004	cd00009	TIGR01242	1	1		1			1	1	1	2	3
arCOG06181	O	Posttranslational modification, protein turnover, c	TrxA	Thiol-disulfide isomerase or thioredoxin	COG00526	pfam00578	cd02966		1	1			1		1	1			
arCOG01341	O	Posttranslational modification, protein turnover, c	GIM5	Predicted prefoldin, molecular chaperone implicated in de novo protein foldi	COG01730	pfam02996	cd00584	TIGR00293	1	1					1	1	1		
arCOG00609	O	Posttranslational modification, protein turnover, c	RseP	Membrane-associated protease RseP, regulator of RpoE activity in bacteria	COG00750	pfam02163	cd06160		1	2	1	1	1	1	1	1	1		
arCOG02959	O	Posttranslational modification, protein turnover, c	Iap	Zn-dependent amino- or carboxypeptidase, M28 family	COG02234	pfam04389	cd05643		1	2					1	1		3	
arCOG00314	O	Posttranslational modification, protein turnover, c	TrxA	Thiol-disulfide isomerase or thioredoxin	COG00526	pfam00578	cd02969		1		1	1	1	1	1	1		1	2
arCOG04463	O	Posttranslational modification, protein turnover, c	-	Presenilin-like membrane protease, A22 family	COG03389	pfam06550			1		1	1	1		1	1	1	1	1
arCOG01257	O	Posttranslational modification, protein turnover, c	GroEL	Chaperonin GroEL, HSP60 family	COG00459	pfam00118	cd03343	TIGR02339	1		1	1		1	1	1	2	3	9
arCOG01833	O	Posttranslational modification, protein turnover, c	IbpA	Molecular chaperone (HSP20 family)	COG00071	pfam00011	cd06464		1			1		1	1	1	1		
arCOG01296	O	Posttranslational modification, protein turnover, c	TrxB	Thioredoxin reductase	COG00492	pfam07992		TIGR01292	2	1	1		1	2	1	1	2	1	4
arCOG04767	O	Posttranslational modification, protein turnover, c	PpiB	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	COG00652				2	2	1	2	1	1	1	1		3	3
arCOG06880	O	Posttranslational modification, protein turnover, c	DnaJ	DnaJ type Zn finger domain	COG00484			TIGR02349	2	2	2		1		1	1	1	1	4
arCOG02553	O	Posttranslational modification, protein turnover, c	AprE	Subtilisin-like serine protease	COG01404	pfam05048				2	1	1	1		1	1			
arCOG00980	O	Posttranslational modification, protein turnover, c	SlpA	FKBP-type peptidyl-prolyl cis-trans isomerase 2	COG01047	pfam00254									1	1	1	1	2
arCOG01139	O	Posttranslational modification, protein turnover, c	Rri1	Proteasome lid subunit RPN8/RPN11, contains Jab1/MPN domain metalloenz	COG01310	pfam14464	cd08072								1	1	1		
arCOG03610	O	Posttranslational modification, protein turnover, c	AprE	Subtilisin-like serine protease	COG01404		cd02619			1			1		1	2			3
arCOG01331	O	Posttranslational modification, protein turnover, c	HtpX	Zn-dependent protease with chaperone function	COG00501	pfam01435			1	1	1	1		1	1				
arCOG00971	O	Posttranslational modification, protein turnover, c	PRE1	20S proteasome, alpha subunit	COG00638	pfam10584,pfam0022	cd03756	TIGR03633	1	1	1		1		1		1	1	1
arCOG02436	O	Posttranslational modification, protein turnover, c	NosY	ABC-type transport system involved in multi-copper enzyme maturation, per	COG01277	pfam12679			1	1	1				1				
arCOG05153	O	Posttranslational modification, protein turnover, c	GroS	Co-chaperonin GroES (HSP10)	COG00234	pfam00166	cd00320		1	1					1				
arCOG05154	O	Posttranslational modification, protein turnover, c	GroEL	Chaperonin GroEL (HSP60 family)	COG00459	pfam00118	cd03344	TIGR02348	1	1					1				
arCOG02816	O	Posttranslational modification, protein turnover, c	MsrA	Peptide methionine sulfoxide reductase	COG00225	pfam01625		TIGR00401	1	2	1				1			1	3
arCOG00970	O	Posttranslational modification, protein turnover, c	PRE1	20S proteasome, beta subunit	COG00638	pfam00227	cd03764	TIGR03634	1		1	1	1	1	1		1	1	5

arCOG00270	O	Posttranslational modification, protein turnover, c	CcmF	Cytochrome c biogenesis factor	COG01138	pfam01578		TIGR00353	1			1			1			1	2
arCOG00310	O	Posttranslational modification, protein turnover, c	Bcp	Peroxiredoxin	COG01225	pfam00578	cd03018	TIGR03137	2	2					1		1	2	11
arCOG04560	O	Posttranslational modification, protein turnover, c	IscA	Fe-S cluster assembly iron-binding protein IscA	COG00316	pfam01521		TIGR00049	2	3		1	1		1			1	4
arCOG03607	O	Posttranslational modification, protein turnover, c	-	Cysteine protease, C1A family	COG04870	pfam00112	cd02619			1	1				1		1		
arCOG01845	O	Posttranslational modification, protein turnover, c	PaaD	Metal-sulfur cluster biosynthetic enzyme	COG02151	pfam01883		TIGR02945		1	1				1		2	1	1
arCOG04236	O	Posttranslational modification, protein turnover, c	SufC	Cysteine desulfurase activator ATPase	COG00396	pfam00005	cd03217	TIGR01978		1	1				1		2	1	1
arCOG04064	O	Posttranslational modification, protein turnover, c	RseP	Membrane-associated protease RseP, regulator of RpoE activity in bacteria	COG00750	pfam02163	cd06159	TIGR00054		1					1		1		2
arCOG01226	O	Posttranslational modification, protein turnover, c	ArgK	Putative periplasmic protein kinase ArgK or related GTPase of G3E family	COG01703	pfam03308	cd03114	TIGR00750							1		1	1	2
arCOG01308	O	Posttranslational modification, protein turnover, c	Cdc48	ATPase of the AAA+ class , CDC48 family	COG00464	pfam00004,pfam0000	cd00009,cd000	TIGR01243							1		2	2	4
arCOG00267	O	Posttranslational modification, protein turnover, c	CcmC	ABC-type transport system involved in cytochrome c biogenesis, permease co	COG00755	pfam01578		TIGR01191							1			1	1
arCOG02607	O	Posttranslational modification, protein turnover, c	GrxC	Glutaredoxin	COG00695	pfam00462	cd02976	TIGR02196							1			1	1
arCOG04957	O	Posttranslational modification, protein turnover, c	CcmE	Cytochrome c-type biogenesis protein CcmE	COG02332										1			1	3
arCOG02438	O	Posttranslational modification, protein turnover, c	NosY	ABC-type transport system involved in multi-copper enzyme maturation, perm	COG01277	pfam12679									1				
arCOG03614	O	Posttranslational modification, protein turnover, c	-	Cysteine protease, C1A family	COG04870	pfam00112	cd02619								1				
arCOG00065	O	Posttranslational modification, protein turnover, c	csdA	Selenocysteine lyase/Cysteine desulfurase	COG00520	pfam00266	cd06453	TIGR01979	3	5	4	1		1	2	1		4	2
arCOG00479	O	Posttranslational modification, protein turnover, c	CyoE	Polyprenyltransferase (cytochrome oxidase assembly factor)	COG00109	pfam01040	cd13957	TIGR01473		1					2	1		1	1
arCOG04142	O	Posttranslational modification, protein turnover, c	DYS1	Deoxyhypusine synthase	COG01899	pfam01916		TIGR00321	2	2	2	2	1	2	2	2	1	2	4
arCOG03669	O	Posttranslational modification, protein turnover, c	-	Subtilase family protease	COG04934	pfam09286	cd11377,cd04056		4	1	1	3	1	2	2	3	1		3
arCOG04772	O	Posttranslational modification, protein turnover, c	GrpE	Molecular chaperone GrpE (heat shock protein)	COG00576	pfam01025	cd00446		1	2	1			1	2		1	1	2
arCOG03060	O	Posttranslational modification, protein turnover, c	DnaK	Chaperone DnaK (HSP70)	COG00443	pfam00012	cd10234	TIGR02350	1	2	1			1	2		1	1	3
arCOG03103	O	Posttranslational modification, protein turnover, c	CtaA	Uncharacterized protein required for cytochrome oxidase assembly	COG01612	pfam02628			2	1	2		2		2			1	1
arCOG01972	O	Posttranslational modification, protein turnover, c	TrxA	Thiol-disulfide isomerase or thioredoxin	COG00526	pfam00085	cd02947	TIGR01068	2	2	1	1		1	2			2	3
arCOG01715	O	Posttranslational modification, protein turnover, c	SufB	Cysteine desulfurase activator SufB	COG00719	pfam01458		TIGR01981		2	2				2		1	2	2
arCOG00702	O	Posttranslational modification, protein turnover, c	AprE	Subtilisin-like serine protease	COG01404	pfam00082	cd07477	TIGR03921	5	6	4	4	4	1	5	2		3	7
arCOG02007	O	Posttranslational modification, protein turnover, c	-	Prenyltransferase family protein containing thioredoxin domain	COG01331	pfam03190	cd02955			1				1		1			
arCOG02834	O	Posttranslational modification, protein turnover, c	RseP	Membrane-associated protease RseP, regulator of RpoE activity in bacteria	COG00750	pfam02163,pfam1318	cd06159,cd009	TIGR00054						1		1		1	
arCOG00976	O	Posttranslational modification, protein turnover, c	Pcm	Protein-L-isoaspartate carboxylmethyltransferase	COG02518	pfam01135	cd02440	TIGR00080								1	1	1	2
arCOG03202	O	Posttranslational modification, protein turnover, c	-	Collagenase family protease	COG00826	pfam01297,pfam01136										1			
arCOG06807	O	Posttranslational modification, protein turnover, c	-	Cytochrome c biogenesis factor	COG01138											1			
arCOG02160	O	Posttranslational modification, protein turnover, c	LonB	Predicted ATP-dependent protease	COG01067	pfam01078,pfam13654,pfam05362		TIGR00764	1	1	1	1					1	1	2
arCOG00312	O	Posttranslational modification, protein turnover, c	AhpC	AhpC/TSA family peroxiredoxin	COG00450	pfam00578,pfam1041	cd03016	TIGR03137	1	1	1	1					1	1	
arCOG01342	O	Posttranslational modification, protein turnover, c	GimC	Prefoldin, chaperonin cofactor	COG01382	pfam01920	cd00632	TIGR02338	1	1							1		1
arCOG01328	O	Posttranslational modification, protein turnover, c	CcmB	ABC-type transport system involved in cytochrome c biogenesis, permease co	COG02386				1	1									
arCOG01846	O	Posttranslational modification, protein turnover, c	PaaD	Metal-sulfur cluster biosynthetic enzyme	COG02151	pfam01883,pfam0914	cd02037	TIGR02945,TIGR	1	1									
arCOG02815	O	Posttranslational modification, protein turnover, c	-	Conserved domain frequently associated with peptide methionine sulfoxide r	COG00229	pfam01641		TIGR00357	1	2									
arCOG00981	O	Posttranslational modification, protein turnover, c	SlpA	FKBP-type peptidyl-prolyl cis-trans isomerase 2	COG01047	pfam00254		TIGR00115	1			1					1	1	1
arCOG03580	O	Posttranslational modification, protein turnover, c	STE14	Putative protein-S-isoprenylcysteine methyltransferase	COG02020	pfam04191			1			1					1		
arCOG06823	O	Posttranslational modification, protein turnover, c	AprE	Subtilisin-like serine protease	COG01404	pfam00082	cd05562	TIGR03921	1									1	1
arCOG02173	O	Posttranslational modification, protein turnover, c	NrdG	Organic radical activating enzyme	COG00602	pfam13394	cd01335	TIGR03963		1							1	1	1
arCOG02962	O	Posttranslational modification, protein turnover, c	Iap	Zn-dependent amino- or carboxypeptidase, M28 family	COG02234	pfam04389	cd02690			1								1	
arCOG02443	O	Posttranslational modification, protein turnover, c	NosY	ABC-type transport system involved in multi-copper enzyme maturation, perm	COG01277	pfam12679				1									
arCOG03028	O	Posttranslational modification, protein turnover, c	NifU	Fe-S cluster biogenesis protein NfuA, 4Fe-4S-binding domain	COG00694	pfam01106		TIGR02000		1									
arCOG01297	O	Posttranslational modification, protein turnover, c	AhpF	Alkyl hydroperoxide reductase, large subunit	COG03634	pfam07992		TIGR03140			1								
arCOG02606	O	Posttranslational modification, protein turnover, c	GrxC	Glutaredoxin	COG00695	pfam00462	cd02976	TIGR02196				1							
arCOG10598	O	Posttranslational modification, protein turnover, c	-	ATP-dependent protease La PUA-like domain		pfam02190								1				1	1
arCOG00185	O	Posttranslational modification, protein turnover, c	GsiA	ABC-type glutathione transport system ATPase component, contains duplicate	COG01123	pfam00005,pfam0000	cd03225,cd032	TIGR03269									1	1	1
arCOG05850	O	Posttranslational modification, protein turnover, c	Pcp	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)	COG02039	pfam01470	cd00501	TIGR00504									1	1	
arCOG00164	O	Posttranslational modification, protein turnover, c	CysU	ABC-type sulfate transport system, permease component	COG00555		cd06261	TIGR02141									1		
arCOG00299	O	Posttranslational modification, protein turnover, c	-	DsbA family protein													1		
arCOG00636	O	Posttranslational modification, protein turnover, c	HypE	Hydrogenase maturation factor	COG00309	pfam00586,pfam0276	cd06061	TIGR02124									1		
arCOG00946	O	Posttranslational modification, protein turnover, c	PflA	Pyruvate-formate lyase-activating enzyme	COG01180	pfam04055	cd01335	TIGR04337									1		
arCOG01187	O	Posttranslational modification, protein turnover, c	HypF	Hydrogenase maturation factor	COG00068	pfam00708,pfam07503,pfam07503,pf		TIGR00143									1		
arCOG01218	O	Posttranslational modification, protein turnover, c	TrxA	Thiol-disulfide isomerase or thioredoxin	COG00526	pfam08484,pfam1319	cd02975,cd029	TIGR02187									1		
arCOG01716	O	Posttranslational modification, protein turnover, c	SufB	Cysteine desulfurase activator SufB	COG00719	pfam01458		TIGR01980									1		
arCOG01832	O	Posttranslational modification, protein turnover, c	IbpA	Molecular chaperone (HSP20 family)	COG00071	pfam00011	cd06464										1		
arCOG02162	O	Posttranslational modification, protein turnover, c	LonB	Predicted ATP-dependent protease	COG01067	pfam01078,pfam1324	cd00009,cd000	TIGR00764									1		
arCOG02737	O	Posttranslational modification, protein turnover, c	-	Predicted Fe-Mo cluster-binding protein, NifX family	COG01433	pfam02579	cd00562										1		
arCOG03689	O	Posttranslational modification, protein turnover, c	NosY	ABC-type transport system involved in multi-copper enzyme maturation, perm	COG01277												1		
arCOG04427	O	Posttranslational modification, protein turnover, c	HypC	Hydrogenase maturation factor	COG00298	pfam01455		TIGR00074									1		
arCOG04428	O	Posttranslational modification, protein turnover, c	HypD	Hydrogenase maturation factor	COG00409	pfam01924		TIGR00075									1		
arCOG00322	O	Posttranslational modification, protein turnover, c	TldE	Inactivated Zn-dependent protease, component of TldD/TldE system	COG00312	pfam01523											2	1	1
arCOG00321	O	Posttranslational modification, protein turnover, c	TldD	Zn-dependent protease, component of TldD/TldE system	COG00312	pfam01523											2	1	
arCOG03685	O	Posttranslational modification, protein turnover, c	-	Predicted redox protein, regulator of disulfide bond formation	COG01765	pfam02566											2	1	
arCOG00952	O	Posttranslational modification, protein turnover, c	PflA	Pyruvate-formate lyase-activating enzyme	COG01180	pfam04055		TIGR02494									2		
arCOG04933	O	Posttranslational modification, protein turnover, c	-	Serine protease inhibitor	COG04826	pfam00079	cd00172										2		
arCOG02734	O	Posttranslational modification, protein turnover, c	-	Predicted Fe-Mo cluster-binding protein, NifX family	COG01433	pfam02579	cd00851										4		
arCOG07441	O	Posttranslational modification, protein turnover, c	SurA	Parvulin-like peptidyl-prolyl isomerase	COG00760	pfam00639		TIGR02933										1	1
arCOG01929	O	Posttranslational modification, protein turnover, c	XdhC	Xanthine and CO dehydrogenase maturation factor, XdhC/CoxF family	COG01975	pfam13478												1	2
arCOG04648	O	Posttranslational modification, protein turnover, c	-	Glutaredoxin-related protein	COG00278	pfam00462	cd03028	TIGR00365										1	2
arCOG02784	O	Posttranslational modification, protein turnover, c	SRAP	Putative SOS response-associated peptidase YedK	COG02135	pfam02586												1	
arCOG02846	O	Posttranslational modification, protein turnover, c	DnaJ	DnaJ-class molecular chaperone	COG00484	pfam00226	cd06257	TIGR02349										1	
arCOG03947	O	Posttranslational modification, protein turnover, c	clpA	ATP-binding subunits of Clp protease and DnaK/DnaJ chaperones	COG00542	pfam02861,pfam0286	cd00009,cd000	TIGR03346										1	
arCOG04712	O	Posttranslational modification, protein turnover, c	ECM4	Predicted glutathione S-transferase	COG00435	pfam13409,pfam1341	cd03190											1	
arCOG03026	O	Posttranslational modification, protein turnover, c	NifU	Fe-S cluster biogenesis protein NfuA, 4Fe-4S-binding domain	COG00694	pfam01106		TIGR02000											1
arCOG01153	T	Signal transduction mechanisms	CpdA	3',5'-cyclic AMP phosphodiesterase CpdA	COG01409	pfam00149,pfam0145	cd07400,cd001	TIGR00040,TIGR02689		1					1	1			
arCOG02985	T	Signal transduction mechanisms	-	Membrane proteinase of CAAX superfamily, regulator of anti-sigma factor	COG02339	pfam13367			2	2	1	1	1		2	1	1	1	2
arCOG04425	T	Signal transduction mechanisms	Wzb	Protein-tyrosine-phosphatase	COG00394	pfam01451	cd00115	TIGR02689		2				1	2	1		1	4
arCOG01171	T	Signal transduction mechanisms	RAD55	RecA-superfamily ATPase implicated in signal transduction	COG00467	pfam06745	cd01124	TIGR03877	2	2					2	2	10	3	
arCOG02967	T	Signal transduction mechanisms	-	NACHT family NTPase fused to HEAT repeats domain	COG05635	pfam13646,pfam13646			1	1	1	2				1		1	
arCOG02053	T	Signal transduction mechanisms	UspA	Nucleotide-binding protein, UspA family	COG00589	pfam00582	cd00293		1							1	1		
arCOG05374	T	Signal transduction mechanisms	-	GAF domain-containing protein	COG01956	pfam13185			1							1			

arCOG06712	T	Signal transduction mechanisms	AtoS	Sensory protein, contains PAS domain	COG02202	pfam13426	cd00130	TIGR00229				1		1		1	3		
arCOG02333	T	Signal transduction mechanisms	-	Signal transduction histidine kinase, contains REC and PAS domains	COG00642	pfam13492,pfam0051	cd00082,cd000	TIGR02966								1			
arCOG04809	T	Signal transduction mechanisms	-	Signal transduction histidine kinase	COG00642	pfam00512,pfam0251	cd00082,cd000	TIGR02956								1			
arCOG01180	T	Signal transduction mechanisms	RIO1	Serine/threonine protein kinase involved in cell cycle control	COG01718	pfam01163	cd05145	TIGR03724	1	1		1					1	1	2
arCOG04820	T	Signal transduction mechanisms	-	SOUL heme-binding protein		pfam04832				1	1	1		1					1
arCOG06193	T	Signal transduction mechanisms	-	Signal transduction histidine kinase and PAS domains	COG00642	pfam13426,pfam1342	cd00130,cd001	TIGR00229,TIGR00229,TI		1									
arCOG04453	T	Signal transduction mechanisms	DisA_N	Diadenylate cyclase (c-di-AMP synthetase), DisA_N domain	COG01624	pfam02457											1	1	
arCOG03799	T	Signal transduction mechanisms	AtoS	GAF, PAS/PAC domains containing signal transduction protein	COG02202	pfam05763											1	2	1
arCOG00449	T	Signal transduction mechanisms	UspA	Nucleotide-binding protein, UspA family	COG00589	pfam00582,pfam0058	cd00293,cd00293										1		
arCOG01172	T	Signal transduction mechanisms	RAD55	RecA-superfamily ATPase implicated in signal transduction	COG00467	pfam06745		TIGR03881									1		
arCOG01173	T	Signal transduction mechanisms	RAD55	RecA-superfamily ATPase implicated in signal transduction	COG00467	pfam06745	cd01393	TIGR03880									1		
arCOG01174	T	Signal transduction mechanisms	RAD55	RecA-superfamily ATPase implicated in signal transduction	COG00467	pfam06745	cd01124	TIGR03877									1		
arCOG02327	T	Signal transduction mechanisms	-	Signal transduction histidine kinase, contains PAS domain	COG00642	pfam13426,pfam0251	cd00130,cd000	TIGR02966									1		
arCOG02385	T	Signal transduction mechanisms	CheY	Rec domain	COG00784	pfam00072	cd00156	TIGR01818									1		
arCOG03803	T	Signal transduction mechanisms	-	Membrane assicated inactivated KaiC-like ATPase, DUF835 family	SC.00096	pfam05763											1		
arCOG03804	T	Signal transduction mechanisms	-	Membrane assicated inactivated KaiC-like ATPase, DUF835 family	SC.00096	pfam05763											1		
arCOG04404	T	Signal transduction mechanisms	-	Cell fate regulator YlbF, YheA/YmcA/DUF963 family (controls sporulation, com	COG03679	pfam06133											1		
arCOG06538	T	Signal transduction mechanisms	-	Signal transduction histidine kinase	COG00642			TIGR00229,TIGR02956									1		
arCOG01143	T	Signal transduction mechanisms	ApaH	Serine/threonine protein phosphatase PP2A family	COG00639	pfam00149	cd00144										2	2	
arCOG01178	T	Signal transduction mechanisms	GvpD	GvpD gas vesicle protein, contains RecA/KaiC family ATPase domain	COG00467	pfam07088	cd01124	TIGR02655									2		
arCOG02391	T	Signal transduction mechanisms	CheY	Rec domain	COG00784	pfam00072	cd00156	TIGR02154									3	1	5
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	
arCOG00451	T	Signal transduction mechanisms	UspA	Nucleotide-binding protein, UspA family	COG00589													2	2
arCOG01992	T	Signal transduction mechanisms	SixA	Phosphohistidine phosphatase SixA	COG02062	pfam00300	cd07067	TIGR00249											1
arCOG04647	T	Signal transduction mechanisms	BolA	Stress-induced morphogen (activity unknown)	COG00271	pfam01722													1
arCOG06801	T	Signal transduction mechanisms	SrkA	Ser/Thr protein kinase RdoA involved in Cpx stress response, MazF antagonist	COG02334	pfam01636	cd05153												3

METABOLISM																			
arCOG01768	E	Amino acid transport and metabolism	GlpG	Membrane associated serine protease	COG00705	pfam01694			1	1	1	1	1		1	1	1	1	1
arCOG04671	E	Amino acid transport and metabolism	HutH	Histidine ammonia-lyase	COG02986	pfam00221	cd00332	TIGR01225	1	1	1	1	1		1	1	1	1	3
arCOG04247	E	Amino acid transport and metabolism	YpwA	Zn-dependent carboxypeptidase, M32 family	COG02317	pfam02074	cd06460		1	1	1		1	2	1	1	1	1	2
arCOG01352	E	Amino acid transport and metabolism	GdhA	Glutamate dehydrogenase/leucine dehydrogenase	COG00334	pfam02812,pfam0020	cd01076		1	1	1				1	1	1	1	2
arCOG00751	E	Amino acid transport and metabolism	DppB	ABC-type dipeptide/oligopeptide/nickel transport system, permease compone	COG00601	pfam00528	cd06261	TIGR02789	1	1		1	1		1	1	5		
arCOG03109	E	Amino acid transport and metabolism	DdaH	N-Dimethylarginine dimethylaminohydrolase	COG01834	pfam02274		TIGR01078	1	2	1	1	1	1	1	1	1	1	3
arCOG06678	E	Amino acid transport and metabolism	Ald	Alanine dehydrogenase	COG00686	pfam05222,pfam0126	cd05304	TIGR00561	1	2	1	1	1	1	1	1		1	5
arCOG09400	E	Amino acid transport and metabolism	PntB	NAD(P) transhydrogenase beta subunit	COG01282	pfam02233			1	2	1	1	1	1	1	1		1	5
arCOG00184	E	Amino acid transport and metabolism	AppF	ABC-type oligopeptide transport system, ATPase component	COG04608	pfam00005	cd03257	TIGR02769	1	2		1	1		1	1	4		
arCOG01700	E	Amino acid transport and metabolism	SpeB	Arginase family enzyme	COG00010	pfam00491	cd11593	TIGR01230	1		1			1	1	1	1	1	3
arCOG05395	E	Amino acid transport and metabolism	FtcD	Formiminotetrahydrofolate cyclodeaminase	COG03404				1		1				1	1	1	2	5
arCOG00181	E	Amino acid transport and metabolism	DppD	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	COG00444	pfam00005	cd03257	TIGR02770	1			1	1		1	1	4		
arCOG01430	E	Amino acid transport and metabolism	CysK	Cysteine synthase	COG00031	pfam00291	cd01561	TIGR01136							1	1	1	1	
arCOG00915	E	Amino acid transport and metabolism	GabT	4-aminobutyrate aminotransferase or related aminotransferase	COG00160	pfam00202	cd00610	TIGR00707							1	1	2		
arCOG00095	E	Amino acid transport and metabolism	GltB	Glutamate synthase domain 1	COG00067	pfam00310	cd01907	TIGR01134							1	1		1	
arCOG04670	E	Amino acid transport and metabolism	HutU	Urocanate hydratase	COG02987	pfam01175		TIGR01228	1	1	1	1			1		1	1	2
arCOG01948	E	Amino acid transport and metabolism	RhtB	Threonine efflux protein	COG01280	pfam01810		TIGR00949	1	1	1	1			1			1	2
arCOG00243	E	Amino acid transport and metabolism	LYS9	Saccharopine dehydrogenase or related enzyme	COG01748	pfam03435			1	1	1	1			1			1	3
arCOG01158	E	Amino acid transport and metabolism	SerB	Phosphoserine phosphatase	COG00560	pfam00702		TIGR01491	1	1	1	1			1			3	2
arCOG01924	E	Amino acid transport and metabolism	AnsB	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D	COG00252	pfam00710	cd08962	TIGR02153	1	1		1			1		1	1	2
arCOG01888	E	Amino acid transport and metabolism	AmpS	Leucyl aminopeptidase (aminopeptidase T)	COG02309	pfam02073			1	1		1			1				2
arCOG04897	E	Amino acid transport and metabolism	-	Aspartate/tyrosine/aromatic aminotransferase	COG00436	pfam00155	cd00609	TIGR01141	1	2	1	1			1				
arCOG00924	E	Amino acid transport and metabolism	LivF	ABC-type branched-chain amino acid transport system, ATPase component	COG00410	pfam00005	cd03224	TIGR03410	1	2			1		1			1	1
arCOG00925	E	Amino acid transport and metabolism	LivG	ABC-type branched-chain amino acid transport system, ATPase component	COG00411	pfam00005	cd03219	TIGR03411	1	2			1		1			1	1
arCOG01021	E	Amino acid transport and metabolism	LivK	ABC-type branched-chain amino acid transport system, periplasmic compone	COG00683	pfam13458	cd06268		1	2			1		1			1	1
arCOG01273	E	Amino acid transport and metabolism	LivM	ABC-type branched-chain amino acid transport system, permease component	COG04177	pfam02653	cd06581		1	2					1			1	
arCOG00912	E	Amino acid transport and metabolism	ArgF	Ornithine carbamoyltransferase	COG00078	pfam02729,pfam00185		TIGR00658	1		1	1	1	1	1		1	1	
arCOG04758	E	Amino acid transport and metabolism	PepF	Oligoendopeptidase F	COG01164	pfam08439,pfam0143	cd09608	TIGR00181	1		1	1	1	1	1				1
arCOG01646	E	Amino acid transport and metabolism	DAP2	Dipeptidyl aminopeptidase/acylaminoacyl-peptidase	COG01506	pfam07859	cd00312		3	2	3	2		1	1		1	2	5
arCOG00071	E	Amino acid transport and metabolism	AsnB	Asparagine synthase (glutamine-hydrolyzing)	COG00367	pfam00733	cd01991	TIGR01536		1	1	1	1	1	1		1	1	2
arCOG00076	E	Amino acid transport and metabolism	GcvP	Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain	COG01003	pfam02347	cd00613	TIGR00461		1	1	1			1		1	1	1
arCOG01319	E	Amino acid transport and metabolism	PutP	Na+/proline symporter	COG00591	pfam00474	cd11474	TIGR00813		1	1				1				1
arCOG04779	E	Amino acid transport and metabolism	IaaA	Isoaspartyl peptidase or L-asparaginase, Ntn-hydrolase superfamily	COG01446	pfam01112	cd14950			1					1		1		1
arCOG00863	E	Amino acid transport and metabolism	ArcC	Carbamate kinase	COG00549	pfam00696	cd04235	TIGR00746							1		1	1	4
arCOG01534	E	Amino acid transport and metabolism	DdpA	ABC-type transport system, periplasmic component	COG00747	pfam00496	cd08519	TIGR02294							1		3		
arCOG04333	E	Amino acid transport and metabolism	-	Aspartate/tyrosine/aromatic aminotransferase	COG00436	pfam00155	cd00609	TIGR03947							1				
arCOG00088	E	Amino acid transport and metabolism	PuuD	Gamma-glutamyl-gamma-aminobutyrate hydrolase PuuD (putrescine degrada	COG02071	pfam07722	cd01745	TIGR00888	1	1	1	1	1	1	2	1			4
arCOG00060	E	Amino acid transport and metabolism	MetC	Cystathionine beta-lyase/cystathionine gamma-synthase	COG00626	pfam01053	cd00614	TIGR02080	1	1					2	1		2	2
arCOG01107	E	Amino acid transport and metabolism	ArgE	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase or relate	COG00624	pfam01546	cd05650	TIGR01910		2					2	1	2		
arCOG02706	E	Amino acid transport and metabolism	GloA	Lactoylglutathione lyase or related enzyme	COG00346	pfam13669	cd07249	TIGR03081	2	1			1	1	2	2	1	1	1
arCOG00096	E	Amino acid transport and metabolism	GltB	Glutamate synthase domain 3	COG00070	pfam01493	cd00981	TIGR03122	1	1	1	1		1	2				1
arCOG05229	E	Amino acid transport and metabolism	PepD	Di- or tripeptidase	COG02195		cd03890	TIGR01893	1	1	1	1		1	2				
arCOG02297	E	Amino acid transport and metabolism	IlvE	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lya	COG00115	pfam01063	cd01558	TIGR01122	2	2	1	1			2			2	2
arCOG01000	E	Amino acid transport and metabolism	PepP	Xaa-Pro aminopeptidase	COG00006	pfam01321,pfam0055	cd01092	TIGR00500	2	1		1			3	1	3	2	5
arCOG01130	E	Amino acid transport and metabolism	-	Aspartate/tyrosine/aromatic aminotransferase	COG00436	pfam00155	cd00609	TIGR03540	2	3	2	1			3		3	2	6
arCOG04490	E	Amino acid transport and metabolism	PdaD	Pyruvoyl-dependent arginine decarboxylase (PvlArgDC)	COG01945	pfam01862		TIGR00286	1	1	1	1	1			1	1		
arCOG01533	E	Amino acid transport and metabolism	DdpA	ABC-type transport system, periplasmic component	COG00747	pfam00496	cd08512		1	1	1	1	2			1			
arCOG01594	E	Amino acid transport and metabolism	CarB	Carbamoylphosphate synthase large subunit	COG00458	pfam00289,pfam02786,pfam02787,pf		TIGR01369	1	1	1		1			1		1	1
arCOG00458	E	Amino acid transport and metabolism	-	Archaemetzincin family protease	COG01913	pfam07998	cd11375		1	1		1				1			
arCOG02165	E	Amino acid transport and metabolism	-	Transglutaminase-like cysteine protease	COG01305	pfam01841			1	1						1	1	1	
arCOG00064	E	Amino acid transport and metabolism	CarA	Carbamoylphosphate synthase small subunit	COG00505	pfam00988,pfam0011	cd01744	TIGR01368	1		1		1			1		1	1

arCOG01431	E	Amino acid transport and metabolism	IlvA	Threonine dehydratase	COG01171	pfam00291	cd01562,cd048	TIGR01127	1		1			1		1			
arCOG00923	E	Amino acid transport and metabolism	GlnQ	ABC-type polar amino acid transport system, ATPase component	COG01126		cd03262	TIGR03005						1		1			2
arCOG00771	E	Amino acid transport and metabolism	-	CubicO group peptidase, beta-lactamase class C family	COG01680	pfam00144										1			
arCOG01798	E	Amino acid transport and metabolism	HisM	ABC-type amino acid transport system, permease component	COG00765	pfam00528	cd06261	TIGR03003						2		2			3
arCOG00914	E	Amino acid transport and metabolism	ArgD	Ornithine/acetylornithine aminotransferase	COG04992	pfam00202	cd00610	TIGR00707	1	1	1	1	1					1	1
arCOG01909	E	Amino acid transport and metabolism	GlnA	Glutamine synthetase	COG00174	pfam00120		TIGR03105	1	1	1	1					2	1	2
arCOG00756	E	Amino acid transport and metabolism	GcvT	Glycine cleavage system T protein (aminomethyltransferase)	COG00404	pfam01571,pfam08669		TIGR00528	1	1		1					1	1	1
arCOG01303	E	Amino acid transport and metabolism	GcvH	Glycine cleavage system H protein (lipoate-binding)	COG00509	pfam01597	cd06848	TIGR00527	1	1		1					1	2	5
arCOG06322	E	Amino acid transport and metabolism	PutA	Proline dehydrogenase	COG00506	pfam01619			1	1		1						1	
arCOG00755	E	Amino acid transport and metabolism	DadA	Glycine/D-amino acid oxidase (deaminating)	COG00665	pfam01266			1	1							1		2
arCOG01947	E	Amino acid transport and metabolism	RhtB	Threonine efflux protein	COG01280	pfam01810			1	2									
arCOG01110	E	Amino acid transport and metabolism	ArgE	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase or relate	COG00624	pfam01546	cd05681	TIGR01910	1		1		1						1
arCOG02767	E	Amino acid transport and metabolism	-	Metal-dependent membrane protease, CAAX family	COG01266	pfam02517			1		1			1					
arCOG03600	E	Amino acid transport and metabolism	-	Transglutaminase-like cysteine protease	COG01305				1		1								
arCOG00177	E	Amino acid transport and metabolism	PotA	ABC-type spermidine/putrescine transport system, ATPase component	COG03842	pfam00005	cd03301	TIGR03265	1			1							1
arCOG03101	E	Amino acid transport and metabolism	GloA	Lactoylglutathione lyase or related enzyme	COG00346	pfam00903	cd08346		1			1							
arCOG14875	E	Amino acid transport and metabolism	-	Aspartyl protease		pfam05618			1				1						1
arCOG01316	E	Amino acid transport and metabolism	PutP	Na+/proline symporter	COG00591	pfam00474	cd10322	TIGR00813	2	1							1	1	3
arCOG00027	E	Amino acid transport and metabolism	MfnA	L-tyrosine decarboxylase, PLP-dependent protein	COG00076	pfam00282	cd06450	TIGR03812		1							1	1	
arCOG07760	E	Amino acid transport and metabolism	-	Peptidase family C25		pfam01364	cd02258			1							1		
arCOG01512	E	Amino acid transport and metabolism	HyuB	N-methylhydantoinase B/acetone carboxylase, alpha subunit	COG00146	pfam02538				1									
arCOG01949	E	Amino acid transport and metabolism	ArgO	Lysine/arginine efflux permease	COG01279	pfam01810		TIGR00948		1									
arCOG05121	E	Amino acid transport and metabolism	TesA	Lysophospholipase L1 or related esterase	COG02755					1									
arCOG00121	E	Amino acid transport and metabolism	AsnB	Asparagine synthase (glutamine-hydrolyzing)	COG00367	pfam00733						1							
arCOG03999	E	Amino acid transport and metabolism	-	Clostripain family peptidase, C11		pfam03415		TIGR02806				1							
arCOG01269	E	Amino acid transport and metabolism	LivH	Branched-chain amino acid ABC-type transport system, permease component	COG00559	pfam02653	cd06582	TIGR03409					1						1
arCOG03611	E	Amino acid transport and metabolism	-	Peptidase C1A subfamily			cd08546,cd14254							1				2	
arCOG01596	E	Amino acid transport and metabolism	CarB	Carbamoylphosphate synthase large subunit	COG00458	pfam15632		TIGR01205						1					
arCOG00077	E	Amino acid transport and metabolism	GcvP	Glycine cleavage system protein P (pyridoxal-binding), N-terminal domain	COG00403	pfam02347	cd00613	TIGR00461									1	1	1
arCOG01434	E	Amino acid transport and metabolism	ThrC	Threonine synthase and cysteate synthase	COG00498	pfam01155,pfam0029	cd01563	TIGR02605,TIGR00260									1	1	1
arCOG00279	E	Amino acid transport and metabolism	SpeD	S-adenosylmethionine decarboxylase/arginine decarboxylase	COG01586	pfam02675		TIGR03330									1	1	2
arCOG00073	E	Amino acid transport and metabolism	CysH	PAPS reductase related enzyme fused to RNA-binding PUA domain and ferred	COG00175	pfam01507	cd01713	TIGR00434									1		2
arCOG00009	E	Amino acid transport and metabolism	PotE	Amino acid transporter	COG00531	pfam00324		TIGR00909									1		
arCOG00050	E	Amino acid transport and metabolism	SpeE	Spermidine synthase	COG00421	pfam01564	cd02440	TIGR00417									1		
arCOG00092	E	Amino acid transport and metabolism	LdcC	Arginine/lysine/ornithine decarboxylase	COG01982	pfam03709,pfam0127	cd00615	TIGR04301									1		
arCOG00304	E	Amino acid transport and metabolism	HIS2	Histidinol phosphatase or related hydrolase of the PHP family	COG01387	pfam02811	cd12110	TIGR01856									1		
arCOG01123	E	Amino acid transport and metabolism	MtnA	Methylthioribose-1-phosphate isomerase (methionine salvage pathway), a pa	COG00182	pfam01008		TIGR00512									1		
arCOG01292	E	Amino acid transport and metabolism	GltD	NADPH-dependent glutamate synthase beta chain or related oxidoreductase	COG00493	pfam07992		TIGR01316									1		
arCOG01647	E	Amino acid transport and metabolism	-	Serine protease of the peptidase family S9A	COG01505	pfam00326											1		
arCOG01678	E	Amino acid transport and metabolism	MetK	Archaeal S-adenosylmethionine synthetase	COG01812	pfam01941											1		
arCOG02167	E	Amino acid transport and metabolism	-	Transglutaminase-like cysteine protease	COG01305	pfam01841											1		
arCOG02766	E	Amino acid transport and metabolism	-	Metal-dependent membrane protease, CAAX family	COG01266	pfam02517											1		
arCOG03602	E	Amino acid transport and metabolism	PepD	Dipeptidase family C69	COG04690	pfam03577											1		
arCOG03672	E	Amino acid transport and metabolism	-	Thermopsin-like protease	SC.00065	pfam05317,pfam06832											1		
arCOG05065	E	Amino acid transport and metabolism	CdsB	L-cysteine desulfidase	COG03681	pfam03313											1		
arCOG05363	E	Amino acid transport and metabolism	-	CAAX family protease, possibly associated with type IV pili like system	COG01266	pfam02517											1		
arCOG05808	E	Amino acid transport and metabolism	DUR1	Allophanate hydrolase subunit 2	COG01984	pfam02626		TIGR00724									1		
arCOG05809	E	Amino acid transport and metabolism	DUR1	Allophanate hydrolase subunit 1	COG02049	pfam02682		TIGR00370									1		
arCOG07546	E	Amino acid transport and metabolism	-	Zincin superfamily protease													1		
arCOG10063	E	Amino acid transport and metabolism	SdaC	Tryptophan/tyrosine permease family	COG00814	pfam03222		TIGR00837									1		
arCOG13501	E	Amino acid transport and metabolism	-	Serine dehydratase beta chain		pfam03315	cd04879	TIGR00719									1		
arCOG00070	E	Amino acid transport and metabolism	GlyA	Glycine/serine hydroxymethyltransferase	COG00112	pfam00464	cd00378										2	1	1
arCOG01698	E	Amino acid transport and metabolism	LeuC	Homoaconitate hydratase/3-isopropylmalate dehydratase large subunit famil	COG00065	pfam00330	cd01583	TIGR02086									3	1	4
arCOG02230	E	Amino acid transport and metabolism	LeuD	3-isopropylmalate dehydratase small subunit	COG00066	pfam00694	cd01577	TIGR02087									3		
arCOG00748	E	Amino acid transport and metabolism	DppC	ABC-type dipeptide/oligopeptide/nickel transport system, permease compone	COG01173	pfam12911,pfam0052	cd06261	TIGR02790									5		
arCOG00494	E	Amino acid transport and metabolism	Asd	Aspartate-semialdehyde dehydrogenase	COG00136	pfam01118,pfam02774		TIGR00978										1	1
arCOG02014	E	Amino acid transport and metabolism	TrpE	Anthranilate/para-aminobenzoate synthase component I	COG00147	pfam04715,pfam00425		TIGR01820										1	1
arCOG02097	E	Amino acid transport and metabolism	AroD	3-dehydroquinate dehydratase	COG00710	pfam01487	cd00502	TIGR01093										1	1
arCOG04134	E	Amino acid transport and metabolism	AroA	5-enolpyruvylshikimate-3-phosphate synthase	COG00128	pfam00275	cd01556	TIGR01356										1	1
arCOG06005	E	Amino acid transport and metabolism	-	Predicted metalloprotease, contains C-terminal PDZ domain	COG03975	pfam05299,pfam1318	cd00990	TIGR02037										1	1
arCOG07384	E	Amino acid transport and metabolism	HisB	Histidinol phosphatase or related phosphatase	COG00241	pfam13242	cd01427	TIGR01656										1	1
arCOG01025	E	Amino acid transport and metabolism	AroK2	Archaeal shikimate kinase	COG01685	pfam00288		TIGR01920										1	2
arCOG01131	E	Amino acid transport and metabolism	-	Aspartate/tyrosine/aromatic aminotransferase	COG00436	pfam00155	cd00609	TIGR01265										1	2
arCOG04133	E	Amino acid transport and metabolism	AroC	Chorismate synthase	COG00082	pfam01264	cd07304	TIGR00033										1	2
arCOG04353	E	Amino acid transport and metabolism	-	3-dehydroquinate synthase	COG01465	pfam01959												1	2
arCOG02092	E	Amino acid transport and metabolism	LeuA	Isopropylmalate/homocitrate/citramalate synthase	COG00119	pfam00682,pfam0103	cd07940	TIGR02146										1	3
arCOG04322	E	Amino acid transport and metabolism	PepB	Leucyl aminopeptidase	COG00260	pfam02789,pfam0088	cd00433											1	3
arCOG01890	E	Amino acid transport and metabolism	AmpS	Leucyl aminopeptidase (aminopeptidase T)	COG02309	pfam02073												1	4
arCOG00861	E	Amino acid transport and metabolism	LysC	Aspartokinase	COG00527													1	
arCOG01459	E	Amino acid transport and metabolism	Tdh	Threonine dehydrogenase or related Zn-dependent dehydrogenase	COG01063	pfam08240,pfam0010	cd08235	TIGR00692										1	
arCOG02769	E	Amino acid transport and metabolism	-	Metal-dependent membrane protease, CAAX family	COG01266	pfam02517												1	
arCOG04044	E	Amino acid transport and metabolism	-	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonic acid synthase, DhnA-aldolase fa	COG01830	pfam01791	cd00958	TIGR01949										2	4
arCOG00619	E	Amino acid transport and metabolism	GltB	Glutamate synthase domain 2 and ferredoxin domain	COG00069	pfam01645	cd02808												1
arCOG01033	E	Amino acid transport and metabolism	AroE	Shikimate 5-dehydrogenase	COG00169	pfam08501,pfam0148	cd01065	TIGR00507											1
arCOG01799	E	Amino acid transport and metabolism	HisJ	ABC-type amino acid transport/signal transduction system, periplasmic compo	COG00834	pfam00497	cd13624	TIGR01096											1
arCOG04273	E	Amino acid transport and metabolism	HisC	Histidinol-phosphate/aromatic aminotransferase or cobyric acid decarboxylas	COG00079	pfam00155	cd00609	TIGR01140											1
arCOG00757	E	Amino acid transport and metabolism	GcvT	Glycine cleavage system T protein (aminomethyltransferase)	COG00404	pfam01571,pfam08669		TIGR00528											2
arCOG01122	G	Carbohydrate transport and metabolism	RpiA	Ribose 5-phosphate isomerase	COG00120	pfam06026	cd01398	TIGR00021	1	1		1			1	1	1	1	3
arCOG00767	G	Carbohydrate transport and metabolism	{ManB}	Phosphomannomutase	COG01109	pfam02878,pfam0287	cd03087	TIGR03990	1		1	1		1	1	1	3	2	3
arCOG00493	G	Carbohydrate transport and metabolism	GapA	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydro	COG00057	pfam00044,pfam02800		TIGR01546	1		1				1	1	1	1	2
arCOG00052	G	Carbohydrate transport and metabolism	Pgi	Glucose-6-phosphate isomerase	COG00166	pfam01380,pfam1043	cd05017,cd056	TIGR02128	1		1				1	1		1	1

arCOG04170	G	Carbohydrate transport and metabolism	GckA	Glycerate kinase	COG02379	pfam13660,pfam05161									1	1	1		
arCOG04961	G	Carbohydrate transport and metabolism	GlpX	Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisphosphatase or related pr	COG01494	pfam03320	cd01516	TIGR00330							1	1		1	4
arCOG00274	G	Carbohydrate transport and metabolism	RhaT	Permease of the drug/metabolite transporter (DMT) superfamily	COG00697	pfam00892,pfam00892		TIGR00950							1	1			2
arCOG01349	G	Carbohydrate transport and metabolism	SuhB	Archaeal fructose-1,6-bisphosphatase or related enzyme of inositol monopho	COG00483	pfam00459	cd01642	TIGR01331	1	1	1		1	1	1	3	1		2
arCOG00014	G	Carbohydrate transport and metabolism	RbsK	Sugar kinase, ribokinase family	COG00524	pfam00294	cd01174	TIGR02152	1	2	1	1	1	1	1	3	1	2	6
arCOG01993	G	Carbohydrate transport and metabolism	GpmA	Phosphoglycerate mutase 1	COG00588	pfam00300	cd07067	TIGR01258	1	1	1		1	2	1			1	2
arCOG04431	G	Carbohydrate transport and metabolism	GlpF	Glycerol uptake facilitator or related permease (Major Intrinsic Protein Family	COG00580	pfam00230	cd00333	TIGR00861	1	1		1			1			1	2
arCOG01087	G	Carbohydrate transport and metabolism	TpiA	Triosephosphate isomerase	COG00149	pfam00121	cd00311	TIGR00419	1	1					1		1	1	1
arCOG05046	G	Carbohydrate transport and metabolism	Rpe	Pentose-5-phosphate-3-epimerase	COG00036	pfam00834	cd00429	TIGR01163		1	1	1			1		1	1	3
arCOG00130	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174			1	1	1			1		4	1	1
arCOG01169	G	Carbohydrate transport and metabolism	Eno	Enolase	COG00148	pfam03952,pfam0011	cd03313	TIGR01060		1		1	1	1	1		1	1	2
arCOG01111	G	Carbohydrate transport and metabolism	PpsA	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	COG00574	pfam01326,pfam00391,pfam02896		TIGR01418	1	2	1	1	1	1	2	1	1		
arCOG00496	G	Carbohydrate transport and metabolism	Pgk	3-phosphoglycerate kinase	COG00126	pfam00162	cd00318		1		1				2	1	1	1	1
arCOG01053	G	Carbohydrate transport and metabolism	TktA1	Transketolase, N-terminal subunit	COG03959	pfam00456	cd02012	TIGR00232	2	2	3	3		2	3	2	1	2	6
arCOG00271	G	Carbohydrate transport and metabolism	RhaT	Permease of the drug/metabolite transporter (DMT) superfamily	COG00697	pfam00892,pfam00892		TIGR00950	4	6	1	1	1	1	3	2	2	3	3
arCOG01420	G	Carbohydrate transport and metabolism	GlgA	Glycogen synthase	COG00297	pfam08323,pfam0053	cd03791	TIGR02095	1	1		1				1			
arCOG03460	G	Carbohydrate transport and metabolism	LmbE	N-acetylglucosaminyl deacetylase, LmbE family	COG02120	pfam02585		TIGR04001	1	2						1	1		
arCOG07581	G	Carbohydrate transport and metabolism	-	Glycosyl hydrolase family 18, contains cellulose binding domain	COG03325	pfam02839,pfam0080	cd12215,cd00146,cd06548		3	3	1	2				1	2	4	4
arCOG02796	G	Carbohydrate transport and metabolism	-	Glucose/sorbosone dehydrogenase	COG02133	pfam07995		TIGR03606								1		1	1
arCOG00138	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477				1	1	1	1	1						
arCOG03641	G	Carbohydrate transport and metabolism	PfkA	6-phosphofructokinase	COG00205	pfam00365	cd00363	TIGR02483	1	1	1	1		1					
arCOG02876	G	Carbohydrate transport and metabolism	CDA1	Peptidoglycan/xylan/chitin deacetylase, PgdA/CDA1 family	COG00726	pfam01522	cd10941	TIGR03006	1		1								
arCOG00147	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174	TIGR00890	1			1		1					2
arCOG04934	G	Carbohydrate transport and metabolism	-	Peptidoglycan/xylan/chitin deacetylase, PgdA/CDA1 family	COG00726				1										
arCOG00143	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174	TIGR00711		1								1	1
arCOG07840	G	Carbohydrate transport and metabolism	-	Glycosyl hydrolase family 18, contains cellulose binding domain	COG03325	pfam02839,pfam0080	cd12215,cd00146,cd06543			1									2
arCOG00754	G	Carbohydrate transport and metabolism	LhgO	L-2-hydroxyglutarate oxidase LhgO	COG00579	pfam01266,pfam04324		TIGR03377						1			1		
arCOG04221	G	Carbohydrate transport and metabolism	NagD	Phosphatase of the HAD superfamily	COG00647	pfam13344,pfam1324	cd01427	TIGR01457									1	1	2
arCOG00135	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam05977	cd06174	TIGR00900									1	1	3
arCOG01051	G	Carbohydrate transport and metabolism	TktA2	Transketolase, C-terminal subunit	COG03958	pfam02779,pfam0278	cd07033	TIGR00204									1	1	3
arCOG01029	G	Carbohydrate transport and metabolism	GalK	Galactokinase	COG00153	pfam10509,pfam08544		TIGR00131									1	1	
arCOG01393	G	Carbohydrate transport and metabolism	-	Glycosyl transferase, related to UDP-glucuronosyltransferase	COG01819												1	1	
arCOG04120	G	Carbohydrate transport and metabolism	PykF	Pyruvate kinase	COG00469	pfam00224,pfam0288	cd00288	TIGR01064									1	1	
arCOG05061	G	Carbohydrate transport and metabolism	TalA	Transaldolase	COG00176	pfam00923	cd00956	TIGR00875									1	1	
arCOG05412	G	Carbohydrate transport and metabolism	BglB	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase	COG02723	pfam00232		TIGR03356									1	1	
arCOG00132	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174										1		
arCOG00136	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam13347	cd06174	TIGR01301,TIGR00895									1		
arCOG00142	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174	TIGR00711									1		
arCOG00144	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174	TIGR00711									1		
arCOG00272	G	Carbohydrate transport and metabolism	RhaT	Permease of the drug/metabolite transporter (DMT) superfamily	COG00697	pfam00892											1		
arCOG00760	G	Carbohydrate transport and metabolism	Mcl/CitE	Beta-methylmalyl-CoA lyase, Citrate lyase beta subunit family	COG02301	pfam03328		TIGR01588									1		
arCOG01696	G	Carbohydrate transport and metabolism	ApgM	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	COG03635	pfam01676		TIGR00306									1		
arCOG02602	G	Carbohydrate transport and metabolism	OxdD	Oxalate decarboxylase/archaeal phosphoglucose isomerase, cupin superfamil	COG02140	pfam06560											1		
arCOG02682	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam00083	cd06174	TIGR00887									1		
arCOG03278	G	Carbohydrate transport and metabolism	-	Glycosyl hydrolase family 57	COG01449	pfam03065	cd10795										1		
arCOG04180	G	Carbohydrate transport and metabolism	-	Bifunctional fructose-1,6-bisphosphate aldolase/phosphatase FBPA/FBPase	COG01980	pfam01950											1		
arCOG04226	G	Carbohydrate transport and metabolism	AraD	Ribulose-5-phosphate 4-epimerase/Fuculose-1-phosphate aldolase	COG00235	pfam00596	cd00398	TIGR03328									1		
arCOG04443	G	Carbohydrate transport and metabolism	RbcL	Ribulose 1,5-bisphosphate carboxylase, large subunit	COG01850	pfam02788,pfam0001	cd08213	TIGR03326									1		
arCOG05728	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174	TIGR00881									1		
arCOG00139	G	Carbohydrate transport and metabolism	-	MFS family permease	COG00477	pfam07690	cd06174										2		
arCOG01518	G	Carbohydrate transport and metabolism	FrvX	Cellulase M or related protein	COG01363	pfam05343	cd05656	TIGR03107									3		
arCOG00210	G	Carbohydrate transport and metabolism	TagH	ABC-type polysaccharide/polyol phosphate transport system, ATPase compon	COG01134	pfam00005	cd03220	TIGR01188										1	1
arCOG04339	G	Carbohydrate transport and metabolism	TagG	ABC-type polysaccharide/polyol phosphate export systems, permease compo	COG01682	pfam01061												1	1
arCOG01967	G	Carbohydrate transport and metabolism	Pgk2	2-phosphoglycerate kinase	COG02074													1	2
arCOG00175	G	Carbohydrate transport and metabolism	MalK	ABC-type sugar transport system, ATPase component	COG03839	pfam00005	cd03299	TIGR03265										1	
arCOG05355	G	Carbohydrate transport and metabolism	GmhA	Phosphoheptose isomerase	COG00279														1
arCOG01490	H	Coenzyme transport and metabolism	FolA	Dihydrofolate reductase	COG00262	pfam00186	cd00209		1	1		1	1		1	1		1	4
arCOG01484	H	Coenzyme transport and metabolism	RibD	Pyrimidine reductase, riboflavin biosynthesis	COG01985	pfam01872		TIGR01508	1	1		1			1	1	1		
arCOG04262	H	Coenzyme transport and metabolism	-	Phosphopantothenate synthetase	COG01701	pfam02006			1	1					1	1	1	1	1
arCOG04538	H	Coenzyme transport and metabolism	FolD	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate	COG00190	pfam00763,pfam0288	cd01080		1	2	1	1		1	1	1	1	1	1
arCOG00476	H	Coenzyme transport and metabolism	UbiA	4-hydroxybenzoate polyprenyltransferase or related prenyltransferase	COG00382	pfam01040	cd13961	TIGR01476	1	3		1			1	1	1	1	
arCOG00034	H	Coenzyme transport and metabolism	PDX2	Predicted glutamine amidotransferase involved in pyridoxine biosynthesis	COG00311	pfam01174	cd01749	TIGR03800	1		1		1		1	1	2	1	2
arCOG00972	H	Coenzyme transport and metabolism	NadR	Nicotinamide mononucleotide adenylyltransferase	COG01056	pfam01467	cd02166	TIGR01527	1			1		1	1	1	1	1	1
arCOG01223	H	Coenzyme transport and metabolism	CAB4	Phosphopantetheine adenylyltransferase	COG01019	pfam01467	cd02164	TIGR00125	1			1			1	1	1		1
arCOG01940	H	Coenzyme transport and metabolism	BirA	Biotin-(acetyl-CoA carboxylase) ligase	COG00340	pfam03099		TIGR00121	1			1			1	1	1		2
arCOG00584	H	Coenzyme transport and metabolism	PanB	Ketopantoate hydroxymethyltransferase	COG00413	pfam02548	cd06557	TIGR00222	2	1	1	1			1	1		1	2
arCOG04139	H	Coenzyme transport and metabolism	ApbA	Ketopantoate reductase	COG01893	pfam02558,pfam08546		TIGR00745			1				1	1	1	1	2
arCOG01320	H	Coenzyme transport and metabolism	RibB	3,4-dihydroxy-2-butanone 4-phosphate synthase	COG00108	pfam00926		TIGR00506	1	1	1	1		1	1		1	1	3
arCOG01323	H	Coenzyme transport and metabolism	RibH	Riboflavin synthase beta-chain	COG00054	pfam00885	cd09211	TIGR00114	1	1	1	1		1	1		1	1	3
arCOG01671	H	Coenzyme transport and metabolism	UbiD	3-polyprenyl-4-hydroxybenzoate decarboxylase or related decarboxylase	COG00043	pfam01977		TIGR03701	1	1	1	1		1	1		1	2	3
arCOG04713	H	Coenzyme transport and metabolism	RibC	Riboflavin synthase alpha chain	COG00307	pfam00677,pfam00677		TIGR00187	1	1	1	1		1	1			1	3
arCOG01703	H	Coenzyme transport and metabolism	UbiX	3-polyprenyl-4-hydroxybenzoate decarboxylase	COG00163	pfam02441		TIGR00421	1	1	1			1	1		1	1	1
arCOG00040	H	Coenzyme transport and metabolism	Hpt1	Hypoxanthine phosphoribosyltransferase	COG02236	pfam00156	cd06223	TIGR01251	1	1		1			1		1		
arCOG00478	H	Coenzyme transport and metabolism	UbiA	4-hydroxybenzoate polyprenyltransferase or related prenyltransferase	COG00382	pfam01040	cd13956	TIGR01475	1	2	1	1			1				
arCOG00113	H	Coenzyme transport and metabolism	BioF	7-keto-8-aminopelargonate synthetase or related enzyme	COG00156	pfam00155	cd06454	TIGR01825	1	2					1		1	1	2
arCOG02939	H	Coenzyme transport and metabolism	PhhB	Pterin-4a-carbinolamine dehydratase	COG02154	pfam01329	cd00488		2	2	1	2	2	1	1				2
arCOG01321	H	Coenzyme transport and metabolism	RibA	GTP cyclohydrolase II	COG00807	pfam00926,pfam0092	cd00641	TIGR00506,TIGR00505		1	1				1			2	4
arCOG01482	H	Coenzyme transport and metabolism	NadC	Nicotinate-nucleotide pyrophosphorylase	COG00157	pfam02749,pfam0172	cd01572	TIGR00078		1		1	1	1	1		1	1	2
arCOG04459	H	Coenzyme transport and metabolism	NadA	Quinolinate synthase	COG00379	pfam02445		TIGR00550		1					1		1	1	4
arCOG04137	H	Coenzyme transport and metabolism	SAM1	S-adenosylhomocysteine hydrolase	COG00499	pfam05221	cd00401	TIGR00936							1		1	1	2
arCOG07444	H	Coenzyme transport and metabolism	MetK	S-adenosylmethionine synthetase	COG00192	pfam00438,pfam02772,pfam02773		TIGR01034							1			1	1

arCOG03838	H	Coenzyme transport and metabolism	PqqD	Coenzyme PQQ synthesis protein D		pfam05402			1	1	1	1	1	1	2	1		1	
arCOG00069	H	Coenzyme transport and metabolism	NadE	NH3-dependent NAD+ synthetase	COG00171	pfam02540	cd00553	TIGR00552	1	2	1	1	1	1	2	1	1	1	3
arCOG01726	H	Coenzyme transport and metabolism	IspA	Geranylgeranyl pyrophosphate synthase	COG00142	pfam00348	cd00685	TIGR02748	2	2	2	2	1	1	2	1	1	2	5
arCOG01942	H	Coenzyme transport and metabolism	LipB	Lipoate-protein ligase B	COG00321	pfam03099		TIGR00214	1	1	1	1	1		2			1	2
arCOG00660	H	Coenzyme transport and metabolism	LipA	Lipoate synthase	COG00320	pfam04055	cd01335	TIGR00510	1	1		1			2			1	2
arCOG01904	H	Coenzyme transport and metabolism	-	CTP-dependent Riboflavin kinase	COG01339	pfam13412,pfam14277,pfam01982			2	1	1		1		2		1	1	2
arCOG00480	H	Coenzyme transport and metabolism	MenA	1,4-dihydroxy-2-naphthoate octaprenyltransferase	COG01575	pfam01040	cd13962	TIGR02235	1	1	1	1	1			1			
arCOG00489	H	Coenzyme transport and metabolism	PduO	Cob(I)alamin adenosyltransferase	COG02096	pfam01923		TIGR00636	1	1	1			1		1		1	
arCOG02172	H	Coenzyme transport and metabolism	QueD	6-pyruvoyl-tetrahydropterin synthase	COG00720	pfam01242	cd00470	TIGR03367	1	1		1				1	1	1	1
arCOG01045	H	Coenzyme transport and metabolism	CoaE	Dephospho-CoA kinase	COG00237		cd02022		1	1		1				1	1	1	2
arCOG02817	H	Coenzyme transport and metabolism	FolC	Folylpolyglutamate synthase and Dihydropteroate synthase	COG00285	pfam08245,pfam0287	cd00739	TIGR01499,TIGR01496		1	1	1		1		1	2	1	1
arCOG01704	H	Coenzyme transport and metabolism	Dfp	Phosphopantothenoylcysteine synthetase/decarboxylase	COG00452	pfam02441,pfam04127		TIGR00521		1						1	1	1	2
arCOG00214	H	Coenzyme transport and metabolism	MoaB	Molybdopterin biosynthesis enzyme	COG00521	pfam00994	cd00886	TIGR02667								1	1	1	2
arCOG00534	H	Coenzyme transport and metabolism	MoaE	Molybdopterin converting factor, large subunit	COG00314	pfam02391	cd00756									1	1	1	4
arCOG00930	H	Coenzyme transport and metabolism	MoaA	Molybdenum cofactor biosynthesis enzyme	COG02896	pfam04055,pfam0646	cd01335	TIGR02668								1	1	1	4
arCOG01530	H	Coenzyme transport and metabolism	MoaC	Molybdenum cofactor biosynthesis enzyme	COG00315	pfam01967	cd01419	TIGR00581								1	1	1	4
arCOG01872	H	Coenzyme transport and metabolism	MobA	Molybdopterin-guanine dinucleotide biosynthesis protein A	COG00746	pfam12804	cd02503									1	1		2
arCOG00217	H	Coenzyme transport and metabolism	MoeA	Molybdopterin biosynthesis enzyme	COG00303	pfam03453,pfam0099	cd00887	TIGR00177								1	1		4
arCOG02199	H	Coenzyme transport and metabolism	Mcr1	NAD(P)H-flavin reductase	COG00543											1	3		
arCOG04263	H	Coenzyme transport and metabolism	-	Pantoate kinase	COG01829	pfam00288			1	1	1	1					1	1	2
arCOG00021	H	Coenzyme transport and metabolism	-	Predicted transcriptional regulator fused phosphomethylpyrimidine kinase, in	COG01992	pfam10120			1	1	1	1						1	
arCOG04075	H	Coenzyme transport and metabolism	SNZ1	Pyridoxine biosynthesis enzyme	COG00214	pfam01680,pfam0569	cd04727	TIGR00343	1	2							1	1	3
arCOG00226	H	Coenzyme transport and metabolism	TbpA	ABC-type thiamine transport system, periplasmic component	COG04143	pfam13343	cd13545	TIGR01254	1			1						1	
arCOG01589	H	Coenzyme transport and metabolism	RimK	Glutathione synthase/glutaminyl transferase/alpha-L-glutamate ligase	COG00189	pfam08443		TIGR02144	1				1					1	2
arCOG04813	H	Coenzyme transport and metabolism	PanD	Aspartate 1-decarboxylase	COG00853	pfam02261	cd06919	TIGR00223	1										1
arCOG03402	H	Coenzyme transport and metabolism	MtbC1	Methanogenic corrinoid protein MtbC1	COG05012	pfam02607,pfam0231	cd02065	TIGR02370	1										
arCOG04542	H	Coenzyme transport and metabolism	FolE	GTP cyclohydrolase I	COG00302	pfam01227	cd00642	TIGR00063		1								1	1
arCOG01522	H	Coenzyme transport and metabolism	HemY	Protoporphyrinogen oxidase	COG01232	pfam01593		TIGR00562		1									
arCOG01676	H	Coenzyme transport and metabolism	ThiF	Dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosyn	COG00476	pfam00899,pfam0523	cd00757	TIGR02356									1	1	2
arCOG01348	H	Coenzyme transport and metabolism	nadF	NAD kinase	COG00061	pfam01513											1	1	
arCOG01754	H	Coenzyme transport and metabolism	SerA	Phosphoglycerate dehydrogenase or related dehydrogenase	COG00111	pfam00389	cd05303	TIGR01327									1	1	
arCOG00020	H	Coenzyme transport and metabolism	ThiD	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	COG00351	pfam08543	cd01169	TIGR00097									1		
arCOG00117	H	Coenzyme transport and metabolism	MenG	Demethylmenaquinone methyltransferase	COG00684	pfam00215,pfam0373	cd04726	TIGR03128,TIGR01935									1		
arCOG00228	H	Coenzyme transport and metabolism	MopI	Molybdopterin-binding protein	COG03585	pfam03459		TIGR00638									1		
arCOG00532	H	Coenzyme transport and metabolism	MobB	Molybdopterin-guanine dinucleotide biosynthesis protein	COG01763	pfam03205	cd03116	TIGR00176									1		
arCOG00574	H	Coenzyme transport and metabolism	THI4	Archaeal ribulose 1,5-bisphosphate synthetase/yeast thiazole synthase	COG01635	pfam01946		TIGR00292									1		
arCOG00613	H	Coenzyme transport and metabolism	LldD	FMN-dependent dehydrogenase, includes L-lactate dehydrogenase and type I	COG01304	pfam01070	cd02811	TIGR02151									1		
arCOG00638	H	Coenzyme transport and metabolism	ThiL	Thiamine monophosphate kinase	COG00611	pfam00586	cd02194	TIGR01379									1		
arCOG01089	H	Coenzyme transport and metabolism	ThiE	Thiamine monophosphate synthase	COG00352	pfam02581	cd00564	TIGR00693									1		
arCOG01322	H	Coenzyme transport and metabolism	RibC2	Archaeal riboflavin synthase	COG01731	pfam00885	cd09210	TIGR01506									1		
arCOG01481	H	Coenzyme transport and metabolism	PncB	Nicotinic acid phosphoribosyltransferase	COG01488	pfam02749,pfam0172	cd01571	TIGR01513									1		
arCOG01939	H	Coenzyme transport and metabolism	LplA	Lipoate-protein ligase A	COG00095	pfam03099		TIGR00545									1		
arCOG02741	H	Coenzyme transport and metabolism	ThiC	Thiamine biosynthesis protein ThiC	COG00422	pfam01964		TIGR00190									1		
arCOG03837	H	Coenzyme transport and metabolism	-	Lipoate-protein ligase A associated domain	COG00095												1		
arCOG04301	H	Coenzyme transport and metabolism	MptA	Fe(2+)-dependent GTP cyclohydrolase	COG01469	pfam02649		TIGR00294									1		
arCOG04536	H	Coenzyme transport and metabolism	ArfB	Creatinine amidohydrolase/Fe(II)-dependent formamide hydrolase involved in	COG01402	pfam02633		TIGR03964									1		
arCOG04678	H	Coenzyme transport and metabolism	BtuR	ATP:corrinoid adenosyltransferase	COG02109	pfam02572	cd00561	TIGR00708									1		
arCOG00536	H	Coenzyme transport and metabolism	MoaD	Molybdopterin converting factor, small subunit	COG01977	pfam02391	cd00754,cd00756										2		
arCOG02250	H	Coenzyme transport and metabolism	EcfT	Energy-coupling factor transporter transmembrane protein EcfT	COG00619												2		
arCOG01485	H	Coenzyme transport and metabolism	RibD	Pyrimidine deaminase and reductase	COG00117	pfam00383,pfam0187	cd01284	TIGR00326										1	1
arCOG01873	H	Coenzyme transport and metabolism	MobA	GT-A family glycosyltransferase involved in molybdopterin guanine dinucleoti	COG02068	pfam12804	cd04182	TIGR03310										1	1
arCOG04348	H	Coenzyme transport and metabolism	UbiE	Ubiquinone/menaquinone biosynthesis C-methylase UbiE	COG02226	pfam08241		TIGR01934										1	1
arCOG00477	H	Coenzyme transport and metabolism	UbiA	4-hydroxybenzoate polyprenyltransferase or related prenyltransferase	COG00382	pfam01040	cd13959	TIGR01475										1	2
arCOG00572	H	Coenzyme transport and metabolism	NadB	Aspartate oxidase	COG00029	pfam00890,pfam02910		TIGR00551										1	4
arCOG02624	H	Coenzyme transport and metabolism	PaaK	Coenzyme F390 synthetase	COG01541			TIGR02304										1	
arCOG00656	H	Coenzyme transport and metabolism	ThiH	Thiamine biosynthesis enzyme ThiH, FO synthase or related uncharacterized	COG01060	pfam04055		TIGR00423										2	7
arCOG04299	H	Coenzyme transport and metabolism	HemC	Porphobilinogen deaminase	COG00181	pfam01379,pfam0390	cd13644	TIGR00212											1
arCOG01548	C	Energy production and conversion	NuoD	NADH dehydrogenase subunit D	COG00649	pfam00346		TIGR01962	1	1	1	1			1	1	1	1	3
arCOG01551	C	Energy production and conversion	NuoC	NADH dehydrogenase subunit C	COG00852	pfam00329		TIGR01961	1	1	1	1			1	1	1	1	3
arCOG01554	C	Energy production and conversion	NuoB	F420H2 dehydrogenase subunit, related to NADH:ubiquinone oxidoreductase	COG00377	pfam01058		TIGR01957	1	1	1	1			1	1	1	1	3
arCOG01543	C	Energy production and conversion	NuoI	NADH dehydrogenase subunit I	COG01143	pfam12838		TIGR01971	1	1	1	1			1	1	2	1	2
arCOG01538	C	Energy production and conversion	NuoM	NADH dehydrogenase subunit M	COG01008	pfam00361		TIGR01972	1	1	1	1			1	1		1	2
arCOG01539	C	Energy production and conversion	NuoL	NADH dehydrogenase subunit L	COG01009	pfam00662,pfam00361		TIGR01974	1	1	1	1			1	1		1	2
arCOG01540	C	Energy production and conversion	NuoN	NADH dehydrogenase subunit N	COG01007	pfam00361		TIGR01770	1	1	1	1			1	1		1	2
arCOG03073	C	Energy production and conversion	NuoK	NADH dehydrogenase subunit 4L (K,kappa)	COG00713				1	1	1	1			1	1		1	2
arCOG04654	C	Energy production and conversion	NuoJ	NADH dehydrogenase subunit J	COG00839				1	1	1	1			1	1		1	2
arCOG01546	C	Energy production and conversion	NuoH	NADH dehydrogenase subunit H	COG01005	pfam00146			1	1	1	1			1	1		1	3
arCOG01557	C	Energy production and conversion	NuoA	NADH dehydrogenase subunit A	COG00838				1	1	1	1			1	1		1	3
arCOG02095	C	Energy production and conversion	OadA1	Pyruvate/oxaloacetate carboxyltransferase	COG05016	pfam00682,pfam0243	cd07937	TIGR01108	1	1		1	1	1	1	1	2	2	3
arCOG09401	C	Energy production and conversion	-	NAD(P) transhydrogenase, subunit alpha		pfam12769		TIGR00561	1	2	1	1	1	1	1	1		1	5
arCOG01697	C	Energy production and conversion	AcnA	Aconitase A	COG01048	pfam00330,pfam0069	cd01586,cd015	TIGR01341	1	2	1	1	1	2	1	1		1	1
arCOG06720	C	Energy production and conversion	FixC	Dehydrogenase (flavoprotein)	COG00644				1		1	1		1	1	1		1	4
arCOG04138	C	Energy production and conversion	NtpI	Archaeal/vacuolar-type H+-ATPase subunit I	COG01269	pfam01496			1		1	1			1	1	1	1	2
arCOG01721	C	Energy production and conversion	QcrB	Cytochrome b subunit of the bc complex	COG01290	pfam13631	cd00284		1		1		1	2	1	1		1	2
arCOG00869	C	Energy production and conversion	NtpE	Archaeal/vacuolar-type H+-ATPase subunit E	COG01390				1			1			1	1	1	1	1
arCOG02455	C	Energy production and conversion	AtpK	Archaeal/vacuolar-type Na+/H+-ATPase, subunit K	COG00636				1			1			1	1	1	1	1
arCOG02459	C	Energy production and conversion	NtpC	Archaeal/vacuolar-type H+-ATPase subunit C	COG01527				1			1			1	1	1	1	1
arCOG04102	C	Energy production and conversion	NtpG	Archaeal/vacuolar-type H+-ATPase subunit F	COG01436	pfam01990			1			1			1	1	1	1	1
arCOG00865	C	Energy production and conversion	NtpB	Archaeal/vacuolar-type H+-ATPase subunit B	COG01156	pfam02874,pfam0000	cd01135	TIGR01041	1						1	1	1	1	1
arCOG00868	C	Energy production and conversion	NtpA	Archaeal/vacuolar-type H+-ATPase subunit A	COG01155	pfam02874,pfam0000	cd01134	TIGR01043	1						1	1	1	1	1
arCOG02200	C	Energy production and conversion	Fpr	Flavodoxin reductase (ferredoxin-NADPH reductase) family 1	COG01018		cd00322	TIGR01941			1				1	1		1	

arCOG00982	C	Energy production and conversion	GldA	Glycerol dehydrogenase or related enzyme	COG00371	pfam13685	cd08173	TIGR01357							1	1	1		
arCOG01755	C	Energy production and conversion	LdhA	Lactate dehydrogenase or related 2-hydroxyacid dehydrogenase	COG01052	pfam00389	cd05301	TIGR01327							1	1	2		
arCOG02460	C	Energy production and conversion	NapF	Ferredoxin	COG01145	pfam09383,pfam1283	cd07030	TIGR02314,TIGR04041							1	1			
arCOG01749	C	Energy production and conversion	FumC	Fumarase	COG00114	pfam00206,pfam1041	cd01596	TIGR00979	1	1				1	1	2		1	1
arCOG01337	C	Energy production and conversion	SucC	Succinyl-CoA synthetase, beta subunit	COG00045	pfam08442,pfam00549		TIGR01016	1	1	1	1			1		1	1	1
arCOG01339	C	Energy production and conversion	SucD	Succinyl-CoA synthetase, alpha subunit	COG00074	pfam02629,pfam00549		TIGR01019	1	1	1	1			1		1	1	1
arCOG01052	C	Energy production and conversion	AcoB	Pyruvate/2-oxoglutarate/acetoin dehydrogenase complex, dehydrogenase (E	COG00022	pfam02779,pfam0278	cd07036	TIGR00204	1	1	1	1			1			1	2
arCOG05014	C	Energy production and conversion	HdrE	CoB--CoM heterodisulfide reductase subunit E	COG02181				1	1	1		1		1			1	2
arCOG01054	C	Energy production and conversion	AcoA	Pyruvate/2-oxoglutarate/acetoin dehydrogenase complex, dehydrogenase (E	COG01071	pfam00676	cd02000	TIGR03181	1	1		1			1			2	5
arCOG06073	C	Energy production and conversion	PckA	Phosphoenolpyruvate carboxykinase (ATP)	COG01866	pfam01293	cd00484	TIGR00224	1	2	1				1			1	1
arCOG00246	C	Energy production and conversion	Mdh	Malate/lactate dehydrogenase	COG00039	pfam00056,pfam0286	cd00300	TIGR01771	1	2	1				1			1	5
arCOG02921	C	Energy production and conversion	PetE	Plastocyanin	COG03794	pfam00127	cd04220	TIGR03102	1	3		1	1	2	1			1	2
arCOG01606	C	Energy production and conversion	PorA	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidored	COG00674	pfam01558,pfam0185	cd07034	TIGR03710	1					1	1			1	1
arCOG04101	C	Energy production and conversion	NtpD	Archaeal/vacuolar-type H+-ATPase subunit D	COG01394	pfam01813		TIGR00309	1						1		1	1	1
arCOG04949	C	Energy production and conversion	OVP1	Na+ or H+-translocating membrane pyrophosphatase	COG03808	pfam03030		TIGR01104	1						1		1	1	3
arCOG01706	C	Energy production and conversion	AceF	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltrans	COG00508	pfam00198		TIGR01349	2	1	1	2			1			1	3
arCOG01068	C	Energy production and conversion	Lpd	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydro	COG01249	pfam07992,pfam02852		TIGR01350		1	1		1		1		2	2	3
arCOG02077	C	Energy production and conversion	IscU	NifU homolog involved in Fe-S cluster formation	COG00822	pfam01592	cd06664	TIGR03419		1	1				1				
arCOG04279	C	Energy production and conversion	-	Swiveling domain associated with predicted aconitase	COG01786	pfam01989	cd01356								1		1		
arCOG04073	C	Energy production and conversion	-	MinD superfamily P-loop ATPase containing an inserted ferredoxin domain	COG01149	pfam01656	cd03110	TIGR01969							1		2		
arCOG00573	C	Energy production and conversion	SdhA	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	COG01053	pfam00890,pfam02910		TIGR02061							1				
arCOG02179	C	Energy production and conversion	NapF	Polyferredoxin	COG01145	pfam12838,pfam12838,pfam12838		TIGR01971,TIGR04105							1				
arCOG02618	C	Energy production and conversion	-	Ferredoxin	COG01146	pfam13187,pfam12139		TIGR02060							1				
arCOG00447	C	Energy production and conversion	FixB	Electron transfer flavoprotein, alpha subunit	COG02025	pfam01012,pfam0076	cd01985		1	1	1		1		2	1		1	2
arCOG01235	C	Energy production and conversion	CyoA	Heme/copper-type cytochrome/quinol oxidase, subunit 2	COG01622	pfam00116	cd13918	TIGR02866	1	1	1		1		2	1			1
arCOG02017	C	Energy production and conversion	RutF	NADH-FMN oxidoreductase RutF, flavin reductase (DIM6/NTAB) family	COG01853	pfam01613		TIGR03615	2	1	1				2	1	1	1	1
arCOG04548	C	Energy production and conversion	-	Ferredoxin	COG01146	pfam13237		TIGR02512		1					2	1			
arCOG00446	C	Energy production and conversion	FixA	Electron transfer flavoprotein, beta subunit	COG02086	pfam01012	cd01714		1	1	1		1		2			1	2
arCOG04237	C	Energy production and conversion	GltA	Citrate synthase	COG00372	pfam00285	cd06118	TIGR01800	1	2	1	1	1	1	2		1	1	2
arCOG01237	C	Energy production and conversion	CyoB	Heme/copper-type cytochrome/quinol oxidase, subunit 1 and 3	COG00843	pfam00115,pfam0051	cd01662,cd003	TIGR02891,TIGR	1	1	1		1		3	2		1	1
arCOG00332	C	Energy production and conversion	GlpC	Membrane associated Fe-S oxidoreductase	COG00247	pfam02754									3				
arCOG01252	C	Energy production and conversion	PutA	Lactaldehyde dehydrogenase, Succinate semialdehyde dehydrogenase or oth	COG01012	pfam00171	cd07088	TIGR01780	3	4	3	2		2	5	1		4	11
arCOG00570	C	Energy production and conversion	FixC	Dehydrogenase (flavoprotein)	COG00644	pfam13450		TIGR02032	8	9	4	5	3	5	8	4	2	4	9
arCOG04594	C	Energy production and conversion	QcrB	Cytochrome b subunit of the bc complex	COG01290				1		1		1	2		1			
arCOG00288	C	Energy production and conversion	NfnB	Nitroreductase	COG00778	pfam00881	cd02150	TIGR02476		2						1	1	1	2
arCOG02929	C	Energy production and conversion	PetE	Plastocyanin	COG03794	pfam00127	cd13921	TIGR02657				1				1			
arCOG00333	C	Energy production and conversion	GlpC	Fe-S oxidoreductase	COG00247	pfam13534,pfam02754										1	1	1	2
arCOG02187	C	Energy production and conversion	NapF	Ferredoxin domain containing protein	COG01145	pfam12838,pfam12838		TIGR04105,TIGR04041								1			
arCOG02398	C	Energy production and conversion	CcdA	Cytochrome c biogenesis protein	COG00785	pfam02683										1			
arCOG02449	C	Energy production and conversion	NapF	Flavodoxin fused to ferredoxin domain	COG01145	pfam12724,pfam13187		TIGR04041								1			
arCOG01458	C	Energy production and conversion	Qor	NADPH:quinone reductase or related Zn-dependent oxidoreductase	COG00604	pfam08240,pfam0010	cd08264	TIGR02824	1	2	2		2	1		2		2	2
arCOG01491	C	Energy production and conversion	BisC	Anaerobic dehydrogenase	COG00243	pfam00384	cd02766	TIGR01591								3	1	1	3
arCOG01500	C	Energy production and conversion	HybA	Fe-S-cluster-containing dehydrogenase component	COG00437	pfam13459,pfam13247		TIGR02951								3			
arCOG00963	C	Energy production and conversion	GlpC	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	COG00479	pfam13085,pfam13183,pfam02754,pf		TIGR00384,TIGR	1	1	1	1						1	2
arCOG01164	C	Energy production and conversion	Icd	Isocitrate dehydrogenase	COG00538	pfam00180		TIGR00183	1	1		1						1	
arCOG04650	C	Energy production and conversion	CyoC	Heme/copper-type cytochrome/quinol oxidase, subunit 3	COG01845	pfam00510	cd00386	TIGR02842	1	1			1					1	1
arCOG01599	C	Energy production and conversion	PorB	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidored	COG01013	pfam02775,pfam1236	cd03375	TIGR02177	1	1				1			1	1	1
arCOG00701	C	Energy production and conversion	UgpQ	Glycerophosphoryl diester phosphodiesterase	COG00584	pfam03009	cd08568		1	2	1	1	1	1			2	1	1
arCOG00340	C	Energy production and conversion	GlcD	FAD/FMN-containing dehydrogenase fused to Heterodisulfide reductase, sub	COG00277	pfam01565,pfam02913,pfam13183		TIGR00387,TIGR	1		1		1	2					
arCOG00571	C	Energy production and conversion	SdhA	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	COG01053	pfam00890,pfam02910		TIGR03378,TIGR	2	1	1	1					1	2	8
arCOG00519	C	Energy production and conversion	FldA	Flavodoxin	COG00716	pfam12682			3	2	3	1	1	4					1
arCOG02410	C	Energy production and conversion	-	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin red	COG02141	pfam00296	cd01097	TIGR03555		1				1					2
arCOG01359	C	Energy production and conversion	-	Radical SAM superfamily enzyme	COG01031	pfam04055		TIGR04013									1	1	1
arCOG00338	C	Energy production and conversion	SdhC	Succinate dehydrogenase subunit C	COG02048	pfam02754,pfam02754		TIGR03288									1	1	2
arCOG03363	C	Energy production and conversion	NtpF	Archaeal/vacuolar-type H+-ATPase subunit H	COG02811												1		1
arCOG00024	C	Energy production and conversion	GlpK	Glycerol kinase	COG00554	pfam00370,pfam0278	cd07786	TIGR01311									1		
arCOG00335	C	Energy production and conversion	LutB	L-lactate utilization protein LutB, contains ferredoxin domain	COG01139	pfam02589,pfam13183		TIGR00273									1		
arCOG00349	C	Energy production and conversion	Fer	Ferredoxin	COG01141	pfam13459											1		
arCOG00509	C	Energy production and conversion	NorV	Flavorubredoxin	COG00426	pfam00753,pfam00258											1		
arCOG00709	C	Energy production and conversion	-	Aldehyde:ferredoxin oxidoreductase	COG02414	pfam02730,pfam01314											1		
arCOG00853	C	Energy production and conversion	SfcA	Malic enzyme	COG00281	pfam00390,pfam0394	cd05311										1		
arCOG00959	C	Energy production and conversion	-	Ferredoxin	COG01146			TIGR02512									1		
arCOG00964	C	Energy production and conversion	HdrC	Heterodisulfide reductase, subunit C	COG01150	pfam13183		TIGR03290									1		
arCOG01097	C	Energy production and conversion	-	Rubrerythrin	COG01592	pfam02915	cd01041										1		
arCOG01338	C	Energy production and conversion	-	Acyl-CoA synthetase, ATP-grasp containing subunit	COG01042	pfam13549											1		
arCOG01356	C	Energy production and conversion	-	Radical SAM superfamily enzyme	COG01032	pfam02310,pfam0405	cd02068,cd013	TIGR02026									1		
arCOG01549	C	Energy production and conversion	FrhA	Coenzyme F420-reducing hydrogenase, alpha subunit	COG03259	pfam00374		TIGR03295									1		
arCOG01552	C	Energy production and conversion	HycE	Ni,Fe-hydrogenase III component G	COG03262	pfam00329		TIGR01961									1		
arCOG01607	C	Energy production and conversion	PorA	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidored	COG00674	pfam01855	cd07034	TIGR03710									1		
arCOG01609	C	Energy production and conversion	-	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunit	COG04231	pfam01855,pfam0277	cd07034,cd020	TIGR03336									1		
arCOG01674	C	Energy production and conversion	AcyP	Acylphosphatase	COG01254	pfam00708											1		
arCOG01711	C	Energy production and conversion	Ppa	Inorganic pyrophosphatase	COG00221	pfam00719	cd00412										1		
arCOG02146	C	Energy production and conversion	-	Desulfoferredoxin	COG02033	pfam01880	cd03172	TIGR00332									1		
arCOG02428	C	Energy production and conversion	CdhA	CO dehydrogenase/acetyl-CoA synthase alpha subunit	COG01152	pfam03063	cd01916	TIGR00314									1		
arCOG02461	C	Energy production and conversion	-	Ferredoxin	COG01146	pfam13237	cd07030	TIGR03224									1		
arCOG02472	C	Energy production and conversion	FrhG	Coenzyme F420-reducing hydrogenase, gamma subunit	COG01941	pfam01058		TIGR03294									1		
arCOG02473	C	Energy production and conversion	FrhG	Coenzyme F420-reducing hydrogenase, gamma subunit	COG01941	pfam01058,pfam12838		TIGR03294									1		
arCOG02475	C	Energy production and conversion	FrhD	Coenzyme F420-reducing hydrogenase, delta subunit	COG01908	pfam02662											1		
arCOG02653	C	Energy production and conversion	FrhB	Coenzyme F420-reducing hydrogenase, beta subunit (with C-terminal ferredo	COG01035	pfam04432,pfam13183											1		
arCOG03626	C	Energy production and conversion	HyfE	Hydrogenase-4 membrane subunit HyfE	COG04237												1		
arCOG04002	C	Energy production and conversion	-	Cytochrome b family protein	SC.00119												1		

arCOG04391	C	Energy production and conversion	-	Rubredoxin	COG01773	pfam00301	cd00730										1		
arCOG04406	C	Energy production and conversion	FumA	Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal dor	COG01838	pfam05683		TIGR00723									1		
arCOG04407	C	Energy production and conversion	TtdA	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal do	COG01951	pfam05681		TIGR00722									1		
arCOG04429	C	Energy production and conversion	HyaD	Ni,Fe-hydrogenase maturation factor	COG00680	pfam01750	cd06067	TIGR00142									1		
arCOG04475	C	Energy production and conversion	OadB	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subu	COG01883	pfam03977		TIGR01109									1		
arCOG04537	C	Energy production and conversion	NuoF	NADH:ubiquinone oxidoreductase, NADH-binding 51 kD subunit (chain F)	COG01894	pfam01512,pfam10589		TIGR01959									1		
arCOG04874	C	Energy production and conversion	AllD	Malate/lactate/ureidoglycolate dehydrogenase, LDH2 family	COG02055	pfam02615		TIGR03175									1		
arCOG04890	C	Energy production and conversion	NuoE	NADH:ubiquinone oxidoreductase 24 kD subunit	COG01905	pfam01257	cd13637,cd030	TIGR01958									1		
arCOG05128	C	Energy production and conversion	NapF	Ferredoxin	COG01145	pfam13746		TIGR02910									1		
arCOG05744	C	Energy production and conversion	HycB	Fe-S-cluster-containing hydrogenase component 2	COG01142	pfam12838		TIGR01971									1		
arCOG05745	C	Energy production and conversion	-	BFD-like [2Fe-2S] binding domain	COG00446	pfam04324		TIGR01372									1		
arCOG05797	C	Energy production and conversion	OadG	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, gamma su	COG03630	pfam04277		TIGR01195									1		
arCOG05865	C	Energy production and conversion	PepCK	Phosphoenolpyruvate carboxykinase, GTP-dependent	COG01274	pfam00821	cd00819										1		
arCOG06124	C	Energy production and conversion	ACH1	Acetyl-CoA hydrolase	COG00427	pfam02550,pfam13336		TIGR03458									1		
arCOG06130	C	Energy production and conversion	PflD	Pyruvate-formate lyase	COG01882	pfam02901,pfam0122	cd01677	TIGR01774									1		
arCOG13546	C	Energy production and conversion	-	ACP (acyl carrier) superfamily protein		pfam06857		TIGR01608									1		
arCOG01605	C	Energy production and conversion	PorD	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidored	COG01144	pfam12838		TIGR02179									2	1	1
arCOG01163	C	Energy production and conversion	LeuB	Isocitrate/isopropylmalate dehydrogenase	COG00473	pfam00180		TIGR02088									2	1	3
arCOG01340	C	Energy production and conversion	-	Acyl-CoA synthetase (NDP forming)	COG01042	pfam13380,pfam13607		TIGR02717									2		
arCOG01357	C	Energy production and conversion	-	Radical SAM superfamily enzyme	COG01032	pfam04055		TIGR04013									2		
arCOG01547	C	Energy production and conversion	HycE	Ni,Fe-hydrogenase III large subunit and subunit G	COG03261	pfam00374,pfam00346		TIGR01962									2		
arCOG01553	C	Energy production and conversion	-	Ni,Fe-hydrogenase III small subunit	COG03260	pfam01058		TIGR01957									2		
arCOG01601	C	Energy production and conversion	PorB	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidored	COG01013	pfam02775	cd03376	TIGR02176									2		
arCOG01602	C	Energy production and conversion	PorG	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidored	COG01014	pfam01558		TIGR03334									2		
arCOG01603	C	Energy production and conversion	PorG	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidored	COG01014	pfam01558		TIGR02175									2		
arCOG01608	C	Energy production and conversion	PorA	Pyruvate:ferredoxin oxidoreductase or related 2-oxoacid:ferredoxin oxidored	COG00674	pfam01855,pfam0278	cd07034	TIGR02176									2		
arCOG02235	C	Energy production and conversion	HdrA	Heterodisulfide reductase, subunit A or related polyferredoxin	COG01148	pfam07992,pfam13183,pfam01266,pf		TIGR03997,TIGR02179,TIGR03143,TIGR02179									2		
arCOG01545	C	Energy production and conversion	HyfC	Formate hydrogenlyase subunit 4	COG00650	pfam00146											3		
arCOG00706	C	Energy production and conversion	-	Aldehyde:ferredoxin oxidoreductase	COG02414	pfam02730,pfam01314											4		
arCOG01537	C	Energy production and conversion	NuoM	NADH:ubiquinone oxidoreductase subunit 4 (chain M)	COG00651	pfam00361		TIGR01972									5		
arCOG00855	C	Energy production and conversion	Pta	Phosphotransacetylase	COG00280	pfam01515		TIGR02706										1	1
arCOG01167	C	Energy production and conversion	CoxL	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homo	COG01529	pfam01315,pfam02738		TIGR02416										1	1
arCOG01925	C	Energy production and conversion	CoxS	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS hom	COG02080	pfam13085,pfam0179	cd00207	TIGR03193										1	1
arCOG01926	C	Energy production and conversion	CoxM	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM h	COG01319	pfam00941,pfam03450		TIGR03195										1	1
arCOG00962	C	Energy production and conversion	FrdB	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	COG00479	pfam13085,pfam13183		TIGR00384										1	2
arCOG04595	C	Energy production and conversion	QcrA	Rieske Fe-S protein	COG00723			TIGR01416										1	2
arCOG00456	C	Energy production and conversion	GpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	COG00240	pfam01210,pfam07479		TIGR03376										1	3
arCOG01617	C	Energy production and conversion	Tas	Aryl-alcohol dehydrogenase related enzyme	COG00667	pfam00248	cd06660	TIGR01293										1	3
arCOG04358	C	Energy production and conversion	FdhD	Uncharacterized protein required for formate dehydrogenase activity	COG01526	pfam02634		TIGR00129										1	3
arCOG01236	C	Energy production and conversion	CyoA	Heme/copper-type cytochrome/quinol oxidase, subunit 2	COG01622	pfam00116	cd13842	TIGR02866										1	
arCOG01502	C	Energy production and conversion	HycB	Fe-S-cluster-containing hydrogenase component 2	COG01142	pfam13247		TIGR02512,TIGR03149										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,pfam13454,pf		TIGR03140,TIGR04105,TIGR03385,TIGR04105										1	
arCOG04522	C	Energy production and conversion	CcdA	Cytochrome c biogenesis protein	COG00785													1	
arCOG02189	C	Energy production and conversion	NapF	HTH containing ranscriptional regulator fused to ferredoxin domain	COG01145			TIGR02179											1
arCOG02842	C	Energy production and conversion	Fdx	Ferredoxin	COG00633	pfam00111	cd00207	TIGR02008											1
arCOG04145	P	Inorganic ion transport and metabolism	TrkG	Trk-type K+ transport system, membrane component	COG00168	pfam02386		TIGR00933	1	1	1	1		1	1	1	1	1	1
arCOG01959	P	Inorganic ion transport and metabolism	TrkA	TrkA, K+ transport system, NAD-binding component	COG00569	pfam02254,pfam02080,pfam02254,pfam02080			1	1	1	1		1	1	1		1	1
arCOG04147	P	Inorganic ion transport and metabolism	SodA	Superoxide dismutase	COG00605	pfam00081,pfam02777			1	1	1				1	1			
arCOG04231	P	Inorganic ion transport and metabolism	CutA	Uncharacterized protein involved in tolerance to divalent cations	COG01324	pfam03091			1	1					1	1		1	3
arCOG02021	P	Inorganic ion transport and metabolism	PspE	Rhodanese-related sulfurtransferase	COG00607	pfam00581	cd00158	TIGR02981	1		1				1	2		5	6
arCOG07775	P	Inorganic ion transport and metabolism	HcaE	Phenylpropionate dioxygenase or related ring-hydroxylating dioxygenase, larg	COG04638	pfam00355,pfam0084	cd03535,cd088	TIGR03229	1	1	1	1	1		1			1	4
arCOG02763	P	Inorganic ion transport and metabolism	-	Heavy-metal-associated domain (HMA)	COG02608	pfam00403	cd00371	TIGR02052	2	1					1			1	2
arCOG02881	P	Inorganic ion transport and metabolism	ECM27	Ca2+/Na+ antiporter	COG00530	pfam01699,pfam01699		TIGR00367		1	1	1			1		1	2	4
arCOG01477	P	Inorganic ion transport and metabolism	CzcD	Co/Zn/Cd efflux system component	COG01230	pfam01545		TIGR01297		2		1	1		1				
arCOG00576	P	Inorganic ion transport and metabolism	-	Predicted divalent heavy-metal cations transporter	COG00428	pfam02535					1		1		2	1			
arCOG00238	P	Inorganic ion transport and metabolism	ArsB	Na+/H+ antiporter NhaD or related arsenite permease	COG01055	pfam03600	cd01117	TIGR00785	2	1	2	1	1		2	2	3	1	2
arCOG02569	P	Inorganic ion transport and metabolism	EriC	Chloride channel protein EriC	COG00038	pfam00654,pfam0057	cd00400,cd045	TIGR01302	1	2	1	1	1	1	2				
arCOG04330	P	Inorganic ion transport and metabolism	FTR1	High-affinity Fe2+/Pb2+ permease	COG00672	pfam03239		TIGR00145							2				
arCOG09746	P	Inorganic ion transport and metabolism	-	Sulfotransferase related protein		pfam00685			1	2			1			1			3
arCOG04750	P	Inorganic ion transport and metabolism	-	Sirohydrochlorin iron chelatase fused to [2Fe-2S] Ferredoxin	COG02138	pfam01903,pfam0190	cd03416,cd03414,cd02980		1		1		1	1		1		1	1
arCOG02499	P	Inorganic ion transport and metabolism	-	Lipoprotein NosD family, contains CASH domains	COG03420	pfam13229,pfam13229		TIGR04247	1							1			
arCOG02265	P	Inorganic ion transport and metabolism	CorA	Mg2+ and Co2+ transporter	COG00598	pfam01544	cd12828	TIGR00383								1	1		
arCOG04397	P	Inorganic ion transport and metabolism	AmtB	Ammonia permease	COG00004	pfam00909		TIGR00836								1	1		
arCOG02267	P	Inorganic ion transport and metabolism	PitA	Phosphate/sulphate permease	COG00306	pfam01384										1	2	1	1
arCOG02640	P	Inorganic ion transport and metabolism	-	Uncharacterized protein YkaA, distantly related to PhoU, UPF0111/DUF47 fan	COG01392											1	2		
arCOG02764	P	Inorganic ion transport and metabolism	CopZ	Copper-ion-binding protein	COG02608	pfam00403	cd00371	TIGR02052								1		1	1
arCOG01474	P	Inorganic ion transport and metabolism	MMT1	Predicted Co/Zn/Cd cation transporter	COG00053	pfam01545		TIGR01297								1			
arCOG02068	P	Inorganic ion transport and metabolism	DsrE	Uncharacterized protein involved in intracellular sulfur reduction	COG01553	pfam02635			1	1		1							
arCOG00173	P	Inorganic ion transport and metabolism	PhnE	ABC-type phosphate/phosphonate transport system, permease component	COG03639	pfam00528	cd06261	TIGR01097	1		1			1				1	3
arCOG00206	P	Inorganic ion transport and metabolism	PhnC	ABC-type phosphate/phosphonate transport system, ATPase component	COG03638	pfam00005	cd03256	TIGR02315	1		1			1				1	3
arCOG01805	P	Inorganic ion transport and metabolism	PhnD	ABC-type phosphate/phosphonate transport system, periplasmic component	COG03221	pfam12974	cd01071	TIGR01098	1		1			1				1	4
arCOG04233	P	Inorganic ion transport and metabolism	FepB	ABC-type Fe3+-hydroxamate transport system, periplasmic component	COG00614	pfam01497	cd01143	TIGR04281	1		1							1	
arCOG00201	P	Inorganic ion transport and metabolism	ZnuC	ABC-type Mn/Zn transport system, ATPase component	COG01121	pfam00005	cd03235	TIGR03771	1			1					1	1	1
arCOG01006	P	Inorganic ion transport and metabolism	ZnuB	ABC-type Mn2+/Zn2+ transport system, permease component	COG01108	pfam00950	cd06550	TIGR03770	1			1					1	1	1
arCOG01005	P	Inorganic ion transport and metabolism	LraI	ABC-type metal ion transport system, periplasmic component/surface adhesi	COG00803	pfam01297	cd01018	TIGR03772,TIGR	1			1					1	1	
arCOG00163	P	Inorganic ion transport and metabolism	ThiP	ABC-type Fe3+ transport system, permease component	COG01178	pfam00528,pfam0052	cd06261,cd062	TIGR03262	1			1						1	
arCOG03127	P	Inorganic ion transport and metabolism	Kch	Ion channel fused to ion transporting domain	COG01226				1								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,pfam0014	cd00649,cd006	TIGR00198		1									

arCOG02497	P	Inorganic ion transport and metabolism	-	Lipoprotein NosD family, contains CASH domains	COG03420	pfam12708		TIGR04247			1						1		
arCOG01578	P	Inorganic ion transport and metabolism	MgtA	Cation transport ATPase	COG00474	pfam00690,pfam00122,pfam00702,pf		TIGR01647									1	1	1
arCOG02050	P	Inorganic ion transport and metabolism	-	Sulfite exporter, TauE/SafE family	COG00730	pfam01925											1	1	2
arCOG00202	P	Inorganic ion transport and metabolism	EcfA2	Energy-coupling factor transporter ATP-binding protein EcfA2	COG01122	pfam00005	cd03225	TIGR01166									1	1	
arCOG01040	P	Inorganic ion transport and metabolism	CysC	Adenylylsulfate kinase or related kinase	COG00529	pfam01583	cd02027	TIGR00455									1		1
arCOG01096	P	Inorganic ion transport and metabolism	CCC1	Predicted Fe2+/Mn2+ transporter, VIT1/CCC1 family	COG01814	pfam02915,pfam0198	cd01044,cd02431										1		1
arCOG00219	P	Inorganic ion transport and metabolism	ModA	ABC-type molybdate transport system, periplasmic component	COG00725	pfam13531	cd13540	TIGR03730									1		
arCOG00359	P	Inorganic ion transport and metabolism	FeoB	Fe2+ transport system protein B	COG00370	pfam02421,pfam0767	cd01879	TIGR00437									1		
arCOG00624	P	Inorganic ion transport and metabolism	MgtE2	Permease, similar to cation transporter	COG01824	pfam01769											1		
arCOG01069	P	Inorganic ion transport and metabolism	-	CoA-dependent NAD(P)H Sulfur Oxidoreductase	COG00446	pfam07992,pfam02852		TIGR03385									1		
arCOG01095	P	Inorganic ion transport and metabolism	Ftn	Ferritin	COG01528	pfam00210	cd01055										1		
arCOG01475	P	Inorganic ion transport and metabolism	MMT1	Predicted Co/Zn/Cd cation transporter	COG00053	pfam01545,pfam0257	cd00851	TIGR01297									1		
arCOG01953	P	Inorganic ion transport and metabolism	KefB	Kef-type K+ transport system, membrane component	COG00475	pfam00999		TIGR00932									1		
arCOG01954	P	Inorganic ion transport and metabolism	KefB	Kef-type K+ transport system, membrane component	COG00475	pfam00999		TIGR00932									1		
arCOG01957	P	Inorganic ion transport and metabolism	TrkA	TrkA, K+ transport system, NAD-binding component	COG00569	pfam02254,pfam02080											1		
arCOG02102	P	Inorganic ion transport and metabolism	FeoA	Fe2+ transport system protein A	COG01918	pfam04023											1		
arCOG02248	P	Inorganic ion transport and metabolism	CbiM	ABC-type Co2+ transport system, permease component	COG00310	pfam01891		TIGR00123									1		
arCOG03077	P	Inorganic ion transport and metabolism	MnhB	Multisubunit Na+/H+ antiporter, MnhB subunit	COG02111												1		
arCOG03159	P	Inorganic ion transport and metabolism	CbiM	ABC-type Co2+ transport system, permease component	COG00310	pfam13190											1		
arCOG04191	P	Inorganic ion transport and metabolism	MET3	ATP sulfurylase (sulfate adenylyltransferase)	COG02046	pfam14306,pfam0174	cd00517	TIGR00339									1		
arCOG04355	P	Inorganic ion transport and metabolism	TehA	Tellurite resistance protein or related permease	COG01275	pfam03595	cd09299	TIGR00816									1		
arCOG05758	P	Inorganic ion transport and metabolism	-	TrkA-C domain contaning protein	COG00490	pfam02080											1		
arCOG05908	P	Inorganic ion transport and metabolism	-	Ferritin-like domain	COG01633	pfam04454											1		
arCOG10427	P	Inorganic ion transport and metabolism	-	Chromate resistance protein	COG04275	pfam09828											1		
arCOG10942	P	Inorganic ion transport and metabolism	-	Sulfotransferase family protein													1		
arCOG01103	P	Inorganic ion transport and metabolism	-	Ferritin-like domain	COG01633	pfam02915	cd01045										2		
arCOG01958	P	Inorganic ion transport and metabolism	Kch	Kef-type K+ transport system, predicted NAD-binding component	COG01226	pfam07885,pfam02254											2		
arCOG01960	P	Inorganic ion transport and metabolism	TrkA	K+ transport system, NAD-binding component fused to Ion channel	COG01226	pfam02254,pfam02080,pfam02254,pfam02080											2		
arCOG01961	P	Inorganic ion transport and metabolism	NhaP	NhaP-type Na+/H+ and K+/H+ antiporter	COG00025	pfam00999		TIGR00831									2		
arCOG02190	P	Inorganic ion transport and metabolism	ACR3	Arsenite efflux pump ACR3 or related permease	COG00798	pfam01758		TIGR00832									2		
arCOG03072	P	Inorganic ion transport and metabolism	MnhC	Multisubunit Na+/H+ antiporter, MnhC subunit	COG01006	pfam00420		TIGR00941									2		
arCOG03078	P	Inorganic ion transport and metabolism	-	Predicted subunit of the Multisubunit Na+/H+ antiporter	COG01563	pfam13244											2		
arCOG03079	P	Inorganic ion transport and metabolism	MnhB	Multisubunit Na+/H+ antiporter, MnhB subunit	COG02111	pfam04039											2		
arCOG03082	P	Inorganic ion transport and metabolism	MnhG	Multisubunit Na+/H+ antiporter, MnhG subunit	COG01320	pfam03334		TIGR01300									2		
arCOG03099	P	Inorganic ion transport and metabolism	MnhE	Multisubunit Na+/H+ antiporter, MnhE subunit	COG01863	pfam01899		TIGR00942									2		
arCOG03121	P	Inorganic ion transport and metabolism	MnhF	Multisubunit Na+/H+ antiporter, MnhF subunit	COG02212	pfam04066											2		
arCOG00318	P	Inorganic ion transport and metabolism	PhoU	Phosphate uptake regulator	COG00704	pfam04014,pfam01895,pfam01895		TIGR02135										1	1
arCOG01576	P	Inorganic ion transport and metabolism	ZntA	Cation transport ATPase	COG02217	pfam00403,pfam0012	cd00371,cd014	TIGR00003,TIGR01511										1	1
arCOG02062	P	Inorganic ion transport and metabolism	TusA	TusA-related sulfurtransferase	COG00425	pfam01206	cd00291											1	1
arCOG02287	P	Inorganic ion transport and metabolism	-	Putative selenium binding protein, beta/alpha-propeller fold	COG00393	pfam01906												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	
arCOG06837	P	Inorganic ion transport and metabolism	-	Lipoprotein NosD family, contains CASH domains	COG03420	pfam05048		TIGR04247,TIGR03024										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
arCOG06728	P	Inorganic ion transport and metabolism	-	Sulfite exporter, TauE/SafE family	COG00730	pfam01925													2
arCOG01709	I	Lipid transport and metabolism	CaiA	Acyl-CoA dehydrogenase	COG01960	pfam02771,pfam0277	cd01158	TIGR03207	1	1		1			1	1			
arCOG04213	I	Lipid transport and metabolism	INO1	Myo-inositol-1-phosphate synthase	COG01260	pfam07994		TIGR03450	1	2	1	1	1	1	1	1			
arCOG06112	I	Lipid transport and metabolism	Acs	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	COG00365	pfam00501	cd05943	TIGR01217	1	2	1				1	1			
arCOG02245	I	Lipid transport and metabolism	-	Cytidylyltransferase family enzyme	COG01836	pfam01940		TIGR00297	1		1	1		1	1	1		1	2
arCOG04106	I	Lipid transport and metabolism	CdsA	CDP-diglyceride synthetase	COG00575	pfam01864			1		1				1	1	1	1	1
arCOG01532	I	Lipid transport and metabolism	UppS	Undecaprenyl pyrophosphate synthase	COG00020	pfam01255	cd00475	TIGR00055	1			1			1	1	1	1	2
arCOG08932	I	Lipid transport and metabolism	LCB5	Diacylglycerol kinase family enzyme	COG01597	pfam00781		TIGR03702		1	1	1			1	1		1	2
arCOG00249	I	Lipid transport and metabolism	FadB	3-hydroxyacyl-CoA dehydrogenase, some fused to Enoyl-CoA hydratase	COG01250	pfam02737,pfam0072	cd06558	TIGR02437,TIGR	3	2	3	2	1	1	1	2		2	4
arCOG13950	I	Lipid transport and metabolism	-	Phosphatidylglycerophosphatase A		pfam04608	cd06971		1	1	1	1	1		1				
arCOG00860	I	Lipid transport and metabolism	-	Isopentenyl phosphate kinase, enzyme of modified mevalonate pathway	COG01608	pfam00696	cd04241	TIGR02075	1	1	1	1			1		2	1	2
arCOG01028	I	Lipid transport and metabolism	ERG12	Mevalonate kinase	COG01577	pfam00288		TIGR00549	1	1	1			1	1		1	1	3
arCOG01843	I	Lipid transport and metabolism	-	Sterol carrier protein	COG03255	pfam02036			1	1	1				1		1		
arCOG01264	I	Lipid transport and metabolism	FabG	Short-chain alcohol dehydrogenase	COG01028	pfam00106	cd05327	TIGR01289	1	1		1			1			1	1
arCOG01085	I	Lipid transport and metabolism	PcrB	(S)-3-O-geranylgeranylglyceryl phosphate synthase, TIM-barrel fold	COG01646	pfam01884	cd02812	TIGR01768	1	1				1	1		1	1	4
arCOG04351	I	Lipid transport and metabolism	-	Predicted membrane associated lipid hydrolase, neutral ceramidase superfam	COG03356	pfam09843			1	1				1	1		1		
arCOG00250	I	Lipid transport and metabolism	FadB	3-hydroxyacyl-CoA dehydrogenase	COG01250	pfam02737,pfam00725		TIGR02279	1		1	1	1	1	1			2	5
arCOG04260	I	Lipid transport and metabolism	HMG1	Hydroxymethylglutaryl-CoA reductase	COG01257	pfam00368	cd00643	TIGR00533	1		1				1		1	1	2
arCOG02936	I	Lipid transport and metabolism	ERG9	Phytoene/squalene synthetase	COG01562	pfam00494	cd00683	TIGR03465	2	2	1				1			3	5
arCOG01710	I	Lipid transport and metabolism	Sbm	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-binding)	COG02185	pfam02310	cd02071	TIGR00640							1		1	1	3
arCOG01590	I	Lipid transport and metabolism	AccC	Biotin carboxylase	COG00439	pfam00289,pfam02786,pfam02785		TIGR00514	1	1	1	1	1	1	2	1		2	7
arCOG02705	I	Lipid transport and metabolism	-	Acetyl-CoA carboxylase, carboxyltransferase component	COG04799	pfam01039		TIGR01117	2	2		1	1	1	2	1	1	4	7
arCOG04232	I	Lipid transport and metabolism	Sbm	Methylmalonyl-CoA mutase	COG01884	pfam01642	cd03680	TIGR00641	2	2		2			2	1	1	2	2
arCOG01259	I	Lipid transport and metabolism	FabG	Short-chain alcohol dehydrogenase	COG01028		cd05233	TIGR01830	6	6	4	1	1	1	2	2	5	6	7
arCOG01081	I	Lipid transport and metabolism	Idi	Isopentenyldiphosphate isomerase	COG01443	pfam00293	cd02885	TIGR02150	1	1	1	1		1	2				
arCOG00773	I	Lipid transport and metabolism	-	Acyl-CoA hydrolase	COG01607	pfam03061,pfam0306	cd03442,cd03442		1	1		1			2			1	3

arCOG00670	I	Lipid transport and metabolism	PgsA	Phosphatidylglycerophosphate synthase	COG00558	pfam01066			1	2	2	2	1		2		1	2	2
arCOG00239	I	Lipid transport and metabolism	CaiD	Enoyl-CoA hydratase/carnithine racemase	COG01024	pfam00378	cd06558	TIGR03210	3		1	2		1	3	1		3	12
arCOG01707	I	Lipid transport and metabolism	CaiA	Acyl-CoA dehydrogenase	COG01960	pfam02771,pfam0277	cd00567	TIGR03207	4	3	3	2	1	1	3	1		4	11
arCOG04199	I	Lipid transport and metabolism	FAA1	Long-chain acyl-CoA synthetase (AMP-forming)	COG01022	pfam00501	cd05907	TIGR01923	1	1	1	2	1			1		1	2
arCOG01137	I	Lipid transport and metabolism	FadM	Acyl-CoA thioesterase FadM	COG00824	pfam13279	cd00586	TIGR00051	1		1	1				1		1	1
arCOG04100	I	Lipid transport and metabolism	CaiA	Acyl-CoA dehydrogenase	COG01960											1			
arCOG01529	I	Lipid transport and metabolism	Acs	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	COG00365	pfam00501	cd05966	TIGR02188	1	1				1		2			
arCOG01282	I	Lipid transport and metabolism	PaaJ	Acetyl-CoA acetyltransferase	COG00183	pfam00108,pfam0280	cd00751	TIGR01930	2	2	2	1				2		3	5
arCOG01767	I	Lipid transport and metabolism	PksG	3-hydroxy-3-methylglutaryl CoA synthase	COG03425	pfam08545,pfam0854	cd00827	TIGR00748	1	1	1	1	1				1	3	2
arCOG01278	I	Lipid transport and metabolism	PaaJ	Acetyl-CoA acetyltransferase	COG00183		cd00829	TIGR01930	1	1	1	1					1	1	
arCOG04761	I	Lipid transport and metabolism	UppP	Undecaprenyl pyrophosphate phosphatase	COG01968	pfam02673		TIGR00753	1	2	1	1	1	1					
arCOG01879	I	Lipid transport and metabolism	-	Dolichol kinase family protein	COG00170				1			1						1	
arCOG01880	I	Lipid transport and metabolism	SEC59	Dolichol kinase	COG00170				1								2		
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										
arCOG04470	I	Lipid transport and metabolism	Psd	Phosphatidylserine decarboxylase	COG00688	pfam02666		TIGR00164	2	1	1	1	1					1	
arCOG00671	I	Lipid transport and metabolism	PssA	Phosphatidylserine synthase	COG01183	pfam01066		TIGR04217	2	1		1	1						
arCOG00242	I	Lipid transport and metabolism	CaiD	Enoyl-CoA hydratase/carnithine racemase	COG01024	pfam00378	cd06558	TIGR02280		1									
arCOG01650	I	Lipid transport and metabolism	PldB	Lysophospholipase, alpha-beta hydrolase superfamily	COG02267	pfam12697		TIGR03695									1		1
arCOG03056	I	Lipid transport and metabolism	PgpB	Membrane-associated phospholipid phosphatase	COG00671	pfam01569	cd03392										1		
arCOG07155	I	Lipid transport and metabolism	IspD	4-diphosphocytidyl-2-methyl-D-erithritol synthase	COG01211	pfam01128	cd02516	TIGR00453									1		
arCOG11863	I	Lipid transport and metabolism	-	Membrane diacylglycerol kinase	COG00818	pfam01219	cd14263										1		
arCOG02228	I	Lipid transport and metabolism	GtrA	GtrA-like flippase	COG02246	pfam04138											2		
arCOG02039	I	Lipid transport and metabolism	Cls	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthase or rel	COG01502	pfam13091,pfam1309	cd07493,cd09127,cd09128										3	1	
arCOG00241	I	Lipid transport and metabolism	CaiD	Enoyl-CoA hydratase/carnithine racemase	COG01024	pfam00378	cd06558	TIGR02280										1	1
arCOG01261	I	Lipid transport and metabolism	FabG	Short-chain alcohol dehydrogenase	COG01028	pfam00106	cd05233	TIGR01830										2	1
arCOG03951	I	Lipid transport and metabolism	PgpB	Membrane-associated phospholipid phosphatase	COG00671	pfam01569	cd03386											2	6
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
arCOG01487	F	Nucleotide transport and metabolism	ComEB	Deoxycytidylate deaminase	COG02131	pfam00383	cd01286	TIGR02571	1	1	1	1			1	1	1	1	1
arCOG00067	F	Nucleotide transport and metabolism	PrsA	Phosphoribosylpyrophosphate synthetase	COG00462	pfam13793,pfam0015	cd06223	TIGR01251	1	1	1				1	1	1	1	1
arCOG03214	F	Nucleotide transport and metabolism	ThyA	Thymidylate synthase	COG00207	pfam00303	cd00351	TIGR03283	1	1		1	1		1	1		1	4
arCOG02824	F	Nucleotide transport and metabolism	PurH	AICAR transformylase/IMP cyclohydrolase PurH	COG00138	pfam02142,pfam0180	cd01421	TIGR00355	1	2	1	1	1	1	1	1	1	1	2
arCOG00689	F	Nucleotide transport and metabolism	AllB	Dihydroorotase or related cyclic amidohydrolase	COG00044	pfam13147	cd01318	TIGR00857	1	2	1	1	1		1	1	1	1	2
arCOG04276	F	Nucleotide transport and metabolism	NrdA	Ribonucleotide reductase, alpha subunit	COG00209	pfam03477,pfam0031	cd02888	TIGR02504	1	2	2	1	1	1	1	1	2	1	3
arCOG01039	F	Nucleotide transport and metabolism	AdkA	Archaeal adenylate kinase	COG02019				1	2				1	1	1	1		
arCOG04184	F	Nucleotide transport and metabolism	RdgB	Inosine/xanthosine triphosphate pyrophosphatase, all-alpha NTP-PPase famil	COG00127	pfam01725	cd00515	TIGR00042	1		1			1	1	1	1	1	4
arCOG00028	F	Nucleotide transport and metabolism	-	Orotate phosphoribosyltransferase homolog	COG00856	pfam00156	cd06223	TIGR02985,TIGR	1		1				1	1	1	1	1
arCOG00639	F	Nucleotide transport and metabolism	PurM	Phosphoribosylaminoimidazole (AIR) synthetase	COG00150	pfam00586,pfam0276	cd02196	TIGR00878	2	2	1	1	1	1	1	1	1	1	1
arCOG00029	F	Nucleotide transport and metabolism	PyrE	Orotate phosphoribosyltransferase	COG00461	pfam00156	cd06223	TIGR00336		1	1	1			1	1	1	1	1
arCOG00692	F	Nucleotide transport and metabolism	SsnA	Cytosine deaminase or related metal-dependent hydrolase	COG00402	pfam01979	cd01305	TIGR02967		1	1				1	1	2		
arCOG00419	F	Nucleotide transport and metabolism	Hit	HIT family hydrolase	COG00537	pfam01230	cd01275			1				1	1	1	1	1	4
arCOG01747	F	Nucleotide transport and metabolism	PurB	Adenylosuccinate lyase	COG00015	pfam00206,pfam1039	cd01360	TIGR00928			1				1	1	1	1	2
arCOG00102	F	Nucleotide transport and metabolism	PurL	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransf	COG00047	pfam13507	cd01740	TIGR01737	1	1				1	1	2	1	1	2
arCOG04313	F	Nucleotide transport and metabolism	Ndk	Nucleoside diphosphate kinase	COG00105	pfam00334	cd04413		1	1				1	1	2	1	1	
arCOG00063	F	Nucleotide transport and metabolism	PyrG	CTP synthase (UTP-ammonia lyase)	COG00504	pfam06418,pfam0011	cd03113,cd017	TIGR00337	1	1	1	1	1	1	1		1	1	3
arCOG04462	F	Nucleotide transport and metabolism	PurS	Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component	COG01828	pfam02700		TIGR00302	1	1	1	1	1		1		1	1	2
arCOG04421	F	Nucleotide transport and metabolism	PurC	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	COG00152	pfam01259	cd01415	TIGR00081	1	1	1	1	1		1		1	1	
arCOG00641	F	Nucleotide transport and metabolism	PurL	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain	COG00046	pfam00586,pfam0276	cd02203,cd022	TIGR01736	1	1	1	1	1		1		1		2
arCOG01565	F	Nucleotide transport and metabolism	NrnA	nanoRNase/pAp phosphatase, hydrolyzes c-di-AMP and oligoRNAs	COG00618	pfam01368			1	1	1		1		1		1	1	1
arCOG00911	F	Nucleotide transport and metabolism	PyrB	Aspartate carbamoyltransferase, catalytic chain	COG00540	pfam02729,pfam00185		TIGR00670	1	2	1	1		1	1		1	1	2
arCOG01034	F	Nucleotide transport and metabolism	THEP1	Nucleoside-triphosphatase THEP1	COG01618	pfam03266	cd00009		1	2	1	1		1	1		1	1	2
arCOG04229	F	Nucleotide transport and metabolism	PyrI	Aspartate carbamoyltransferase, regulatory subunit	COG01781	pfam01948,pfam02748		TIGR00240	1	2	1	1		1	1		1	1	2
arCOG04048	F	Nucleotide transport and metabolism	Dcd	Deoxycytidine deaminase	COG00717	pfam00692	cd07557	TIGR02274	1		1				1		1	1	2
arCOG04387	F	Nucleotide transport and metabolism	PurA	Adenylosuccinate synthase	COG00104	pfam00709	cd03108	TIGR00184	1		1				1		1	1	2
arCOG04415	F	Nucleotide transport and metabolism	PurD	Phosphoribosylamine-glycine ligase	COG00151	pfam02844,pfam01071,pfam02843		TIGR00877		1	1	1			1		1	1	1
arCOG01038	F	Nucleotide transport and metabolism	Fap7	Broad-specificity NMP kinase	COG01936	pfam13238				1	1	1			1		1	1	2
arCOG00018	F	Nucleotide transport and metabolism	Nnr2	NAD(P)H-hydrate repair enzyme Nnr, NAD(P)H-hydrate dehydratase domain	COG00063	pfam03853,pfam0125	cd01171	TIGR00197,TIGR00196		1	1	1			1		1		
arCOG00085	F	Nucleotide transport and metabolism	GuaA	GMP synthase, PP-ATPase domain/subunit	COG00519	pfam02540,pfam0095	cd01997	TIGR00884		1	1			1	1		1	1	1
arCOG00090	F	Nucleotide transport and metabolism	GuaA	GMP synthase - Glutamine amidotransferase domain	COG00518	pfam00117	cd01741	TIGR00888		1					1				3
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	1	1	1	1	1	2	1	1	1	4
arCOG01037	F	Nucleotide transport and metabolism	Cmk	Cytidylate kinase	COG01102	pfam13189	cd02020	TIGR02173	1	2	1				2	1	1	1	1
arCOG00087	F	Nucleotide transport and metabolism	GuaA	GMP synthase - Glutamine amidotransferase domain	COG00518	pfam00117	cd01742	TIGR00888	2	1	1	2			2	1	1	1	1
arCOG01891	F	Nucleotide transport and metabolism	Tmk	Thymidylate kinase	COG00125	pfam02223	cd01672	TIGR00041	2	1		1		1	2	1	1	1	2
arCOG00093	F	Nucleotide transport and metabolism	PurF	Glutamine phosphoribosylpyrophosphate amidotransferase	COG00034	pfam00310,pfam0015	cd00715,cd062	TIGR01134	3	3				1	2	2	1	1	2
arCOG02825	F	Nucleotide transport and metabolism	PurN	Folate-dependent phosphoribosylglycinamide formyltransferase PurN	COG00299				3	2	1	1		2	3	2	1	2	3
arCOG02464	F	Nucleotide transport and metabolism	PurE	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase	COG00041	pfam00731		TIGR01162	1	1		1				1	1	1	1
arCOG00612	F	Nucleotide transport and metabolism	GuaB	IMP dehydrogenase/GMP reductase	COG00516	pfam00478	cd00381	TIGR01302	2	2		2				1	1		3
arCOG02807	F	Nucleotide transport and metabolism	AzgA	Xanthine/uracil/vitamin C permease, AzgA family	COG02252	pfam00860				1	1	1				1	1		2
arCOG05252	F	Nucleotide transport and metabolism	-	Predicted secreted endonuclease distantly related to archaeal Holliday junctic	COG04741	pfam10107										1			
arCOG00030	F	Nucleotide transport and metabolism	Apt	Adenine/guanine phosphoribosyltransferase or related PRPP-binding protein	COG00503	pfam00156	cd06223	TIGR01090	1	1		1				4	1	1	4
arCOG00081	F	Nucleotide transport and metabolism	PyrF	Orotidine-5'-phosphate decarboxylase	COG00284	pfam00215	cd04725	TIGR01740	1	2							1	1	2
arCOG03575	F	Nucleotide transport and metabolism	-	Polyphosphate kinase 2	COG02326	pfam03976,pfam0397	cd01672	TIGR03708	1			1		1					
arCOG00858	F	Nucleotide transport and metabolism	PyrH	Uridylate kinase	COG00528	pfam00696	cd04253	TIGR02076									1	1	1
arCOG04541	F	Nucleotide transport and metabolism	MIS1	Formyltetrahydrofolate synthetase	COG02759	pfam01268	cd00477										1	1	2
arCOG01350	F	Nucleotide transport and metabolism	-	Predicted inorganic polyphosphate/ATP-NAD kinase	COG03199	pfam01513											1	1	3
arCOG02013	F	Nucleotide transport and metabolism	DeoA	Thymidine phosphorylase	COG00213	pfam01568,pfam02885,pfam00591,pf		TIGR03327									1	1	
arCOG04311	F	Nucleotide transport and metabolism	-	5'-deoxynucleotidase, HD superfamily hydrolase	COG01896	pfam13023											1	1	
arCOG01075	F	Nucleotide transport and metabolism	-	NUDIX family hydrolase	COG01051	pfam00293	cd04673										1	4	8
arCOG04320	F	Nucleotide transport and metabolism	DeoC	Deoxyribose-phosphate aldolase	COG00274	pfam01791	cd00959	TIGR00126									1		1

arCOG01324	F	Nucleotide transport and metabolism	Udp	Uridine phosphorylase	COG02820	pfam01048		TIGR01718									1		
arCOG01723	F	Nucleotide transport and metabolism	CyaB	Adenylate cyclase, class 2 (thermophilic)	COG01437	pfam01928	cd07890	TIGR00318									1		
arCOG01883	F	Nucleotide transport and metabolism	THY1	Thymidylate synthase	COG01351	pfam02511		TIGR02170									1		
arCOG04173	F	Nucleotide transport and metabolism	Cdd	Cytidine deaminase	COG00295	pfam00383	cd01283	TIGR01354									1		
arCOG04298	F	Nucleotide transport and metabolism	-	Adenosine/AMP kinase	COG01839	pfam04008											1		
arCOG04309	F	Nucleotide transport and metabolism	-	S-adenosyl-l-methionine hydroxide adenosyltransferase	COG01912	pfam01887											1		
arCOG04889	F	Nucleotide transport and metabolism	NrdD	Oxygen-sensitive ribonucleoside-triphosphate reductase	COG01328	pfam13597	cd01675	TIGR02487									1		
arCOG05133	F	Nucleotide transport and metabolism	Udk	Uridine kinase	COG00572	pfam00485	cd02026	TIGR00235									1		
arCOG01327	F	Nucleotide transport and metabolism	Pnp	Purine nucleoside phosphorylase	COG00005	pfam01048		TIGR01694									2	1	2
arCOG00695	F	Nucleotide transport and metabolism	SsnA	Cytosine deaminase or related metal-dependent hydrolase	COG00402	pfam01979	cd01298	TIGR03314									2	2	2
arCOG03658	F	Nucleotide transport and metabolism	NrdF	Ribonucleotide reductase, beta subunit (ferritin domain)	COG00208	pfam00268	cd01049	TIGR04171										1	1
arCOG01046	F	Nucleotide transport and metabolism	Adk	Adenylate kinase or related kinase	COG00563	pfam00406	cd01428	TIGR01351										1	2
arCOG14568	F	Nucleotide transport and metabolism	-	Pseudouridine synthase		pfam00849	cd02554	TIGR00093										1	2
arCOG01566	F	Nucleotide transport and metabolism	NrnA	nanoRNase/pAp phosphatase, hydrolyzes c-di-AMP and oligoRNAs	COG00618	pfam02254,pfam01368,pfam02272												1	
arCOG06976	Q	Secondary metabolites biosynthesis, transport an	HmgA	Homogentisate 1,2-dioxygenase	COG03508				1	1			1	1	1	1			
arCOG00696	Q	Secondary metabolites biosynthesis, transport an	HutI	Imidazolonepropionase or related amidohydrolase	COG01228	pfam13147	cd01296	TIGR01224	1			1		1	1	1	2	1	2
arCOG00235	Q	Secondary metabolites biosynthesis, transport an	MhpD	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (c	COG00179	pfam01557		TIGR02303	2	1		1	1	1	1	1	1	1	1
arCOG04347	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR01934	3	2	1	1		2	1				
arCOG01730	Q	Secondary metabolites biosynthesis, transport an	-	Aromatic ring-opening dioxygenase, catalytic LigB subunit related enzyme	COG03384	pfam02900	cd07363	TIGR02298							1				
arCOG04340	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam13489	cd02440	TIGR02081							1				
arCOG06106	Q	Secondary metabolites biosynthesis, transport an	-	Predicted ring-cleavage extradiol dioxygenase	COG02514	pfam12681,pfam1268	cd07255,cd072	TIGR03211								1			
arCOG03570	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam12847	cd02440	TIGR02021	1	1	1	1		1					1
arCOG01791	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam12847	cd02440	TIGR02021	1	1		1	1	1			1		
arCOG01792	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR01934	1	1		1							
arCOG01781	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR02072	1	1			1	1				1	2
arCOG00777	Q	Secondary metabolites biosynthesis, transport an	PaaI	HGG motif-containing thioesterase, possibly involved in aromatic compounds	COG02050	pfam03061	cd03443	TIGR00369	1	2	1	1	1					1	2
arCOG01521	Q	Secondary metabolites biosynthesis, transport an	-	Phytoene dehydrogenase or related enzyme	COG01233	pfam13450			1	2				1				1	3
arCOG03914	Q	Secondary metabolites biosynthesis, transport an	SufI	Multicopper oxidase	COG02132	pfam07732	cd11024	TIGR02376	1		1		1						
arCOG01523	Q	Secondary metabolites biosynthesis, transport an	-	Phytoene dehydrogenase or related enzyme	COG01233	pfam01593		TIGR03467	1		1			1				1	1
arCOG01778	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR02072		1	1		1	1					
arCOG01782	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR01934			1								
arCOG05015	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam12847	cd02440	TIGR03534									1		1
arCOG01229	Q	Secondary metabolites biosynthesis, transport an	-	Cyclic 2, 3-diphosphoglycerate synthetase	COG02403												1		
arCOG01400	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam05050	cd02440,cd021	TIGR01444									1		
arCOG01729	Q	Secondary metabolites biosynthesis, transport an	-	Aromatic ring-opening dioxygenase, LigB subunit	COG03885	pfam02900	cd07952										1		
arCOG01773	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam08241		TIGR01934									1		
arCOG02702	Q	Secondary metabolites biosynthesis, transport an	-	SAM-dependent methyltransferase	COG00500	pfam08241	cd02440	TIGR02072									1		
arCOG03688	Q	Secondary metabolites biosynthesis, transport an	osmC	Organic hydroperoxide reductase	COG01764	pfam02566		TIGR03561									1		
arCOG01943	Q	Secondary metabolites biosynthesis, transport an	PncA	Amidase related to nicotinamidase	COG01335	pfam00857	cd00431	TIGR03614									2	1	
arCOG04786	Q	Secondary metabolites biosynthesis, transport an	-	1,2-phenylacetyl-CoA epoxidase, catalytic subunit	COG03396	pfam05138		TIGR02158										1	3
arCOG06169	Q	Secondary metabolites biosynthesis, transport an	-	Arylsulfotransferase family protein		pfam05935												1	
arCOG01402	Q	Secondary metabolites biosynthesis, transport an	AglP	SAM-dependent methyltransferase	COG00500	pfam05050		TIGR01444										2	2

POORLY CHARACTERIZED																			
arCOG02177	S	Function unknown	-	Uncharacterized membrane protein	COG01967	pfam01889			1	1	1	1	1	1	1	1		1	2
arCOG04565	S	Function unknown	-	Predicted membrane protein, DUF368 family	COG02035	pfam04018			1	1	1	1		1	1	1			
arCOG05517	S	Function unknown	-	Uncharacterized protein					1	1	1	1			1	1	1		1
arCOG04619	S	Function unknown	-	Uncharacterized membrane protein, contains bPH2 (bacterial pleckstrin hom	COG03428	pfam03703,pfam03703,pfam03703			1	1	1	1			1	1			1
arCOG05368	S	Function unknown	-	Uncharacterized protein	SC.00138				1	1		1	1	1	1	1			1
arCOG04521	S	Function unknown	-	Uncharacterized membrane protein, predicted permease	SC.00496				1		1	1		1	1	1	1	1	2
arCOG04596	S	Function unknown	-	Uncharacterized membrane protein					1		1			1	1	1			
arCOG03678	S	Function unknown	-	Uncharacterized protein	SC.00067				1		1				1	1	1	1	3
arCOG04308	S	Function unknown	-	Uncharacterized protein	COG01698	pfam03685			1			1			1	1	1	1	1
arCOG03729	S	Function unknown	-	Metal-binding cluster containing protein						1					1	1			
arCOG13537	S	Function unknown	-	Uncharacterized protein					1	1	1		1	2	1		1		
arCOG11014	S	Function unknown	-	HTH-domain containing transcriptional regulator	SC.00234	pfam06224			1	1	1				1			1	1
arCOG01224	S	Function unknown	-	Uncharacterized protein	COG01849	pfam04010			1	1		1			1		1	1	2
arCOG02142	S	Function unknown	-	Pheromone shutdown protein TraB, contains GTxH motif	COG01916	pfam01963		TIGR00261	1	2	1	1			1		1	1	1
arCOG03124	S	Function unknown	-	Pentapeptide repeats containing protein	COG01357	pfam00805,pfam00805			1	2	1	1			1			2	3
arCOG03633	S	Function unknown	-	Uncharacterized membrane protein YckC, RDD family	COG01714	pfam06271			1	2					1		1		
arCOG10198	S	Function unknown	-	Uncharacterized membrane protein, DUF2899 family		pfam11449			1	2					1				1
arCOG07412	S	Function unknown	-	Uncharacterized protein					1		1			1	1		1		
arCOG05495	S	Function unknown	-	Uncharacterized protein, contains N-terminal coiled-coil domain	COG04911	pfam09969			1			1			1				
arCOG04076	S	Function unknown	-	Uncharacterized protein, DUF359 family	COG01909	pfam04019			1						1		1	1	3
arCOG07813	S	Function unknown	-	LamG-like jellyroll fold domain	SC.00184	pfam13385			1						1			1	
arCOG04370	S	Function unknown	-	Uncharacterized membrane protein	COG03503	pfam07786			1						1				
arCOG04412	S	Function unknown	-	Uncharacterized protein	COG04004					1	1	1			1		1	1	
arCOG08231	S	Function unknown	-	Periplasmic protein with immunoglobin-like fold		pfam00932				1					1		1	1	
arCOG05330	S	Function unknown	-	Uncharacterized protein						1					1		1		
arCOG02546	S	Function unknown	-	Secreted protein, contains PKD repeats and vWA domain	COG03291	pfam05048,pfam0504	cd00146,cd001	TIGR04247,TIGR04247,TI		1					1				2
arCOG03606	S	Function unknown	-	Uncharacterized protein	SC.00401							1			1				
arCOG01917	S	Function unknown	-	Zn-ribbon domain containing protein											1		3		1
arCOG02998	S	Function unknown	-	Cupin domain containing protein	COG01917	pfam07883									1			1	2
arCOG02492	S	Function unknown	-	Secreted protein, with PKD repeat domain	COG03291										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 a	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	2	2	2	1	1		2	1	2	2	5
arCOG01314	S	Function unknown	-	Uncharacterized membrane anchored protein with extracellular flavodoxin-lik	SC.00272				2	1	1	1			2	2		1	
arCOG08673	S	Function unknown	-	Uncharacterized protein					1	1	1	1			2			1	

arCOG05351	S	Function unknown	-	Uncharacterized membrane protein		pfam11433				2					2		1		
arCOG01907	S	Function unknown	AIM24	Uncharacterized protein, AIM24 family	COG02013	pfam01987		TIGR00266	3	3	3	3		3	3	3	1		1
arCOG03232	S	Function unknown	-	VanZ like family protein	COG05652	pfam04892			1	1		1				1	1		
arCOG07442	S	Function unknown	-	Uncharacterized protein					1	1						1			
arCOG02087	S	Function unknown	-	Predicted membrane protein	COG01470	pfam10633,pfam13620,pfam10633			1	2		1		1		1			2
arCOG04214	S	Function unknown	-	Uncharacterized protein	COG00432	pfam01894		TIGR00149	1		1		1			1	1	1	
arCOG10338	S	Function unknown	-	Uncharacterized protein	SC.00914	pfam13517,pfam13517,pfam13517,pfam13517				2	1		1			1	1		
arCOG05338	S	Function unknown	-	Uncharacterized protein							1		1			1		1	2
arCOG02081	S	Function unknown	-	Predicted membrane protein	COG01470	pfam10633						1				1		2	2
arCOG02206	S	Function unknown	-	Uncharacterized membrane protein										1		1	1		1
arCOG01330	S	Function unknown	-	Uncharacterized membrane protein	COG02426	pfam06695										1	2	1	3
arCOG04269	S	Function unknown	-	Protein, predicted to be involved in DNA repair	COG01602	pfam04894,pfam04895										1	2		
arCOG02565	S	Function unknown	-	Secreted uncharacterized protein	COG05276											1			
arCOG06429	S	Function unknown	-	Uncharacterized protein, contains NRDE domain	COG03332	pfam05742										1			
arCOG02508	S	Function unknown	-	Secreted protein, with PKD repeat domain	COG03291	pfam00801,pfam0080	cd00146,cd001	TIGR00864	1	1	2			1		3		1	
arCOG02884	S	Function unknown	-	Membrane associated protein with extracellular Ig-like domain, a component	COG04743				1	1	1	1		1			2		
arCOG04618	S	Function unknown	-	Uncharacterized protein, DUF2237 family	COG03651	pfam09996			1	1		1	1					1	2
arCOG10444	S	Function unknown	-	Uncharacterized protein					1	1		1	1						4
arCOG12677	S	Function unknown	-	Uncharacterized protein					1	1			1	1					
arCOG04693	S	Function unknown	-	Uncharacterized protein					1	1									1
arCOG03888	S	Function unknown	-	Uncharacterized membrane protein					1	1									
arCOG03949	S	Function unknown	-	Uncharacterized membrane protein	COG03815	pfam09858			1	2	1	1	1	1			1		2
arCOG07680	S	Function unknown	-	Uncharacterized membrane protein	COG02832	pfam04304			1	2	1			1				1	3
arCOG10153	S	Function unknown	-	Uncharacterized membrane protein, DUF4112 family		pfam13430			1	2		1							
arCOG04364	S	Function unknown	-	Uncharacterized protein	COG01772	pfam04407			1	3	1	1	1	2					
arCOG02491	S	Function unknown	-	WD40 repeats containing protein	COG02319	pfam13360			1		1	1		2				1	
arCOG01119	S	Function unknown	-	GYD domain, alpha/beta barrel superfamily	COG04274	pfam08734			1		1	1							
arCOG08355	S	Function unknown	-	Uncharacterized membrane protein					1		1		1	1					
arCOG04566	S	Function unknown	-	Uncharacterized protein					1			1							
arCOG02966	S	Function unknown	-	HEAT repeats containing protein	COG01413				1				1	1					
arCOG03749	S	Function unknown	-	Uncharacterized membrane protein	COG04243	pfam07884	cd12918		1				1						
arCOG06533	S	Function unknown	-	Uncharacterized membrane protein					1					2					
arCOG05022	S	Function unknown	-	Uncharacterized protein, contains PQ loop repeat	COG04095				1									1	1
arCOG11882	S	Function unknown	-	Uncharacterized membrane protein					1										2
arCOG05839	S	Function unknown	-	Uncharacterized protein				TIGR04292	2	1	2		2	2					
arCOG08211	S	Function unknown	-	Uncharacterized membrane protein	SC.00448					1	1			1					
arCOG08977	S	Function unknown	-	Uncharacterized membrane protein	COG04270					1	1							1	2
arCOG09475	S	Function unknown	-	Uncharacterized protein	SC.00862					1									
arCOG06958	S	Function unknown	-	Uncharacterized protein						2							1		2
arCOG04006	S	Function unknown	-	HEAT repeats containing protein	COG01413	pfam13646				2								1	3
arCOG04579	S	Function unknown	-	Uncharacterized protein, DUF2071 family	COG03361	pfam09844					1		1	1				1	2
arCOG06742	S	Function unknown	-	NosD-like cell surface protein							1		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					2		
arCOG04662	S	Function unknown	-	Uncharacterized membrane protein	SC.00128												1	1	
arCOG05345	S	Function unknown	-	Uncharacterized protein													1	1	
arCOG04500	S	Function unknown	-	Uncharacterized protein with Ig-like domain													1	2	1
arCOG02170	S	Function unknown	-	Uncharacterized protein	SC.00300	pfam13559											1		1
arCOG09426	S	Function unknown	-	Uncharacterized membrane protein													1		2
arCOG01302	S	Function unknown	-	Uncharacterized protein	COG01531	pfam04457											1		
arCOG01336	S	Function unknown	AMMECR1	Uncharacterized protein	COG02078	pfam01871		TIGR04335									1		
arCOG01472	S	Function unknown	-	Hemerythrin HHE cation binding domain containing protein	COG02461	pfam04282,pfam01814,pfam13596											1		
arCOG01921	S	Function unknown	-	Uncharacterized protein, DUF61 family	COG02083	pfam01886											1		
arCOG02148	S	Function unknown	-	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase su	COG00599	pfam02627		TIGR04169									1		
arCOG02159	S	Function unknown	-	Uncharacterized membrane protein	COG04089	pfam07758											1		
arCOG02264	S	Function unknown	-	Uncharacterized membrane protein	COG01808	pfam04087		TIGR00341									1		
arCOG02566	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG02717	S	Function unknown	-	Predicted membrane protein, DUF131 family	COG02034	pfam01998											1		
arCOG02991	S	Function unknown	-	Uncharacterized protein, DUF1850 family	COG04729	pfam08905											1		
arCOG03107	S	Function unknown	-	Uncharacterized protein, YigZ/IMPACT family	COG01739	pfam01205,pfam09186		TIGR00257									1		
arCOG03128	S	Function unknown	-	Pentapeptide repeats containing protein	COG01357	pfam13599,pfam13599											1		
arCOG03165	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG03379	S	Function unknown	-	Uncharacterized protein													1		
arCOG03397	S	Function unknown	-	Uncharacterized protein													1		
arCOG03573	S	Function unknown	-	Uncharacterized protein, DUF1015 family	COG04198	pfam06245											1		
arCOG03677	S	Function unknown	-	Uncharacterized protein	SC.00067												1		
arCOG03768	S	Function unknown	-	Uncharacterized membrane protein, DUF973 family	SC.00418	pfam06157											1		
arCOG03776	S	Function unknown	-	Zn finger protein	SC.00092												1		
arCOG03853	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG04051	S	Function unknown	-	Uncharacterized protein	COG02412	pfam04242											1		
arCOG04079	S	Function unknown	-	Uncharacterized protein													1		
arCOG04132	S	Function unknown	-	Uncharacterized protein	COG04697	pfam09910											1		
arCOG04140	S	Function unknown	-	Uncharacterized protein	COG01888	pfam02680											1		
arCOG04253	S	Function unknown	-	Uncharacterized protein	COG01415	pfam05559											1		
arCOG04361	S	Function unknown	-	Predicted metal-binding protein	COG05423	pfam10050											1		
arCOG04373	S	Function unknown	-	Uncharacterized protein YqgV, UPF0045/DUF77 family	COG00011	pfam01910		TIGR00106									1		
arCOG04390	S	Function unknown	-	Uncharacterized protein containing a Zn-ribbon	COG04068	pfam09889											1		
arCOG04424	S	Function unknown	-	Uncharacterized protein	COG03377	pfam08827											1		
arCOG04484	S	Function unknown	-	Uncharacterized membrane protein, DUF1648 family	COG05658	pfam07853,pfam13630											1		
arCOG04555	S	Function unknown	-	Uncharacterized membrane protein related to bactofilin		pfam04519,pfam04519											1		
arCOG04705	S	Function unknown	-	Uncharacterized protein	COG02098	pfam04036,pfam04038											1		

arCOG04938	S	Function unknown	-	Uncharacterized membrane protein	SC.00516												1		
arCOG05238	S	Function unknown	-	Uncharacterized protein													1		
arCOG05308	S	Function unknown	-	Uncharacterized membrane protein	SC.00137												1		
arCOG05325	S	Function unknown	-	Uncharacterized protein													1		
arCOG05327	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG05352	S	Function unknown	-	Uncharacterized protein													1		
arCOG05357	S	Function unknown	-	Uncharacterized protein													1		
arCOG05358	S	Function unknown	-	Uncharacterized protein													1		
arCOG05389	S	Function unknown	-	Uncharacterized protein													1		
arCOG05460	S	Function unknown	-	Uncharacterized Zn-finger protein	COG01326												1		
arCOG05631	S	Function unknown	-	Uncharacterized protein													1		
arCOG05717	S	Function unknown	-	Uncharacterized protein	SC.00530												1		
arCOG05739	S	Function unknown	-	Uncharacterized protein with conserved CXXC pairs, DUF1667 family	COG03862	pfam07892											1		
arCOG05759	S	Function unknown	-	Uncharacterized protein		pfam12646											1		
arCOG05783	S	Function unknown	-	Uncharacterized protein													1		
arCOG05800	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG05803	S	Function unknown	-	Uncharacterized protein													1		
arCOG06053	S	Function unknown	-	Uncharacterized protein													1		
arCOG06113	S	Function unknown	-	Zn finger protein, C2C2 type	SC.00488												1		
arCOG06115	S	Function unknown	-	Pleckstrin homology domain containing proteins	SC.00612	pfam14470,pfam09851											1		
arCOG06521	S	Function unknown	-	Uncharacterized protein													1		
arCOG06692	S	Function unknown	-	Uncharacterized protein													1		
arCOG06939	S	Function unknown	-	WbqC-like protein family		pfam08889											1		
arCOG07169	S	Function unknown	-	Uncharacterized protein													1		
arCOG07353	S	Function unknown	-	Zn-ribbon protein													1		
arCOG07356	S	Function unknown	-	Uncharacterized protein													1		
arCOG07411	S	Function unknown	-	Uncharacterized membrane protein	SC.00711												1		
arCOG08157	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG08946	S	Function unknown	-	Uncharacterized protein													1		
arCOG09581	S	Function unknown	-	Uncharacterized membrane protein, DUF1700 family	COG04709	pfam08006											1		
arCOG09752	S	Function unknown	-	Uncharacterized membrane protein, DUF2068	COG03305												1		
arCOG10088	S	Function unknown	-	Uncharacterized protein	COG05504												1		
arCOG10150	S	Function unknown	-	Uncharacterized protein	SC.00215												1		
arCOG10658	S	Function unknown	-	Uncharacterized protein													1		
arCOG10671	S	Function unknown	-	Uncharacterized protein													1		
arCOG10940	S	Function unknown	-	Uncharacterized membrane protein	SC.00942												1		
arCOG11614	S	Function unknown	-	Uncharacterized protein													1		
arCOG11996	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13491	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13492	S	Function unknown	-	Uncharacterized protein													1		
arCOG13493	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13494	S	Function unknown	-	Uncharacterized protein													1		
arCOG13495	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13496	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13498	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13499	S	Function unknown	-	Uncharacterized protein, DUF4125 family		pfam13526											1		
arCOG13500	S	Function unknown	-	Uncharacterized protein													1		
arCOG13502	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13503	S	Function unknown	-	Uncharacterized protein													1		
arCOG13507	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13508	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13509	S	Function unknown	-	Uncharacterized protein													1		
arCOG13511	S	Function unknown	-	Uncharacterized protein													1		
arCOG13515	S	Function unknown	-	Uncharacterized protein													1		
arCOG13516	S	Function unknown	-	Uncharacterized protein													1		
arCOG13517	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13518	S	Function unknown	-	Uncharacterized protein													1		
arCOG13520	S	Function unknown	-	Uncharacterized protein		pfam02677											1		
arCOG13521	S	Function unknown	-	Uncharacterized membrane protein	SC.01004												1		
arCOG13523	S	Function unknown	-	Uncharacterized protein													1		
arCOG13524	S	Function unknown	-	Uncharacterized protein	SC.00667												1		
arCOG13525	S	Function unknown	-	Uncharacterized protein													1		
arCOG13526	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13527	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13528	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13529	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13530	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13533	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13534	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13535	S	Function unknown	-	Uncharacterized protein													1		
arCOG13539	S	Function unknown	-	Uncharacterized protein													1		
arCOG13540	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13541	S	Function unknown	-	Uncharacterized protein													1		
arCOG13542	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13543	S	Function unknown	-	Uncharacterized membrane protein													1		
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arCOG13545	S	Function unknown	-	Uncharacterized protein													1		
arCOG13547	S	Function unknown	-	Uncharacterized protein													1		
arCOG13548	S	Function unknown	-	Uncharacterized protein													1		
arCOG13549	S	Function unknown	-	Uncharacterized protein													1		
arCOG13551	S	Function unknown	-	Uncharacterized membrane protein													1		

arCOG13552	S	Function unknown	-	Uncharacterized protein													1		
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arCOG13559	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13560	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13561	S	Function unknown	-	Uncharacterized protein													1		
arCOG13562	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13563	S	Function unknown	-	Uncharacterized protein													1		
arCOG13564	S	Function unknown	-	Uncharacterized membrane protein	SC.01004												1		
arCOG13565	S	Function unknown	-	Uncharacterized protein													1		
arCOG13566	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG13567	S	Function unknown	-	Uncharacterized protein													1		
arCOG15190	S	Function unknown	-	Uncharacterized membrane protein													1		
arCOG02545	S	Function unknown	-	Secreted protein, with PKD repeat domain	COG03291	pfam13229,pfam13229,pfam00801		TIGR04247									2		
arCOG03338	S	Function unknown	-	Uncharacterized membrane protein	SC.00033												2		
arCOG03817	S	Function unknown	-	Uncharacterized protein	SC.00100												2		
arCOG05407	S	Function unknown	-	Uncharacterized protein													2		
arCOG05805	S	Function unknown	-	Uncharacterized protein	SC.00141												2		
arCOG08126	S	Function unknown	-	Uncharacterized membrane protein	SC.00775												2		
arCOG09431	S	Function unknown	-	Uncharacterized protein		pfam14478											2		
arCOG10041	S	Function unknown	-	Uncharacterized membrane protein HdeD, DUF308 family	COG03247												2		
arCOG12007	S	Function unknown	-	Uncharacterized protein													2		
arCOG13538	S	Function unknown	-	Uncharacterized membrane protein	SC.00702												2		
arCOG02994	S	Function unknown	-	Cupin domain containing protein	COG01917	pfam07883											3		
arCOG10113	S	Function unknown	-	Uncharacterized protein													3		
arCOG10161	S	Function unknown	-	Uncharacterized protein													3		
arCOG03118	S	Function unknown	-	Membrane protein DegA family	COG01238	pfam09335												1	1
arCOG07655	S	Function unknown	-	Uncharacterized protein														1	1
arCOG01713	S	Function unknown	-	Uncharacterized protein	COG05440	pfam10061												1	3
arCOG02561	S	Function unknown	-	WD40 repeats containing protein	COG02319	pfam13191,pfam1160	cd00200,cd002	TIGR02794,TIGR02800,TIGR02800										1	3
arCOG00620	S	Function unknown	-	Uncharacterized conserved DUF39 domain fused to CBS domain	COG01900	pfam01837,pfam0057	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
arCOG04987	S	Function unknown	-	Uncharacterized protein															1
arCOG05100	S	Function unknown	-	Uncharacterized membrane protein	COG02364														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
arCOG02614	S	Function unknown	-	Uncharacterized conserved protein															2
arCOG10301	S	Function unknown	-	Uncharacterized protein	COG03011	pfam04134													2
arCOG02284	R	General function prediction only	-	Secreted protein containing C-terminal beta-propeller domain distantly relate	COG04880	pfam09826			1	1	1		1	1	1	1		1	1
arCOG08640	R	General function prediction only	-	Predicted RNA-binding protein containing PUA-domain	COG02947	pfam01878			1	1	2			1	1	1		1	4
arCOG06896	R	General function prediction only	RRM	RNA-binding protein, RRM domain	COG00724	pfam00076	cd12399	TIGR01622	1	1		1			1	1			
arCOG00833	R	General function prediction only	RimI	Acetyltransferase (GNAT) family	COG00456	pfam00583	cd04301	TIGR01575	1	1					1	1	1	1	
arCOG02452	R	General function prediction only	-	KaiC-like protein ATPase	COG00467				1	1					1	1	3	1	
arCOG04430	R	General function prediction only	-	HD superfamily phosphohydrolase	COG01078	pfam01966	cd00077		1	2	1	1	1	1	1	1	1	1	2
arCOG02680	R	General function prediction only	-	Uncharacterized archaeal Zn-finger protein	COG01326				1	2	1	1	1	1	1	1	1	1	
arCOG04227	R	General function prediction only	-	Predicted CoA-binding protein	COG01832	pfam13380		TIGR02717	1	2	1	1			1	1		1	1
arCOG00557	R	General function prediction only	Lhr	Lhr-like helicase	COG01201	pfam00270,pfam0027	cd00046,cd000	TIGR04121	1		1	1	1		1	1	2	1	2
arCOG01150	R	General function prediction only	-	Predicted phosphohydrolase, MPP superfamily	COG01407		cd07391	TIGR00024	1		1	1	1		1	1	2		
arCOG01857	R	General function prediction only	-	SpoU rRNA Methylase family enzyme	COG01303	pfam01994			1		1	1		1	1	1	1	1	2
arCOG04151	R	General function prediction only	-	ABC-type multidrug transport system, permease component	COG02237	pfam04123			1		1	1		1	1	1	1	1	2
arCOG09205	R	General function prediction only	-	Predicted metal-dependent hydrolase	COG01547	pfam03745			1		1		1	1	1	1			
arCOG09415	R	General function prediction only	-	Membrane associated metal-binding domain fused to Reeler domain		pfam02014	cd08544		1		1			2	1	1		2	6
arCOG00626	R	General function prediction only	TlyC	Hemolysins or related protein containing CBS domains	COG01253	pfam01595,pfam0057	cd04590	TIGR03520	1			1			1	1		1	2
arCOG02291	R	General function prediction only	-	HAD superfamily hydrolase	COG01011	pfam13419	cd01427	TIGR02252							1	1	2		
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	1				1	1	2		1	1
arCOG04807	R	General function prediction only	OPT	Uncharacterized membrane protein, oligopeptide transporter (OPT) family	COG01297	pfam03169		TIGR00733	2	3	1	1			1	2		2	1
arCOG00517	R	General function prediction only	-	Rhodanese Homology Domain fused to Zn-dependent hydrolase of beta-lacta	COG00491	pfam00753		TIGR03413	1	2	1				1	3		2	1
arCOG01360	R	General function prediction only	-	MiaB family, Radical SAM enzyme	COG01244	pfam04055	cd01335	TIGR01210	1	1	1	1		1	1		1	1	1
arCOG04278	R	General function prediction only	-	Predicted aconitase	COG01679	pfam04412	cd01355		1	1	1	1		1	1		1	1	1
arCOG00215	R	General function prediction only	CinA	Predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis	COG01058	pfam00994	cd00885	TIGR00200	1	1	1	1		1	1				
arCOG00505	R	General function prediction only	-	Metal-dependent hydrolase of the beta-lactamase superfamily II	COG00491	pfam00753		TIGR03413	1	1	1	1		1	1				
arCOG01641	R	General function prediction only	-	Predicted RNA-binding protein, contains TRAM domain	COG03269				1	1	1	1			1		1		1
arCOG00504	R	General function prediction only	-	Metal-dependent hydrolase of the beta-lactamase superfamily II	COG00491	pfam00753		TIGR03413	1	1	1	1			1			3	1
arCOG00348	R	General function prediction only	-	Archaeal enzyme of ATP-grasp superfamily	COG02047	pfam09754		TIGR00162	1	1		1	1	1	1		1	1	2
arCOG04055	R	General function prediction only	-	SHS2 domain protein implicated in nucleic acid metabolism	COG01371	pfam01951			1	1		1			1		1	1	1
arCOG00313	R	General function prediction only	Sco1	Cytochrome oxidase Cu insertion factor, SCO1/SenC/PrrC family	COG01999	pfam02630	cd02968		1	1			1		1			2	

arCOG00893	R	General function prediction only	-	Predicted metal-dependent hydrolase (urease superfamily)	COG01831	pfam01026			1	1					1		1	1	2
arCOG00543	R	General function prediction only	-	Predicted metal-dependent RNase, consists of a metallo-beta-lactamase dom	COG01782	pfam00753,pfam1099	cd02410	TIGR03675	1		1	1	1	1	1		1	1	5
arCOG01093	R	General function prediction only	-	Protein distantly related to bacterial ferritins	COG02406	pfam00210	cd01052		1			1			1				
arCOG00347	R	General function prediction only	-	Archaeal enzyme of ATP-grasp superfamily	COG01938	pfam09754		TIGR00161	2		1	1	1	1	1		1	2	1
arCOG04628	R	General function prediction only	-	Predicted metal-dependent hydrolase	COG01547	pfam03745				1	1	1			1				
arCOG02579	R	General function prediction only	-	Fe-S-cluster containining protein	COG00727					1					1			2	1
arCOG03096	R	General function prediction only	-	NAD dependent epimerase/dehydratase family enzyme	COG01090	pfam01370,pfam0833	cd05242	TIGR01777		2				1	1			1	3
arCOG03991	R	General function prediction only	-	PKD repeats containing protein	COG03291	pfam00801	cd00146	TIGR00864,TIGR04213					1		1				2
arCOG04212	R	General function prediction only	-	Predicted DNA-binding protein with PD1-like DNA-binding motif	COG01661	pfam03479	cd11378								1		1	1	1
arCOG06747	R	General function prediction only	-	SIR2 superfamily protein	COG00846	pfam02146,pfam1328	cd01406								1				
arCOG06769	R	General function prediction only	-	GTPase SAR1 family domain fused to Leucine-rich repeats domain	COG01100	pfam13855,pfam1385	cd00116,cd099	TIGR00231							1				
arCOG00499	R	General function prediction only		Metal-dependent hydrolase of the beta-lactamase superfamily	COG01235	pfam12706		TIGR02651	1	1	1	1	1	1	2	1	1	1	1
arCOG01225	R	General function prediction only	-	GTPase SAR1 or related small G protein	COG01100	pfam03029	cd02027,cd00880		1	1	1	1	1	1	2	1	1	1	
arCOG04444	R	General function prediction only	-	ACT domain containing protein	COG04747	pfam01842,pfam0184	cd04908,cd04908		1	1	1	1	1		2	1			2
arCOG00062	R	General function prediction only	-	Predicted amidohydrolase	COG00388	pfam00795	cd07197	TIGR03381	1	2	1	1	1	1	2	1	2		
arCOG02293	R	General function prediction only	-	HAD superfamily hydrolase	COG00637	pfam13419	cd01427	TIGR02009	2	3	1	2	1	2	2	1	2		
arCOG02742	R	General function prediction only	-	Uncharacterized membrane anchored protein with extracellular vWF domain	COG01721	pfam01882			2	1	1	2			2	2	1	2	4
arCOG04303	R	General function prediction only	-	Uncharacterized Rossmann fold enzyme	COG01634	pfam01973	cd07995		1	1	1		1		2		1	1	1
arCOG03450	R	General function prediction only	-	Predicted surface protease of transglutaminase family					1	2	1	1		1	2		1		
arCOG04466	R	General function prediction only	-	Na+-dependent transporter of the SNF family	COG00733	pfam00209	cd10336		1	2		1		1	2			1	3
arCOG04950	R	General function prediction only	YggS	Uncharacterized pyridoxal phosphate-containing protein, affects Ilv metabolis	COG00325	pfam01168	cd00635	TIGR00044	1						2		1		
arCOG04624	R	General function prediction only	-	Multimeric flavodoxin WrbA	COG00431				1						2			1	1
arCOG02155	R	General function prediction only	-	Protein implicated in RNA metabolism, contains PRC-barrel domain	COG01873	pfam05239			1	1	1	1	1	1	4	1	2	1	2
arCOG03682	R	General function prediction only	SPS1	Membrane associated serine/threonine protein kinase	COG00515	pfam00069	cd14014		2	3	2	1	2		4	2		1	
arCOG02174	R	General function prediction only	-	Predicted exporter of the RND superfamily	COG01033	pfam03176,pfam03176		TIGR00921	4	4	4	3		3	5	1	1	6	11
arCOG01848	R	General function prediction only	WbbJ	Acetyltransferase (isoleucine patch superfamily)	COG00110	pfam00132,pfam0013	cd03358	TIGR03570	1	2				1		1		1	1
arCOG06534	R	General function prediction only	-	Cohesin domain containing secreted protein		pfam00963	cd08547		1			1				1		1	
arCOG07590	R	General function prediction only	-	Predicted acyl esterase	COG02936	pfam02129,pfam08530		TIGR00976	3	4	1	2	2	2		1		2	5
arCOG05343	R	General function prediction only	-	GTPase SAR1 or related small G protein	COG01100	pfam00071	cd00154	TIGR00231				1		1		1	1		
arCOG03439	R	General function prediction only	-	vWFa domain containing protein								2				1	1	2	3
arCOG04179	R	General function prediction only	PDCD5	DNA-binding TFAR19-related protein, PDSD5 family	COG02118	pfam01984										1	1	1	
arCOG00601	R	General function prediction only	-	Protein containing two CBS domains (some fused to C-terminal double-strand	COG00517	pfam00571,pfam0057	cd04633,cd046	TIGR01302,TIGR01302								1	1		
arCOG02935	R	General function prediction only	-	Pirin-related protein	COG01741	pfam02678,pfam05726										1		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,pfam0080	cd14251,cd001	TIGR04247,TIGR04275,TIGR04275,TIGR04275,TIGR04275,TIGR04275,TIGR04275,TIGR04								1			
arCOG06897	R	General function prediction only	-	Predicted ATP-grasp enzyme	COG03919	pfam15632		TIGR01369	3	3	1		1	1		4			
arCOG03038	R	General function prediction only	-	TPR repeats containing protein	COG00457				1	2	1	2	1	1		5	4	2	3
arCOG01285	R	General function prediction only	-	OB-fold domain and Zn-ribbon containing protein, possible acyl-CoA-binding p	COG01545	pfam12172,pfam01796			1	1	1	1					1		
arCOG01651	R	General function prediction only	-	Alpha/beta superfamily hydrolase	COG01073	pfam08538			1	1	1	2					2		2
arCOG02812	R	General function prediction only	-	Bacteriorhodopsin	COG05524	pfam01036			1	1	1								1
arCOG00352	R	General function prediction only	Nog1	GTP-binding protein, GTP1/Obg family	COG01084	pfam01926	cd01897	TIGR02729	1	1		1					1	1	1
arCOG01108	R	General function prediction only	AbgB	Metal-dependent amidase/aminoacylase/carboxypeptidase	COG01473	pfam01546	cd03886	TIGR01891	1	1		1					1		1
arCOG07416	R	General function prediction only	MhpC	Alpha/beta superfamily hydrolase	COG00596	pfam12695		TIGR03695	1	1								1	1
arCOG05195	R	General function prediction only	-	TPR repeats containing protein	COG00457	pfam13414	cd00189	TIGR02521	1	1									2
arCOG02889	R	General function prediction only	-	Predicted deacylase	COG03608	pfam04952	cd06252	TIGR02994	1	1									
arCOG01425	R	General function prediction only	-	RecB family nuclease with coiled-coil N-terminal domain	SC.00001				1		1	1	1						1
arCOG02259	R	General function prediction only	-	Zn-finger domain containing protein	SC.00304				1			1	1	1					
arCOG01234	R	General function prediction only	-	GTPase, G3E family	COG00523	pfam02492,pfam0768	cd03112	TIGR02475	1			1							2
arCOG01141	R	General function prediction only	-	ICC-like phosphoesterase	COG00622	pfam12850	cd00841	TIGR00040	1								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										
arCOG01622	R	General function prediction only	MviM	Predicted dehydrogenase	COG00673	pfam01408,pfam02894			2					1				1	
arCOG03509	R	General function prediction only	-	Cell surface protein, containing PKD repeats	COG03291	pfam10102				1	1								
arCOG00614	R	General function prediction only	SpoIVFB	Zn-dependent protease	COG01994		cd06158			1							1	1	2
arCOG03015	R	General function prediction only	-	Uncharacterized protein YbjT, contains NAD(P)-binding and DUF2867 domains	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		2									1
arCOG03048	R	General function prediction only	-	TPR repeats containing protein	COG00457	pfam13414,pfam1343	cd00189,cd001	TIGR02917			1	1	1						
arCOG04932	R	General function prediction only	-	Cell surface protein	COG01470						1			1					
arCOG01213	R	General function prediction only	Cof	HAD superfamily hydrolase	COG00561	pfam08282	cd01427	TIGR01487			1							1	2
arCOG03850	R	General function prediction only	-	Predicted O-methyltransferase YrrM	COG04122	pfam13578								1					
arCOG00302	R	General function prediction only	-	Metal-dependent phosphoesterase (PHP family)	COG00613	pfam02811,pfam1326	cd07432										1	1	1
arCOG00353	R	General function prediction only	HflX	GTP-binding protein protease modulator	COG02262	pfam13167,pfam0192	cd01878	TIGR03156									1	1	1
arCOG01043	R	General function prediction only	-	Predicted RNA binding protein with dsRBD fold	COG01931	pfam01877											1	1	1
arCOG04589	R	General function prediction only	CinA	Uncharacterized protein (competence- and mitomycin-induced)	COG01546	pfam02464		TIGR00199									1	1	1
arCOG05137	R	General function prediction only	-	TPR repeats containing protein	COG00457	pfam13414,pfam1341	cd00189,cd001	TIGR02917									1	1	1
arCOG00932	R	General function prediction only	-	Uncharacterized protein related to pyruvate formate-lyase activating enzyme	COG02108	pfam04055	cd01335										1	1	2
arCOG04116	R	General function prediction only	-	ATPase (PilT family)	COG01855	pfam00437	cd09878,cd01130										1	1	2
arCOG04265	R	General function prediction only	-	C4-type Zn-finger protein	COG01779	pfam03367		TIGR00340									1	1	3
arCOG01084	R	General function prediction only	MazG	Predicted pyrophosphatase	COG01694	pfam03819	cd11535										1	1	
arCOG02448	R	General function prediction only	-	Uncharacterized Fe-S center protein	COG02768	pfam04015,pfam12838		TIGR01971									1		2
arCOG00254	R	General function prediction only	-	Predicted dinucleotide-utilizing enzyme	COG01712	pfam03447,pfam01958		TIGR03855									1		
arCOG00600	R	General function prediction only	-	CBS domain	COG00517	pfam00571,pfam0057	cd04623,cd046	TIGR01302,TIGR00393									1		
arCOG00662	R	General function prediction only	-	Biotin synthase-related protein, radical SAM superfamily	COG02516	pfam04055	cd01335	TIGR04317,TIGR04043									1		
arCOG00691	R	General function prediction only	-	Predicted metal-dependent hydrolase with the TIM-barrel fold	COG01574	pfam07969	cd01300										1		
arCOG00769	R	General function prediction only	ThiJ	Putative intracellular protease/amidase	COG00693	pfam01965	cd03134	TIGR01382									1		
arCOG00828	R	General function prediction only	-	Acetyltransferase GNAT superfamily	COG03393	pfam08445		TIGR01575									1		
arCOG00913	R	General function prediction only	-	Predicted methyltransferase	COG01568	pfam01861											1		
arCOG00933	R	General function prediction only	-	Radical SAM superfamily enzyme	COG01964	pfam04055	cd01335	TIGR02666									1		

arCOG00940	R	General function prediction only	-	Radical SAM superfamily enzyme	COG00535	pfam04055,pfam1318	cd01335	TIGR04055									1		
arCOG00969	R	General function prediction only	-	Predicted hydrolase (metallo-beta-lactamase superfamily)	COG02248	pfam12706											1		
arCOG01145	R	General function prediction only	-	Phosphohydrolase, Icc/MPP superfamily	COG02129	pfam00149	cd07392										1		
arCOG01263	R	General function prediction only	DltE	Short-chain dehydrogenase	COG00300		cd05233	TIGR01830									1		
arCOG01294	R	General function prediction only	HcaD	NAD(FAD)-dependent dehydrogenase	COG00446	pfam13510,pfam0799	cd00207,cd052	TIGR01372									1		
arCOG01295	R	General function prediction only	HcaD	NAD(FAD)-dependent dehydrogenase	COG00446	pfam07992		TIGR01292									1		
arCOG01377	R	General function prediction only	-	Phosphodiesterase of AP superfamily	COG03379	pfam01663											1		
arCOG01378	R	General function prediction only	-	Uncharacterized protein of the AP superfamily	COG01524	pfam01663											1		
arCOG01455	R	General function prediction only	AdhP	Zn-dependent alcohol dehydrogenase	COG01064	pfam08240,pfam0010	cd08259	TIGR02824									1		
arCOG01492	R	General function prediction only	YjgC	Predicted molibdopterin-dependent oxidoreductase YjgC	COG03383	pfam13510,pfam1058	cd00207,cd027	TIGR02512,TIGR01591									1		
arCOG01728	R	General function prediction only	Mho1	Predicted class III extradiol dioxygenase, MEMO1 family	COG01355	pfam01875	cd07361	TIGR04336									1		
arCOG01801	R	General function prediction only	Imp	TRAP-type uncharacterized transport system, periplasmic component	COG02358	pfam12974	cd13567	TIGR02122									1		
arCOG01849	R	General function prediction only	PaaY	Isoleucine patch superfamily protein	COG00663		cd04650	TIGR02287									1		
arCOG01906	R	General function prediction only	-	TRAP-type uncharacterized transport system, fused permease component	COG04666	pfam06808		TIGR02123									1		
arCOG02008	R	General function prediction only	-	Uncharacterized membrane protein, a putative transporter component	COG03371	pfam06197											1		
arCOG02238	R	General function prediction only	-	Predicted DNA-binding protein	COG01342	pfam02001		TIGR02937									1		
arCOG02317	R	General function prediction only	-	Predicted regulator of amino acid metabolism, contains ACT domain	COG02150												1		
arCOG02431	R	General function prediction only	-	Predicted Rossmann fold nucleotide-binding protein	COG01611			TIGR00725									1		
arCOG02444	R	General function prediction only	-	Predicted permease	COG03368	pfam09847											1		
arCOG02828	R	General function prediction only	-	NAD dependent epimerase/dehydratase family	COG03367	pfam07755											1		
arCOG02900	R	General function prediction only	-	vWFA domain containing protein	COG02304	pfam00092	cd00198										1		
arCOG02902	R	General function prediction only	-	vWFA domain containing protein	COG02304	pfam13519	cd01467										1		
arCOG03045	R	General function prediction only	-	TPR repeats containing protein	COG00457	pfam13424	cd00189,cd00189										1		
arCOG03427	R	General function prediction only	-	DMT superfamily transporter	COG02510												1		
arCOG03639	R	General function prediction only	-	Predicted glutamine amidotransferase	COG00121		cd01908										1		
arCOG03691	R	General function prediction only	-	Cell surface protein													1		
arCOG04065	R	General function prediction only	PqqL	Zn-dependent peptidase	COG00612	pfam00675,pfam05193											1		
arCOG04115	R	General function prediction only	SfsA	DNA-binding protein, stimulates sugar fermentation	COG01489	pfam03749		TIGR00230									1		
arCOG04230	R	General function prediction only	-	HD supefamily hydrolase	COG03294												1		
arCOG04290	R	General function prediction only	-	PIN-domain and Zn ribbon	COG01656	pfam01927											1		
arCOG04291	R	General function prediction only	-	Sugar isomerase related protein	COG01801	pfam01904											1		
arCOG04331	R	General function prediction only	-	Thioesterase-like protein	COG05496		cd03440										1		
arCOG04354	R	General function prediction only	-	Tripartite tricarboxylate transporter (TTT) class transporter	COG01906	pfam04165		TIGR00529									1		
arCOG04359	R	General function prediction only	-	Predicted RNA-binding protein containing a C-terminal EMAP domain	COG02517	pfam01588	cd02796	TIGR00472									1		
arCOG04410	R	General function prediction only	-	Predicted ATP-grasp domain fused to redox center	COG01578	pfam01937											1		
arCOG04418	R	General function prediction only	-	Predicted HTH domain, homologous to N-terminal domain of RPA1 protein fa	COG03612	pfam09999											1		
arCOG04426	R	General function prediction only	HybF	Zn finger protein HypA/HybF (possibly regulating hydrogenase expression)	COG00375	pfam01155		TIGR00100									1		
arCOG04477	R	General function prediction only	-	Predicted metal binding protein, contains two cysteine clusters	COG01860	pfam03684											1		
arCOG05097	R	General function prediction only	-	CBS domain	COG00517	pfam00571,pfam0057	cd02205	TIGR01302									1		
arCOG05366	R	General function prediction only	-	Cell surface protein	COG01572	pfam07705											1		
arCOG05810	R	General function prediction only	-	Uncharacterized protein, homolog of lactam utilization protein B	COG01540	pfam03746	cd10787										1		
arCOG05825	R	General function prediction only	-	Radical SAM superfamily enzyme	COG01856	pfam04055	cd01335										1		
arCOG07368	R	General function prediction only	-	Cell surface protein	COG01572	pfam07705											1		
arCOG11082	R	General function prediction only	-	Uncharacterized membrane protein, a component of a putative secretion system													1		
arCOG00497	R	General function prediction only	-	Zn-dependent hydrolase of the beta-lactamase fold	COG02220	pfam13483											2	1	
arCOG00606	R	General function prediction only	-	CBS domain	COG00517	pfam00478	cd04623	TIGR01302									2	1	
arCOG04469	R	General function prediction only	-	Tripartite tricarboxylate transporter (TTT) class transporter	COG01784	pfam01970											2	1	
arCOG03032	R	General function prediction only	-	TPR repeats containing protein	COG00457	pfam13414,pfam1341	cd00189	TIGR02917									2		1
arCOG00503	R	General function prediction only	-	Metal-dependent hydrolase of the beta-lactamase superfamily II	COG01237	pfam00753		TIGR03675									2		
arCOG01688	R	General function prediction only	-	Predicted transcriptional regulator, contains HTH and 4VR domain	COG01719	pfam02830											2		
arCOG01963	R	General function prediction only	-	PhoU-like domain fused to TrkA-C domain	COG03273	pfam01895,pfam02080											2		
arCOG02292	R	General function prediction only	Gph	HAD superfamily hydrolase	COG00546	pfam13419	cd01427	TIGR03351									2		
arCOG02603	R	General function prediction only	-	Roadblock/LC7 domain	COG02018												2		
arCOG03167	R	General function prediction only	-	Predicted ATPase, AAA+ superfamily	COG01373	pfam13173,pfam13635											2		
arCOG03400	R	General function prediction only	-	Predicted RNA-binding protein, contains TRAM domain	COG04085	pfam01336	cd04485										2		
arCOG04409	R	General function prediction only	-	Predicted nuclease (RNAse H fold)	COG02410	pfam04250											2		
arCOG07997	R	General function prediction only	-	Predicted OB fold RNA-binding domain fused metal-dependent hydrolase	COG01988	pfam01336,pfam04307											2		
arCOG00938	R	General function prediction only	-	Radical SAM superfamily enzyme	COG00535	pfam04055,pfam1318	cd01335	TIGR04084									5		
arCOG02175	R	General function prediction only	-	Predicted transporter of the RND superfamily	COG02409	pfam03176,pfam03176		TIGR00833,TIGR00833										1	1
arCOG10597	R	General function prediction only	-	Hemocyanin family protein, binds copper ions		pfam00264												1	1
arCOG11383	R	General function prediction only	-	MOCS domain, sulfur-carrier protein	COG02258	pfam03473												1	1
arCOG00498	R	General function prediction only	-	Metal-dependent hydrolase of the beta-lactamase superfamily II	COG00491	pfam00753		TIGR03413										1	2
arCOG00500	R	General function prediction only	ElaC	Metal-dependent hydrolase of the beta-lactamase superfamily	COG01234	pfam12706		TIGR02651										1	2
arCOG00502	R	General function prediction only	PhnP	Metal-dependent hydrolase of the beta-lactamase superfamily	COG01235													1	2
arCOG02642	R	General function prediction only	PerM	Predicted PurR-regulated permease PerM	COG00628	pfam01594		TIGR02872										1	2
arCOG02890	R	General function prediction only	-	Predicted deacylase	COG03608	pfam04952	cd06251	TIGR02994										1	2
arCOG04743	R	General function prediction only	-	Helicase associated uncharacterized terminal domain		pfam05854												1	2
arCOG00654	R	General function prediction only	-	Predicted periplasmic solute-binding protein	COG02107	pfam02621	cd13534											1	3
arCOG00655	R	General function prediction only	-	Predicted periplasmic solute-binding protein	COG01427	pfam02621	cd13634											1	3
arCOG01189	R	General function prediction only	AarF	Predicted unusual protein kinase	COG00661	pfam03109	cd05121	TIGR01982										1	3
arCOG01030	R	General function prediction only	-	Predicted kinase related to galactokinase and mevalonate kinase	COG02605													1	6
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	
arCOG03241	R	General function prediction only	-	ATPase AAA family	COG04637	pfam13304,pfam13304												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,pfam0143	cd14955											2	

arCOG07781	R	General function prediction only	-	Cell surface protein														2	
arCOG02562	R	General function prediction only	-	Beta-propeller repeat containing protein	COG03391													3	1
arCOG02810	R	General function prediction only	-	Bacteriorhodopsin	COG05524	pfam01036													1
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
arCOG02316	R	General function prediction only	-	Predicted regulator of amino acid metabolism, contains ACT domain	COG02150														2
arCOG02560	R	General function prediction only	-	Secreted protein with beta-propeller repeat domain	COG03391		cd05819	TIGR03866											2
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	1
arCOG01446	VK		Csa3	CRISPR-Cas assicated transcriptional regulator, contains CARF and HTH domai	COG00640		cd09655	TIGR01884									1		