

Additional file 6. The 283 arCOGs present in both Nanoarchaeota

arCOG	COG	Gene	Function code		Acc1	# genomes in	# genomes in
			(as in COGs)	Annotation		Crenarchaeota	Euryarchaeota
						(35 max)	(78 max)
arCOG00349	COG01141	Fer	C	Ferredoxin	0	19	42
arCOG01711	COG00221	Ppa	C	Inorganic pyrophosphatase	1	27	47
arCOG02201	COG00206	FtsZ	D	Cell division GTPase	0	0	76
arCOG02263	COG02450	-	D	Predicted cell division protein, SepF homolog	0	0	76
arCOG01924	COG00252	AnsB	E	L-asparaginase/archaeal Glu-tRNA ^{Gln} amidotransferase subunit D	1	35	78
arCOG01700	COG00010	SpeB	E	Arginase family enzyme	1	35	75
arCOG01107	COG00624	ArgE	E	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase or related deacylase	1	35	62
arCOG00255	COG00077	PheA	E	Prephenate dehydratase	1	26	65
arCOG04048	COG00717	Dcd	F	Deoxycytidine deaminase	1	35	78
arCOG00419	COG00537	Hit	F	HIT family hydrolase	1	35	71
arCOG01038	COG01936	-	F	Predicted nucleotide kinase (CMP/AMP kinase related)	1	33	78
arCOG04313	COG00105	Ndk	F	Nucleoside diphosphate kinase	1	30	78
arCOG01039	COG02019	AdkA	F	Archaeal adenylate kinase	1	28	48
arCOG01111	COG00574	PpsA	G	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	1	34	78
arCOG01676	COG00476	ThiF	H	Dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis	1	35	68
arCOG00535	COG02104	ThiS	H	Sulfur transfer protein involved in thiamine biosynthesis	1	14	64
arCOG00807	COG00060	IleS	J	Isoleucyl-tRNA synthetase	1	35	78
arCOG01719	COG02511	GatE	J	Archaeal Glu-tRNA ^{Gln} amidotransferase subunit E (contains GAD domain)	1	35	78
arCOG01701	COG01676	SEN2	J	tRNA splicing endonuclease	1	35	78
arCOG00810	COG00143	MetG	J	Methionyl-tRNA synthetase	1	35	78
arCOG01255	COG00013	AlaS	J	Alanyl-tRNA synthetase	1	35	78
arCOG00042	COG00037	MesJ	J	tRNA(Ile)-lysidine synthase MesJ	1	35	77
arCOG00809	COG00495	LeuS	J	Leucyl-tRNA synthetase	1	35	71
arCOG00973	COG00144	Sun	J	tRNA or rRNA cytosine-C5-methylase	1	35	54
arCOG00357	COG00012	-	J	Predicted GTPase, probable translation factor	1	35	78
arCOG00402	COG00442	ProS	J	Prolyl-tRNA synthetase	1	35	78
arCOG00405	COG00423	GRS1	J	Glycyl-tRNA synthetase (class II)	1	35	78
arCOG01887	COG00180	TrpS	J	Tryptophanyl-tRNA synthetase	1	35	78
arCOG04112	COG01736	DPH2	J	Diphthamide synthase subunit DPH2	1	35	78
arCOG00401	COG00441	ThrS	J	Threonyl-tRNA synthetase	1	35	78
arCOG00033	COG02520	Trm5	J	Wybutosine (yW) biosynthesis enzyme, Trm5 methyltransferase	1	35	78
arCOG00078	COG01889	NOP1	J	Fibrillar-like rRNA methylase	1	35	78
arCOG00403	COG00172	SerS	J	Seryl-tRNA synthetase	1	35	78
arCOG00404	COG00124	HisS	J	Histidyl-tRNA synthetase	1	35	78
arCOG00406	COG00017	AsnS	J	Aspartyl/asparaginyl-tRNA synthetase	1	35	78
arCOG00410	COG00016	PheS	J	Phenylalanyl-tRNA synthetase alpha subunit	1	35	78
arCOG00412	COG00072	PheT	J	Phenylalanyl-tRNA synthetase beta subunit	1	35	78
arCOG00487	COG00018	ArgS	J	Arginyl-tRNA synthetase	1	35	78
arCOG00779	COG00200	RplO	J	Ribosomal protein L15	1	35	78
arCOG00780	COG01727	RPL18A	J	Ribosomal protein L18E	1	35	78
arCOG00782	COG00199	RpsN	J	Ribosomal protein S14	1	35	78
arCOG00808	COG00525	ValS	J	Valyl-tRNA synthetase	1	35	78
arCOG01001	COG00024	Map	J	Methionine aminopeptidase	1	35	78
arCOG01179	COG00361	InfA	J	Translation initiation factor 1 (IF-1)	1	35	78
arCOG01219	COG01867	TRM1	J	N2,N2-dimethylguanosine tRNA methyltransferase	1	35	78
arCOG01344	COG02238	RPS19A	J	Ribosomal protein S19E (S16A)	1	35	78
arCOG01559	COG00480	FusA	J	Translation elongation factor G, EF-G (GTPase)	1	35	78
arCOG01560	COG00532	InfB	J	Translation initiation factor 2 (IF-2; GTPase)	1	35	78
arCOG01561	COG05256	TEF1	J	Translation elongation factor EF-1alpha (GTPase)	1	35	78
arCOG01563	COG05257	GCD11	J	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)	1	35	78
arCOG01640	COG01601	GCD7	J	Translation initiation factor 2, beta subunit (eIF-2beta)/eIF-5 N-terminal domain	1	35	78
arCOG01722	COG00099	RpsM	J	Ribosomal protein S13	1	35	78
arCOG01741	COG01537	PelA	J	Release factor eRF1	1	35	78
arCOG01751	COG01358	RPL8A	J	Ribosomal protein L7AE	1	35	78
arCOG01758	COG00051	RpsJ	J	Ribosomal protein S10	1	35	78
arCOG01885	COG01383	RPS17A	J	Ribosomal protein S17E	1	35	78
arCOG01886	COG00162	TyrS	J	Tyrosyl-tRNA synthetase	1	35	78
arCOG01923	COG01498	SIK1	J	Protein implicated in ribosomal biogenesis, Nop56p homolog	1	35	78
arCOG01946	COG02125	RPS6A	J	Ribosomal protein S6E (S10)	1	35	78
arCOG01988	COG02092	EFB1	J	Translation elongation factor EF-1beta	1	35	78
arCOG04067	COG00090	RplB	J	Ribosomal protein L2	1	35	78
arCOG04070	COG00087	RplC	J	Ribosomal protein L3	1	35	78
arCOG04071	COG00088	RplD	J	Ribosomal protein L4	1	35	78
arCOG04072	COG00089	RplW	J	Ribosomal protein L23	1	35	78
arCOG04086	COG01841	RpmD	J	Ribosomal protein L30	1	35	78
arCOG04087	COG00098	RpsE	J	Ribosomal protein S5	1	35	78
arCOG04088	COG00256	RplR	J	Ribosomal protein L18	1	35	78
arCOG04089	COG02147	RPL19A	J	Ribosomal protein L19E	1	35	78
arCOG04090	COG00097	RplF	J	Ribosomal protein L6P	1	35	78
arCOG04091	COG00096	RpsH	J	Ribosomal protein S8	1	35	78
arCOG04092	COG00094	RplE	J	Ribosomal protein L5	1	35	78
arCOG04093	COG01471	RPS4A	J	Ribosomal protein S4E	1	35	78

arCOG04094	COG00198	RplX	J	Ribosomal protein L24	1	35	78
arCOG04095	COG00093	RplN	J	Ribosomal protein L14	1	35	78
arCOG04096	COG00186	RpsQ	J	Ribosomal protein S17	1	35	78
arCOG04097	COG00092	RpsC	J	Ribosomal protein S3	1	35	78
arCOG04098	COG00091	RplV	J	Ribosomal protein L22	1	35	78
arCOG04099	COG00185	RpsS	J	Ribosomal protein S19	1	35	78
arCOG04107	COG01093	SUI2	J	Translation initiation factor 2, alpha subunit (eIF-2alpha)	1	35	78
arCOG04109	COG01631	RPL42A	J	Ribosomal protein L44E	1	35	78
arCOG04113	COG00197	RplP	J	Ribosomal protein L10AE/L16	1	35	78
arCOG04129	COG02139	RPL21A	J	Ribosomal protein L21E	1	35	78
arCOG04182	COG02004	RPS24A	J	Ribosomal protein S24E	1	35	78
arCOG04185	COG00184	RpsO	J	Ribosomal protein S15P	1	35	78
arCOG04208	COG01997	RPL43A	J	Ribosomal protein L37AE/L43A	1	35	78
arCOG04223	COG00023	SUI1	J	Translation initiation factor 1 (eIF-1/SUI1)	1	35	78
arCOG04228	COG01990	pth2	J	Peptidyl-tRNA hydrolase	1	35	78
arCOG04239	COG00522	RpsD	J	Ribosomal protein S4 or related protein	1	35	78
arCOG04242	COG00102	RplM	J	Ribosomal protein L13	1	35	78
arCOG04243	COG00103	Rpsi	J	Ribosomal protein S9	1	35	78
arCOG04245	COG00052	RpsB	J	Ribosomal protein S2	1	35	78
arCOG04249	COG01746	CCA1	J	tRNA nucleotidyltransferase (CCA-adding enzyme)	1	35	78
arCOG04254	COG00049	RpsG	J	Ribosomal protein S7	1	35	78
arCOG04255	COG00048	RpsL	J	Ribosomal protein S12	1	35	78
arCOG04287	COG02058	RPP1A	J	Ribosomal protein L12E/L44/L45/RPP1/RPP2	1	35	78
arCOG04288	COG00244	RplJ	J	Ribosomal protein L10	1	35	78
arCOG04289	COG00081	RplA	J	Ribosomal protein L1	1	35	78
arCOG04302	COG00008	GlnS	J	Glutamyl- or glutaminyl-tRNA synthetase	1	35	78
arCOG04314	COG02053	RPS28A	J	Ribosomal protein S28E/S33	1	35	78
arCOG04372	COG00080	RplK	J	Ribosomal protein L11	1	35	78
arCOG00781	COG01717	RPL32	J	Ribosomal protein L32E	1	35	78
arCOG01950	COG02075	RPL24A	J	Ribosomal protein L24E	1	35	78
arCOG04049	COG01552	RPL40A	J	Ribosomal protein L40E	1	35	78
arCOG04186	COG01890	RPS1A	J	Ribosomal protein S3AE	1	35	78
arCOG04473	COG02097	RPL31A	J	Ribosomal protein L31E	1	35	78
arCOG04177	COG02167	RPL39	J	Ribosomal protein L39E	1	35	78
arCOG04126	COG02126	RPL37A	J	Ribosomal protein L37E	1	35	78
arCOG01742	COG01503	eRF1	J	Peptide chain release factor 1 (eRF1)	1	35	78
arCOG04161	COG01798	DPH5	J	Diphthamide biosynthesis methyltransferase	1	35	78
arCOG04149	COG01499	NMD3	J	NMD protein affecting ribosome stability and mRNA decay	1	35	78
arCOG00109	COG02890	HemK	J	Methylase of polypeptide chain release factors	1	35	77
arCOG00985	COG02016	-	J	Predicted RNA-binding protein (contains PUA domain)	1	35	77
arCOG00989	COG00343	Tgt	J	Queuine/archaeosine tRNA-ribosyltransferase	1	35	77
arCOG01358	COG00621	MiaB	J	2-methylthioadenine synthetase	1	35	77
arCOG04130	COG01491	-	J	Predicted RNA-binding protein	1	35	77
arCOG04176	COG01976	TIF6	J	Translation initiation factor 6 (eIF-6)	1	35	77
arCOG04187	COG01500	-	J	Predicted exosome subunit	1	35	77
arCOG00991	COG01370	-	J	tRNA modification protein, contains pre-PUA and PUA domains	1	35	77
arCOG00906	COG02260	-	J	Predicted Zn-ribbon RNA-binding protein	1	35	77
arCOG01989	COG02888	-	J	Predicted Zn-ribbon RNA-binding protein with a function in translation	1	35	76
arCOG01736	COG01514	LigT	J	2'-5' RNA ligase	1	35	75
arCOG00978	COG02519	GCD14	J	tRNA(1-methyladenosine) methyltransferase	1	35	73
arCOG04174	COG00731	TYW3	J	Wybutosine (yW) biosynthesis enzyme, Fe-S oxidoreductase	1	35	73
arCOG01042	COG01325	-	J	Exosome subunit, RNA binding protein with dsRBD fold	1	35	68
arCOG04175	COG02157	RPL20A	J	Ribosomal protein L20A (L18A)	1	35	67
arCOG00486	COG00215	CysS	J	CysteinyI-tRNA synthetase	1	35	62
arCOG01752	COG01911	RPL30	J	Ribosomal protein L30E	1	35	58
arCOG04318	COG02178	-	J	Predicted RNA-binding protein of the translin family	1	35	43
arCOG01574	COG02123	-	J	RNase PH-related exoribonuclease	1	35	41
arCOG01575	COG00689	Rph	J	Ribonuclease PH	1	35	40
arCOG04167	COG02163	RPL14A	J	Ribosomal protein L14E/L6E/L27E	1	35	36
arCOG04305	COG04830	RPS26B	J	Ribosomal protein S26	1	35	3
arCOG04246	COG01690	RtcB	J	RNA 3'-P ligase, RtcB family protein	1	34	78
arCOG00785	COG00255	RpmC	J	Ribosomal protein L29	1	34	78
arCOG00678	COG01097	RRP4	J	RNA-binding protein Rrp4 or related protein (contain S1 domain and KH domain)	1	34	39
arCOG04252	COG00585	-	J	tRNA pseudouridine synthase D	1	33	78
arCOG00038	COG00301	Thil	J	tRNA S(4)U 4-thiouridine synthase	1	33	76
arCOG04183	COG01998	RPS31	J	Ribosomal protein S27AE	1	33	73
arCOG04156	COG01590	TYW3	J	Wybutosine (yW) biosynthesis enzyme	1	33	33
arCOG04168	COG02174	RPL34A	J	Ribosomal protein L34E	0	32	36
arCOG00987	COG00130	TruB	J	Pseudouridine synthase	1	30	78
arCOG00967	COG02419	-	J	tRNA m(1)G methyltransferase	1	29	17
arCOG01018	COG00565	LasT	J	rRNA methylase	1	25	72
arCOG04304	COG02451	-	J	Ribosomal protein L35AE/L33A	0	10	13
arCOG04449	COG00101	TruA	J	Pseudouridylate synthase	0	9	77
arCOG00546	COG00595	-	J	mRNA degradation ribonuclease J1/J2 (metallo-beta-lactamase superfamily)	0	0	69
arCOG02285	COG03270	-	J	Ribosome biogenesis protein, NOL1/NOP2/fmu family	0	0	15
arCOG00122	COG02265	TrmA	J	SAM-dependent methyltransferase related to tRNA (uracil-5-)-methyltransferase	0	0	12
arCOG06624	-	-	J	Ribosomal protein L41E	0	0	10

arCOG01695	COG01293	-	K	Predicted RNA-binding protein homologous to eukaryotic snRNP	1	35	78
arCOG01762	COG00085	RpoB/Rpo2	K	DNA-directed RNA polymerase subunit B	1	35	78
arCOG04241	COG00202	RpoA/Rpo1	K	DNA-directed RNA polymerase subunit D	1	35	78
arCOG01981	COG01405	SUA7	K	Transcription initiation factor TFIIB, Brf1 subunit/Transcription initiation factor TFIIB	1	35	78
arCOG00675	COG01095	RPB7	K	DNA-directed RNA polymerase, subunit E'	1	35	78
arCOG01016	COG01460	-	K	DNA-directed RNA polymerase, subunit F (rpoF)	1	35	78
arCOG01268	COG01758	rpoZ	K	DNA-directed RNA polymerase, subunit K/omega	1	35	78
arCOG01920	COG00250	NusG	K	Transcription antiterminator NusG	1	35	78
arCOG04244	COG01644	RPB10	K	DNA-directed RNA polymerase, subunit N (RpoN/RPB10)	1	35	78
arCOG04256	COG00086	RpoC/Rpo11	K	DNA-directed RNA polymerase subunit A''	1	35	78
arCOG04257	COG00086	RpoC/Rpo3	K	DNA-directed RNA polymerase subunit A'	1	35	78
arCOG04111	COG01761	RPB11	K	DNA-directed RNA polymerase, subunit L	1	35	78
arCOG04341	COG01996	RPC10	K	DNA-directed RNA polymerase, subunit RPC10 (contains C4-type Zn-finger)	1	35	78
arCOG01863	COG01813	-	K	Predicted transcription factor, homolog of eukaryotic MBF1	1	35	78
arCOG01580	COG01522	Lrp	K	Transcriptional regulator, IclR family	1	35	77
arCOG00579	COG01594	RPB9	K	DNA-directed RNA polymerase, subunit M/Transcription elongation factor TFIIS	1	35	77
arCOG04258	COG02012	RPB5	K	DNA-directed RNA polymerase, subunit H, RpoH/RPB5	1	35	77
arCOG01764	COG02101	SPT15	K	TATA-box binding protein (TBP), component of TFIID and TFIIB	1	35	74
arCOG04270	COG01675	TFA1	K	Transcription initiation factor IIE, alpha subunit	1	35	73
arCOG01753	COG01581	Ssh10b	K	Archaeal DNA-binding protein	1	35	53
arCOG04077	COG02093	Spt4	K	Transcription elongation factor Spt4/RpoE2, zinc finger protein	1	32	78
arCOG02037	COG01378	-	K	Sugar-specific transcriptional regulator TrmB	1	25	61
arCOG00921	COG01318	-	K	Predicted transcriptional regulator	0	19	22
arCOG01526	COG01110	-	L	Reverse gyrase	1	35	28
arCOG02144	COG02036	HHT1	L	Histones H3 and H4	0	4	73
arCOG01527	COG00550	TopA	L	Topoisomerase IA	1	35	78
arCOG01183	COG00533	Kae1/QRI7	L	Subunit of KEOPS complex, contains a domain with ASKHA fold and RIO-type kinase (AP-endonuclease activity)	1	35	78
arCOG01347	COG01793	CDC9	L	ATP-dependent DNA ligase	1	35	76
arCOG00891	COG00084	TatD	L	Mg-dependent DNase	1	34	46
arCOG00488	COG00592	DnaN	L	DNA polymerase sliding clamp subunit (PCNA homolog)	1	35	78
arCOG00328	COG00417	PolB	L	DNA polymerase elongation subunit (family B)	1	35	78
arCOG00439	COG01241	MCM2	L	Predicted ATPase involved in replication control, Cdc46/Mcm family	1	35	78
arCOG00469	COG00470	HolB	L	ATPase involved in DNA replication HolB, small subunit	1	35	78
arCOG00470	COG00470	HolB	L	ATPase involved in DNA replication HolB, large subunit	1	35	78
arCOG00551	COG01711	-	L	DNA replication initiation complex subunit, GINS15 family	1	35	78
arCOG03013	COG02219	PR12	L	Eukaryotic-type DNA primase, large subunit	1	35	78
arCOG04121	COG00164	RnhB	L	Ribonuclease HII	1	35	78
arCOG04281	COG00358	DnaG	L	DNA primase (bacterial type)	1	35	78
arCOG04050	COG00258	Exo	L	5'-3' exonuclease (including N-terminal domain of Poll)	1	35	78
arCOG00280	COG00433	-	L	HerA helicase	1	35	77
arCOG00397	COG00420	SbcD	L	DNA repair exonuclease, SbcD	1	35	77
arCOG01165	COG01389	-	L	DNA topoisomerase VI, subunit B	1	35	74
arCOG04143	COG01697	-	L	DNA topoisomerase VI, subunit A	1	35	74
arCOG00928	COG01628	-	L	Endonuclease V homolog	1	35	71
arCOG00467	COG01474	CDC6	L	Cdc6-related protein, AAA superfamily ATPase	1	35	62
arCOG00919	COG01591	-	L	Holliday junction resolvase	1	35	61
arCOG00905	COG01573	-	L	Uracil-DNA glycosylase	1	35	47
arCOG00368	COG00419	SbcC	L	ATPase involved in DNA repair, SbcC	1	34	77
arCOG01894	COG00648	Nfo	L	Endonuclease IV	1	34	76
arCOG00284	COG00433	-	L	HerA helicase	1	27	7
arCOG01510	COG01599	RFA1	L	Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subunit or related ssDNA-binding protein	1	24	78
arCOG04144	COG04047	-	L	8-oxoguanine DNA glycosylase	0	22	24
arCOG00048	COG00116	-	L	Predicted N6-adenine-specific DNA methylase	0	17	26
arCOG00424	COG00608	-	L	DHH superfamily phosphohydrolase/exonuclease	0	12	8
arCOG04447	COG01933	-	L	Archaeal DNA polymerase II, large subunit	0	0	78
arCOG04455	COG01311	HYS2	L	Archaeal DNA polymerase II, small subunit/DNA polymerase delta, subunit B	0	0	77
arCOG00872	COG01111	MPH1	L	ERCC4-like helicase	0	0	76
arCOG00663	COG01208	GCD1	M	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunit	1	35	20
arCOG02079	COG01361	-	M	S-layer domain	1	5	55
arCOG04064	COG00750	-	M	Predicted membrane-associated Zn-dependent protease	1	35	78
arCOG03199	COG00472	Rfe	M	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	1	35	39
arCOG01817	COG00630	VirB11	N	Type IV secretory pathway, VirB11 component, or related ATPase involved in archaeal flagella biosynthesis	1	35	64
arCOG01814	COG00630	VirB11	N	Type II secretion system protein F	0	0	19
arCOG01818	COG00630	VirB11	N	Type IV secretory pathway, VirB11 component, or related ATPase involved in archaeal flagella biosynthesis	0	7	25
arCOG01308	COG00464	Cdc48	O	ATPase of the AAA+ class, CDC48 family	4	35	78
arCOG00970	COG00638	PRE1	O	20S proteasome, beta subunit	1	35	78
arCOG01257	COG00459	GroL	O	Chaperonin GroEL (HSP60 family)	1	35	78
arCOG00980	COG01047	SlpA	O	FKBP-type peptidyl-prolyl cis-trans isomerase 2	1	35	78

arCOG01341	COG01730	GIM5	O	Predicted prefoldin, molecular chaperone implicated in de novo protein folding	1	35	78
arCOG01342	COG01382	GimC	O	Prefoldin, chaperonin cofactor	1	35	78
arCOG04142	COG01899	DYS1	O	Deoxyhypusine synthase	1	35	78
arCOG00971	COG00638	PRE1	O	20S proteasome, alpha subunit	1	35	77
arCOG01296	COG00492	TrxB	O	Thioredoxin reductase	1	35	74
arCOG01218	COG00526	TrxA	O	Thiol-disulfide isomerase or thioredoxin	1	35	32
arCOG00312	COG00450	AhpC	O	Peroxioredoxin	1	34	56
arCOG01832	COG00071	IbpA	O	Molecular chaperone (HSP20 family)	1	27	78
arCOG02160	COG01067	LonB	O	Predicted ATP-dependent protease	0	0	77
arCOG04347	COG00500	-	Q	SAM-dependent methyltransferase	0	3	49
arCOG01937	COG01750	-	R	Archaeal serine protease	0	25	33
arCOG00557	COG01201	Lhr	R	Lhr-like helicase	1	35	75
arCOG01204	COG01708	-	R	Minimal nucleotidyltransferase	1	25	11
arCOG01951	COG01444	-	R	Predicted P-loop ATPase fused to an acetyltransferase	1	35	36
arCOG02155	COG01873	-	R	Protein implicated in RNA metabolism, contains PRC-barrel domain	0	0	76
arCOG00589	COG00455	-	R	CobQ/CobB/MinD/ParA ATPase	0	8	60
arCOG00187	COG01245	-	R	Predicted ATPase, RNase L inhibitor (RLI) homolog	1	35	78
arCOG00358	COG01163	DRG	R	Predicted GTPase	1	35	78
arCOG00501	COG01234	ElaC	R	Metal-dependent hydrolase of the beta-lactamase superfamily	1	35	78
arCOG00543	COG01782	-	R	Predicted metal-dependent RNase, consists of a metallo-beta-lactamase domain and an RNA-binding KH domain	1	35	78
arCOG04116	COG01855	-	R	ATPase (PiT family)	1	35	78
arCOG04150	COG01094	-	R	Predicted RNA-binding protein (contains KH domains)	1	35	78
arCOG04179	COG02118	-	R	DNA-binding protein	1	35	78
arCOG00035	COG02102	-	R	Predicted ATPase of PP-loop superfamily	1	35	78
arCOG00352	COG01084	-	R	Predicted GTPase	1	35	78
arCOG04312	COG01412	-	R	PIN domain containing protein	1	35	77
arCOG01150	COG01407	-	R	Predicted ICC-like phosphoesterase	1	35	74
arCOG04055	COG01371	-	R	SHS2 domain protein implicated in nucleic acid metabolism	1	35	74
arCOG01728	COG01355	-	R	Predicted dioxygenase	1	35	63
arCOG01845	COG02151	PaaD	R	Predicted metal-sulfur cluster biosynthetic enzyme	1	35	56
arCOG04219	COG02433	-	R	Possible nuclease of RNase H fold, RuvC/YggF family	1	35	53
arCOG00969	COG02248	-	R	Predicted hydrolase (metallo-beta-lactamase superfamily)	1	35	30
arCOG04265	COG01779	-	R	C4-type Zn-finger protein	1	34	62
arCOG00324	COG00123	AcuC	R	Deacetylase, including yeast histone deacetylase and acetoin utilization protein	1	34	51
arCOG02044	COG01287	-	R	Uncharacterized membrane protein, required for N-linked glycosylation	1	34	39
arCOG00350	COG01161	-	R	Predicted GTPase	1	34	33
arCOG01145	COG02129	-	R	Icc family phosphoesterase	1	33	65
arCOG00017	COG02522	-	R	Predicted transcriptional regulator	1	32	33
arCOG02960	COG04882	-	R	Predicted aminopeptidase, lap family	1	32	0
arCOG04702	COG01881	-	R	Phospholipid-binding protein	1	25	46
arCOG00769	COG00693	ThiJ	R	Putative intracellular protease/amidase	1	24	69
arCOG02209	COG02244	RfbX	R	Polysaccharide biosynthesis protein, Mvin family	0	21	76
arCOG02900	COG02304	-	R	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain	1	19	21
arCOG00601	COG00517	-	R	Protein containing two CBS domains (some fused to C-terminal double-stranded RNA-binding domain of RaiA family)	1	18	57
arCOG01744	COG01988	-	R	Membrane-bound metal-dependent hydrolase	0	9	29
arCOG01688	COG01719	-	R	Predicted transcriptional regulator, contains HTH and 4VR domain	0	7	40
arCOG00438	COG01239	-	R	AAA family ATPase	0	5	50
arCOG02261	-	-	R	Protein containing OB-fold-like and PCI domains	0	0	16
arCOG01159	COG01340	-	S	Uncharacterized archaeal coiled-coil protein	1	35	66
arCOG01572	-	-	S	Uncharacterized conserved membrane protein	1	28	17
arCOG04214	COG00432	-	S	Uncharacterized conserved protein	1	35	65
arCOG00398	COG02411	-	S	ASCH domain, predicted RNA-binding domain	0	20	24
arCOG01994	COG01300	SpoIIM	S	Uncharacterized membrane protein	0	6	64
arCOG06946	-	-	S	Uncharacterized conserved membrane protein	0	3	0
arCOG05037	-	-	S	Uncharacterized conserved protein	0	0	27
arCOG01180	COG01718	RIO1	T	Serine/threonine protein kinase involved in cell cycle control	1	35	78
arCOG01185	COG03642	-	T	Mn2+-dependent serine/threonine protein kinase	1	35	78
arCOG01182	COG02112	-	T	Predicted Ser/Thr protein kinase	1	34	31
arCOG01171	COG00467	RAD55	T	RecA-superfamily ATPase implicated in signal transduction	1	33	58
arCOG04471	COG04083	-	U	Exosortase	0	2	55
arCOG04169	COG00201	SecY	U	Preprotein translocase subunit SecY	1	35	78
arCOG02204	COG02443	Sss1	U	Preprotein translocase subunit Sss1	1	35	78
arCOG01739	COG00681	LepB	U	Signal peptidase I	1	33	77
arCOG03054	COG00341	SecF	U	Preprotein translocase subunit SecF	0	0	68
arCOG03055	COG00342	SecD	U	Preprotein translocase subunit SecD	0	0	68
arCOG00793	COG01468	-	V	CRISPR-associated protein, Cas4 family, PD-(D/E)XK superfamily nuclease	0	0	28