Table S8 - RNA-seq expression of *A. baumannii* AB6870155 coculture biofilms with *K. pneumoniae* KP6870155 in SLMM versus AB6870155 monoculture biofilms grown in SLMM

locus_tag	gene	log2FoldChange	padj	product	eC_number	eggnog_gene	eggnog_product
COJEPEMI_(	COJEPE	5.82362	2.24E-110	hypothetical p	NA	0	Thioesterase superfamily
COJEPEMI_(	napA	5.56872	3.66E-115	Periplasmic ni	1.9.6.1	0	Molybdopterin oxidoreductase Fe4S4 domain
COJEPEMI_(	COJEPE	5.35958	7.50E-38	hypothetical p	NA	0	Chlorhexidine efflux transporter
COJEPEMI_(	COJEPE	4.85208	1.87E-90	hypothetical p	NA	0	Endoribonuclease L-PSP
COJEPEMI_(	bauA	4.39035	8.93E-33	Beta-alanine--	2.6.1.18	aptA	Aminotransferase class-III
COJEPEMI_(	mmgC_	4.18296	5.72E-61	Acyl-CoA dehy	1.3.99.-	gcdH	Acyl-CoA dehydrogenase, middle domain
COJEPEMI_(	groS	4.14717	2.12E-55	10 kDa chaper	NA	groS	Binds to Cpn60 in the presence of Mg-ATP and suppresses the ATPase a
COJEPEMI_(	COJEPE	3.81157	8.15E-67	hypothetical p	NA	0	Spore Coat Protein U domain
COJEPEMI_(	COJEPE	3.78781	2.28E-26	hypothetical p	NA	0	COG3209 Rhs family protein
COJEPEMI_(	yjhB_3	3.75612	1.47E-47	Putative meta	NA	0	MFS/sugar transport protein
COJEPEMI_(	COJEPE	3.70968	3.15E-29	hypothetical p	NA	0	DUF218 domain
COJEPEMI_(	puuE	3.62202	7.07E-25	4-aminobutyra	2.6.1.19	gabT	Belongs to the class-III pyridoxal-phosphate-dependent aminotransfera
COJEPEMI_(	dnaJ	3.60187	1.22E-65	Chaperone pro	NA	dnaJ	ATP binding to DnaK triggers the release of the substrate protein, thus
COJEPEMI_(	grpE	3.59429	3.10E-29	Protein GrpE	NA	grpE	Participates actively in the response to hyperosmotic and heat shock by
COJEPEMI_(	COJEPE	3.57385	1.25E-60	putative trans	NA	0	Major facilitator Superfamily
COJEPEMI_(	COJEPE	3.56715	3.57E-28	hypothetical p	NA	0	
COJEPEMI_(	panD	3.50266	2.36E-50	Aspartate 1-de	4.1.1.11	panD	Catalyzes the pyruvoyl-dependent decarboxylation of aspartate to prod
COJEPEMI_(	COJEPE	3.46208	3.43E-27	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	3.43394	5.56E-08	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	3.43052	6.75E-49	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	3.42946	5.85E-32	hypothetical p	NA	tsx	Nucleoside-specific channel-forming protein, Tsx
COJEPEMI_(	COJEPE	3.32763	8.33E-28	hypothetical p	NA	0	
COJEPEMI_(	rhtB_4	3.26921	3.90E-12	Homoserine/h	NA	0	LysE type translocator
COJEPEMI_(	groL	3.21314	3.18E-35	60 kDa chaper	NA	groL	Prevents misfolding and promotes the refolding and proper assembly o
COJEPEMI_(	COJEPE	3.14059	1.55E-13	hypothetical p	NA	0	Protein of unknown function (DUF2938)

COJEPEMI_(	smf-1_1	3.10146	1.06E-24	Major fimbrial	NA	fimA	Type-1 fimbrial protein, A
COJEPEMI_(	prr	3.02545	3.13E-08	Gamma-amin	1.2.1.19	ydcW	Aldehyde dehydrogenase family
COJEPEMI_(	uctC_2	2.91589	4.75E-42	Acetyl-CoA:oxa	2.8.3.19	caiB	CoA-transferase family III
COJEPEMI_(	COJEPE	2.90401	1.51E-36	hypothetical p	NA	yyaM	EamA-like transporter family
COJEPEMI_(	pntAA	2.90281	1.94E-33	NAD(P) transh	7.1.1.1	pntAA	Alanine dehydrogenase/PNT, N-terminal domain
COJEPEMI_(	pntA	2.88466	2.13E-22	NAD(P) transh	7.1.1.1	pntAB	4TM region of pyridine nucleotide transhydrogenase, mitoch
COJEPEMI_(	xpt	2.84683	5.69E-32	Xanthine phos	2.4.2.22	xpt	Converts the preformed base xanthine, a product of nucleic acid breakd
COJEPEMI_(	COJEPE	2.83466	1.36E-15	hypothetical p	NA	0	
COJEPEMI_(	dnaK	2.7967	3.66E-25	Chaperone pro	NA	dnaK	Heat shock 70 kDa protein
COJEPEMI_(	COJEPE	2.77312	2.01E-23	hypothetical p	NA	0	
COJEPEMI_(	fldP_1	2.7585	1.11E-14	Flavodoxin Fld	NA	0	NADPH-dependent FMN reductase
COJEPEMI_(	COJEPE	2.73109	8.74E-32	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	2.73031	5.35E-48	hypothetical p	NA	0	Serine aminopeptidase, S33
COJEPEMI_(	COJEPE	2.70933	1.81E-14	hypothetical p	NA	0	
COJEPEMI_(	rpsL	2.68867	5.17E-43	30S ribosomal	NA	0	structural constituent of ribosome
COJEPEMI_(	rpsG	2.62675	1.61E-27	30S ribosomal	NA	rpsG	One of the primary rRNA binding proteins, it binds directly to 16S rRNA
COJEPEMI_(	COJEPE	2.59168	9.22E-30	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	2.56844	7.39E-33	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	2.53704	4.64E-26	hypothetical p	NA	0	Protein of unknown function (DUF3144)
COJEPEMI_(	COJEPE	2.49821	4.71E-26	hypothetical p	NA	0	Phage late control gene D protein (GPD)
COJEPEMI_(	rlmD	2.49779	2.40E-42	23S rRNA (ura	2.1.1.190	rlmD	Catalyzes the formation of 5-methyl-uridine at position 1939 (m5U193
COJEPEMI_(	COJEPE	2.48656	3.94E-24	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	2.46572	1.69E-33	hypothetical p	NA	cvpA	membrane protein, required for colicin V production
COJEPEMI_(	mgtA	2.45228	1.96E-17	Magnesium-tr	7.2.2.14	mgtA	Cation transporter/ATPase, N-terminus
COJEPEMI_(	ribB	2.43629	1.14E-14	3,4-dihydroxy-	4.1.99.12	ribB	Catalyzes the conversion of D-ribulose 5-phosphate to formate and 3,4-
COJEPEMI_(	COJEPE	2.41516	1.88E-11	hypothetical p	NA	sdh	NAD dependent epimerase/dehydratase family
COJEPEMI_(	pntB	2.40742	3.24E-40	NAD(P) transh	7.1.1.1	pntB	The transhydrogenation between NADH and NADP is coupled to respira
COJEPEMI_(	cbdB	2.38304	1.20E-06	2-halobenzoat	1.14.12.1	benB	Ring hydroxylating beta subunit
COJEPEMI_(	htpG	2.37436	3.68E-10	Chaperone pro	NA	htpG	Molecular chaperone. Has ATPase activity
COJEPEMI_(	rplA	2.36809	3.04E-20	50S ribosomal	NA	rplA	Binds directly to 23S rRNA. The L1 stalk is quite mobile in the ribosome

COJEPEMI_(	bauC	2.35964	3.00E-13	Putative 3-oxo	1.2.1.-	mmsA	Aldehyde dehydrogenase family
COJEPEMI_(	COJEPE	2.35626	6.81E-09	NADPH oxidor	1.-.-.-	0	Oxidoreductase NAD-binding domain
COJEPEMI_(	rplK	2.34736	1.12E-23	50S ribosomal	NA	rplK	Forms part of the ribosomal stalk which helps the ribosome interact wi
COJEPEMI_(	acr1	2.32403	3.94E-22	Fatty acyl-CoA	1.2.1.-	acr1	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	COJEPE	2.32269	5.97E-57	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	2.31529	2.97E-20	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	2.29086	5.74E-29	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	ytcD	2.28531	2.82E-17	putative HTH-t	NA	0	HxlR-like helix-turn-helix
COJEPEMI_(	gloA	2.27386	1.54E-28	Lactoylglutathi	4.4.1.5	gloA	Catalyzes the conversion of hemimercaptal, formed from methylglyoxa
COJEPEMI_(	COJEPE	2.27212	2.19E-24	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	2.27043	1.09E-11	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	2.2609	8.48E-16	hypothetical p	NA	0	
COJEPEMI_(	pliG	2.25684	1.32E-07	Inhibitor of g-t	NA	0	
COJEPEMI_(	COJEPE	2.23467	4.26E-05	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	grxC	2.23369	7.39E-24	Glutaredoxin 3	NA	grxC	Has a glutathione-disulfide oxidoreductase activity in the presence of N
COJEPEMI_(	COJEPE	2.22889	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	cinA_1	2.22231	1.69E-11	Putative comp	NA	0	Belongs to the CinA family
COJEPEMI_(	hslO	2.21812	1.86E-20	33 kDa chaper	NA	hslO	Redox regulated molecular chaperone. Protects both thermally unfoldir
COJEPEMI_(	COJEPE	2.20855	3.60E-18	hypothetical p	NA	0	lysine exporter protein (LysE YggA)
COJEPEMI_(	desA3_	2.1996	1.09E-05	NADPH-depen	1.14.19.-	0	Fatty acid desaturase
COJEPEMI_(	rpmG	2.19161	5.37E-24	50S ribosomal	NA	rpmG	Belongs to the bacterial ribosomal protein bL33 family
COJEPEMI_(	COJEPE	2.18822	0.00022	hypothetical p	NA	0	Spore Coat Protein U domain
COJEPEMI_(	trmB_2	2.15898	1.50E-07	tRNA (guanine	2.1.1.33	0	Putative methyltransferase
COJEPEMI_(	mrdB	2.1466	1.85E-18	Peptidoglycan	2.4.1.129	mrdB	Peptidoglycan polymerase that is essential for cell wall elongation
COJEPEMI_(	COJEPE	2.14401	2.08E-08	hypothetical p	NA	0	
COJEPEMI_(	fusA	2.14275	5.83E-19	Elongation fac	NA	fusA	Catalyzes the GTP-dependent ribosomal translocation step during trans
COJEPEMI_(	cysH	2.134	4.04E-34	Phosphoadeno	1.8.4.8	cysH	Reduction of activated sulfate into sulfite
COJEPEMI_(	COJEPE	2.12998	2.93E-10	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	2.11617	3.46E-16	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	2.10731	5.59E-08	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family

COJEPEMI_(	rhtC_3	2.10215	1.12E-16	Threonine effl	NA	0	LysE type translocator
COJEPEMI_(	nuoB	2.10132	1.26E-42	NADH-quinone	7.1.1.-	nuoB	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) c
COJEPEMI_(	mutS2	2.09453	2.73E-13	Endonuclease	3.1.-.-	smrA	Smr domain
COJEPEMI_(	rplD	2.08563	3.62E-25	50S ribosomal	NA	rplD	Forms part of the polypeptide exit tunnel
COJEPEMI_(	COJEPE	2.0723	0.000984	hypothetical p	NA	ycgI	Domain of unknown function (DUF1989)
COJEPEMI_(	gltR_2	2.07171	4.84E-08	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	mshB	2.0703	3.95E-17	1D-myo-inosit	3.5.1.103	0	GlcNAc-PI de-N-acetylase
COJEPEMI_(	COJEPE	2.06206	2.43E-12	hypothetical p	NA	0	Stress-induced bacterial acidophilic repeat motif
COJEPEMI_(	ant1_2	2.0619	4.14E-05	Streptomycin 3	2.7.7.47	aadA4	Mediates bacterial resistance to the antibiotics streptomycin and spect
COJEPEMI_(	COJEPE	2.05169	1.28E-20	hypothetical p	NA	0	Glutathione S-transferase N-terminal domain
COJEPEMI_(	secB	2.05158	1.11E-28	Protein-export	NA	secB	One of the proteins required for the normal export of preproteins out o
COJEPEMI_(	rpsB	2.03431	6.90E-14	30S ribosomal	NA	rpsB	Belongs to the universal ribosomal protein uS2 family
COJEPEMI_(	rplC	2.02801	1.23E-17	50S ribosomal	NA	rplC	One of the primary rRNA binding proteins, it binds directly near the 3'-e
COJEPEMI_(	uvrC	2.02732	1.33E-24	UvrABC systen	NA	uvrC	The UvrABC repair system catalyzes the recognition and processing of I
COJEPEMI_(	COJEPE	2.01864	1.48E-44	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	2.01735	1.84E-09	hypothetical p	NA	yicG	UPF0126 domain
COJEPEMI_(	COJEPE	2.01591	1.05E-15	hypothetical p	NA	0	Phage Mu protein F like protein
COJEPEMI_(	COJEPE	2.0038	2.58E-17	hypothetical p	NA	0	acyl-CoA dehydrogenase
COJEPEMI_(	yqeY	1.99623	4.64E-27	putative prote	NA	yqeY	Yqey-like protein
COJEPEMI_(	COJEPE	1.99395	9.52E-13	hypothetical p	NA	0	
COJEPEMI_(	rpsJ	1.98452	2.44E-18	30S ribosomal	NA	rpsJ	Involved in the binding of tRNA to the ribosomes
COJEPEMI_(	COJEPE	1.96546	1.33E-11	hypothetical p	NA	rssA	Patatin-like phospholipase
COJEPEMI_(	COJEPE	1.96011	1.41E-22	hypothetical p	NA	hit	Scavenger mRNA decapping enzyme C-term binding
COJEPEMI_(	COJEPE	1.95923	3.62E-07	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.95089	1.08E-11	hypothetical p	NA	0	
COJEPEMI_(	rpsQ	1.94896	5.33E-40	30S ribosomal	NA	rpsQ	One of the primary rRNA binding proteins, it binds specifically to the 5'
COJEPEMI_(	COJEPE	1.93042	2.04E-05	hypothetical p	NA	0	Short repeat of unknown function (DUF308)
COJEPEMI_(	COJEPE	1.92401	2.43E-14	hypothetical p	NA	ygiW	Bacterial OB fold (BOF) protein
COJEPEMI_(	COJEPE	1.92247	6.53E-23	hypothetical p	NA	VY92_06	Belongs to the pirin family
COJEPEMI_(	yibN	1.92193	5.76E-14	putative prote	NA	yibN	Rhodanese Homology Domain

COJEPEMI_(	COJEPE	1.92103	1.09E-15	hypothetical p	NA	IV02_136	Belongs to the UPF0149 family
COJEPEMI_(	ydaD	1.92062	8.65E-13	General stress	1.-.-.-	ydaD	Enoyl-(Acyl carrier protein) reductase
COJEPEMI_(	COJEPE	1.9051	8.02E-12	hypothetical p	NA	pru	Spore Coat Protein U domain
COJEPEMI_(	ychF	1.90377	2.22E-13	Ribosome-bin	NA	ychF	ATPase that binds to both the 70S ribosome and the 50S ribosomal sub
COJEPEMI_(	otsB	1.8955	4.18E-11	Trehalose-6-pl	3.1.3.12	otsB	Removes the phosphate from trehalose 6-phosphate to produce free tr
COJEPEMI_(	COJEPE	1.89377	5.62E-05	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.88822	3.57E-19	Zinc-type alcol	NA	0	Belongs to the zinc-containing alcohol dehydrogenase family. Quinone
COJEPEMI_(	COJEPE	1.88644	8.53E-17	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2171)
COJEPEMI_(	rpmC	1.8678	5.85E-32	50S ribosomal	NA	rpmC	Belongs to the universal ribosomal protein uL29 family
COJEPEMI_(	rpmB	1.86406	2.61E-17	50S ribosomal	NA	rpmB	Belongs to the bacterial ribosomal protein bL28 family
COJEPEMI_(	yeaW	1.86195	1.75E-10	Carnitine mon	1.14.13.2	0	Ring hydroxylating alpha subunit (catalytic domain)
COJEPEMI_(	rplW	1.86156	3.57E-24	50S ribosomal	NA	rplW	One of the early assembly proteins it binds 23S rRNA. One of the prote
COJEPEMI_(	COJEPE	1.86054	1.61E-32	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	nuoF	1.85704	6.49E-29	NADH-quinone	7.1.1.-	nuoF	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) c
COJEPEMI_(	rplP	1.85397	2.28E-39	50S ribosomal	NA	rplP	Binds 23S rRNA and is also seen to make contacts with the A and possi
COJEPEMI_(	COJEPE	1.85045	NA	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	rpoD	1.84962	3.70E-18	RNA polymera	NA	rpoD	Sigma factors are initiation factors that promote the attachment of RN
COJEPEMI_(	COJEPE	1.84353	2.20E-19	hypothetical p	NA	0	Catalase
COJEPEMI_(	COJEPE	1.84116	6.08E-07	hypothetical p	NA	0	
COJEPEMI_(	rplB	1.83268	2.67E-31	50S ribosomal	NA	rplB	One of the primary rRNA binding proteins. Required for association of t
COJEPEMI_(	COJEPE	1.83151	5.81E-18	hypothetical p	NA	sigE	Belongs to the sigma-70 factor family. ECF subfamily
COJEPEMI_(	COJEPE	1.82463	0.000221	hypothetical p	NA	0	Glycosyl hydrolase 108
COJEPEMI_(	lgt	1.82335	2.23E-16	Phosphatidylgl	2.5.1.145	lgt	Transfers the N-acyl diglyceride group on what will become the N-term
COJEPEMI_(	rpsS	1.81684	4.07E-26	30S ribosomal	NA	rpsS	Protein S19 forms a complex with S13 that binds strongly to the 16S rib
COJEPEMI_(	COJEPE	1.8095	1.10E-16	hypothetical p	NA	0	
COJEPEMI_(	rpsC	1.80492	8.70E-38	30S ribosomal	NA	rpsC	Binds the lower part of the 30S subunit head. Binds mRNA in the 70S ri
COJEPEMI_(	uvrA	1.80292	2.81E-13	UvrABC systen	NA	uvrA	The UvrABC repair system catalyzes the recognition and processing of I
COJEPEMI_(	ndhC	1.80238	2.50E-25	NAD(P)H-quin	7.1.1.-	nuoA	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) c
COJEPEMI_(	rpsU	1.79788	2.74E-23	30S ribosomal	NA	rpsU	Belongs to the bacterial ribosomal protein bS21 family
COJEPEMI_(	rplV	1.79738	9.77E-32	50S ribosomal	NA	rplV	The globular domain of the protein is located near the polypeptide exit

COJEPEMI_(	COJEPE	1.78843	8.16E-07	hypothetical p	NA	osmB	COG3668 Plasmid stabilization system protein
COJEPEMI_(	rpmH	1.78688	9.23E-15	50S ribosomal	NA	rpmH	Belongs to the bacterial ribosomal protein bL34 family
COJEPEMI_(	COJEPE	1.78481	1.20E-06	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.7813	NA	Putative nickel	NA	nikR	NikR C terminal nickel binding domain
COJEPEMI_(	tgnD_2	1.77842	4.09E-05	(E)-2-((N-metl	3.5.1.-	0	Ndr family
COJEPEMI_(	norW	1.77801	5.84E-11	Nitric oxide re	1.18.1.-	nirB	Rieske-like [2Fe-2S] domain
COJEPEMI_(	COQ3_1	1.77572	1.90E-11	Ubiquinone bi	2.1.1.222	0	Nodulation protein S (NodS)
COJEPEMI_(	COJEPE	1.76709	1.30E-15	hypothetical p	NA	0	OmpW family
COJEPEMI_(	COJEPE	1.76559	0.001155	hypothetical p	NA	0	
COJEPEMI_(	nuoE	1.76425	2.92E-14	NADH-quinone	7.1.1.-	nuoE	Thioredoxin-like [2Fe-2S] ferredoxin
COJEPEMI_(	nemR	1.76301	7.85E-15	HTH-type trans	NA	nemR	Bacterial transcriptional repressor C-terminal
COJEPEMI_(	COJEPE	1.74691	2.11E-10	hypothetical p	NA	0	HPP family
COJEPEMI_(	COJEPE	1.74486	5.92E-26	hypothetical p	NA	0	
COJEPEMI_(	yhhW_1	1.74153	1.08E-15	Quercetin 2,3-	1.13.11.2	MA20_0(	Belongs to the pirin family
COJEPEMI_(	rpmE	1.73915	2.26E-07	50S ribosomal	NA	rpmE	Binds the 23S rRNA
COJEPEMI_(	COJEPE	1.73891	3.22E-05	hypothetical p	NA	0	
COJEPEMI_(	purF	1.72423	1.87E-24	Amidophospho	2.4.2.14	purF	Catalyzes the formation of phosphoribosylamine from phosphoribosylp
COJEPEMI_(	nusG	1.72401	4.38E-14	Transcription t	NA	nusG	Participates in transcription elongation, termination and antiterminatic
COJEPEMI_(	COJEPE	1.71927	NA	hypothetical p	NA	rci	Phage integrase family
COJEPEMI_(	COJEPE	1.71889	1.42E-09	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.70856	4.54E-14	hypothetical p	NA	0	Protein of unknown function (DUF3106)
COJEPEMI_(	rplY	1.70634	2.30E-19	50S ribosomal	NA	ctc	This is one of the proteins that binds to the 5S RNA in the ribosome wh
COJEPEMI_(	tdh_1	1.70479	7.16E-20	L-threonine 3-(	1.1.1.103	mecR	Alcohol dehydrogenase GroES-like domain
COJEPEMI_(	COJEPE	1.70414	6.92E-13	hypothetical p	NA	0	AraC-binding-like domain
COJEPEMI_(	leuA	1.69973	0.000198	2-isopropylma	2.3.3.13	leuA	Catalyzes the condensation of the acetyl group of acetyl-CoA with 3-me
COJEPEMI_(	COJEPE	1.69945	6.07E-10	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	COJEPE	1.69748	5.56E-14	hypothetical p	NA	0	
COJEPEMI_(	rpsP	1.68851	3.08E-15	30S ribosomal	NA	rpsP	Belongs to the bacterial ribosomal protein bS16 family
COJEPEMI_(	prs	1.68525	2.73E-18	Ribose-phosph	2.7.6.1	prs	Involved in the biosynthesis of the central metabolite phospho-alpha-D-
COJEPEMI_(	COJEPE	1.68257	0.011851	hypothetical p	NA	0	

COJEPEMI_(	baiA	1.6813	4.05E-06	3-alpha-hydro	1.1.1.392	baiA2	Enoyl-(Acyl carrier protein) reductase
COJEPEMI_(	bacC_1	1.67577	0.003039	Dihydroantica	1.1.1.385	0	short-chain dehydrogenase
COJEPEMI_(	rplJ	1.67543	8.96E-17	50S ribosomal	NA	rplJ	Forms part of the ribosomal stalk, playing a central role in the interacti
COJEPEMI_(	blh_2	1.67541	0.007888	Beta-lactamas	3.-.-.-	0	Metallo-beta-lactamase superfamily
COJEPEMI_(	czcC	1.66878	0.000325	Cobalt-zinc-ca	NA	czcC	Outer membrane efflux protein
COJEPEMI_(	purM	1.66137	3.38E-11	Phosphoribosy	6.3.3.1	purM	Phosphoribosylformylglycinamidine cyclo-ligase
COJEPEMI_(	COJEPE	1.6597	6.18E-19	hypothetical p	NA	0	
COJEPEMI_(	trmB_1	1.65753	3.38E-14	tRNA (guanine	2.1.1.33	trmB	Catalyzes the formation of N(7)-methylguanine at position 46 (m7G46)
COJEPEMI_(	COJEPE	1.65238	4.25E-09	hypothetical p	NA	0	EamA-like transporter family
COJEPEMI_(	cbpM	1.64327	1.78E-28	Chaperone mo	NA	cbpM	MerR HTH family regulatory protein
COJEPEMI_(	sdhD	1.64309	1.85E-16	Succinate deh	NA	sdhD	Succinate dehydrogenase hydrophobic membrane anchor subunit
COJEPEMI_(	COJEPE	1.63151	2.61E-24	hypothetical p	NA	0	YARHG
COJEPEMI_(	COJEPE	1.63058	0.000523	hypothetical p	NA	0	
COJEPEMI_(	rpe	1.61295	8.27E-11	Ribulose-phos	5.1.3.1	rpe	Belongs to the ribulose-phosphate 3-epimerase family
COJEPEMI_(	gltD	1.61249	7.96E-18	Glutamate syr	1.4.1.13	gltD	glutamate synthase
COJEPEMI_(	rpsR	1.6095	4.79E-11	30S ribosomal	NA	rpsR	Binds as a heterodimer with protein S6 to the central domain of the 16
COJEPEMI_(	COJEPE	1.60338	NA	hypothetical p	NA	0	
COJEPEMI_(	proC_1	1.59919	0.001019	Pyrroline-5-ca	1.5.1.2	proC	Catalyzes the reduction of 1-pyrroline-5-carboxylate (PCA) to L-proline
COJEPEMI_(	otsA	1.59347	1.56E-09	Trehalose-6-pl	2.4.1.15	otsA	Glycosyltransferase family 20
COJEPEMI_(	gbsA	1.5919	1.23E-09	Betaine aldeh	1.2.1.8	0	Aldehyde dehydrogenase family
COJEPEMI_(	fumB	1.58222	3.86E-11	Fumarate hyd	4.2.1.2	fumA	Catalyzes the reversible hydration of fumarate to (S)- malate
COJEPEMI_(	COJEPE	1.57359	2.82E-16	hypothetical p	NA	0	
COJEPEMI_(	oatA	1.57226	1.35E-08	O-acetyltransf	2.3.1.-	0	Acyltransferase family
COJEPEMI_(	COJEPE	1.56548	1.35E-05	Baeyer-Villige	1.14.13.-	0	Flavin-binding monooxygenase-like
COJEPEMI_(	COJEPE	1.56505	0.002481	Bacterioheme	NA	0	Hemerythrin HHE cation binding domain
COJEPEMI_(	COJEPE	1.56196	6.02E-15	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	sodB	1.55983	1.30E-21	Superoxide dis	1.15.1.1	sodB	Destroys radicals which are normally produced within the cells and whi
COJEPEMI_(	typA	1.55844	1.55E-12	GTP-binding p	NA	typA	GTP-binding protein TypA
COJEPEMI_(	COJEPE	1.55634	9.89E-19	hypothetical p	NA	0	Sensors of blue-light using FAD
COJEPEMI_(	katE	1.55498	5.32E-18	Catalase HPII	1.11.1.6	katE	serves to protect cells from the toxic effects of hydrogen peroxide

COJEPEMI_(	COJEPE	1.54273	6.50E-10	hypothetical p	NA	0	
COJEPEMI_(	rplL	1.5398	8.46E-16	50S ribosomal	NA	rplL	Forms part of the ribosomal stalk which helps the ribosome interact wi
COJEPEMI_(	nadX	1.53563	3.91E-05	L-aspartate de	1.4.1.21	nadX	Specifically catalyzes the NAD or NADP-dependent dehydrogenation of
COJEPEMI_(	nuoI	1.52915	3.16E-12	NADH-quinone	7.1.1.-	nuoI	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) c
COJEPEMI_(	COJEPE	1.52372	7.82E-09	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.52168	9.07E-11	hypothetical p	NA	0	
COJEPEMI_(	yhhW_2	1.5168	2.17E-08	Quercetin 2,3-	1.13.11.2	0	Belongs to the pirin family
COJEPEMI_(	nuoG	1.51348	7.73E-16	NADH-quinone	7.1.1.-	nuoG	COG1034 NADH dehydrogenase NADH ubiquinone oxidoreductase 75 kD
COJEPEMI_(	COJEPE	1.51295	4.96E-07	hypothetical p	NA	0	
COJEPEMI_(	dusC	1.50192	1.20E-06	tRNA-dihydrou	1.3.1.-	dusC	Catalyzes the synthesis of 5,6-dihydrouridine (D), a modified base foun
COJEPEMI_(	pyrB	1.49658	5.68E-07	Aspartate carb	2.1.3.2	pyrB	Belongs to the ATCase OTCase family
COJEPEMI_(	iscU	1.49565	0.000327	Iron-sulfur clus	NA	iscU	A scaffold on which IscS assembles Fe-S clusters. It is likely that Fe-S c
COJEPEMI_(	cysN	1.49341	0.000309	Sulfate adenyl	2.7.7.4	cysN	Belongs to the TRAFAC class translation factor GTPase superfamily. Cla
COJEPEMI_(	wbpA	1.49284	4.23E-08	UDP-N-acetyl-	1.1.1.136	0	Belongs to the UDP-glucose GDP-mannose dehydrogenase family
COJEPEMI_(	COJEPE	1.49017	5.85E-06	hypothetical p	NA	0	SnoaL-like polyketide cyclase
COJEPEMI_(	COJEPE	1.4885	0.000208	hypothetical p	NA	0	Putative diguanylate phosphodiesterase
COJEPEMI_(	COJEPE	1.48818	8.27E-11	hypothetical p	NA	0	
COJEPEMI_(	nuoC	1.48203	8.00E-19	NADH-quinone	7.1.1.-	nuoC	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) c
COJEPEMI_(	xanP	1.48201	3.09E-06	Xanthine perm	NA	xanP	Permease family
COJEPEMI_(	purL	1.48163	5.24E-18	Phosphoribosy	6.3.5.3	purL	Phosphoribosylformylglycinamidine synthase involved in the purines bio
COJEPEMI_(	COJEPE	1.47945	1.91E-08	hypothetical p	NA	0	
COJEPEMI_(	rpsH	1.47781	7.14E-13	30S ribosomal	NA	rpsH	One of the primary rRNA binding proteins, it binds directly to 16S rRNA
COJEPEMI_(	COJEPE	1.47587	0.000529	hypothetical p	NA	0	Bacterial protein of unknown function (Gcw_chp)
COJEPEMI_(	COJEPE	1.46884	2.41E-12	hypothetical p	NA	0	
COJEPEMI_(	lon_2	1.46724	1.29E-09	Lon protease	3.4.21.53	lon	ATP-dependent serine protease that mediates the selective degradatio
COJEPEMI_(	rplU	1.46414	2.01E-13	50S ribosomal	NA	rplU	This protein binds to 23S rRNA in the presence of protein L20
COJEPEMI_(	gabP_1	1.46171	4.91E-11	GABA permea	NA	gabP	Amino acid permease
COJEPEMI_(	hslR	1.46085	5.58E-12	Heat shock pro	NA	hslR	Belongs to the HSP15 family
COJEPEMI_(	comR	1.45735	6.70E-09	HTH-type trans	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	cbdA	1.45575	1.85E-07	2-halobenzoat	1.14.12.1	benA	Ring hydroxylating alpha subunit (catalytic domain)

COJEPEMI_(	rplF	1.45156	1.08E-12	50S ribosomal	NA	rplF	This protein binds to the 23S rRNA, and is important in its secondary st
COJEPEMI_(	anoR	1.44902	1.51E-06	Transcriptiona	NA	sdiA	Transcriptional activator protein
COJEPEMI_(	modA	1.4487	1.02E-08	Molybdate-bin	NA	modA	Bacterial extracellular solute-binding protein
COJEPEMI_(	COJEPE	1.44752	0.008391	hypothetical p	NA	0	Ring hydroxylating beta subunit
COJEPEMI_(	COJEPE	1.4468	2.65E-07	hypothetical p	NA	0	Thioesterase superfamily
COJEPEMI_(	benC	1.44401	0.000173	Benzoate 1,2-(	NA	benC	Oxidoreductase FAD-binding domain
COJEPEMI_(	slyX	1.4409	6.94E-10	Protein SlyX	NA	slyX	SlyX
COJEPEMI_(	smvA	1.4399	5.23E-14	Methyl viologe	NA	smvA	Major Facilitator Superfamily
COJEPEMI_(	pld1	1.43842	4.29E-05	Pyridoxal 4-de	1.1.1.107	0	Aldo Keto reductase
COJEPEMI_(	COJEPE	1.4345	2.05E-06	hypothetical p	NA	0	
COJEPEMI_(	rpmA	1.43011	2.07E-12	50S ribosomal	NA	rpmA	Belongs to the bacterial ribosomal protein bL27 family
COJEPEMI_(	COJEPE	1.42596	1.67E-07	hypothetical p	NA	0	Ankyrin repeat
COJEPEMI_(	COJEPE	1.42421	5.57E-05	hypothetical p	NA	0	Phage late control gene D protein (GPD)
COJEPEMI_(	COJEPE	1.42294	1.46E-09	hypothetical p	NA	0	Protein of unknown function (DUF1315)
COJEPEMI_(	ygiN	1.42231	0.000184	putative quino	1.-.-.-	ygiN	Antibiotic biosynthesis monooxygenase
COJEPEMI_(	COJEPE	1.4216	6.45E-18	hypothetical p	NA	0	Bax inhibitor 1 like
COJEPEMI_(	gabD_1	1.42099	5.83E-09	Succinate-sem	1.2.1.79	gabD	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat
COJEPEMI_(	COJEPE	1.4165	4.78E-06	hypothetical p	NA	0	Sulfite exporter TauE/SafE
COJEPEMI_(	COJEPE	1.4158	0.049225	hypothetical p	NA	0	
COJEPEMI_(	rpsF	1.40513	1.77E-09	30S ribosomal	NA	rpsF	Binds together with S18 to 16S ribosomal RNA
COJEPEMI_(	COJEPE	1.40456	0.0076	hypothetical p	NA	0	
COJEPEMI_(	fadH_3	1.40416	2.59E-07	2,4-dienoyl-Co	1.3.1.34	fadH	2,4-dienoyl-coA reductase
COJEPEMI_(	COJEPE	1.40218	0.000214	hypothetical p	NA	0	Iron-containing redox enzyme
COJEPEMI_(	glpE_1	1.40087	1.03E-07	Thiosulfate su	2.8.1.1	yceA	Belongs to the UPF0176 family
COJEPEMI_(	COJEPE	1.3998	8.69E-06	hypothetical p	NA	papD	Pili and flagellar-assembly chaperone, PapD N-terminal domain
COJEPEMI_(	nfuA	1.39654	1.73E-11	Fe/S biogenes	NA	nfuA	Involved in iron-sulfur cluster biogenesis. Binds a 4Fe- 4S cluster, can t
COJEPEMI_(	infA	1.39645	1.39E-08	Translation ini	NA	infA	One of the essential components for the initiation of protein synthesis.
COJEPEMI_(	COJEPE	1.394	0.154476	hypothetical p	NA	0	
COJEPEMI_(	nuoH	1.39377	1.31E-10	NADH-quinone	7.1.1.-	nuoH	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) c
COJEPEMI_(	COJEPE	1.39177	1.02E-07	hypothetical p	NA	0	

COJEPEMI_(	COJEPE	1.38906	0.024141	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.38543	0.022122	hypothetical p	NA	0	Uncharacterised MFS-type transporter YbfB
COJEPEMI_(	yacG	1.37826	7.15E-12	DNA gyrase in	NA	yacG	Inhibits all the catalytic activities of DNA gyrase by preventing its intera
COJEPEMI_(	COJEPE	1.37602	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	1.37501	1.02E-05	hypothetical p	NA	0	
COJEPEMI_(	rsxB	1.37179	5.19E-05	Ion-translocati	7.-.-.-	rnfB	Part of a membrane complex involved in electron transport
COJEPEMI_(	COJEPE	1.37152	1.04E-11	hypothetical p	NA	0	
COJEPEMI_(	antA_1	1.37115	0.001792	Anthranilate 1	1.14.12.1	antA	Ring hydroxylating alpha subunit (catalytic domain)
COJEPEMI_(	dedA_1	1.36253	5.22E-08	Protein DedA	NA	dedA	SNARE associated Golgi protein
COJEPEMI_(	rpmD	1.35383	9.96E-10	50S ribosomal	NA	rpmD	Ribosomal protein L30
COJEPEMI_(	COJEPE	1.35069	0.000572	hypothetical p	NA	0	
COJEPEMI_(	tpiA	1.34477	1.22E-14	Triosephospha	5.3.1.1	tpiA	Involved in the gluconeogenesis. Catalyzes stereospecifically the conver
COJEPEMI_(	sotB	1.34277	0.004813	sugar efflux tr	NA	ynfM_2	Major facilitator Superfamily
COJEPEMI_(	menF	1.34052	0.000702	Isochorismate	5.4.4.2	pabB	chorismate binding enzyme
COJEPEMI_(	uup	1.33689	3.07E-06	ABC transport	NA	uup	COG0488 ATPase components of ABC transporters with duplicated ATP
COJEPEMI_(	cysD	1.33526	0.008638	Sulfate adenyl	2.7.7.4	cysD	Sulfate adenylyltransferase subunit 2
COJEPEMI_(	COJEPE	1.33336	9.13E-08	hypothetical p	NA	0	
COJEPEMI_(	fabG_2	1.33233	0.000131	3-oxoacyl-[acy	1.1.1.100	fabG_1	KR domain
COJEPEMI_(	COJEPE	1.32909	NA	hypothetical p	NA	0	SnoaL-like domain
COJEPEMI_(	COJEPE	1.32644	1.27E-10	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	1.3254	0.000813	hypothetical p	NA	0	Belongs to the UPF0250 family
COJEPEMI_(	COJEPE	1.32458	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.32338	9.70E-09	hypothetical p	NA	0	Fibronectin type 3 domain
COJEPEMI_(	tsaD	1.32193	7.65E-07	tRNA N6-aden	2.3.1.234	tsaD	Required for the formation of a threonylcarbamoyl group on adenosine
COJEPEMI_(	COJEPE	1.3181	0.100734	hypothetical p	NA	eamB	LysE type translocator
COJEPEMI_(	COJEPE	1.31684	NA	IS6 family trar	NA	0	Transposase IS66 family
COJEPEMI_(	COJEPE	1.31608	1.48E-06	hypothetical p	NA	0	Enoyl-(Acyl carrier protein) reductase
COJEPEMI_(	iutA_1	1.31591	3.95E-07	Ferric aerobac	NA	aleB	TonB dependent receptor
COJEPEMI_(	COJEPE	1.31567	3.13E-12	hypothetical p	NA	0	OsmC-like protein
COJEPEMI_(	COJEPE	1.31286	0.037111	hypothetical p	NA	0	

COJEPEMI_(	lolA	1.31134	6.41E-09	Outer-membra	NA	lolA	Participates in the translocation of lipoproteins from the inner membra
COJEPEMI_(	rplR	1.30999	1.59E-09	50S ribosomal	NA	rplR	This is one of the proteins that binds and probably mediates the attach
COJEPEMI_(	rubA	1.30701	9.72E-15	Rubredoxin	NA	rubA	Rubredoxin
COJEPEMI_(	pcaK_4	1.30224	0.000173	4-hydroxybenz	NA	benK	Major facilitator Superfamily
COJEPEMI_(	COJEPE	1.30186	1.64E-06	hypothetical p	NA	0	
COJEPEMI_(	gabP_2	1.29545	7.16E-06	GABA permea	NA	gabP	Amino acid permease
COJEPEMI_(	COJEPE	1.28752	NA	hypothetical p	NA	0	Helix-turn-helix domain
COJEPEMI_(	COJEPE	1.28231	0.001132	hypothetical p	NA	0	
COJEPEMI_(	tnpR	1.28001	2.36E-05	Transposon Tn	NA	0	Resolvase, N terminal domain
COJEPEMI_(	COJEPE	1.27968	8.94E-08	hypothetical p	NA	0	Phage late control gene D protein (GPD)
COJEPEMI_(	COJEPE	1.27392	0.000227	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.26813	0.000556	hypothetical p	NA	0	Glycosyl transferase family 2
COJEPEMI_(	COJEPE	1.26063	0.002857	hypothetical p	NA	0	Domain of unknown function (DUF4142)
COJEPEMI_(	rplI	1.25351	6.10E-06	50S ribosomal	NA	rplI	Binds to the 23S rRNA
COJEPEMI_(	tusA_2	1.25342	4.61E-09	Sulfur carrier p	NA	tusA	Belongs to the sulfur carrier protein TusA family
COJEPEMI_(	COJEPE	1.24884	0.032444	hypothetical p	NA	0	Membrane bound YbgT-like protein
COJEPEMI_(	secA	1.24291	3.62E-07	Protein translc	NA	secA	Part of the Sec protein translocase complex. Interacts with the SecYEG
COJEPEMI_(	rpsN	1.24254	1.16E-07	30S ribosomal	NA	rpsN	Binds 16S rRNA, required for the assembly of 30S particles and may als
COJEPEMI_(	COJEPE	1.24108	0.235173	hypothetical p	NA	0	
COJEPEMI_(	rpsE	1.23974	2.31E-07	30S ribosomal	NA	rpsE	Located at the back of the 30S subunit body where it stabilizes the conf
COJEPEMI_(	COJEPE	1.23711	0.000434	hypothetical p	NA	0	Dienelactone hydrolase family
COJEPEMI_(	COJEPE	1.23585	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.23383	1.49E-09	hypothetical p	NA	0	
COJEPEMI_(	asd	1.23065	2.28E-07	Aspartate-sem	1.2.1.11	asd	Catalyzes the NADPH-dependent formation of L-aspartate- semialdehy
COJEPEMI_(	acnA	1.2284	4.47E-05	Aconitate hydr	4.2.1.3	acnA	Catalyzes the isomerization of citrate to isocitrate via cis-aconitate
COJEPEMI_(	sdhA	1.22486	4.14E-08	Succinate deh	1.3.5.1	sdhA	Belongs to the FAD-dependent oxidoreductase 2 family. FRD SDH subfa
COJEPEMI_(	COJEPE	1.22401	0.021626	hypothetical p	NA	0	Competence protein
COJEPEMI_(	COJEPE	1.22158	0.000172	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	leuC	1.22112	0.019314	3-isopropylma	4.2.1.33	leuC	Catalyzes the isomerization between 2-isopropylmalate and 3-isopropy
COJEPEMI_(	COJEPE	1.21082	0.001046	hypothetical p	NA	0	

COJEPEMI_(	miaA	1.21016	2.81E-14	tRNA dimethy	2.5.1.75	miaA	Catalyzes the transfer of a dimethylallyl group onto the adenine at posi
COJEPEMI_(	COJEPE	1.21007	0.00067	hypothetical p	NA	MA20_15	Elongator protein 3, MiaB family, Radical SAM
COJEPEMI_(	COJEPE	1.20353	5.95E-07	hypothetical p	NA	0	
COJEPEMI_(	yiaD	1.20023	1.41E-06	putative lipopr	NA	yiaD	Belongs to the ompA family
COJEPEMI_(	bfrD	1.19897	5.30E-07	putative TonB-	NA	bfrD_2	TonB dependent receptor
COJEPEMI_(	pth	1.19787	9.58E-13	Peptidyl-tRNA	3.1.1.29	pth	The natural substrate for this enzyme may be peptidyl- tRNAs which dr
COJEPEMI_(	mtnN_2	1.193	3.61E-05	5'-methylthioa	3.2.2.9	0	Phosphorylase superfamily
COJEPEMI_(	COJEPE	1.19246	0.03884	hypothetical p	NA	0	
COJEPEMI_(	betB_1	1.19224	0.001099	NAD/NADP-de	1.2.1.8	aldA	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat
COJEPEMI_(	COJEPE	1.19096	0.002519	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2213)
COJEPEMI_(	COJEPE	1.19094	8.29E-05	hypothetical p	NA	0	Sh3 type 3 domain protein
COJEPEMI_(	yciC	1.18638	0.289741	Putative meta	NA	yciC	Cobalamin synthesis protein cobW C-terminal domain
COJEPEMI_(	uvrB_1	1.18224	0.000178	UvrABC systen	NA	uvrB	damaged site, the DNA wraps around one UvrB monomer. DNA wrap is
COJEPEMI_(	prlC_1	1.17789	5.34E-05	Oligopeptidas	3.4.24.70	prlC	Peptidase family M3
COJEPEMI_(	rsfS	1.17708	1.50E-11	Ribosomal sile	NA	rsfS	Functions as a ribosomal silencing factor. Interacts with ribosomal prot
COJEPEMI_(	COJEPE	1.17535	1.85E-16	hypothetical p	NA	0	
COJEPEMI_(	merR	1.1714	4.16E-05	Mercuric resis	NA	merR	MerR, DNA binding
COJEPEMI_(	leuD	1.1699	0.011382	3-isopropylma	4.2.1.33	leuD	Catalyzes the isomerization between 2-isopropylmalate and 3-isopropy
COJEPEMI_(	guaD_2	1.16947	2.67E-05	Guanine deam	3.5.4.3	guaD	MafB19-like deaminase
COJEPEMI_(	mtnN_1	1.16728	3.04E-05	5'-methylthioa	3.2.2.9	0	Phosphorylase superfamily
COJEPEMI_(	rpoH	1.16304	1.66E-11	RNA polymera	NA	rpoH	RNA polymerase sigma factor RpoH
COJEPEMI_(	paaA	1.16276	0.00022	1,2-phenylacet	1.14.13.1	paaA	Phenylacetic acid catabolic protein
COJEPEMI_(	COJEPE	1.16246	8.16E-07	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.16043	0.00096	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.15475	0.055318	hypothetical p	NA	0	Pyridine nucleotide-disulphide oxidoreductase
COJEPEMI_(	COJEPE	1.15457	0.000174	hypothetical p	NA	MA20_36	Putative cyclase
COJEPEMI_(	paaD	1.15378	0.002821	Putative 1,2-pl	NA	paaD	Iron-sulfur cluster assembly protein
COJEPEMI_(	sdhB	1.14923	5.98E-05	Succinate deh	1.3.5.1	sdhB	succinate dehydrogenase
COJEPEMI_(	comM_	1.14883	0.006231	Competence p	NA	comM	Magnesium chelatase, subunit ChlI
COJEPEMI_(	recX	1.14861	6.41E-05	Regulatory prc	NA	recX	Regulatory protein recX

COJEPEMI_(	mdaB	1.14846	0.041529	NADPH:quinon	1.6.5.10	mdaB	Flavodoxin-like fold
COJEPEMI_(	COJEPE	1.1477	1.14E-09	hypothetical p	NA	ygiQ	UPF0313 protein
COJEPEMI_(	ycjY	1.14685	7.95E-07	putative prote	NA	0	BAAT / Acyl-CoA thioester hydrolase C terminal
COJEPEMI_(	blh_1	1.14664	4.57E-09	Beta-lactamas	3.-.-.-	0	Putative phosphatase (DUF442)
COJEPEMI_(	dxs	1.14402	3.08E-15	1-deoxy-D-xylu	2.2.1.7	dxs	Catalyzes the acyloin condensation reaction between C atoms 2 and 3 c
COJEPEMI_(	erpA	1.14398	7.40E-06	Iron-sulfur clus	NA	erpA	Iron-sulfur cluster insertion protein ErpA
COJEPEMI_(	fbp_1	1.14385	1.52E-05	Fructose-1,6-b	3.1.3.11	fbp	D-fructose-1,6-bisphosphate 1-phosphohydrolase class 1
COJEPEMI_(	egtB	1.14333	0.020747	Hercynine oxyg	1.14.99.5	pkn1	Sulfatase-modifying factor enzyme 1
COJEPEMI_(	phnX	1.13984	0.014256	Phosphonoace	3.11.1.1	phnX	Belongs to the HAD-like hydrolase superfamily. PhnX family
COJEPEMI_(	COJEPE	1.13664	0.000652	hypothetical p	NA	mgtC	MgtC family
COJEPEMI_(	nuoJ	1.13028	0.000164	NADH-quinone	7.1.1.-	nuoJ	Belongs to the complex I subunit 6 family
COJEPEMI_(	thrH	1.12928	5.33E-06	Phosphoserine	3.1.3.3	thrH	haloacid dehalogenase-like hydrolase
COJEPEMI_(	COJEPE	1.12916	0.001768	hypothetical p	NA	0	Domain of unknown function (DUF4902)
COJEPEMI_(	yheS_1	1.12854	7.95E-06	putative ABC t	NA	yheS	COG0488 ATPase components of ABC transporters with duplicated ATP
COJEPEMI_(	rnpA	1.12488	3.61E-05	Ribonuclease I	3.1.26.5	rnpA	RNaseP catalyzes the removal of the 5'-leader sequence from pre-tRN/
COJEPEMI_(	ilvB	1.12463	0.002717	Acetolactate s	2.2.1.6	0	Thiamine pyrophosphate enzyme, central domain
COJEPEMI_(	nuoK	1.12305	0.000212	NADH-quinone	7.1.1.-	nuoK	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) c
COJEPEMI_(	COJEPE	1.12094	3.99E-10	Thioredoxin C-	NA	trxA	Belongs to the thioredoxin family
COJEPEMI_(	COJEPE	1.12028	1.05E-06	hypothetical p	NA	0	LysE type translocator
COJEPEMI_(	rplN	1.11979	9.93E-11	50S ribosomal	NA	rplN	Binds to 23S rRNA. Forms part of two intersubunit bridges in the 70S ri
COJEPEMI_(	secE	1.11776	1.14E-06	Protein translc	NA	secE	Essential subunit of the Sec protein translocation channel SecYEG. Clan
COJEPEMI_(	hcaB_3	1.11697	0.009274	3-phenylpropic	1.3.1.87	0	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	sdhC	1.11254	1.17E-06	Succinate deh	NA	sdhC	succinate dehydrogenase
COJEPEMI_(	antC	1.10847	0.000783	Anthranilate 1	NA	antC	Oxidoreductase FAD-binding domain
COJEPEMI_(	tufA_1	1.10759	3.59E-05	Elongation fac	NA	tuf	This protein promotes the GTP-dependent binding of aminoacyl-tRNA t
COJEPEMI_(	COJEPE	1.10648	NA	IS5 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	rnz	1.10618	0.017091	Ribonuclease Z	3.1.26.11	rnz	Zinc phosphodiesterase, which displays some tRNA 3'- processing endc
COJEPEMI_(	COJEPE	1.10617	1.91E-12	hypothetical p	NA	0	Peptidase M15
COJEPEMI_(	fabG_1	1.10449	0.000418	3-oxoacyl-[acy	1.1.1.100	MA20_3	Enoyl-(Acyl carrier protein) reductase
COJEPEMI_(	yafP	1.10362	2.08E-08	putative N-ace	2.3.1.-	0	-acetyltransferase

COJEPEMI_(	dtd	1.10282	1.25E-07	D-aminoacyl-t	3.1.1.96	dtd	rejects L-amino acids rather than detecting D-amino acids in the active
COJEPEMI_(	paaC	1.10116	0.002578	1,2-phenylacet	NA	paaC	Phenylacetic acid catabolic protein
COJEPEMI_(	paaB	1.10033	0.000885	1,2-phenylacet	NA	paaB	Phenylacetic acid degradation B
COJEPEMI_(	rplE	1.09699	3.64E-06	50S ribosomal	NA	rplE	This is 1 of the proteins that binds and probably mediates the attachme
COJEPEMI_(	paaE	1.09693	0.014956	1,2-phenylacet	1.-.-.-	paaE	Oxidoreductase FAD-binding domain
COJEPEMI_(	yeaX	1.0966	0.003407	Carnitine mon	1.14.13.2	0	2Fe-2S iron-sulfur cluster binding domain
COJEPEMI_(	namA_1	1.08439	2.37E-05	NADPH dehydr	1.6.99.1	0	NADH:flavin oxidoreductase / NADH oxidase family
COJEPEMI_(	dacD	1.08375	6.40E-05	D-alanyl-D-ala	3.4.16.4	dacD	Belongs to the peptidase S11 family
COJEPEMI_(	pckG	1.0833	0.00055	Phosphoenolpy	4.1.1.32	pckG	Catalyzes the conversion of oxaloacetate (OAA) to phosphoenolpyruvat
COJEPEMI_(	ssb	1.08115	0.013915	Single-strande	NA	ssb	Single-strand binding protein family
COJEPEMI_(	clpB	1.08017	0.005361	Chaperone pro	NA	clpB	Part of a stress-induced multi-chaperone system, it is involved in the re
COJEPEMI_(	COJEPE	1.07611	0.062424	hypothetical p	NA	0	Phosphate acyltransferases
COJEPEMI_(	rplX	1.07518	1.64E-07	50S ribosomal	NA	rplX	One of the proteins that surrounds the polypeptide exit tunnel on the o
COJEPEMI_(	COJEPE	1.07156	0.254735	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.07059	0.021697	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	iscA	1.06794	0.01972	Iron-binding p	NA	iscA	Is able to transfer iron-sulfur clusters to apo- ferredoxin. Multiple cycle
COJEPEMI_(	gabR_2	1.06734	1.11E-07	HTH-type trans	NA	gabR_1	helix_turn_helix gluconate operon transcriptional repressor
COJEPEMI_(	COJEPE	1.0627	5.78E-05	hypothetical p	NA	0	Transcriptional regulator
COJEPEMI_(	truA	1.06251	0.000455	tRNA pseudou	5.4.99.12	truA	Formation of pseudouridine at positions 38, 39 and 40 in the anticodon
COJEPEMI_(	relA	1.06177	3.06E-09	GTP pyrophosp	2.7.6.5	relA	In eubacteria ppGpp (guanosine 3'-diphosphate 5-' diphosphate) is a m
COJEPEMI_(	rocC_1	1.05744	0.000131	Amino-acid pe	NA	mmuP	amino acid
COJEPEMI_(	pepN_2	1.05661	1.92E-10	Aminopeptida	3.4.11.2	pepN	Domain of unknown function (DUF3458_C) ARM repeats
COJEPEMI_(	COJEPE	1.05476	0.09455	hypothetical p	NA	0	BRO family, N-terminal domain
COJEPEMI_(	efp	1.0503	7.42E-10	Elongation fac	NA	efp	Involved in peptide bond synthesis. Alleviates ribosome stalling that oc
COJEPEMI_(	yfiH	1.05021	1.67E-05	Polyphenol oxi	1.10.3.-	yfiH	Belongs to the multicopper oxidase YfiH RL5 family
COJEPEMI_(	dksA	1.0451	2.11E-05	RNA polymera	NA	dksA	Transcription factor that acts by binding directly to the RNA polymerase
COJEPEMI_(	COJEPE	1.04345	0.073613	hypothetical p	NA	0	VRR-NUC domain
COJEPEMI_(	cbpA	1.03375	4.45E-12	Curved DNA-bi	NA	cbpA	DnaJ molecular chaperone homology domain
COJEPEMI_(	COJEPE	1.03326	0.064405	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.03039	0.112556	hypothetical p	NA	0	

COJEPEMI_(	COJEPE	1.03026	5.73E-09	hypothetical p	NA	0	
COJEPEMI_(	hemE	1.02827	2.61E-05	Uroporphyrino	4.1.1.37	hemE	Catalyzes the decarboxylation of four acetate groups of uroporphyrinog
COJEPEMI_(	rsmJ	1.02504	0.000964	Ribosomal RN	2.1.1.242	rsmJ	Specifically methylates the guanosine in position 1516 of 16S rRNA
COJEPEMI_(	rpsT	1.02181	5.96E-06	30S ribosomal	NA	rpsT	Binds directly to 16S ribosomal RNA
COJEPEMI_(	COJEPE	1.02083	0.001841	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	1.01917	0.004634	hypothetical p	NA	MA20_23	Protein of unknown function (DUF1304)
COJEPEMI_(	norG_1	1.01792	0.00706	HTH-type trans	NA	0	helix_turn_helix gluconate operon transcriptional repressor
COJEPEMI_(	COJEPE	1.01492	0.108753	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	1.01369	0.004634	hypothetical p	NA	0	
COJEPEMI_(	styA	1.01184	0.01052	Styrene mono(	1.14.14.1	0	oxidoreductase
COJEPEMI_(	COJEPE	1.00994	0.01497	putative prote	NA	0	Bacterial OB fold (BOF) protein
COJEPEMI_(	nimR_3	1.00978	0.001423	HTH-type trans	NA	0	helix_turn_helix, arabinose operon control protein
COJEPEMI_(	rcsC_7	1.00815	0.000289	Sensor histidir	2.7.13.3	MA20_23	PhoQ Sensor
COJEPEMI_(	COJEPE	1.00433	1.24E-05	hypothetical p	NA	0	Copper resistance protein B precursor (CopB)
COJEPEMI_(	COJEPE	1.0041	0.076862	hypothetical p	NA	0	Interacts with outer membrane receptor proteins that carry out high-af
COJEPEMI_(	rluA_1	1.00408	0.013097	Dual-specificit	5.4.99.28	rluA	Responsible for synthesis of pseudouridine from uracil
COJEPEMI_(	carA	0.99997	0.001973	Carbamoyl-ph(	6.3.5.5	carA	Belongs to the CarA family
COJEPEMI_(	COJEPE	0.99399	0.004135	hypothetical p	NA	nrdA	Provides the precursors necessary for DNA synthesis. Catalyzes the bios
COJEPEMI_(	gatA_2	0.99378	NA	Glutamyl-tRN/	6.3.5.7	0	Amidase
COJEPEMI_(	kdpC	0.99276	0.007925	Potassium-tra	NA	kdpC	Part of the high-affinity ATP-driven potassium transport (or Kdp) syster
COJEPEMI_(	hscB	0.9903	5.20E-07	Co-chaperone	NA	hscB	Co-chaperone involved in the maturation of iron-sulfur cluster-containi
COJEPEMI_(	COJEPE	0.98899	0.002837	hypothetical p	NA	0	In eubacteria ppGpp (guanosine 3'-diphosphate 5-' diphosphate) is a m
COJEPEMI_(	azoR	0.98657	0.11968	FMN-depende	1.7.1.17	azoR	Catalyzes the reductive cleavage of azo bond in aromatic azo compoun
COJEPEMI_(	COJEPE	0.98537	0.024177	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.98391	0.004132	hypothetical p	NA	0	
COJEPEMI_(	antA_2	0.97998	0.00603	Anthranilate 1	1.14.12.1	antA	Ring hydroxylating alpha subunit (catalytic domain)
COJEPEMI_(	coq7	0.978	9.87E-05	3-demethoxyu	1.14.99.6	coq7	Oxygenase that introduces the hydroxyl group at carbon five of 2-nonap
COJEPEMI_(	bolA	0.97729	1.94E-06	DNA-binding t	NA	bolA	Belongs to the BolA IbaG family
COJEPEMI_(	dsbA	0.97689	3.92E-05	Thiol:disulfide	NA	dsbA	Thiol disulfide interchange protein
COJEPEMI_(	COJEPE	0.97289	1.02E-06	hypothetical p	NA	sdhE	Flavinator of succinate dehydrogenase

COJEPEMI_(	COJEPE	0.97102	3.95E-07	hypothetical p	NA	0	Domain of unknown function (DUF4440)
COJEPEMI_(	COJEPE	0.97062	0.001192	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.96606	0.108558	hypothetical p	NA	csuC	Pili and flagellar-assembly chaperone, PapD N-terminal domain
COJEPEMI_(	COJEPE	0.96585	7.25E-08	hypothetical p	NA	0	Protein of unknown function (DUF962)
COJEPEMI_(	COJEPE	0.96547	0.000291	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	fgd	0.96196	5.96E-06	F420-depende	1.1.98.2	yhbW	Luciferase-like monooxygenase
COJEPEMI_(	COJEPE	0.96152	4.14E-05	hypothetical p	NA	0	
COJEPEMI_(	trpC	0.96133	1.50E-06	Indole-3-glyce	4.1.1.48	trpC	Belongs to the TrpC family
COJEPEMI_(	COJEPE	0.96007	0.009456	hypothetical p	NA	MA20_28	Fatty acid desaturase
COJEPEMI_(	COJEPE	0.95962	0.027751	hypothetical p	NA	hemN1	SMART Elongator protein 3 MiaB NifB
COJEPEMI_(	tsf	0.95881	0.001297	Elongation fac	NA	tsf	Associates with the EF-Tu.GDP complex and induces the exchange of G
COJEPEMI_(	gloC	0.95775	1.11E-08	Hydroxyacylglu	3.1.2.6	ycbL	Metallo-beta-lactamase superfamily
COJEPEMI_(	nasD	0.95768	0.000948	Nitrite reducta	1.7.1.4	nirB	Belongs to the nitrite and sulfite reductase 4Fe-4S domain family
COJEPEMI_(	COJEPE	0.95584	1.59E-06	hypothetical p	NA	MA20_30	Alpha/beta hydrolase family
COJEPEMI_(	COJEPE	0.95417	1.45E-07	hypothetical p	NA	0	Nickel/cobalt transporter regulator
COJEPEMI_(	COJEPE	0.95198	0.00493	hypothetical p	NA	trbI	conjugation TrbI family protein
COJEPEMI_(	COJEPE	0.95048	1.03E-06	hypothetical p	NA	0	Tim44
COJEPEMI_(	soxA	0.94878	0.12716	Monomeric sa	1.5.3.1	0	FAD dependent oxidoreductase
COJEPEMI_(	rpiA	0.94638	0.025812	Ribose-5-phos	5.3.1.6	rpiA	Catalyzes the reversible conversion of ribose-5- phosphate to ribulose 5
COJEPEMI_(	xerC_5	0.94422	0.00522	Tyrosine recon	NA	0	Phage integrase, N-terminal SAM-like domain
COJEPEMI_(	purE	0.94385	2.30E-05	N5-carboxyam	5.4.99.18	purE	Catalyzes the conversion of N5-carboxyaminoimidazole ribonucleotide
COJEPEMI_(	metH	0.94251	6.30E-05	Methionine sy	2.1.1.13	metH	B12 binding domain
COJEPEMI_(	COJEPE	0.94211	0.029067	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.94204	0.018369	hypothetical p	NA	0	
COJEPEMI_(	rpmE2	0.94059	0.417914	50S ribosomal	NA	rpmE2	Ribosomal protein L31
COJEPEMI_(	COJEPE	0.93867	0.173454	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.93569	0.0014	hypothetical p	NA	0	Putative methionine and alanine importer, small subunit
COJEPEMI_(	COJEPE	0.9343	6.11E-05	hypothetical p	NA	0	Glycoside hydrolase family 24
COJEPEMI_(	ygiD	0.93194	0.000828	4,5-DOPA diox	1.13.11.2	0	Catalytic LigB subunit of aromatic ring-opening dioxygenase
COJEPEMI_(	exoX	0.93156	0.001588	Exodeoxyribon	3.1.11.-	exoX	3'-5' exonuclease activity on single or double-strand DNA

COJEPEMI_(	cspG_2	0.92963	0.005362	Cold shock-like	NA	cspV	Cold shock protein domain
COJEPEMI_(	hmrR_2	0.92402	1.38E-05	HTH-type trans	NA	cueR	helix_turn_helix, mercury resistance
COJEPEMI_(	COJEPE	0.92036	0.121248	Putative unive	NA	uspA	Universal stress protein
COJEPEMI_(	COJEPE	0.91982	NA	hypothetical p	NA	0	Domain of unknown function (DUF1833)
COJEPEMI_(	phnW	0.91867	0.010946	2-aminoethylp	2.6.1.37	phnW	Belongs to the class-V pyridoxal-phosphate-dependent aminotransfera
COJEPEMI_(	COJEPE	0.9167	NA	hypothetical p	NA	0	
COJEPEMI_(	arsC_1	0.91534	0.002287	Arsenate redu	1.20.4.1	arsC	ArsC family
COJEPEMI_(	rpsK	0.91506	0.000984	30S ribosomal	NA	rpsK	Located on the platform of the 30S subunit, it bridges several disparate
COJEPEMI_(	yheS_2	0.9149	0.006125	putative ABC t	NA	ydiF	ABC transporter
COJEPEMI_(	nadC	0.91471	0.001298	Nicotinate-nuc	2.4.2.19	nadC	Belongs to the NadC ModD family
COJEPEMI_(	rep_1	0.91438	0.001394	ATP-dependen	3.6.4.12	rep	it can initiate unwinding at a nick in the DNA. It binds to the single-stra
COJEPEMI_(	tgnD_1	0.91181	0.115534	(E)-2-((N-metl	3.5.1.-	0	Serine aminopeptidase, S33
COJEPEMI_(	mnmE	0.91009	8.98E-07	tRNA modifica	3.6.-.-	mnmE	Exhibits a very high intrinsic GTPase hydrolysis rate. Involved in the add
COJEPEMI_(	COJEPE	0.90977	8.57E-05	hypothetical p	NA	0	
COJEPEMI_(	paaF_4	0.90928	0.049238	2,3-dehydroad	4.2.1.17	paaF	Enoyl-CoA hydratase/isomerase
COJEPEMI_(	COJEPE	0.90775	7.78E-06	hypothetical p	NA	Z012_04	Belongs to the pirin family
COJEPEMI_(	rubB_1	0.90749	0.006012	Rubredoxin-N	1.18.1.1	rubB	Pyridine nucleotide-disulphide oxidoreductase
COJEPEMI_(	queH	0.90487	2.72E-06	Epoxyqueuosir	1.17.99.6	queH	Catalyzes the conversion of epoxyqueuosine (oQ) to queuosine (Q), whi
COJEPEMI_(	COJEPE	0.90375	0.000565	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.90353	0.002228	hypothetical p	NA	uxpB	Bacterial protein of unknown function (DUF839)
COJEPEMI_(	gcvA_3	0.90241	0.000428	Glycine cleava	NA	gcdR	LysR substrate binding domain
COJEPEMI_(	paaF_1	0.89874	0.006709	2,3-dehydroad	4.2.1.17	0	Enoyl-CoA hydratase/isomerase
COJEPEMI_(	C1-hpaH	0.89813	0.028533	p-hydroxyphen	1.5.1.36	ntaB	Flavin reductase like domain
COJEPEMI_(	COJEPE	0.89777	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.89374	9.05E-05	hypothetical p	NA	0	Enoyl-(Acyl carrier protein) reductase
COJEPEMI_(	COJEPE	0.89291	0.046799	hypothetical p	NA	0	Forms passive diffusion pores that allow small molecular weight hydro
COJEPEMI_(	COJEPE	0.88962	0.002634	hypothetical p	NA	sodC	Destroys radicals which are normally produced within the cells and whi
COJEPEMI_(	COJEPE	0.88906	0.190854	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	nagR_3	0.88691	0.136837	HTH-type trans	NA	0	UTRA
COJEPEMI_(	COJEPE	0.88644	0.189193	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family

COJEPEMI_(	tcdA	0.88639	5.03E-06	tRNA threonyl	6.1.-.-	ygdL	COG1179 Dinucleotide-utilizing enzymes involved in molybdopterin anc
COJEPEMI_(	fatA_2	0.88572	0.000951	Ferric-anguiba	NA	0	TonB dependent receptor
COJEPEMI_(	gluQ	0.88268	0.003955	Glutamyl-Q tR	6.1.1.-	gluQ	Catalyzes the tRNA-independent activation of glutamate in presence of
COJEPEMI_(	COJEPE	0.88187	0.174213	hypothetical p	NA	0	Domain of unknown function (DUF4124)
COJEPEMI_(	COJEPE	0.88049	0.003568	hypothetical p	NA	0	Protein of unknown function (DUF2789)
COJEPEMI_(	yciK	0.87953	5.48E-08	putative oxido	1.-.-.-	yciK	KR domain
COJEPEMI_(	COJEPE	0.87489	NA	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	rplQ	0.87356	0.00337	50S ribosomal	NA	rplQ	Ribosomal protein L17
COJEPEMI_(	COJEPE	0.87351	0.00054	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.87293	0.000336	hypothetical p	NA	0	Heavy-metal-associated domain
COJEPEMI_(	merC	0.87224	0.011771	Mercuric trans	NA	merC	PFAM MerC mercury resistance protein
COJEPEMI_(	potE	0.87159	0.049878	Putrescine tra	NA	eat	Amino acid permease
COJEPEMI_(	zitB_2	0.87045	4.74E-08	Zinc transporte	NA	0	Cation efflux family
COJEPEMI_(	COJEPE	0.86997	0.00021	hypothetical p	NA	0	Phage regulatory protein Rha (Phage_pRha)
COJEPEMI_(	trxC	0.86991	4.90E-05	Thioredoxin 2	1.8.1.8	trxC	Thioredoxin
COJEPEMI_(	COJEPE	0.86962	0.006687	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.86582	0.000798	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	COJEPE	0.86533	0.019934	hypothetical p	NA	0	
COJEPEMI_(	oqxB7	0.8649	0.003067	multidrug effl	NA	bepE_1	Protein export membrane protein
COJEPEMI_(	COJEPE	0.86407	0.01815	hypothetical p	NA	0	
COJEPEMI_(	yrdA_1	0.86071	1.51E-06	Protein YrdA	NA	yrdA	Bacterial transferase hexapeptide (six repeats)
COJEPEMI_(	adc	0.85858	0.117955	acetoacetate d	4.1.1.4	0	Acetoacetate decarboxylase (ADC)
COJEPEMI_(	murI	0.85818	0.000175	Glutamate rac	5.1.1.3	murI	Provides the (R)-glutamate required for cell wall biosynthesis
COJEPEMI_(	pyrC'	0.8571	0.004338	Dihydroorotase	NA	pyrC	dihydroorotase
COJEPEMI_(	COJEPE	0.85584	0.111273	hypothetical p	NA	0	DJ-1/PfpI family
COJEPEMI_(	catC	0.85378	0.045286	Muconolacton	5.3.3.4	catC	Muconolactone delta-isomerase
COJEPEMI_(	COJEPE	0.85259	0.000677	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	lexA_1	0.85249	0.000272	LexA repressor	3.4.21.88	CI	Helix-turn-helix XRE-family like proteins
COJEPEMI_(	emrA_2	0.85069	0.026817	Colistin resista	NA	emrA	HlyD membrane-fusion protein of T1SS
COJEPEMI_(	dsdA	0.85044	0.003209	D-serine dehyd	4.3.1.18	dsdA	Belongs to the serine threonine dehydratase family. DsdA subfamily

COJEPEMI_(	COJEPE	0.85034	0.001728	hypothetical p	NA	0	META domain
COJEPEMI_(	COJEPE	0.8503	0.000297	hypothetical p	NA	fokIM	D12 class N6 adenine-specific DNA methyltransferase
COJEPEMI_(	emrE_1	0.84974	0.001854	Multidrug tran	NA	qacE	Small Multidrug Resistance protein
COJEPEMI_(	COJEPE	0.84935	0.072628	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	anoI	0.84913	0.176719	Acyl-homoseri	2.3.1.184	solI	Involved in the synthesis of the acyl-homoserine lactone (AHL) signal N
COJEPEMI_(	yfdC	0.84905	0.000256	Inner membra	NA	yfdC	Formate/nitrite transporter
COJEPEMI_(	yveA	0.84712	0.035186	Aspartate-prot	NA	yveA	Amino acid permease
COJEPEMI_(	ygfZ	0.84682	3.96E-05	tRNA-modifyir	NA	ygfZ	Aminomethyltransferase folate-binding domain
COJEPEMI_(	COJEPE	0.84648	0.00206	hypothetical p	NA	0	
COJEPEMI_(	rpsM	0.84641	0.002333	30S ribosomal	NA	rpsM	Located at the top of the head of the 30S subunit, it contacts several he
COJEPEMI_(	rpmJ	0.8459	0.000317	50S ribosomal	NA	rpmJ	Belongs to the bacterial ribosomal protein bL36 family
COJEPEMI_(	COJEPE	0.84477	0.000668	hypothetical p	NA	ugd2	Belongs to the UDP-glucose GDP-mannose dehydrogenase family
COJEPEMI_(	COJEPE	0.8438	0.005308	hypothetical p	NA	0	Patatin-like phospholipase
COJEPEMI_(	cntO_3	0.8428	9.49E-05	Metal-pseudo	NA	0	TonB dependent receptor
COJEPEMI_(	COJEPE	0.84174	0.023181	hypothetical p	NA	0	Cupin
COJEPEMI_(	pdxA	0.84014	5.81E-06	4-hydroxythre	1.1.1.262	pdxA	Catalyzes the NAD(P)-dependent oxidation of 4- (phosphohydroxy)-L-thr
COJEPEMI_(	COJEPE	0.84004	0.000572	hypothetical p	NA	0	Antitoxin component of a toxin-antitoxin (TA) module
COJEPEMI_(	slyD	0.83422	1.46E-06	FKBP-type pep	5.2.1.8	slyD	Peptidyl-prolyl cis-trans
COJEPEMI_(	COJEPE	0.83208	0.012608	hypothetical p	NA	0	
COJEPEMI_(	rocC_2	0.83119	0.002465	Amino-acid pe	NA	mmuP	amino acid
COJEPEMI_(	catM	0.83098	4.25E-05	HTH-type trans	NA	benM	Transcriptional regulator
COJEPEMI_(	COJEPE	0.82956	0.128829	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.82805	0.008358	hypothetical p	NA	0	
COJEPEMI_(	rpmF	0.82401	2.03E-06	50S ribosomal	NA	rpmF	Belongs to the bacterial ribosomal protein bL32 family
COJEPEMI_(	COJEPE	0.82397	2.50E-07	hypothetical p	NA	sndH	Glucose / Sorbosone dehydrogenase
COJEPEMI_(	COJEPE	0.82214	NA	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	tesB	0.82204	0.000373	Acyl-CoA thioe	3.1.2.-	tesB	Acyl-CoA thioesterase
COJEPEMI_(	dut	0.82129	0.01305	Deoxyuridine 5	3.6.1.23	dut	This enzyme is involved in nucleotide metabolism it produces dUMP, th
COJEPEMI_(	COJEPE	0.81986	0.001686	hypothetical p	NA	0	
COJEPEMI_(	infC	0.81817	2.06E-05	Translation ini	NA	infC	IF-3 binds to the 30S ribosomal subunit and shifts the equilibrum betw

COJEPEMI_(	amiE	0.81748	0.011851	N-acetylmurar	3.5.1.28	0	Beta-lactamase
COJEPEMI_(	catA	0.8165	0.027384	Catechol 1,2-d	1.13.11.1	catA	Catechol dioxygenase N terminus
COJEPEMI_(	dmlR_1	0.81615	0.007356	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	fabI	0.81026	0.001415	Enoyl-[acyl-ca	1.3.1.9	fabI	Enoyl- acyl-carrier-protein reductase NADH
COJEPEMI_(	COJEPE	0.80992	1.48E-06	hypothetical p	NA	0	COG1366 Anti-anti-sigma regulatory factor (antagonist of anti-sigma f
COJEPEMI_(	COJEPE	0.8094	0.008343	putative zinc-b	1.1.1.1	ybdR	Alcohol dehydrogenase GroES-like domain
COJEPEMI_(	yadV_2	0.80896	NA	putative fimbr	NA	cupB4	Pili assembly chaperone PapD, C-terminal domain
COJEPEMI_(	purK	0.80878	6.56E-05	N5-carboxyam	6.3.4.18	purK	Catalyzes the ATP-dependent conversion of 5- aminoimidazole ribonucl
COJEPEMI_(	ahpC	0.80725	2.45E-05	Alkyl hydroper	1.11.1.15	ahpC	Alkyl hydroperoxide reductase
COJEPEMI_(	bamE	0.80596	0.001285	Outer membra	NA	bamE	Part of the outer membrane protein assembly complex, which is involv
COJEPEMI_(	C1-hpah	0.80331	0.000885	p-hydroxyphen	1.5.1.36	C1-hpah	Flavin reductase like domain
COJEPEMI_(	nit1	0.79541	0.001192	Deaminated g	3.5.1.128	ramA	Carbon-nitrogen hydrolase
COJEPEMI_(	COJEPE	0.79369	8.55E-05	hypothetical p	NA	0	Glycosyltransferase family 25 (LPS biosynthesis protein)
COJEPEMI_(	nemA	0.79299	8.37E-05	N-ethylmalein	1.3.1.-	xenB	NADH:flavin oxidoreductase / NADH oxidase family
COJEPEMI_(	dsbB	0.79279	0.000107	Disulfide bond	NA	dsbB	Required for disulfide bond formation in some periplasmic proteins. Ac
COJEPEMI_(	hisP_2	0.79252	0.026163	Histidine trans	NA	hisP	ABC transporter, ATP-binding protein
COJEPEMI_(	COJEPE	0.79214	0.001607	hypothetical p	NA	0	DNA-templated transcription, initiation
COJEPEMI_(	tatC	0.79089	0.007728	Sec-independe	NA	tatC	Part of the twin-arginine translocation (Tat) system that transports lar
COJEPEMI_(	eutC	0.7906	0.020023	Ethanolamine	4.3.1.7	eutC	Ethanolamine ammonia-lyase light chain (EutC)
COJEPEMI_(	rpsD	0.78932	0.005548	30S ribosomal	NA	rpsD	One of the primary rRNA binding proteins, it binds directly to 16S rRNA
COJEPEMI_(	glyA	0.78898	0.000108	Serine hydroxy	2.1.2.1	glyA	Catalyzes the reversible interconversion of serine and glycine with tetra
COJEPEMI_(	COJEPE	0.78747	0.000526	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.78691	0.112556	hypothetical p	NA	0	
COJEPEMI_(	alkB	0.78659	0.087126	Alkane 1-mon	1.14.15.3	alkM	Fatty acid desaturase
COJEPEMI_(	hipO	0.78454	0.01014	Hippurate hyd	3.5.1.32	amaA	Peptidase dimerisation domain
COJEPEMI_(	rhaS_6	0.78326	0.000572	HTH-type trans	NA	tetD	helix_turn_helix, arabinose operon control protein
COJEPEMI_(	lptC	0.78285	0.000376	Lipopolysaccha	NA	lptC	Lipopolysaccharide-assembly, LptC-related
COJEPEMI_(	aacC1	0.78184	0.004228	Gentamicin 3-	2.3.1.60	0	FR47-like protein
COJEPEMI_(	rimM	0.78088	0.000159	Ribosome mat	NA	rimM	An accessory protein needed during the final step in the assembly of 3(
COJEPEMI_(	paaF_3	0.78045	0.006672	2,3-dehydroad	4.2.1.17	0	Enoyl-CoA hydratase/isomerase

COJEPEMI_(	COJEPE	0.78006	0.00954	hypothetical p	NA	0	Polyketide cyclase / dehydrase and lipid transport
COJEPEMI_(	COJEPE	0.77994	0.006727	hypothetical p	NA	0	Cyd operon protein YbgE (Cyd_oper_YbgE)
COJEPEMI_(	COJEPE	0.77989	0.055548	hypothetical p	NA	csuD	Outer membrane usher protein
COJEPEMI_(	aroP_4	0.77851	0.009468	Aromatic amir	NA	pheP	Amino acid permease
COJEPEMI_(	pdtaR	0.77768	NA	putative trans(	NA	nasT	ANTAR
COJEPEMI_(	gltA	0.77436	0.001056	Citrate syntha:	2.3.3.16	gltA	Belongs to the citrate synthase family
COJEPEMI_(	ilvD	0.77391	5.77E-08	Dihydroxy-acid	4.2.1.9	ilvD	Belongs to the IlvD Edd family
COJEPEMI_(	COJEPE	0.77149	0.012775	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.77017	0.023046	hypothetical p	NA	0	GDSL-like Lipase/Acylhydrolase family
COJEPEMI_(	exbD_2	0.76949	0.169244	Biopolymer tra	NA	exbD1	Biopolymer transport protein ExbD/TolR
COJEPEMI_(	aidA_2	0.76779	0.313469	Quorum-quen(	NA	0	Acetyl xylan esterase (AXE1)
COJEPEMI_(	dctA_3	0.76717	0.065572	Aerobic C4-dic	NA	dctA1	Belongs to the dicarboxylate amino acid cation symporter (DAACS) (TC
COJEPEMI_(	COJEPE	0.76532	0.002085	hypothetical p	NA	0	Short-chain dehydrogenase reductase Sdr
COJEPEMI_(	kdsD	0.76414	0.003146	Arabinose 5-pl	5.3.1.13	kdsD	Arabinose 5-phosphate isomerase
COJEPEMI_(	tenA	0.7624	0.001045	Aminopyrimid	3.5.99.2	tenA	Catalyzes an amino-pyrimidine hydrolysis reaction at the C5' of the pyri
COJEPEMI_(	ant1_1	0.76209	6.00E-05	Streptomycin 3	2.7.7.47	aadA	Domain of unknown function (DUF4111)
COJEPEMI_(	yhjQ	0.76166	0.007474	putative cystei	NA	#N/A	#N/A
COJEPEMI_(	rhaS_5	0.76145	0.000425	HTH-type trans	NA	0	AraC-binding-like domain
COJEPEMI_(	drgA	0.76109	0.00394	Protein DrgA	NA	drgA	Nitroreductase family
COJEPEMI_(	dkgB	0.76068	0.042991	2,5-diketo-D-g	1.1.1.346	dkgB	Aldo/keto reductase family
COJEPEMI_(	COJEPE	0.75953	0.194709	hypothetical p	NA	0	PspC domain
COJEPEMI_(	tgnB	0.75909	0.001579	Flavin-depend	1.14.14.-	0	Luciferase-like monooxygenase
COJEPEMI_(	ttgC	0.75852	0.01428	putative efflux	NA	0	Outer membrane efflux protein
COJEPEMI_(	aroE	0.75794	0.054014	Shikimate deh	1.1.1.25	aroE	Involved in the biosynthesis of the chorismate, which leads to the biosy
COJEPEMI_(	dgt	0.75663	0.018685	Deoxyguanosir	3.1.5.1	dgt	Deoxyguanosinetriphosphate triphosphohydrolase-like protein
COJEPEMI_(	COJEPE	0.75567	0.001574	hypothetical p	NA	0	Outer membrane usher protein
COJEPEMI_(	rluD	0.75384	1.83E-05	Ribosomal lar	5.4.99.23	rluD	Responsible for synthesis of pseudouridine from uracil
COJEPEMI_(	COJEPE	0.75325	9.24E-05	hypothetical p	NA	MA20_23	Protein of unknown function (DUF1345)
COJEPEMI_(	araC_1	0.75166	0.009903	L-arabonate de	4.2.1.25	IV02_106	Dehydratase family
COJEPEMI_(	COJEPE	0.75092	0.009161	hypothetical p	NA	0	Exonuclease VII small subunit

COJEPEMI_(	pgk	0.75039	0.001055	Phosphoglycer	2.7.2.3	pgk	Belongs to the phosphoglycerate kinase family
COJEPEMI_(	COJEPE	0.74993	0.26437	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.74862	0.004412	hypothetical p	NA	0	
COJEPEMI_(	ubiG	0.74855	0.000641	Ubiquinone bi	2.1.1.222	ubiG	O-methyltransferase that catalyzes the 2 O-methylation steps in the ul
COJEPEMI_(	carC	0.74853	0.24324	Caffeyl-CoA re	1.3.1.108	yngJ	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	grxD	0.74841	9.43E-06	Glutaredoxin 4	NA	grxD	Belongs to the glutaredoxin family. Monothiol subfamily
COJEPEMI_(	nsrR	0.74752	0.130236	HTH-type trans	NA	nsrR	Transcriptional regulator
COJEPEMI_(	corA	0.74675	0.000722	Magnesium tr	NA	corA	CorA-like Mg2+ transporter protein
COJEPEMI_(	COJEPE	0.74203	NA	hypothetical p	NA	gpI	Phage tail protein (Tail_P2_I)
COJEPEMI_(	eutQ	0.74149	0.129728	Ethanolamine	NA	0	Ethanolamine utilisation protein EutQ
COJEPEMI_(	COJEPE	0.74142	0.000971	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.74138	0.002734	hypothetical p	NA	0	
COJEPEMI_(	mdtE	0.73888	0.055991	Multidrug resi	NA	mexE	Barrel-sandwich domain of CusB or HlyD membrane-fusion
COJEPEMI_(	COJEPE	0.73864	0.135264	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.73785	0.151802	hypothetical p	NA	0	Nickel/cobalt transporter regulator
COJEPEMI_(	COJEPE	0.73735	0.093199	hypothetical p	NA	0	Protein of unknown function (DUF2750)
COJEPEMI_(	mtcA2	0.73714	2.02E-05	Carbonic anhy	4.2.1.1	cynT	Reversible hydration of carbon dioxide
COJEPEMI_(	COJEPE	0.73699	0.145077	hypothetical p	NA	0	mannose-ethanolamine phosphotransferase activity
COJEPEMI_(	guaB	0.7369	4.34E-06	Inosine-5'-mo	1.1.1.205	guaB	Catalyzes the conversion of inosine 5'-phosphate (IMP) to xanthosine 5'
COJEPEMI_(	COJEPE	0.73557	0.140199	hypothetical p	NA	nlpE	NlpE N-terminal domain
COJEPEMI_(	COJEPE	0.73546	0.023381	hypothetical p	NA	0	Glutathione-dependent formaldehyde-activating enzyme
COJEPEMI_(	COJEPE	0.73427	6.95E-05	hypothetical p	NA	0	
COJEPEMI_(	sir	0.73419	0.12717	Sulfite reducta	1.8.7.1	cysI	Belongs to the nitrite and sulfite reductase 4Fe-4S domain family
COJEPEMI_(	COJEPE	0.73406	0.168241	hypothetical p	NA	fxsA	FxsA cytoplasmic membrane protein
COJEPEMI_(	COJEPE	0.73405	0.003266	hypothetical p	NA	0	Sporulation related domain
COJEPEMI_(	clpX	0.73304	9.45E-06	ATP-dependen	NA	clpX	ATP-dependent specificity component of the Clp protease. It directs the
COJEPEMI_(	COJEPE	0.73266	6.88E-05	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.73194	NA	hypothetical p	NA	0	
COJEPEMI_(	lutR	0.73172	0.039161	HTH-type trans	NA	IV02_293	FCD
COJEPEMI_(	COJEPE	0.72881	0.007212	hypothetical p	NA	#N/A	#N/A

COJEPEMI_(	nrtP	0.72853	0.037997	Nitrate/nitrite	NA	narK	Major Facilitator Superfamily
COJEPEMI_(	COJEPE	0.72674	0.000212	hypothetical p	NA	0	LysM domain
COJEPEMI_(	COJEPE	0.72661	0.005101	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	pcaJ_2	0.72634	0.096214	3-oxoadipate (	2.8.3.6	pcaJ	3-oxoadipate CoA-transferase activity
COJEPEMI_(	COJEPE	0.72586	0.018038	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	yybR_2	0.7255	0.039102	putative HTH-t	NA	ytfH	HxlR-like helix-turn-helix
COJEPEMI_(	rimI	0.72535	0.094238	[Ribosomal pr	2.3.1.266	rimI	This enzyme acetylates the N-terminal alanine of ribosomal protein S1
COJEPEMI_(	COJEPE	0.72508	0.07502	hypothetical p	NA	0	outer membrane porin, OprD family
COJEPEMI_(	COJEPE	0.72494	0.000622	hypothetical p	NA	0	Helix-turn-helix XRE-family like proteins
COJEPEMI_(	COJEPE	0.72377	0.021582	hypothetical p	NA	0	Inovirus Gp2
COJEPEMI_(	COJEPE	0.72352	0.001253	hypothetical p	NA	0	Glyoxalase-like domain
COJEPEMI_(	ybjG	0.72325	0.226106	Putative unde	3.6.1.27	ybjG	Acid phosphatase homologues
COJEPEMI_(	eutB	0.72316	0.023392	Ethanolamine	4.3.1.7	eutB	Ethanolamine ammonia lyase large subunit (EutB)
COJEPEMI_(	sadH_2	0.72291	0.11833	Putative oxido	1.-.-.-	sadH_1	KR domain
COJEPEMI_(	COJEPE	0.71964	NA	hypothetical p	NA	0	Protein conserved in bacteria
COJEPEMI_(	COJEPE	0.71834	0.000564	hypothetical p	NA	MA20_15	Activator of Hsp90 ATPase homolog 1-like protein
COJEPEMI_(	COJEPE	0.71759	0.002243	hypothetical p	NA	Z012_01	Domain of unknown function (DUF927)
COJEPEMI_(	COJEPE	0.71753	0.026817	hypothetical p	NA	0	Ankyrin repeats (many copies)
COJEPEMI_(	hemB	0.71744	0.002058	Delta-aminole	4.2.1.24	hemB	Belongs to the ALAD family
COJEPEMI_(	rimO	0.71637	0.001633	Ribosomal pro	2.8.4.4	rimO	Catalyzes the methylthiolation of an aspartic acid residue of ribosomal
COJEPEMI_(	infB	0.71634	0.000136	Translation ini	NA	infB	One of the essential components for the initiation of protein synthesis.
COJEPEMI_(	bioB	0.71573	0.002531	Biotin synthas	2.8.1.6	bioB	Catalyzes the conversion of dethiobiotin (DTB) to biotin by the insertior
COJEPEMI_(	cmk	0.71548	0.008682	Cytidylate kina	2.7.4.25	cmk	Belongs to the cytidylate kinase family. Type 1 subfamily
COJEPEMI_(	COJEPE	0.71304	0.171138	Long-chain-fat	6.2.1.-	0	AMP-binding enzyme
COJEPEMI_(	COJEPE	0.71292	0.00153	hypothetical p	NA	uspA	Universal stress protein family
COJEPEMI_(	bigR	0.71215	0.001539	Biofilm growtl	NA	bigR	helix_turn_helix, Arsenical Resistance Operon Repressor
COJEPEMI_(	COJEPE	0.71184	0.006493	hypothetical p	NA	0	Protein of unknown function (DUF475)
COJEPEMI_(	COJEPE	0.71159	0.085296	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.71115	0.000252	Peptidyl-prolyl	5.2.1.8	ppiB	PPIases accelerate the folding of proteins. It catalyzes the cis-trans isoı
COJEPEMI_(	galE_2	0.71002	0.022751	UDP-glucose 4	5.1.3.2	0	RmlD substrate binding domain

COJEPEMI_(	COJEPE	0.7097	0.001703	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.70949	0.000429	hypothetical p	NA	IV02_106	Outer membrane lipoprotein-sorting protein
COJEPEMI_(	nth	0.70927	0.019224	Endonuclease	4.2.99.18	nth	DNA repair enzyme that has both DNA N-glycosylase activity and AP-lya
COJEPEMI_(	COJEPE	0.70406	0.095934	hypothetical p	NA	0	Methylene-tetrahydrofolate reductase C terminal
COJEPEMI_(	ribE	0.70333	0.0001	Riboflavin synt	2.5.1.9	ribE	Lumazine binding domain
COJEPEMI_(	panB	0.70181	0.002572	3-methyl-2-ox	2.1.2.11	panB	Catalyzes the reversible reaction in which hydroxymethyl group from 5,
COJEPEMI_(	bamD	0.70116	0.010937	Outer membra	NA	bamD	Part of the outer membrane protein assembly complex, which is involv
COJEPEMI_(	tsaB	0.70057	0.055405	tRNA threonyl	NA	yeaZ	Glycoprotease family
COJEPEMI_(	betB_2	0.69943	0.017707	NAD/NADP-de	1.2.1.8	betB	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat
COJEPEMI_(	zur	0.69898	0.070646	Zinc uptake re	NA	zur	Belongs to the Fur family
COJEPEMI_(	COJEPE	0.69806	7.97E-05	hypothetical p	NA	0	Protein of unknown function (DUF3108)
COJEPEMI_(	aaeA	0.69662	0.042661	p-hydroxybenz	NA	fusE	Barrel-sandwich domain of CusB or HlyD membrane-fusion
COJEPEMI_(	COJEPE	0.69629	0.142365	hypothetical p	NA	0	
COJEPEMI_(	gap2	0.69403	0.004282	Glyceraldehyd	1.2.1.-	gap	Belongs to the glyceraldehyde-3-phosphate dehydrogenase family
COJEPEMI_(	COJEPE	0.68982	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	chbG	0.68746	0.304539	Chitooligosacc	3.5.1.105	0	YdjC-like protein
COJEPEMI_(	COJEPE	0.6868	0.124678	hypothetical p	NA	0	Protein of unknown function (DUF971)
COJEPEMI_(	panC	0.68611	0.000358	Pantothenate	6.3.2.1	panC	Catalyzes the condensation of pantoate with beta-alanine in an ATP-de
COJEPEMI_(	COJEPE	0.68573	0.063869	putative glyco	2.4.-.-	MA20_05	Glycosyltransferase like family 2
COJEPEMI_(	dinB	0.68357	0.003907	DNA polymera	2.7.7.7	dinB	Poorly processive, error-prone DNA polymerase involved in untargeted
COJEPEMI_(	COJEPE	0.6825	0.210167	hypothetical p	NA	0	Transcriptional regulator
COJEPEMI_(	COJEPE	0.68058	0.14125	hypothetical p	NA	0	
COJEPEMI_(	frr	0.6804	0.002634	Ribosome-rec	NA	frr	Responsible for the release of ribosomes from messenger RNA at the t
COJEPEMI_(	COJEPE	0.67659	0.002229	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.67613	1.86E-06	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2147)
COJEPEMI_(	yaeQ	0.67611	0.036141	putative prote	NA	yaeQ	YaeQ
COJEPEMI_(	hpd	0.67581	0.224704	4-hydroxyphen	1.13.11.2	hppD	Hydroxyphenylpyruvate dioxygenase, HPPD, N-terminal
COJEPEMI_(	COJEPE	0.67556	0.11833	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.67555	0.309901	hypothetical p	NA	0	Forms passive diffusion pores that allow small molecular weight hydro
COJEPEMI_(	COJEPE	0.67431	0.030874	hypothetical p	NA	0	COG0457 FOG TPR repeat

COJEPEMI_(	COJEPE	0.67414	0.002312	Ferredoxin 1	NA	fdxA	Ferredoxins are iron-sulfur proteins that transfer electrons in a wide va
COJEPEMI_(	nusA	0.67296	0.000554	Transcription t	NA	nusA	Participates in both transcription termination and antitermination
COJEPEMI_(	hpxO	0.67272	0.184862	FAD-depender	1.14.13.1	hpxO	FAD binding domain
COJEPEMI_(	COJEPE	0.66956	0.000297	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	rpoA	0.66933	0.019224	DNA-directed	2.7.7.6	rpoA	DNA-dependent RNA polymerase catalyzes the transcription of DNA int
COJEPEMI_(	COJEPE	0.66926	0.210101	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.66908	0.086333	hypothetical p	NA	0	Sulfite exporter TauE/SafE
COJEPEMI_(	COJEPE	0.66761	0.398723	IS6 family trar	NA	0	Transposase IS66 family
COJEPEMI_(	panZ	0.66682	0.002572	PanD regulato	NA	0	Acetyltransferase (GNAT) domain
COJEPEMI_(	hsrA	0.66664	0.000376	putative trans	NA	mdtD	Major facilitator Superfamily
COJEPEMI_(	COJEPE	0.66498	0.378564	hypothetical p	NA	0	
COJEPEMI_(	astA_1	0.6643	0.014601	Arginine N-suc	2.3.1.109	astA	Arginine N-succinyltransferase beta subunit
COJEPEMI_(	COJEPE	0.66421	0.174213	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.66378	NA	hypothetical p	NA	0	Acyl-CoA dehydrogenase, middle domain
COJEPEMI_(	htpX_1	0.66233	0.000781	Protease HtpX	3.4.24.-	htpX	Belongs to the peptidase M48B family
COJEPEMI_(	moeB	0.66177	0.020329	Molybdopterin	2.7.7.80	moeB	COG0476 Dinucleotide-utilizing enzymes involved in molybdopterin anc
COJEPEMI_(	COJEPE	0.66042	6.36E-05	hypothetical p	NA	0	N-6 DNA Methylase
COJEPEMI_(	era	0.65995	1.12E-05	GTPase Era	NA	era	An essential GTPase that binds both GDP and GTP, with rapid nucleotic
COJEPEMI_(	COJEPE	0.65907	0.018087	hypothetical p	NA	arsR	Helix-turn-helix domain
COJEPEMI_(	COJEPE	0.65809	0.000524	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.65749	0.000124	hypothetical p	NA	0	COG1112 Superfamily I DNA and RNA helicases and helicase subunits
COJEPEMI_(	cca	0.65694	0.000548	Multifunctiona	NA	cca	Catalyzes the addition and repair of the essential 3'- terminal CCA sequ
COJEPEMI_(	pphB	0.65671	0.182674	Serine/threoni	3.1.3.16	pphA	Calcineurin-like phosphoesterase
COJEPEMI_(	algC_2	0.6561	0.000701	Phosphomann	5.4.2.2	algC	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domai
COJEPEMI_(	COJEPE	0.65609	0.120089	hypothetical p	NA	ygaH	Branched-chain amino acid transport protein (AzlD)
COJEPEMI_(	nrdR	0.65565	0.007888	Transcriptiona	NA	nrdR	Negatively regulates transcription of bacterial ribonucleotide reductase
COJEPEMI_(	ribD	0.65451	0.001177	Riboflavin bios	NA	ribD	Converts 2,5-diamino-6-(ribosylamino)-4(3h)-pyrimidinone 5'-phosphat
COJEPEMI_(	dapB	0.65178	0.000113	4-hydroxy-tetr	1.17.1.8	dapB	Catalyzes the conversion of 4-hydroxy- tetrahydrodipicolinate (HTPA) to
COJEPEMI_(	COJEPE	0.65132	0.013073	hypothetical p	NA	arsR	Bacterial regulatory protein, arsR family
COJEPEMI_(	COJEPE	0.65046	0.004938	hypothetical p	NA	ycgN	Belongs to the UPF0260 family

COJEPEMI_(	COJEPE	0.64905	0.372508	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.64874	0.000222	hypothetical p	NA	vdlD	Thioesterase superfamily
COJEPEMI_(	iscR_2	0.64835	0.004292	HTH-type trans	NA	iscR	Transcriptional regulator
COJEPEMI_(	nadA	0.6452	0.001446	Quinolinate sy	2.5.1.72	nadA	Catalyzes the condensation of iminoaspartate with dihydroxyacetone p
COJEPEMI_(	COJEPE	0.64489	0.185878	hypothetical p	NA	0	haloacid dehalogenase-like hydrolase
COJEPEMI_(	rcnR	0.64366	0.010398	Transcriptiona	NA	rcnR	Metal-sensitive transcriptional repressor
COJEPEMI_(	COJEPE	0.64365	0.003277	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.64269	0.039773	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.64257	0.279541	hypothetical p	NA	0	Glycosyl hydrolase 108
COJEPEMI_(	COJEPE	0.6421	NA	hypothetical p	NA	0	
COJEPEMI_(	gltX	0.64073	0.001344	Glutamate--tR	6.1.1.17	gltX	Catalyzes the attachment of glutamate to tRNA(Glu) in a two-step rea
COJEPEMI_(	fdx_2	0.64025	0.00078	Ferredoxin	NA	fdx1	Ferredoxin
COJEPEMI_(	COJEPE	0.63809	0.043262	hypothetical p	NA	copD	Copper resistance protein D
COJEPEMI_(	COJEPE	0.63723	0.126794	hypothetical p	NA	0	Glutamine amidotransferase class-I
COJEPEMI_(	ubiK	0.63722	0.008417	Ubiquinone bi	NA	0	Membrane fusogenic activity
COJEPEMI_(	lipA_1	0.63664	0.001572	Lipoyl synthas	2.8.1.8	lipA	Catalyzes the radical-mediated insertion of two sulfur atoms into the C
COJEPEMI_(	COJEPE	0.63663	0.019178	putative HTH-t	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	COJEPE	0.63624	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	puuB_1	0.63465	0.027272	Gamma-gluta	1.4.3.-	0	FAD dependent oxidoreductase
COJEPEMI_(	ygiC	0.63442	0.117927	Putative acid--	6.3.1.-	ygiC	Glutathionylspermidine synthase preATP-grasp
COJEPEMI_(	tetR	0.63327	0.068937	Tetracycline re	NA	tetR	Tetracycline repressor protein
COJEPEMI_(	COJEPE	0.63324	0.141509	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.63071	0.086114	hypothetical p	NA	0	GH3 auxin-responsive promoter
COJEPEMI_(	paaG	0.63008	0.278946	1,2-epoxyphen	5.3.3.18	paaG	Enoyl-CoA hydratase/isomerase
COJEPEMI_(	lptA	0.62793	0.012964	Lipopolysaccha	NA	lptA	Involved in the assembly of lipopolysaccharide (LPS). Required for the t
COJEPEMI_(	COJEPE	0.62728	0.03293	putative phosp	3.1.3.-	cicA	haloacid dehalogenase-like hydrolase
COJEPEMI_(	fadH_2	0.62667	0.107309	2,4-dienoyl-Co	1.3.1.34	fadH	2,4-dienoyl-coA reductase
COJEPEMI_(	COJEPE	0.62615	0.002607	hypothetical p	NA	fabG	KR domain
COJEPEMI_(	purN	0.62571	0.054562	Phosphoribosy	2.1.2.2	purN	Catalyzes the transfer of a formyl group from 10- formyltetrahydrofola
COJEPEMI_(	teaD	0.62438	0.122867	TRAP-T-associ	NA	0	Universal stress protein family

COJEPEMI_(	COJEPE	0.62404	0.345183	hypothetical p	NA	gpJ	Baseplate J-like protein
COJEPEMI_(	COJEPE	0.624	0.333164	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ttuB_3	0.62301	0.193754	Putative tartra	NA	0	COG0477 Permeases of the major facilitator superfamily
COJEPEMI_(	fghA	0.62241	0.001128	S-formylglutat	3.1.2.12	fghA	Serine hydrolase involved in the detoxification of formaldehyde
COJEPEMI_(	COJEPE	0.62212	0.021311	hypothetical p	NA	frnE	DSBA-like thioredoxin domain
COJEPEMI_(	COJEPE	0.62192	0.301865	hypothetical p	NA	0	Belongs to the UPF0319 family
COJEPEMI_(	sadH_1	0.62139	0.226352	Putative oxido	1.-.-.-	0	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	ypjD	0.62074	0.004507	Inner membra	NA	ypjD	Cytochrome C assembly protein
COJEPEMI_(	dmlR_1	0.6205	0.003888	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	xerC_1	0.61948	0.223861	Tyrosine recon	NA	rci	Belongs to the 'phage' integrase family
COJEPEMI_(	COJEPE	0.61866	0.014729	hypothetical p	NA	0	long-chain fatty acid transport protein
COJEPEMI_(	rhaS_1	0.61862	0.004292	HTH-type trans	NA	0	helix_turn_helix, arabinose operon control protein
COJEPEMI_(	COJEPE	0.61619	0.036304	hypothetical p	NA	0	Putative general bacterial porin
COJEPEMI_(	bfr_2	0.61579	0.038604	Bacterioferriti	1.16.3.1	bfrA	Iron-storage protein, whose ferroxidase center binds Fe(2) ions, oxidiz
COJEPEMI_(	COJEPE	0.61381	0.006069	hypothetical p	NA	0	Invasion gene expression up-regulator, SirB
COJEPEMI_(	COJEPE	0.61323	0.436873	hypothetical p	NA	0	
COJEPEMI_(	secY	0.61126	0.014518	Protein translc	NA	secY	The central subunit of the protein translocation channel SecYEG. Consis
COJEPEMI_(	hemC	0.6112	0.000865	Porphobilinoge	2.5.1.61	hemC	Tetrapolymerization of the monopyrrole PBG into the hydroxymethylbil
COJEPEMI_(	bfd	0.61035	0.014317	Bacterioferriti	NA	bfd	BFD-like [2Fe-2S] binding domain
COJEPEMI_(	secG	0.60851	0.000857	Protein-export	NA	secG	Preprotein translocase SecG subunit
COJEPEMI_(	iscS	0.60842	0.006694	Cysteine desul	2.8.1.7	iscS	Master enzyme that delivers sulfur to a number of partners involved in
COJEPEMI_(	hscA	0.60808	0.006387	Chaperone pro	NA	hscA	Chaperone involved in the maturation of iron-sulfur cluster-containing p
COJEPEMI_(	hisH	0.60564	0.004135	Imidazole glyc	4.3.2.10	hisH	IGPS catalyzes the conversion of PRFAR and glutamine to IGP, AICAR a
COJEPEMI_(	COJEPE	0.60354	0.014538	hypothetical p	NA	IV01_086	UPF0391 membrane protein
COJEPEMI_(	ydhP_1	0.60252	0.080904	Inner membra	NA	ydhP	Major facilitator Superfamily
COJEPEMI_(	COJEPE	0.60119	0.006509	hypothetical p	NA	0	
COJEPEMI_(	tcyP	0.59919	0.036874	L-cystine uptal	NA	ydjN	Belongs to the dicarboxylate amino acid cation symporter (DAACS) (TC
COJEPEMI_(	COJEPE	0.599	0.292394	hypothetical p	NA	0	Protein of unknown function (DUF523)
COJEPEMI_(	COJEPE	0.5973	0.049602	hypothetical p	NA	0	Patatin-like phospholipase
COJEPEMI_(	rlmE	0.59701	0.009099	Ribosomal RN	2.1.1.166	ftsJ	Specifically methylates the uridine in position 2552 of 23S rRNA at the

COJEPEMI_(	rplO	0.59641	0.033954	50S ribosomal	NA	rplO	binds to the 23S rRNA
COJEPEMI_(	COJEPE	0.59598	0.249461	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.59424	0.124987	NADH oxidase	1.-.-.-	0	NADH:flavin oxidoreductase / NADH oxidase family
COJEPEMI_(	aatA	0.59205	0.062417	Aspartate/pre	2.6.1.1	aspB	DegT/DnrJ/EryC1/StrS aminotransferase family
COJEPEMI_(	dhbF	0.59187	0.088568	Dimodular nor	NA	0	Pfam:HxxPF_rpt
COJEPEMI_(	COJEPE	0.591	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.59037	0.036063	hypothetical p	NA	0	Bacterial protein of unknown function (DUF934)
COJEPEMI_(	nanT_1	0.58958	0.260812	Sialic acid trar	NA	0	Organic Anion Transporter Polypeptide (OATP) family
COJEPEMI_(	puuA	0.58822	0.174737	Gamma-gluta	6.3.1.11	puuA	Glutamine synthetase, catalytic domain
COJEPEMI_(	COJEPE	0.58796	0.28069	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.58777	8.48E-05	hypothetical p	NA	0	SnoaL-like domain
COJEPEMI_(	rbfA	0.58613	0.03089	30S ribosome-	NA	rbfA	One of several proteins that assist in the late maturation steps of the f
COJEPEMI_(	ndk	0.58418	0.046915	Nucleoside dip	2.7.4.6	ndk	Major role in the synthesis of nucleoside triphosphates other than ATP.
COJEPEMI_(	pheA2	0.58391	0.047731	Secreted chori	5.4.99.5	pheA2	Catalyzes the Claisen rearrangement of chorismate to prephenate
COJEPEMI_(	dapD	0.58236	0.003687	2,3,4,5-tetrahy	2.3.1.117	dapD	Belongs to the transferase hexapeptide repeat family
COJEPEMI_(	COJEPE	0.58194	0.000568	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.5819	0.324055	hypothetical p	NA	0	
COJEPEMI_(	hsaA	0.5818	0.436993	Flavin-depend	1.14.14.1	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	COJEPE	0.5818	0.004431	hypothetical p	NA	0	Bacterial protein of unknown function (DUF924)
COJEPEMI_(	yqjI	0.58117	0.20717	Transcriptiona	NA	yqjI	Transcriptional regulator PadR-like family
COJEPEMI_(	btuB_4	0.58096	0.074445	Vitamin B12 tı	NA	0	TonB dependent receptor
COJEPEMI_(	recA	0.58006	0.071857	Protein RecA	NA	recA	Can catalyze the hydrolysis of ATP in the presence of single-stranded D
COJEPEMI_(	arsC_2	0.5797	0.012385	Arsenate redu	1.20.4.4	0	Low molecular weight phosphotyrosine protein phosphatase
COJEPEMI_(	COJEPE	0.579	0.004507	hypothetical p	NA	0	Iron-containing redox enzyme
COJEPEMI_(	COJEPE	0.57745	0.003798	putative prote	NA	0	Beta-lactamase superfamily domain
COJEPEMI_(	pyrD	0.57647	0.005224	Dihydroorotate	1.3.5.2	pyrD	Catalyzes the conversion of dihydroorotate to orotate with quinone as e
COJEPEMI_(	puuB_2	0.57559	0.2009	Gamma-gluta	1.4.3.-	0	FAD dependent oxidoreductase
COJEPEMI_(	btuB_3	0.5746	0.042457	Vitamin B12 tı	NA	yncD	TonB dependent receptor
COJEPEMI_(	nasA	0.57421	0.006502	Nitrate reduct	1.7.-.-	nasA	Belongs to the prokaryotic molybdopterin-containing oxidoreductase fa
COJEPEMI_(	COJEPE	0.57289	NA	hypothetical p	NA	#N/A	#N/A

COJEPEMI_(	COJEPE	0.57001	0.001309	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.56999	0.23907	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ruvA	0.56996	0.045806	Holliday juncti	3.6.4.12	ruvA	The RuvA-RuvB complex in the presence of ATP renatures cruciform str
COJEPEMI_(	pcaF_2	0.56743	0.16376	Beta-ketoadip	2.3.1.174	pcaF	Belongs to the thiolase family
COJEPEMI_(	ppsC	0.56695	0.010757	Phthiocerol sy	2.3.1.41	qor	Zinc-binding dehydrogenase
COJEPEMI_(	dapF	0.56427	0.005336	Diaminopimel	5.1.1.7	dapF	Catalyzes the stereoinversion of LL-2,6- diaminoheptanedioate (L,L-DAF
COJEPEMI_(	COJEPE	0.56396	0.095154	hypothetical p	NA	yeaQ	Transglycosylase associated protein
COJEPEMI_(	ydgC	0.56323	0.236291	Inner membra	NA	ydgC	GlpM protein
COJEPEMI_(	COJEPE	0.56171	0.422246	hypothetical p	NA	0	COG3209 Rhs family protein
COJEPEMI_(	mymA	0.56121	0.028887	Putative FAD-c	1.14.13.-	almA	Flavin-binding monooxygenase-like
COJEPEMI_(	lspA_2	0.56114	0.375921	Lipoprotein sig	3.4.23.36	lspA	This protein specifically catalyzes the removal of signal peptides from p
COJEPEMI_(	COJEPE	0.56053	0.187529	hypothetical p	NA	0	OsmC-like protein
COJEPEMI_(	COJEPE	0.56048	0.010921	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.55989	NA	hypothetical p	NA	0	Phage Mu protein F like protein
COJEPEMI_(	COJEPE	0.55665	0.055548	hypothetical p	NA	glcG	Haem-degrading
COJEPEMI_(	emrE_2	0.5549	0.0674	Multidrug tran	NA	0	Small Multidrug Resistance protein
COJEPEMI_(	phoB	0.55479	0.002338	Phosphate reg	NA	phoB	phosphate regulon transcriptional regulatory protein PhoB
COJEPEMI_(	queG	0.55433	0.021683	Epoxyqueuosir	1.17.99.6	queG	Catalyzes the conversion of epoxyqueuosine (oQ) to queuosine (Q), whi
COJEPEMI_(	COJEPE	0.55373	0.285325	hypothetical p	NA	0	Transporter Component
COJEPEMI_(	COJEPE	0.55109	NA	hypothetical p	NA	0	
COJEPEMI_(	norG_2	0.54886	0.051583	HTH-type trans	NA	0	helix_turn_helix gluconate operon transcriptional repressor
COJEPEMI_(	COJEPE	0.54838	0.170756	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.54817	0.021626	hypothetical p	NA	phnB	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
COJEPEMI_(	catD_2	0.54768	0.124958	3-oxoadipate e	3.1.1.24	pcaD	Alpha/beta hydrolase family
COJEPEMI_(	algC_1	0.54493	0.012699	Phosphomann	5.4.2.2	manB	Phosphoglucomutase/phosphomannomutase, C-terminal domain
COJEPEMI_(	COJEPE	0.54475	0.072876	hypothetical p	NA	0	Predicted membrane protein (DUF2339)
COJEPEMI_(	cysM	0.54457	0.01683	Cysteine synth	2.5.1.47	cysM	Belongs to the cysteine synthase cystathionine beta- synthase family
COJEPEMI_(	pnuC	0.54407	0.273002	Nicotinamide	NA	pnuC	Nicotinamide mononucleotide transporter
COJEPEMI_(	pgrR_4	0.54401	0.256456	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	queA	0.54343	0.104022	S-adenosylme	2.4.99.17	queA	Transfers and isomerizes the ribose moiety from AdoMet to the 7-amir

COJEPEMI_(	rplS	0.54306	0.024649	50S ribosomal	NA	rplS	This protein is located at the 30S-50S ribosomal subunit interface and r
COJEPEMI_(	mdh	0.54255	0.022935	Malate dehydr	1.1.1.37	mdh	Catalyzes the reversible oxidation of malate to oxaloacetate
COJEPEMI_(	COJEPE	0.54237	NA	hypothetical p	NA	0	
COJEPEMI_(	pksN	0.54203	NA	Polyketide syn	2.3.1.-	pksP	Phosphopantetheine attachment site
COJEPEMI_(	COJEPE	0.54183	0.004292	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.5407	0.366834	hypothetical p	NA	phnA	Alkylphosphonate utilization operon protein PhnA
COJEPEMI_(	hcaB_2	0.54057	0.167845	3-phenylpropic	1.3.1.87	0	KR domain
COJEPEMI_(	COJEPE	0.54044	0.029942	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.53986	0.230186	hypothetical p	NA	yoqW	SOS response associated peptidase (SRAP)
COJEPEMI_(	COJEPE	0.5369	0.617507	hypothetical p	NA	0	Peptidase M15
COJEPEMI_(	COJEPE	0.53597	0.065738	hypothetical p	NA	0	
COJEPEMI_(	lexA_2	0.53591	0.304951	LexA repressor	3.4.21.88	umuD	Peptidase S24-like
COJEPEMI_(	COJEPE	0.53557	0.432613	hypothetical p	NA	0	
COJEPEMI_(	leuE_3	0.53557	0.237293	Leucine efflux	NA	0	LysE type translocator
COJEPEMI_(	COJEPE	0.53423	0.022782	hypothetical p	NA	0	
COJEPEMI_(	tsaC	0.5328	0.106815	Threonylcarba	2.7.7.87	tsaC	Required for the formation of a threonylcarbamoyl group on adenosine
COJEPEMI_(	hchA_2	0.53223	0.081157	Protein/nuclei	3.5.1.124	0	ThiJ/PfpI family-like
COJEPEMI_(	COJEPE	0.53164	0.212974	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.531	0.110658	hypothetical p	NA	yneE	Bestrophin, RFP-TM, chloride channel
COJEPEMI_(	COJEPE	0.5305	0.105878	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	yrfG	0.5302	0.017153	GMP/IMP nucl	3.1.3.5	yrfG	Haloacid dehalogenase-like hydrolase
COJEPEMI_(	COJEPE	0.53009	0.006727	putative acyl-C	3.1.2.-	yciA	Thioesterase superfamily
COJEPEMI_(	djlA	0.52837	0.168969	Co-chaperone	NA	0	DnaJ molecular chaperone homology domain
COJEPEMI_(	rapZ	0.52796	0.036615	RNase adapte	NA	rapZ	Displays ATPase and GTPase activities
COJEPEMI_(	COJEPE	0.52774	0.156673	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.52761	NA	hypothetical p	NA	gpU	Phage P2 GpU
COJEPEMI_(	COJEPE	0.52542	0.041654	hypothetical p	NA	0	KTSC domain
COJEPEMI_(	ethR	0.52456	0.016026	HTH-type trans	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	0.52133	0.159014	IS5 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	aidA_1	0.52129	0.024163	Quorum-quenc	NA	0	X-Pro dipeptidyl-peptidase (S15 family)

COJEPEMI_(	yddG_1	0.52045	0.5858	Aromatic amir	NA	yddG	EamA-like transporter family
COJEPEMI_(	emrB_1	0.52041	0.307072	Colistin resista	NA	vceB	Major Facilitator Superfamily
COJEPEMI_(	valS	0.52037	0.027644	Valine--tRNA l	6.1.1.9	valS	amino acids such as threonine, to avoid such errors, it has a posttransfe
COJEPEMI_(	pabC	0.52012	0.047334	Aminodeoxych	4.1.3.38	pabC	Branched-chain amino acid aminotransferase 4-amino-4-deoxychorism
COJEPEMI_(	COJEPE	0.51816	0.02459	hypothetical p	NA	0	Alpha beta hydrolase
COJEPEMI_(	dmlR_1	0.51756	0.159088	HTH-type trans	NA	yeaT	LysR substrate binding domain
COJEPEMI_(	ureG	0.51732	0.119124	Urease access	NA	ureG	Facilitates the functional incorporation of the urease nickel metallocen
COJEPEMI_(	pyrF	0.51729	0.031253	Orotidine 5'-pl	4.1.1.23	pyrF	Catalyzes the decarboxylation of orotidine 5'- monophosphate (OMP) to
COJEPEMI_(	ydcO_2	0.51707	0.228531	Inner membra	NA	benE	Benzoate membrane transport protein
COJEPEMI_(	COJEPE	0.51652	0.074215	hypothetical p	NA	0	Cold shock protein domain
COJEPEMI_(	COJEPE	0.51628	0.156162	putative transp	NA	0	Major facilitator Superfamily
COJEPEMI_(	COJEPE	0.51575	0.360799	hypothetical p	NA	0	Belongs to the SOS response-associated peptidase family
COJEPEMI_(	yddE_3	0.51486	0.291896	putative isome	5.1.-.-	yddE	Phenazine biosynthesis-like protein
COJEPEMI_(	COJEPE	0.51447	0.007728	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.51422	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	trpA	0.51295	0.045284	Tryptophan syı	4.2.1.20	trpA	The alpha subunit is responsible for the aldol cleavage of indoleglycero
COJEPEMI_(	intS	0.51166	0.10256	Prophage integ	NA	0	Arm DNA-binding domain
COJEPEMI_(	COJEPE	0.51114	0.07727	hypothetical p	NA	0	
COJEPEMI_(	nuoL	0.50973	0.019322	NADH-quinone	7.1.1.-	nuoL	COG1009 NADH ubiquinone oxidoreductase subunit 5 (chain L) Multisul
COJEPEMI_(	metN_1	0.50933	0.349923	Methionine im	3.6.3.-	metN	Part of the ABC transporter complex MetNIQ involved in methionine im
COJEPEMI_(	COJEPE	0.50927	0.067662	hypothetical p	NA	0	Membrane
COJEPEMI_(	COJEPE	0.50721	0.106815	hypothetical p	NA	0	VIT family
COJEPEMI_(	nrdB	0.50703	0.110065	Ribonucleoside	1.17.4.1	nrdB	Provides the precursors necessary for DNA synthesis. Catalyzes the bios
COJEPEMI_(	COJEPE	0.50645	0.051366	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	yegS	0.50568	0.008343	lipid kinase Ye	2.7.1.-	bmrU	Diacylglycerol kinase catalytic domain (presumed)
COJEPEMI_(	dapA_1	0.50547	0.19348	4-hydroxy-tetra	4.3.3.7	dapA1	Dihydrodipicolinate synthetase family
COJEPEMI_(	COJEPE	0.50501	0.023852	hypothetical p	NA	yjeE	Threonylcarbamoyl adenosine biosynthesis protein TsaE
COJEPEMI_(	accA_2	0.50496	0.026566	Acetyl-coenzyr	2.1.3.15	accA	Component of the acetyl coenzyme A carboxylase (ACC) complex. First,
COJEPEMI_(	COJEPE	0.50387	0.009903	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	hmrR_1	0.50383	0.029159	HTH-type trans	NA	cueR	helix_turn_helix, mercury resistance

COJEPEMI_(	COJEPE	0.50347	0.073185	hypothetical p	NA	0	
COJEPEMI_(	mpl	0.5025	0.015778	UDP-N-acetylr	6.3.2.45	mpl	Reutilizes the intact tripeptide L-alanyl-gamma-D- glutamyl-meso-diar
COJEPEMI_(	COJEPE	0.50111	0.371877	hypothetical p	NA	0	Protein of unknown function (DUF1003)
COJEPEMI_(	COJEPE	0.50061	0.055878	hypothetical p	NA	0	protein domain associated with
COJEPEMI_(	COJEPE	0.50041	NA	hypothetical p	NA	0	
COJEPEMI_(	merA	0.49971	0.177591	Mercuric redu	1.16.1.1	merA	Resistance to Hg(2) in bacteria appears to be governed by a specialize
COJEPEMI_(	yigZ	0.49834	0.217617	IMPACT family	NA	yigZ	Uncharacterized protein family UPF0029
COJEPEMI_(	COJEPE	0.49711	0.042974	Renalase	1.6.3.5	0	Flavin containing amine oxidoreductase
COJEPEMI_(	argB	0.49649	0.005061	Acetylglutama	2.7.2.8	argB	Belongs to the acetylglutamate kinase family. ArgB subfamily
COJEPEMI_(	COJEPE	0.49559	0.273959	hypothetical p	NA	0	Terminase RNaseH-like domain
COJEPEMI_(	slt	0.49406	0.003525	Soluble lytic m	4.2.2.-	slt	COG0741 Soluble lytic murein transglycosylase and related regulatory p
COJEPEMI_(	hisF	0.4938	0.016766	Imidazole glyc	4.3.2.10	hisF	IGPS catalyzes the conversion of PRFAR and glutamine to IGP, AICAR a
COJEPEMI_(	sutR_2	0.49258	0.171311	HTH-type trans	NA	0	Cupin domain
COJEPEMI_(	folK	0.4919	0.094554	2-amino-4-hyc	2.7.6.3	folK	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (HPPK)
COJEPEMI_(	COJEPE	0.49174	0.095035	putative HTH-t	NA	0	HxlR-like helix-turn-helix
COJEPEMI_(	glpE_2	0.49143	0.483434	Thiosulfate su	2.8.1.1	pspE	Rhodanese Homology Domain
COJEPEMI_(	COJEPE	0.49114	0.001977	hypothetical p	NA	LA2027	Protein of unknown function (DUF2797)
COJEPEMI_(	COJEPE	0.48932	0.003578	hypothetical p	NA	ampG	Acetyl-coenzyme A transporter 1
COJEPEMI_(	puuP	0.48799	0.333398	Putrescine imp	NA	0	Amino acid permease
COJEPEMI_(	COJEPE	0.48764	0.208027	DNA base-flip	NA	ybaZ	6-O-methylguanine DNA methyltransferase, DNA binding domain
COJEPEMI_(	COJEPE	0.48676	0.09506	putative HTH-t	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	COJEPE	0.48633	0.326567	hypothetical p	NA	yybR_1	HxlR-like helix-turn-helix
COJEPEMI_(	COJEPE	0.48554	0.454306	hypothetical p	NA	0	Protein of unknown function (DUF1624)
COJEPEMI_(	paaH_2	0.48375	0.33613	3-hydroxyadip	1.1.1.-	paaH	3-hydroxyacyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	ufaA1	0.48371	0.36698	Tuberculostea	2.1.1.-	cfa	Mycolic acid cyclopropane synthetase
COJEPEMI_(	COJEPE	0.4836	0.064892	NADH:quinone	1.6.5.11	MA20_07	Nitronate monooxygenase
COJEPEMI_(	cysE	0.48327	0.065381	Serine acetyltr	2.3.1.30	cysE	Serine acetyltransferase, N-terminal
COJEPEMI_(	yobA	0.48324	0.156673	Protein YobA	NA	copC	CopC domain
COJEPEMI_(	COJEPE	0.48283	0.144402	Tn3 family tra	NA	tnpA	Transposase
COJEPEMI_(	COJEPE	0.48229	0.536023	hypothetical p	NA	0	

COJEPEMI_(	COJEPE	0.48227	0.134481	hypothetical p	NA	0	Phage-related minor tail protein
COJEPEMI_(	thiD	0.48118	0.031097	Hydroxymethy	2.7.1.49	thiD	Phosphomethylpyrimidine kinase
COJEPEMI_(	COJEPE	0.4811	0.36446	hypothetical p	NA	0	Iron-containing redox enzyme
COJEPEMI_(	COJEPE	0.481	0.059898	hypothetical p	NA	0	Protein conserved in bacteria
COJEPEMI_(	yceJ_2	0.48027	0.079891	Cytochrome b5	NA	0	Prokaryotic cytochrome b561
COJEPEMI_(	COJEPE	0.47911	0.485363	hypothetical p	NA	0	Protein of unknown function (DUF1365)
COJEPEMI_(	tolC	0.47795	0.047731	Outer membra	NA	tolC	Outer membrane efflux protein
COJEPEMI_(	ppa	0.47672	0.021086	Inorganic pyro	3.6.1.1	ppa	Catalyzes the hydrolysis of inorganic pyrophosphate (PPi) forming two p
COJEPEMI_(	ddl_2	0.47588	0.102775	D-alanine--D-a	6.3.2.4	uca	Allophanate hydrolase subunit 2
COJEPEMI_(	thrS	0.47562	0.029065	Threonine--tRI	6.1.1.3	thrS	Catalyzes the attachment of threonine to tRNA(Thr) in a two-step reac
COJEPEMI_(	COJEPE	0.47533	0.374864	hypothetical p	NA	0	Flavin reductase like domain
COJEPEMI_(	COJEPE	0.47473	0.060785	L-lactate trans	NA	yhjX_2	Major Facilitator Superfamily
COJEPEMI_(	ssuB_2	0.47392	0.284572	Aliphatic sulfo	3.6.3.-	0	ATPases associated with a variety of cellular activities
COJEPEMI_(	COJEPE	0.47346	0.001657	hypothetical p	NA	queD	6-pyruvoyl tetrahydropterin synthase
COJEPEMI_(	lrp_1	0.47332	0.381281	Leucine-respo	NA	lrp	Lrp/AsnC ligand binding domain
COJEPEMI_(	COJEPE	0.47324	0.11968	hypothetical p	NA	0	
COJEPEMI_(	choD	0.47258	0.01873	Cholesterol ox	1.1.3.6	0	GMC oxidoreductase
COJEPEMI_(	mlaC	0.47127	0.009366	Intermembran	NA	mlaC	MlaC protein
COJEPEMI_(	norG_3	0.4709	0.063509	HTH-type trans	NA	norG	helix_turn_helix gluconate operon transcriptional repressor
COJEPEMI_(	COJEPE	0.47069	0.018911	hypothetical p	NA	0	Probable metal-binding protein (DUF2387)
COJEPEMI_(	upp	0.46923	0.249043	Uracil phospho	2.4.2.9	upp	Catalyzes the conversion of uracil and 5-phospho-alpha- D-ribose 1-dipl
COJEPEMI_(	COJEPE	0.46867	0.131847	hypothetical p	NA	0	Peptidase S24-like
COJEPEMI_(	acdA	0.46781	0.029443	Acyl-CoA dehy	1.3.99.-	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	COJEPE	0.46655	0.445129	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.46621	0.186106	hypothetical p	NA	0	membrane transporter protein
COJEPEMI_(	COJEPE	0.46618	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.46436	0.032809	hypothetical p	NA	0	Protein of unknown function (DUF1289)
COJEPEMI_(	COJEPE	0.46299	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.46295	0.103025	hypothetical p	NA	0	Arc-like DNA binding domain
COJEPEMI_(	tetA_2	0.46292	0.218484	Tetracycline re	NA	tetA	Sugar (and other) transporter

COJEPEMI_(	gcvA_1	0.46102	0.136308	Glycine cleava	NA	0	LysR substrate binding domain
COJEPEMI_(	nadK	0.46095	0.012608	NAD kinase	2.7.1.23	nadK	Involved in the regulation of the intracellular balance of NAD and NADF
COJEPEMI_(	umuC	0.46089	0.1905	Protein UmuC	NA	umuC	DNA polymerase
COJEPEMI_(	mupP	0.46067	0.099707	N-acetylmurar	3.1.3.105	gph	Phosphoglycolate phosphatase
COJEPEMI_(	entS	0.46057	0.142904	Enterobactin e	NA	0	Major facilitator Superfamily
COJEPEMI_(	lpxK	0.45977	0.06344	Tetraacyldisac	2.7.1.130	lpxK	Transfers the gamma-phosphate of ATP to the 4'-position of a tetraacy
COJEPEMI_(	COJEPE	0.45864	0.422858	hypothetical p	NA	0	
COJEPEMI_(	czcB	0.45737	0.095057	Cobalt-zinc-ca	NA	czcB	Barrel-sandwich domain of CusB or HlyD membrane-fusion
COJEPEMI_(	ygaZ	0.45609	0.161039	Inner membra	NA	ygaZ	AzlC protein
COJEPEMI_(	crcB	0.45564	0.544776	Putative fluori	NA	crcB	Important for reducing fluoride concentration in the cell, thus reducing
COJEPEMI_(	rutG	0.45527	0.116591	Putative pyrim	NA	rutG	Permease family
COJEPEMI_(	COJEPE	0.45426	0.226477	hypothetical p	NA	0	Cache domain
COJEPEMI_(	serB2	0.4515	0.043157	Phosphoserine	3.1.3.3	serB	phosphoserine phosphatase
COJEPEMI_(	tdeA	0.45119	0.059307	Toxin and drug	NA	ttgC_1	Outer membrane efflux protein
COJEPEMI_(	namA_1	0.45015	0.078018	NADPH dehydr	1.6.99.1	namA	NADH:flavin oxidoreductase / NADH oxidase family
COJEPEMI_(	COJEPE	0.45005	0.156341	hypothetical p	NA	0	TonB C terminal
COJEPEMI_(	COJEPE	0.44958	0.089397	hypothetical p	NA	0	Rieske [2Fe-2S] domain
COJEPEMI_(	COJEPE	0.44936	0.071678	hypothetical p	NA	0	Ion channel
COJEPEMI_(	COJEPE	0.44895	0.335867	hypothetical p	NA	mae1	Voltage-dependent anion channel
COJEPEMI_(	yfcF	0.44858	0.094748	Glutathione S-	2.5.1.18	yfcF	Glutathione S-transferase, C-terminal domain
COJEPEMI_(	exbD_3	0.44858	0.210039	Biopolymer tra	NA	exbD2	Biopolymer transport protein ExbD/TolR
COJEPEMI_(	COJEPE	0.44679	0.130896	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.44638	0.333683	hypothetical p	NA	0	Acetyltransferase (GNAT) domain
COJEPEMI_(	dhaT_2	0.44556	0.247787	1,3-propanedi	1.1.1.202	adhB	alcohol dehydrogenase
COJEPEMI_(	COJEPE	0.44556	0.193522	hypothetical p	NA	0	
COJEPEMI_(	doxA	0.4453	0.530774	Naphthalene 1	NA	ndoA	Rieske-like [2Fe-2S] domain
COJEPEMI_(	hisB	0.44446	0.021289	Histidine biosy	NA	hisB	imidazoleglycerol-phosphate dehydratase
COJEPEMI_(	COJEPE	0.44356	0.020762	Electron transf	1.5.5.1	etfD	Electron transfer flavoprotein-ubiquinone oxidoreductase
COJEPEMI_(	ppnP	0.44271	0.019356	Pyrimidine/pu	2.4.2.2	ppnP	Catalyzes the phosphorolysis of diverse nucleosides, yielding D-ribose 1
COJEPEMI_(	COJEPE	0.44235	0.560843	hypothetical p	NA	pcaC	Carboxymuconolactone decarboxylase family

COJEPEMI_(	tolR	0.44226	0.165484	Tol-Pal system	NA	0	Biopolymer transport protein ExbD/TolR
COJEPEMI_(	COJEPE	0.44114	0.114092	hypothetical p	NA	0	Domain of unknown function (DUF4010)
COJEPEMI_(	alr1	0.44104	0.22722	Alanine racem	5.1.1.1	alr	Catalyzes the interconversion of L-alanine and D- alanine. May also act
COJEPEMI_(	COJEPE	0.43899	0.539297	hypothetical p	NA	sohB	Peptidase family S49 N-terminal
COJEPEMI_(	paaZ	0.43808	0.239499	Bifunctional p	NA	paaN	MaoC like domain
COJEPEMI_(	accD	0.43788	0.113027	Acetyl-coenzyr	2.1.3.15	accD	Component of the acetyl coenzyme A carboxylase (ACC) complex. Biotir
COJEPEMI_(	pgpA	0.43757	0.156673	Phosphatidylgl	3.1.3.27	pgpA	Lipid phosphatase which dephosphorylates phosphatidylglycerophospha
COJEPEMI_(	carB_1	0.43734	0.17157	Carbamoyl-ph	6.3.5.5	carB	Carbamoyl-phosphate synthetase ammonia chain
COJEPEMI_(	benM_1	0.4363	0.097724	HTH-type trans	NA	benM	Transcriptional regulator
COJEPEMI_(	COJEPE	0.43624	0.43878	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	zntR	0.43553	0.382693	HTH-type trans	NA	zntR	helix_turn_helix, mercury resistance
COJEPEMI_(	fpr_2	0.43545	0.128829	Flavodoxin/fer	1.18.1.2	fpr	Oxidoreductase NAD-binding domain
COJEPEMI_(	COJEPE	0.43532	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ftsH	0.43504	0.086114	ATP-dependen	3.4.24.-	ftsH	Acts as a processive, ATP-dependent zinc metallopeptidase for both cyt
COJEPEMI_(	yabJ	0.43464	0.041654	2-iminobutanc	3.5.99.10	tdcF	Endoribonuclease L-PSP
COJEPEMI_(	COJEPE	0.43415	0.065386	hypothetical p	NA	0	Serine aminopeptidase, S33
COJEPEMI_(	COJEPE	0.43399	0.040155	hypothetical p	NA	0	Ion transport protein
COJEPEMI_(	COJEPE	0.43324	0.021933	hypothetical p	NA	yqgE	Belongs to the UPF0301 (AlgH) family
COJEPEMI_(	macA	0.43322	0.073119	Macrolide exp	NA	macA	Belongs to the membrane fusion protein (MFP) (TC 8.A.1) family
COJEPEMI_(	COJEPE	0.43315	0.175397	hypothetical p	NA	0	
COJEPEMI_(	pal_1	0.4324	0.173299	Peptidoglycan-	NA	pal	Belongs to the ompA family
COJEPEMI_(	COJEPE	0.43001	0.436873	hypothetical p	NA	0	SnoaL-like domain
COJEPEMI_(	kdsB	0.42957	0.140185	3-deoxy-mann	2.7.7.38	kdsB	Activates KDO (a required 8-carbon sugar) for incorporation into bacter
COJEPEMI_(	COJEPE	0.42927	0.242503	hypothetical p	NA	0	
COJEPEMI_(	serA	0.42919	0.105062	D-3-phosphogl	1.1.1.95	serA	Belongs to the D-isomer specific 2-hydroxyacid dehydrogenase family
COJEPEMI_(	tig	0.42896	0.012786	Trigger factor	5.2.1.8	tig	Involved in protein export. Acts as a chaperone by maintaining the new
COJEPEMI_(	bcr_2	0.42744	0.019266	Bicyclomycin r	NA	bcr	Major facilitator Superfamily
COJEPEMI_(	COJEPE	0.4274	0.133808	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.42706	0.053421	hypothetical p	NA	0	Protein of unknown function (DUF962)
COJEPEMI_(	tolQ_2	0.42649	0.221624	Tol-Pal system	NA	exbB	MotA/TolQ/ExbB proton channel family

COJEPEMI_(	COJEPE	0.42624	0.353255	hypothetical p	NA	VY92_02	Protein of unknown function (DUF1073)
COJEPEMI_(	gltC_4	0.42609	0.146239	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	rnc	0.42608	0.037235	Ribonuclease 3	3.1.26.3	rnc	Digests double-stranded RNA. Involved in the processing of primary rR
COJEPEMI_(	COQ5_1	0.42584	0.085881	2-methoxy-6-p	2.1.1.163	ubiE	Methyltransferase required for the conversion of demethylmenaquinol
COJEPEMI_(	parA	0.42568	0.061626	Chromosome p	NA	parA	Anion-transporting ATPase
COJEPEMI_(	ubiA	0.42431	0.065157	4-hydroxybenz	2.5.1.39	ubiA	Catalyzes the prenylation of para-hydroxybenzoate (PHB) with an all-tra
COJEPEMI_(	COJEPE	0.42397	0.052228	hypothetical p	NA	lys	Saccharopine dehydrogenase NADP binding domain
COJEPEMI_(	queC_1	0.42201	0.137928	7-cyano-7-dea	6.3.4.20	queC	Catalyzes the ATP-dependent conversion of 7-carboxy-7- deazaguanine
COJEPEMI_(	COJEPE	0.4215	0.51704	hypothetical p	NA	0	Zinc dependent phospholipase C
COJEPEMI_(	COJEPE	0.42087	0.333398	3-beta-hydroxy	1.1.1.393	benD	Enoyl-(Acyl carrier protein) reductase
COJEPEMI_(	baiN	0.41964	0.360161	3-dehydro-bile	1.3.1.114	0	HI0933-like protein
COJEPEMI_(	COJEPE	0.4192	0.173454	hypothetical p	NA	0	Spore Coat Protein U domain
COJEPEMI_(	tolB	0.41894	0.193551	Tol-Pal system	NA	tolB	Involved in the TonB-independent uptake of proteins
COJEPEMI_(	COJEPE	0.41767	NA	hypothetical p	NA	IV02_092	Domain of unknown function (DUF1989)
COJEPEMI_(	amtB_1	0.41583	0.227734	Ammonia cha	NA	0	Ammonium Transporter Family
COJEPEMI_(	COJEPE	0.41562	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.41351	NA	hypothetical p	NA	fimT	Pfam:N_methyl_2
COJEPEMI_(	ydeN	0.41248	0.203577	Putative hydro	3.-.-.-	ydeN	Serine hydrolase
COJEPEMI_(	COJEPE	0.41236	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	guaA	0.41224	0.137898	GMP synthase	6.3.5.2	guaA	Catalyzes the synthesis of GMP from XMP
COJEPEMI_(	argG	0.41154	0.119116	Argininosuccin	6.3.4.5	argG	Belongs to the argininosuccinate synthase family. Type
COJEPEMI_(	COJEPE	0.41136	0.406971	hypothetical p	NA	0	Zonular occludens toxin (Zot)
COJEPEMI_(	COJEPE	0.41127	0.14024	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.41071	0.080742	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.41031	NA	hypothetical p	NA	0	transcriptional regulator
COJEPEMI_(	COJEPE	0.41016	0.332011	hypothetical p	NA	ykgJ	Fe-S-cluster oxidoreductase
COJEPEMI_(	COJEPE	0.40957	0.230597	RutC family pr	NA	IV02_055	Endoribonuclease L-PSP
COJEPEMI_(	atzF	0.4095	0.361437	Allophanate hy	3.5.1.54	atzF	Amidase
COJEPEMI_(	rutR	0.40892	0.075982	HTH-type trans	NA	rutR	YcdC-like protein, C-terminal region
COJEPEMI_(	znuB	0.40775	0.119962	High-affinity z	NA	znuB	ABC 3 transport family

COJEPEMI_(	ptsO	0.40605	0.114564	Phosphocarrie	NA	ptsH	PTS HPr component phosphorylation site
COJEPEMI_(	COJEPE	0.40466	0.295678	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.40437	0.063992	Putative gluta	4.4.1.22	0	Glutathione-dependent formaldehyde-activating enzyme
COJEPEMI_(	caiA	0.40386	0.049996	Crotonobetain	1.3.8.13	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	kdpB	0.40386	0.172562	Potassium-tra	7.2.2.6	kdpB	Part of the high-affinity ATP-driven potassium transport (or Kdp) syster
COJEPEMI_(	rhlB	0.40365	0.01681	ATP-dependen	3.6.4.13	rhlB	DEAD-box RNA helicase involved in RNA degradation. Has RNA-depend
COJEPEMI_(	COJEPE	0.4033	0.293268	hypothetical p	NA	0	Phage replication protein CRI
COJEPEMI_(	COJEPE	0.4031	0.424225	hypothetical p	NA	0	Acetyltransferase (GNAT) domain
COJEPEMI_(	ybdG	0.40275	0.190854	Miniconductar	NA	ybdG	Mechanosensitive ion channel
COJEPEMI_(	kup	0.40266	0.074671	Low affinity pc	NA	kup	Transport of potassium into the cell
COJEPEMI_(	COJEPE	0.4023	0.304088	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.40222	NA	hypothetical p	NA	0	Domain of unknown function (DUF932)
COJEPEMI_(	rhtB_1	0.39926	0.455256	Homoserine/h	NA	rhtB	LysE type translocator
COJEPEMI_(	COJEPE	0.3991	0.212608	hypothetical p	NA	yybR	HxlR-like helix-turn-helix
COJEPEMI_(	COJEPE	0.39889	0.547768	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.39888	0.197902	hypothetical p	NA	0	Polyketide cyclase / dehydrase and lipid transport
COJEPEMI_(	COJEPE	0.39668	0.025057	hypothetical p	NA	0	
COJEPEMI_(	cas6f	0.39651	0.062347	CRISPR-associ	3.1.-.-	csy4	CRISPR-associated protein (Cas_Csy4)
COJEPEMI_(	ansB	0.39617	0.230804	Glutaminase-a	3.5.1.38	ansB	Asparaginase
COJEPEMI_(	fucA	0.39505	NA	L-fuculose pho	4.1.2.17	fucA_3	Class II Aldolase and Adducin N-terminal domain
COJEPEMI_(	COJEPE	0.39472	0.485363	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.39411	NA	hypothetical p	NA	0	
COJEPEMI_(	namA_1	0.39397	0.152121	NADPH dehydr	1.6.99.1	0	NADH:flavin oxidoreductase / NADH oxidase family
COJEPEMI_(	COJEPE	0.3934	0.498859	hypothetical p	NA	0	hemolysin activation secretion protein
COJEPEMI_(	COJEPE	0.39333	0.136308	hypothetical p	NA	0	TRAP-type C4-dicarboxylate transport system periplasmic component
COJEPEMI_(	COJEPE	0.39259	0.428477	hypothetical p	NA	0	
COJEPEMI_(	copA_2	0.3916	0.049711	Copper resista	NA	copA	Multicopper oxidase
COJEPEMI_(	COJEPE	0.39147	0.417968	hypothetical p	NA	0	Domain of unknown function (DUF4062)
COJEPEMI_(	COJEPE	0.39037	0.293752	hypothetical p	NA	pgaB	Hypothetical glycosyl hydrolase family 13
COJEPEMI_(	katG	0.39036	0.163897	Catalase-pero	1.11.1.21	katG	Bifunctional enzyme with both catalase and broad- spectrum peroxidas

COJEPEMI_(	COJEPE	0.39007	0.576207	hypothetical p	NA	0	
COJEPEMI_(	bcr_1	0.38862	0.131851	Bicyclomycin r	NA	0	Major facilitator Superfamily
COJEPEMI_(	degS	0.38858	0.192005	Serine endopr	3.4.21.10	degS	COG0265 Trypsin-like serine proteases, typically periplasmic, contain C
COJEPEMI_(	COJEPE	0.3883	0.190941	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.38639	0.037403	hypothetical p	NA	0	Hemerythrin HHE cation binding domain
COJEPEMI_(	COJEPE	0.3859	0.134164	Glucosaminat	4.3.1.9	trxB	Belongs to the class-II pyridine nucleotide-disulfide oxidoreductase fam
COJEPEMI_(	srrA	0.38526	0.139662	Transcriptiona	NA	0	Transcriptional regulatory protein, C terminal
COJEPEMI_(	cobS	0.38518	0.19856	Adenosylcobin	2.7.8.26	cobS	Joins adenosylcobinamide-GDP and alpha-ribazole to generate adenosy
COJEPEMI_(	betI_3	0.38251	0.304883	HTH-type trans	NA	betI	Repressor involved in choline regulation of the bet genes
COJEPEMI_(	COJEPE	0.38144	0.255807	Catechol O-me	2.1.1.6	mdmC	O-methyltransferase
COJEPEMI_(	hcaR_5	0.3805	0.067353	Hca operon tra	NA	hcaR	LysR substrate binding domain
COJEPEMI_(	trpS2	0.38047	0.042476	Tryptophan--tF	6.1.1.2	trpS	Belongs to the class-I aminoacyl-tRNA synthetase family
COJEPEMI_(	COJEPE	0.37895	0.110763	hypothetical p	NA	glt	Belongs to the glutamate synthase family
COJEPEMI_(	yajR	0.3782	0.018823	Inner membra	NA	yajR	Major facilitator Superfamily
COJEPEMI_(	ygfA	0.37772	0.433974	5-formyltetrah	6.3.3.2	ygfA	Belongs to the 5-formyltetrahydrofolate cyclo-ligase family
COJEPEMI_(	htrE_2	0.37769	0.454551	Outer membra	NA	mrkC	usher protein
COJEPEMI_(	tsaM1	0.37734	0.446105	Toluene-4-sulf	1.14.14.-	vanA	Rieske [2Fe-2S] domain
COJEPEMI_(	COJEPE	0.37582	0.666406	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.37547	NA	hypothetical p	NA	0	
COJEPEMI_(	dcd	0.37481	0.048085	dCTP deamina	3.5.4.13	dcd	Belongs to the dCTP deaminase family
COJEPEMI_(	hxlR_1	0.37428	0.564074	HTH-type trans	NA	0	HxlR-like helix-turn-helix
COJEPEMI_(	msrA	0.37425	0.129603	Peptide methi	1.8.4.11	msrA	Has an important function as a repair enzyme for proteins that have be
COJEPEMI_(	COJEPE	0.37419	0.230597	hypothetical p	NA	0	TRAP-type C4-dicarboxylate transport system periplasmic component
COJEPEMI_(	COJEPE	0.37404	0.184493	hypothetical p	NA	0	phosphate-selective porin O and P
COJEPEMI_(	ansA	0.37332	0.105505	L-asparaginas	3.5.1.1	ansA	Asparaginase
COJEPEMI_(	ypeA	0.37326	0.13134	Acetyltransfer	2.3.1.-	ypeA	FR47-like protein
COJEPEMI_(	btuB_5	0.37313	0.136665	Vitamin B12 t	NA	0	TonB dependent receptor
COJEPEMI_(	fldP_3	0.3727	0.141983	Flavodoxin Fld	NA	0	Flavodoxin domain
COJEPEMI_(	COJEPE	0.37192	0.20928	hypothetical p	NA	0	PepSY-associated TM region
COJEPEMI_(	COJEPE	0.37096	0.280116	hypothetical p	NA	0	

COJEPEMI_(	COJEPE	0.37051	0.120835	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.3698	NA	hypothetical p	NA	0	Chalcone isomerase-like
COJEPEMI_(	ydfG	0.36959	0.16501	NADP-depend	1.1.1.381	ydfG	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	tolQ_1	0.36945	0.136308	Tol-Pal system	NA	tolQ	MotA/TolQ/ExbB proton channel family
COJEPEMI_(	arsH	0.3693	0.195954	NADPH-depen	1.-.-.-	arsH	NADPH-dependent FMN reductase
COJEPEMI_(	guaD_1	0.36697	0.217051	Guanine deam	3.5.4.3	guaD	Amidohydrolase family
COJEPEMI_(	COJEPE	0.36674	0.143061	hypothetical p	NA	sppA	signal peptide peptidase SppA
COJEPEMI_(	acpP	0.36587	0.067987	Acyl carrier pr	NA	acpP	Carrier of the growing fatty acid chain in fatty acid biosynthesis
COJEPEMI_(	rhtC_2	0.36456	0.070366	Threonine effl	NA	rhtC	LysE type translocator
COJEPEMI_(	actP_2	0.36428	0.178296	Copper-transp	7.2.2.9	actP	P-type ATPase
COJEPEMI_(	COJEPE	0.36307	0.635254	hypothetical p	NA	traC	Domain of unknown function (DUF1738)
COJEPEMI_(	COJEPE	0.36068	0.105195	hypothetical p	NA	0	
COJEPEMI_(	xerC_3	0.36061	0.189902	Tyrosine recon	NA	rci	Phage integrase family
COJEPEMI_(	ruvB_1	0.3605	0.311489	Holliday juncti	3.6.4.12	ruvB	The RuvA-RuvB complex in the presence of ATP renatures cruciform str
COJEPEMI_(	COJEPE	0.35861	0.404178	GTP cyclohydr	NA	0	protein conserved in bacteria
COJEPEMI_(	COJEPE	0.35767	0.608015	hypothetical p	NA	0	Protein conserved in bacteria
COJEPEMI_(	COJEPE	0.35731	0.172527	hypothetical p	NA	0	macromolecule glycosylation
COJEPEMI_(	pcnB	0.35713	0.297618	Poly(A) polym	2.7.7.19	pcnB	Adds poly(A) tail to the 3' end of many RNAs, which usually targets the
COJEPEMI_(	pcaI_2	0.35687	0.408858	3-oxoadipate (	2.8.3.6	pcaI	3-oxoadipate CoA-transferase activity
COJEPEMI_(	aarA	0.35537	0.228581	Rhomboid pro	3.4.21.10	aarA	membrane protein (homolog of Drosophila rhomboid)
COJEPEMI_(	bcp	0.35516	0.335867	Peroxiredoxin	1.11.1.15	bcp	Redoxin
COJEPEMI_(	map_1	0.35444	0.058219	Methionine an	3.4.11.18	map	Methionine aminopeptidase
COJEPEMI_(	COJEPE	0.35344	0.10216	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.35234	0.23429	hypothetical p	NA	0	Has lipid A 3-O-deacylase activity. Hydrolyzes the ester bond at the 3 p
COJEPEMI_(	bepC	0.35178	0.622757	Outer membra	NA	0	Outer membrane efflux protein
COJEPEMI_(	folC	0.35164	0.208377	Dihydrofolate	6.3.2.12	folC	Belongs to the folylpolyglutamate synthase family
COJEPEMI_(	nuoM	0.34984	0.182319	NADH-quinone	7.1.1.-	nuoM	COG1008 NADH ubiquinone oxidoreductase subunit 4 (chain M)
COJEPEMI_(	eamB	0.34537	NA	Cysteine/O-ac	NA	eamB	LysE type translocator
COJEPEMI_(	aprA	0.34507	0.534064	Adenylylsulfat	1.8.99.2	MA20_14	Fumarate reductase flavoprotein C-term
COJEPEMI_(	COJEPE	0.34487	0.595646	hypothetical p	NA	0	

COJEPEMI_(	kdgR	0.34466	0.088569	Transcriptiona	NA	0	helix_turn_helix isocitrate lyase regulation
COJEPEMI_(	pheA	0.34349	0.191095	Bifunctional cl	NA	pheA	chorismate mutase
COJEPEMI_(	COJEPE	0.34311	0.516243	hypothetical p	NA	0	
COJEPEMI_(	pucK	0.34263	0.432613	Uric acid perm	NA	pbuX	Permease family
COJEPEMI_(	pyrE	0.34223	0.14106	Orotate phosp	2.4.2.10	pyrE	Catalyzes the transfer of a ribosyl phosphate group from 5-phosphoribc
COJEPEMI_(	COJEPE	0.34167	0.083022	hypothetical p	NA	0	Bacterial TniB protein
COJEPEMI_(	COJEPE	0.34084	0.328709	NAD(P)H dehy	1.6.5.2	wrbA	Belongs to the WrbA family
COJEPEMI_(	COJEPE	0.34071	NA	hypothetical p	NA	csuB	Spore Coat Protein U domain
COJEPEMI_(	COJEPE	0.33935	0.426685	hypothetical p	NA	phoX	Bacterial protein of unknown function (DUF839)
COJEPEMI_(	COJEPE	0.33796	0.528535	hypothetical p	NA	0	
COJEPEMI_(	dat	0.33726	0.237108	Diaminobutyra	2.6.1.76	dat	Belongs to the class-III pyridoxal-phosphate-dependent aminotransfera
COJEPEMI_(	COJEPE	0.33708	0.635254	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.33692	0.311489	hypothetical p	NA	0	outer membrane porin, OprD family
COJEPEMI_(	mrpG	0.3364	0.327212	Na(+)/H(+) an	NA	phaG	Na+/H+ antiporter subunit
COJEPEMI_(	COJEPE	0.3359	0.30076	hypothetical p	NA	0	
COJEPEMI_(	dapA_3	0.33586	0.138053	4-hydroxy-tetr	4.3.3.7	0	Dihydrodipicolinate synthetase family
COJEPEMI_(	fabD_2	0.33466	0.18953	Malonyl CoA-a	2.3.1.39	fabD	malonyl CoA-acyl carrier protein transacylase
COJEPEMI_(	COJEPE	0.33458	0.241614	hypothetical p	NA	0	
COJEPEMI_(	rsmD	0.33418	0.302951	Ribosomal RN	2.1.1.171	rsmD	Specifically methylates the guanine in position 966 of 16S rRNA in the a
COJEPEMI_(	COJEPE	0.33417	0.543836	hypothetical p	NA	0	KilA-N
COJEPEMI_(	cntI	0.33156	0.298822	Pseudopaline e	NA	0	EamA-like transporter family
COJEPEMI_(	COJEPE	0.33034	0.105878	hypothetical p	NA	0	A predicted alpha-helical domain with a conserved ER motif.
COJEPEMI_(	COJEPE	0.3291	0.140105	putative FAD-l	1.-.-.-	IV02_256	FAD linked oxidases, C-terminal domain
COJEPEMI_(	COJEPE	0.32851	0.451395	putative trans	NA	0	Major facilitator Superfamily
COJEPEMI_(	ribBA	0.32833	0.344964	Riboflavin bios	NA	ribB	Catalyzes the conversion of D-ribulose 5-phosphate to formate and 3,4-
COJEPEMI_(	bpt	0.32775	0.227734	Aspartate/glut	2.3.2.29	ate	May conjugate Arg from its aminoacyl-tRNA to the N- termini of protei
COJEPEMI_(	dmlR_5	0.32765	0.280041	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	0.32728	0.124313	hypothetical p	NA	0	N-acetylmuramoyl-L-alanine amidase activity
COJEPEMI_(	COJEPE	0.32722	0.635859	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ybeZ	0.32653	0.291576	PhoH-like prot	NA	ybeZ	PhoH-like protein

COJEPEMI_(	COJEPE	0.32623	0.265197	hypothetical p	NA	yohN	Nickel/cobalt transporter regulator
COJEPEMI_(	COJEPE	0.32594	0.607394	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.32577	0.119031	hypothetical p	NA	0	FCD
COJEPEMI_(	COJEPE	0.32497	0.072876	hypothetical p	NA	0	Regulator of ribonuclease activity B
COJEPEMI_(	feaB	0.32489	0.323387	Phenylacetald	1.2.1.39	feaB	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat
COJEPEMI_(	paaJ	0.32445	0.538548	3-oxoadipyl-Cc	2.3.1.174	pcaF	Belongs to the thiolase family
COJEPEMI_(	COJEPE	0.32398	0.610865	hypothetical p	NA	0	
COJEPEMI_(	lolE	0.32392	0.183805	Lipoprotein-re	NA	lolE	MacB-like periplasmic core domain
COJEPEMI_(	COJEPE	0.32371	0.319841	hypothetical p	NA	plsC2	Phosphate acyltransferases
COJEPEMI_(	ephA	0.32358	0.175098	Epoxide hydrol	3.3.2.10	0	Serine aminopeptidase, S33
COJEPEMI_(	cas1	0.32226	0.292711	CRISPR-associ	3.1.-.-	cas1	CRISPR (clustered regularly interspaced short palindromic repeat), is ar
COJEPEMI_(	iolS	0.32172	0.162322	Aldo-keto redu	1.1.1.-	0	Aldo/keto reductase family
COJEPEMI_(	yjhB_2	0.32157	0.519819	Putative meta	NA	mucK	Major facilitator Superfamily
COJEPEMI_(	radA	0.32128	0.192005	DNA repair pro	3.6.4.-	radA	DNA-dependent ATPase involved in processing of recombination interm
COJEPEMI_(	COJEPE	0.32091	0.619064	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.32085	0.508075	hypothetical p	NA	pilX	
COJEPEMI_(	COJEPE	0.31926	0.243113	hypothetical p	NA	0	DNA glycosylase
COJEPEMI_(	coaD	0.31916	0.111049	Phosphopante	2.7.7.3	coaD	Reversibly transfers an adenylyl group from ATP to 4'- phosphopanteth
COJEPEMI_(	lptB	0.31795	0.280216	Lipopolysaccha	3.6.3.-	lptB	ABC transporter
COJEPEMI_(	COJEPE	0.31791	0.413212	hypothetical p	NA	0	4-amino-4-deoxy-alpha-L-arabinopyranosyl undecaprenyl phosphate bio
COJEPEMI_(	ybgC	0.31711	0.422246	Acyl-CoA thioe	3.1.2.-	ybgC	Thioesterase-like superfamily
COJEPEMI_(	fmt	0.31597	0.294294	Methionyl-tRN	2.1.2.9	fmt	Attaches a formyl group to the free amino group of methionyl-tRNA(fM
COJEPEMI_(	fadI	0.31577	0.2037	3-ketoacyl-CoA	2.3.1.16	fadI	Belongs to the thiolase family
COJEPEMI_(	COJEPE	0.31554	0.316667	Peroxiredoxin	1.11.1.15	lsfA	C-terminal domain of 1-Cys peroxiredoxin
COJEPEMI_(	metQ_2	0.31511	0.499093	D-methionine-	NA	metQ3	NLPA lipoprotein
COJEPEMI_(	COJEPE	0.3141	0.136837	hypothetical p	NA	0	dienelactone hydrolase
COJEPEMI_(	nimT	0.31168	0.293268	2-nitroimidazo	NA	cynX	Major Facilitator Superfamily
COJEPEMI_(	apaH	0.31046	0.17122	Bis(5'-nucleos	3.6.1.41	apaH	Hydrolyzes diadenosine 5',5'''-P1,P4-tetraphosphate to yield ADP
COJEPEMI_(	lemA	0.3099	0.080711	Protein LemA	NA	lemA	LemA family
COJEPEMI_(	COJEPE	0.30954	0.373095	hypothetical p	NA	0	Histidine phosphatase superfamily (branch 2)

COJEPEMI_(	COJEPE	0.30806	0.609389	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	COJEPE	0.30664	0.508075	hypothetical p	NA	0	Phage tail-collar fibre protein
COJEPEMI_(	COJEPE	0.30631	0.625571	hypothetical p	NA	0	
COJEPEMI_(	mlaD	0.30571	0.105878	Intermembran	NA	mlaD	MlaD protein
COJEPEMI_(	wbpD	0.30554	0.217051	UDP-2-acetam	2.3.1.201	wbpD	Hexapeptide repeat of succinyl-transferase
COJEPEMI_(	COJEPE	0.3037	0.065381	hypothetical p	NA	0	Tetratricopeptide repeat
COJEPEMI_(	pucI	0.30355	0.470512	putative allant	NA	pucI	Permease for cytosine/purines, uracil, thiamine, allantoin
COJEPEMI_(	znuC	0.30348	0.52027	Zinc import AT	7.2.2.-	znuC	Part of the ABC transporter complex ZnuABC involved in zinc import. Re
COJEPEMI_(	COJEPE	0.30337	0.139887	hypothetical p	NA	0	Capsule assembly protein Wzi
COJEPEMI_(	clpV1	0.30245	0.502919	Protein ClpV1	NA	clpV	C-terminal, D2-small domain, of ClpB protein
COJEPEMI_(	antB	0.30221	0.53099	Anthranilate 1	1.14.12.1	antB	Ring hydroxylating beta subunit
COJEPEMI_(	COJEPE	0.30218	0.323179	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.30194	0.590104	hypothetical p	NA	0	Terminase RNaseH-like domain
COJEPEMI_(	COJEPE	0.30153	0.593834	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.30145	0.363583	hypothetical p	NA	yeaL	Protein of unknown function (DUF441)
COJEPEMI_(	coaBC	0.30134	0.226099	Coenzyme A bi	NA	coaBC	Catalyzes two steps in the biosynthesis of coenzyme A. In the first step
COJEPEMI_(	pgrR_1	0.30071	0.259424	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	ald1	0.29912	0.591972	Long-chain-alc	1.2.1.48	aldB	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat
COJEPEMI_(	trmR	0.29895	0.43624	tRNA 5-hydrox	2.1.1.-	mdmC	O-methyltransferase
COJEPEMI_(	COJEPE	0.29879	0.396735	hypothetical p	NA	0	Peptidase C39 family
COJEPEMI_(	tesA	0.29737	0.232307	Esterase TesA	3.1.1.1	tesA	GDSL-like Lipase/Acylhydrolase family
COJEPEMI_(	COJEPE	0.29735	0.268646	hypothetical p	NA	0	Sporulation related domain
COJEPEMI_(	COJEPE	0.29634	0.404605	putative glycin	NA	0	BCCT, betaine/carnitine/choline family transporter
COJEPEMI_(	ttcA	0.29632	0.363583	tRNA-cytidine(	2.8.1.-	ttcA	Catalyzes the ATP-dependent 2-thiolation of cytidine in position 32 of t
COJEPEMI_(	topA_1	0.29629	0.252634	DNA topoisom	5.6.2.1	topA	Releases the supercoiling and torsional tension of DNA, which is introd
COJEPEMI_(	lldR	0.29618	0.228732	Putative L-lact	NA	lldR	FCD
COJEPEMI_(	COJEPE	0.29534	0.200438	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.295	0.382693	hypothetical p	NA	0	Auxin Efflux Carrier
COJEPEMI_(	COJEPE	0.29452	0.153437	hypothetical p	NA	MA20_32	Proteasome subunit
COJEPEMI_(	mnmG	0.29452	0.240491	tRNA uridine 5	NA	gidA	NAD-binding protein involved in the addition of a carboxymethylaminor

COJEPEMI_(	tdcB	0.29412	0.190854	L-threonine an	4.3.1.19	tdcB	Pyridoxal-phosphate dependent enzyme
COJEPEMI_(	fbp_2	0.29332	0.323253	FK506-binding	5.2.1.8	fbp	Peptidyl-prolyl cis-trans
COJEPEMI_(	COJEPE	0.29298	0.516577	hypothetical p	NA	0	Domain of unknown function (DUF4401)
COJEPEMI_(	COJEPE	0.29148	0.579161	hypothetical p	NA	0	
COJEPEMI_(	ihfA	0.29069	0.302951	Integration ho	NA	himA	This protein is one of the two subunits of integration host factor, a spe
COJEPEMI_(	glpQ	0.29021	0.552712	Glycerophosph	3.1.4.46	glpQ	Glycerophosphoryl diester phosphodiesterase family
COJEPEMI_(	COJEPE	0.2901	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.28949	0.407192	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.28938	0.168969	hypothetical p	NA	aspH	Aspartyl/Asparaginyl beta-hydroxylase
COJEPEMI_(	COJEPE	0.28934	0.369001	hypothetical p	NA	0	ORF6N domain
COJEPEMI_(	thiE_1	0.2885	0.222398	Thiamine-phos	2.5.1.3	thiE	Condenses 4-methyl-5-(beta-hydroxyethyl)thiazole monophosphate (TH
COJEPEMI_(	COJEPE	0.28836	0.452128	hypothetical p	NA	0	YCII-related domain
COJEPEMI_(	COJEPE	0.28832	0.310017	hypothetical p	NA	0	Protein of unknown function (DUF454)
COJEPEMI_(	COJEPE	0.28646	NA	IS4 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	COJEPE	0.28583	0.364648	hypothetical p	NA	rbpA	RNA recognition motif
COJEPEMI_(	COJEPE	0.28495	0.120534	hypothetical p	NA	0	
COJEPEMI_(	yejK	0.28495	0.413177	Nucleoid-asso	NA	ndpA	37-kD nucleoid-associated bacterial protein
COJEPEMI_(	ureA	0.28459	0.612816	Urease subuni	3.5.1.5	ureA	Belongs to the urease gamma subunit family
COJEPEMI_(	COJEPE	0.28446	0.590035	hypothetical p	NA	0	
COJEPEMI_(	sbp_1	0.28357	0.535526	Sulfate-bindin	NA	sbp	sulfate ABC transporter
COJEPEMI_(	COJEPE	0.28357	0.335867	hypothetical p	NA	0	RelB antitoxin
COJEPEMI_(	rhtB_2	0.28185	0.412902	Homoserine/h	NA	yrhP	LysE type translocator
COJEPEMI_(	fabB	0.28106	0.432613	3-oxoacyl-[acy	2.3.1.41	fabB	Belongs to the beta-ketoacyl-ACP synthases family
COJEPEMI_(	COJEPE	0.28039	0.617507	hypothetical p	NA	csuE	Spore Coat Protein U domain
COJEPEMI_(	IMPDH	0.27989	0.483179	Inosine-5'-mo	1.1.1.205	yhcV	Domain in cystathionine beta-synthase and other proteins.
COJEPEMI_(	trpD_1	0.27973	0.220514	Anthranilate p	2.4.2.18	trpD	Catalyzes the transfer of the phosphoribosyl group of 5- phosphorylribo
COJEPEMI_(	panS	0.27924	0.360161	Pantothenate	NA	yocS	SBF-like CPA transporter family (DUF4137)
COJEPEMI_(	COJEPE	0.27883	0.41699	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2218)
COJEPEMI_(	fabG_6	0.27812	0.47352	3-oxoacyl-[acy	1.1.1.100	sdhX	KR domain
COJEPEMI_(	ndh	0.27777	0.231612	NADH dehydro	1.6.99.3	ndh	Pyridine nucleotide-disulphide oxidoreductase

COJEPEMI_(	bla	0.2773	0.316385	Beta-lactamas	3.5.2.6	penP	Beta-lactamase
COJEPEMI_(	tatB	0.27698	0.685274	Sec-independe	NA	tatB	Part of the twin-arginine translocation (Tat) system that transports larg
COJEPEMI_(	pac	0.27644	0.533582	Penicillin G ac	3.5.1.11	pac	Penicillin amidase
COJEPEMI_(	COJEPE	0.27272	0.620535	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.2708	0.625105	Baeyer-Villige	1.14.13.-	0	Flavin-binding monooxygenase-like
COJEPEMI_(	COJEPE	0.27047	0.418669	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.27042	0.299221	hypothetical p	NA	hrpA	Helicase associated domain (HA2) Add an annotation
COJEPEMI_(	czcD_1	0.2702	0.519487	Cadmium, cob	NA	czcD2	Cation efflux family
COJEPEMI_(	COJEPE	0.26994	0.198341	hypothetical p	NA	yeeZ	NAD(P)H-binding
COJEPEMI_(	surE_1	0.26905	0.313957	5'-nucleotidas	3.1.3.5	surE	Nucleotidase that shows phosphatase activity on nucleoside 5'-monoph
COJEPEMI_(	csaA	0.26854	0.396529	putative chape	NA	csaA	Putative tRNA binding domain
COJEPEMI_(	cbbA	0.26695	0.300397	Fructose-bisph	4.1.2.13	fba	Fructose-bisphosphate aldolase class-II
COJEPEMI_(	COJEPE	0.26668	0.394609	hypothetical p	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	trpF	0.2666	0.268242	N-(5'-phospho	5.3.1.24	trpF	Belongs to the TrpF family
COJEPEMI_(	COJEPE	0.26511	0.316118	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.26447	0.549311	hypothetical p	NA	0	Glutathione-dependent formaldehyde-activating enzyme
COJEPEMI_(	astE	0.26423	0.295678	Succinylglutam	3.5.1.96	astE	Belongs to the AspA AstE family. Succinylglutamate desuccinylase subf
COJEPEMI_(	COJEPE	0.26181	0.672525	hypothetical p	NA	0	Ketosteroid isomerase-related protein
COJEPEMI_(	COJEPE	0.26168	0.461101	hypothetical p	NA	mepM_1	Peptidase family M23
COJEPEMI_(	msbA	0.26163	0.317643	Lipid A export	7.5.2.6	msbA	Involved in lipid A export and possibly also in glycerophospholipid expor
COJEPEMI_(	arsC_3	0.26079	0.790892	Arsenate redu	1.20.4.1	arsC	ArsC family
COJEPEMI_(	COJEPE	0.26049	0.603171	hypothetical p	NA	0	DNA RNA non-specific endonuclease
COJEPEMI_(	COJEPE	0.26006	0.175098	Glucosaminate	4.3.1.9	trxB	Belongs to the class-II pyridine nucleotide-disulfide oxidoreductase fam
COJEPEMI_(	COJEPE	0.26006	NA	hypothetical p	NA	tniB	Bacterial TniB protein
COJEPEMI_(	COJEPE	0.25934	0.262039	hypothetical p	NA	0	Alpha/beta hydrolase family
COJEPEMI_(	COJEPE	0.25923	0.129588	hypothetical p	NA	0	Peptidase C13 family
COJEPEMI_(	COJEPE	0.25881	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	lrpC	0.25847	0.343571	HTH-type trans	NA	0	helix_turn_helix ASNC type
COJEPEMI_(	COJEPE	0.25771	0.64332	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	dapE	0.25563	0.291801	Succinyl-diami	3.5.1.18	dapE	Catalyzes the hydrolysis of N-succinyl-L,L- diaminopimelic acid (SDAP),

COJEPEMI_(	rsmI	0.25468	0.381358	Ribosomal RN	2.1.1.198	rsmI	Catalyzes the 2'-O-methylation of the ribose of cytidine 1402 (C1402) i
COJEPEMI_(	phzS	0.2533	0.452773	5-methylphen	1.14.13.2	0	FAD binding domain
COJEPEMI_(	hemL	0.25251	0.152488	Glutamate-1-s	5.4.3.8	hemL	Glutamate-1-semialdehyde aminotransferase
COJEPEMI_(	COJEPE	0.25175	0.685274	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	pobA	0.25169	0.441649	p-hydroxybenz	1.14.13.2	pobA	FAD binding domain
COJEPEMI_(	hemF	0.2506	0.425298	Oxygen-depen	1.3.3.3	hemF	Involved in the heme biosynthesis. Catalyzes the aerobic oxidative deca
COJEPEMI_(	mazG	0.24863	0.43878	Nucleoside tri	3.6.1.8	mazG	Nucleoside triphosphate pyrophosphohydrolase
COJEPEMI_(	COJEPE	0.24846	0.422713	hypothetical p	NA	0	EamA-like transporter family
COJEPEMI_(	mrkD_1	0.248	0.333164	Fimbria adhes	NA	mrkD	Fimbrial protein
COJEPEMI_(	COJEPE	0.2478	0.658861	hypothetical p	NA	0	
COJEPEMI_(	rlmN	0.24744	0.190854	Dual-specificit	2.1.1.192	rlmN	Specifically methylates position 2 of adenine 2503 in 23S rRNA and pos
COJEPEMI_(	ahpF_1	0.24737	0.374864	Alkyl hydroper	1.8.1.-	ahpF	Alkyl hydroperoxide reductase
COJEPEMI_(	ada	0.24735	0.383707	Bifunctional tr	NA	ada	6-O-methylguanine DNA methyltransferase, DNA binding domain
COJEPEMI_(	COJEPE	0.24699	0.345386	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.24556	0.237648	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.24483	0.60699	PKHD-type hyd	1.14.11.-	ybiX	monosaccharide binding
COJEPEMI_(	COJEPE	0.24477	0.690439	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.24361	0.71224	hypothetical p	NA	0	PFAM KAP P-loop domain protein
COJEPEMI_(	COJEPE	0.24301	NA	hypothetical p	NA	0	
COJEPEMI_(	tgnC	0.24264	0.382427	(Z)-2-((N-metl	1.2.1.-	dhaS	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat
COJEPEMI_(	nadB	0.24263	0.410023	L-aspartate ox	1.4.3.16	nadB	Catalyzes the oxidation of L-aspartate to iminoaspartate
COJEPEMI_(	dmoA_1	0.24112	0.422198	Dimethyl-sulfi	1.14.13.1	0	Luciferase-like monooxygenase
COJEPEMI_(	ybhR	0.24054	0.533052	putative multi	NA	0	ABC-2 family transporter protein
COJEPEMI_(	tufA_2	0.2405	0.361376	Elongation fac	NA	tuf	This protein promotes the GTP-dependent binding of aminoacyl-tRNA t
COJEPEMI_(	COJEPE	0.24026	0.681616	hypothetical p	NA	0	Cation efflux family
COJEPEMI_(	COJEPE	0.23991	0.74738	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.23877	0.64973	hypothetical p	NA	0	Domain of unknown function (DUF4882)
COJEPEMI_(	dnaB_3	0.23803	0.492906	Replicative DN	3.6.4.12	dnaB	it exhibits DNA-dependent ATPase activity and contains distinct active s
COJEPEMI_(	COJEPE	0.23791	0.821776	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.23785	0.552473	hypothetical p	NA	0	Protein of unknown function (DUF1176)

COJEPEMI_(	plcN_2	0.23743	0.432765	Non-hemolytic	3.1.4.3	plcN	Phosphoesterase family
COJEPEMI_(	allA	0.23666	0.465957	Ureidoglycolat	4.3.2.3	allA	Ureidoglycolate lyase
COJEPEMI_(	COJEPE	0.23649	0.513253	hypothetical p	NA	nrt	NMT1-like family
COJEPEMI_(	COJEPE	0.23615	0.432481	hypothetical p	NA	MA20_3(	Thioesterase superfamily
COJEPEMI_(	cpdA_3	0.23537	0.450359	3',5'-cyclic ade	3.1.4.53	sbcD	SbcCD cleaves DNA hairpin structures. These structures can inhibit DNA
COJEPEMI_(	COJEPE	0.23461	0.514969	hypothetical p	NA	0	alpha/beta hydrolase fold
COJEPEMI_(	rppH	0.23438	0.556146	RNA pyrophos	3.6.1.-	nudH	Accelerates the degradation of transcripts by removing pyrophosphate
COJEPEMI_(	COJEPE	0.23357	0.690439	hypothetical p	NA	0	EamA-like transporter family
COJEPEMI_(	folE	0.23308	0.4032	GTP cyclohydr	3.5.4.16	folE	GTP cyclohydrolase
COJEPEMI_(	modB	0.2316	0.530774	Molybdenum t	NA	modB	COG4149 ABC-type molybdate transport system, permease component
COJEPEMI_(	yggS	0.23151	0.26527	Pyridoxal phos	NA	yggS	Pyridoxal 5'-phosphate (PLP)-binding protein, which is involved in PLP h
COJEPEMI_(	nudC_1	0.23083	0.353747	NADH pyropho	3.6.1.22	nudC	NADH pyrophosphatase zinc ribbon domain
COJEPEMI_(	COJEPE	0.23017	0.458087	hypothetical p	NA	0	Lysozyme inhibitor LprI
COJEPEMI_(	ybaB	0.22865	0.538508	Nucleoid-asso	NA	ybaB	Binds to DNA and alters its conformation. May be involved in regulation
COJEPEMI_(	gltI	0.22805	0.492866	Glutamate/as	NA	gltI	Bacterial periplasmic substrate-binding proteins
COJEPEMI_(	fadB	0.22755	0.518493	Fatty acid oxid	NA	fadB	Involved in the aerobic and anaerobic degradation of long-chain fatty a
COJEPEMI_(	COJEPE	0.2269	0.533101	hypothetical p	NA	0	
COJEPEMI_(	paaF_5	0.22641	0.372116	2,3-dehydroad	4.2.1.17	0	Enoyl-CoA hydratase/isomerase
COJEPEMI_(	menH_	0.22594	0.567828	2-succinyl-6-hy	4.2.99.20	0	Male sterility protein
COJEPEMI_(	fkpA	0.22565	0.2407	putative FKBP-	5.2.1.8	fkpA	Domain amino terminal to FKBP-type peptidyl-prolyl isomerase
COJEPEMI_(	COJEPE	0.22563	0.592062	hypothetical p	NA	0	Transcriptional regulator
COJEPEMI_(	rpsA	0.2254	0.380233	30S ribosomal	NA	rpsA	thus facilitating recognition of the initiation point. It is needed to trans
COJEPEMI_(	COJEPE	0.2252	0.480849	hypothetical p	NA	phoD	PhoD-like phosphatase
COJEPEMI_(	COJEPE	0.22437	0.444865	hypothetical p	NA	0	
COJEPEMI_(	exbD_1	0.22416	0.551103	Biopolymer tra	NA	tolR	Biopolymer transport protein ExbD/TolR
COJEPEMI_(	COJEPE	0.22392	0.381513	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.22392	0.432765	hypothetical p	NA	0	Transport and Golgi organisation 2
COJEPEMI_(	COJEPE	0.22342	0.569424	hypothetical p	NA	0	Phage Mu protein F like protein
COJEPEMI_(	COJEPE	0.22228	0.343571	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.22037	0.520103	hypothetical p	NA	#N/A	#N/A

COJEPEMI_(	rpmI	0.21972	0.569424	50S ribosomal	NA	rpmI	Belongs to the bacterial ribosomal protein bL35 family
COJEPEMI_(	hmrR_3	0.21942	0.408195	HTH-type trans	NA	0	helix_turn_helix, mercury resistance
COJEPEMI_(	COJEPE	0.21899	0.775451	hypothetical p	NA	0	Haem-degrading
COJEPEMI_(	COJEPE	0.21873	0.781651	hypothetical p	NA	0	Flavin containing amine oxidoreductase
COJEPEMI_(	COJEPE	0.21785	0.700931	hypothetical p	NA	comB	Type IV Pilus-assembly protein W
COJEPEMI_(	COJEPE	0.21728	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	corC	0.21715	0.388107	Magnesium ar	NA	corC	Transporter associated domain
COJEPEMI_(	COJEPE	0.21663	0.583587	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.21624	0.564823	hypothetical p	NA	0	membrane
COJEPEMI_(	argA	0.21577	0.454306	Amino-acid ac	2.3.1.1	argA	Belongs to the acetyltransferase family. ArgA subfamily
COJEPEMI_(	catB	0.21556	0.523968	Muconate cycl	5.5.1.1	catB	Mandelate racemase / muconate lactonizing enzyme, C-terminal doma
COJEPEMI_(	COJEPE	0.21471	0.486144	hypothetical p	NA	0	Putative member of DMT superfamily (DUF486)
COJEPEMI_(	COJEPE	0.21451	0.498081	hypothetical p	NA	prtN	Pyocin activator protein PrtN
COJEPEMI_(	COJEPE	0.21441	0.55933	hypothetical p	NA	uspA	Belongs to the universal stress protein A family
COJEPEMI_(	COJEPE	0.21366	0.540169	hypothetical p	NA	yidB	Bacterial protein of unknown function (DUF937)
COJEPEMI_(	COJEPE	0.21325	0.518493	hypothetical p	NA	porB	Gram-negative porin
COJEPEMI_(	hvrA	0.21319	0.602943	Trans-acting re	NA	hvrA	Domain in histone-like proteins of HNS family
COJEPEMI_(	tyrS	0.21297	0.436658	Tyrosine--tRN/	6.1.1.1	tyrS	Catalyzes the attachment of tyrosine to tRNA(Tyr) in a two-step reactio
COJEPEMI_(	tgnE	0.21223	0.677975	Succinate sem	1.2.1.24	gabD2	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat
COJEPEMI_(	COJEPE	0.2122	0.552473	hypothetical p	NA	yqiA	Uncharacterised protein family (UPF0227)
COJEPEMI_(	engB	0.21206	0.352827	GTP-binding p	NA	engB	Necessary for normal cell division and for the maintenance of normal s
COJEPEMI_(	COJEPE	0.21152	NA	hypothetical p	NA	0	
COJEPEMI_(	nnr	0.21023	0.449981	Bifunctional N	NA	nnrD	Bifunctional enzyme that catalyzes the epimerization of the S- and R-fo
COJEPEMI_(	COJEPE	0.21023	0.504185	hypothetical p	NA	0	Putative diguanylate phosphodiesterase
COJEPEMI_(	fdx_1	0.20913	0.431124	2Fe-2S ferredo	NA	fdx	Ferredoxin, 2Fe-2S type, ISC system
COJEPEMI_(	cydA	0.20709	0.729311	Cytochrome bo	1.10.3.-	cydA	oxidase, subunit
COJEPEMI_(	ribF	0.20569	0.373563	Bifunctional ri	NA	ribF	Belongs to the ribF family
COJEPEMI_(	mutY	0.20505	0.654732	Adenine DNA g	3.2.2.31	mutY	A G-specific
COJEPEMI_(	COJEPE	0.20385	0.521516	hypothetical p	NA	MA20_21	HIT domain
COJEPEMI_(	hisP_1	0.2032	0.705932	Histidine trans	NA	hisP	ABC transporter, ATP-binding protein

COJEPEMI_(	COJEPE	0.20315	0.814667	hypothetical p	NA	0	
COJEPEMI_(	pgaC_1	0.20281	0.617009	Poly-beta-1,6-	2.4.1.-	pgaC	Glycosyl transferase family 21
COJEPEMI_(	gdx	0.20263	0.402572	Guanidinium e	NA	sugE	Small Multidrug Resistance protein
COJEPEMI_(	COJEPE	0.20121	0.794892	hypothetical p	NA	0	
COJEPEMI_(	rtcB	0.19957	0.495173	RNA-splicing l	6.5.1.-	rtcB	tRNA-splicing ligase RtcB
COJEPEMI_(	COJEPE	0.19927	0.498002	hypothetical p	NA	0	helix_turn_helix multiple antibiotic resistance protein
COJEPEMI_(	msrB	0.19858	0.367765	Peptide methi	1.8.4.12	msrB	Belongs to the MsrB Met sulfoxide reductase family
COJEPEMI_(	mfd	0.19776	0.396529	Transcription-r	3.6.4.-	mfd	Couples transcription and DNA repair by recognizing RNA polymerase (
COJEPEMI_(	COJEPE	0.19765	0.498181	hypothetical p	NA	0	
COJEPEMI_(	sphX	0.1968	0.399026	Protein SphX	NA	pstS	PBP superfamily domain
COJEPEMI_(	COJEPE	0.19619	0.64332	hypothetical p	NA	0	COG3209 Rhs family protein
COJEPEMI_(	COJEPE	0.19618	0.619722	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.19526	0.776168	hypothetical p	NA	0	Protein of unknown function (DUF1427)
COJEPEMI_(	mrdA	0.19518	0.587301	Peptidoglycan	3.4.16.4	mrdA	Belongs to the transpeptidase family. MrdA subfamily
COJEPEMI_(	COJEPE	0.19497	0.501805	hypothetical p	NA	algZ	Histidine kinase
COJEPEMI_(	COJEPE	0.19433	0.754736	hypothetical p	NA	0	
COJEPEMI_(	prfC	0.19249	0.377244	Peptide chain	NA	prfC	Increases the formation of ribosomal termination complexes and stimu
COJEPEMI_(	lipB	0.19241	0.508986	Octanoyltransf	2.3.1.181	lipB	Catalyzes the transfer of endogenously produced octanoic acid from oc
COJEPEMI_(	COJEPE	0.19198	0.516727	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.19161	0.567828	Bifunctional N	NA	0	Cytidylyltransferase-like
COJEPEMI_(	COJEPE	0.19077	0.540738	hypothetical p	NA	yfeH	SBF-like CPA transporter family (DUF4137)
COJEPEMI_(	COJEPE	0.18884	0.717319	hypothetical p	NA	eamA1	EamA-like transporter family
COJEPEMI_(	COJEPE	0.18801	0.726616	hypothetical p	NA	0	MarC family integral membrane protein
COJEPEMI_(	nagR_2	0.18786	0.444405	HTH-type trans	NA	0	UTRA
COJEPEMI_(	COJEPE	0.18728	0.42186	putative prote	NA	MA20_32	Bacterial transglutaminase-like N-terminal region
COJEPEMI_(	COJEPE	0.18692	0.607982	hypothetical p	NA	0	Chlorhexidine efflux transporter
COJEPEMI_(	mutL	0.18461	0.506154	DNA mismatcl	NA	mutL	This protein is involved in the repair of mismatches in DNA. It is require
COJEPEMI_(	ureB	0.18451	0.813041	Urease subuni	3.5.1.5	ureB	Belongs to the urease beta subunit family
COJEPEMI_(	pepD	0.18341	0.541842	Cytosol non-sp	3.4.13.18	pepD	Peptidase family M20/M25/M40
COJEPEMI_(	nfdA	0.18338	0.566173	N-substituted	3.5.1.91	nfdA	Amidohydrolase family

COJEPEMI_(	COJEPE	0.18266	0.645256	hypothetical p	NA	atpI	ATP synthase I chain
COJEPEMI_(	COJEPE	0.18171	0.608015	hypothetical p	NA	hemD	Uroporphyrinogen-III synthase
COJEPEMI_(	proA	0.18142	0.308438	Gamma-gluta	1.2.1.41	proA	Catalyzes the NADPH-dependent reduction of L-glutamate 5-phosphate
COJEPEMI_(	COJEPE	0.1805	0.763191	hypothetical p	NA	0	Domain of unknown function (DUF1737)
COJEPEMI_(	COJEPE	0.17983	0.649097	hypothetical p	NA	0	
COJEPEMI_(	yihG	0.17976	0.52672	putative acyltr	2.3.-.-	yihG	Phosphate acyltransferases
COJEPEMI_(	clsC_1	0.17883	0.523939	Cardiolipin syn	2.7.8.-	0	Phospholipase D
COJEPEMI_(	trpE	0.17863	0.391853	Anthranilate s	4.1.3.27	trpE	Part of a heterotetrameric complex that catalyzes the two-step biosynt
COJEPEMI_(	rluB	0.1773	0.389525	Ribosomal lar	5.4.99.22	rluB	Belongs to the pseudouridine synthase RsuA family
COJEPEMI_(	caiT	0.17714	0.721783	L-carnitine/ga	NA	yeaV	BCCT, betaine/carnitine/choline family transporter
COJEPEMI_(	ihfB	0.17643	0.353747	Integration ho	NA	himD	This protein is one of the two subunits of integration host factor, a spe
COJEPEMI_(	COJEPE	0.17608	0.605978	dITP/XTP pyro	3.6.1.66	rdgB	Pyrophosphatase that catalyzes the hydrolysis of nucleoside triphospha
COJEPEMI_(	COJEPE	0.17543	0.619722	Putative acety	2.3.1.-	lacA	Hexapeptide repeat of succinyl-transferase
COJEPEMI_(	COJEPE	0.17401	0.605978	hypothetical p	NA	0	Region found in RelA / SpoT proteins
COJEPEMI_(	mshA_2	0.17374	0.542365	D-inositol-3-ph	2.4.1.250	capM	Glycosyl transferase 4-like domain
COJEPEMI_(	COJEPE	0.17365	0.719359	hypothetical p	NA	0	self proteolysis
COJEPEMI_(	acr3_1	0.17359	0.57289	Arsenical-resis	NA	arsB	Sodium Bile acid symporter family
COJEPEMI_(	COJEPE	0.17268	0.715811	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.17254	0.552516	hypothetical p	NA	adeT	TRAP-type C4-dicarboxylate transport system periplasmic component
COJEPEMI_(	ftsZ	0.17225	0.387555	Cell division pr	NA	ftsZ	Essential cell division protein that forms a contractile ring structure (Z
COJEPEMI_(	lrp_5	0.17164	0.762157	Leucine-respo	NA	lrp	helix_turn_helix ASNC type
COJEPEMI_(	COJEPE	0.1715	0.617507	hypothetical p	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	0.1712	0.748294	hypothetical p	NA	0	EamA-like transporter family
COJEPEMI_(	COJEPE	0.16912	0.702952	hypothetical p	NA	0	Domain of unknown function (DUF4055)
COJEPEMI_(	gdhA_1	0.169	0.546227	Glutamate del	1.4.1.3	gdhA	Belongs to the Glu Leu Phe Val dehydrogenases family
COJEPEMI_(	COJEPE	0.1689	0.679083	hypothetical p	NA	0	Diphthamide synthase
COJEPEMI_(	rcsC_2	0.1688	0.546227	Sensor histidir	2.7.13.3	0	PhoQ Sensor
COJEPEMI_(	rstA	0.16765	0.399906	Transcriptiona	NA	rstA	COG0745 Response regulators consisting of a CheY-like receiver domai
COJEPEMI_(	cntB	0.16685	0.729311	Carnitine mon	1.14.13.2	yeaX	2Fe-2S iron-sulfur cluster binding domain
COJEPEMI_(	COJEPE	0.16674	NA	hypothetical p	NA	0	

COJEPEMI_(	COJEPE	0.16665	0.645285	hypothetical p	NA	0	
COJEPEMI_(	thiM	0.16643	0.619435	Hydroxyethylth	2.7.1.50	thiM	Catalyzes the phosphorylation of the hydroxyl group of 4-methyl-5-beta
COJEPEMI_(	gatC	0.16613	0.47855	Glutamyl-tRN/	6.3.5.-	gatC	Allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(
COJEPEMI_(	map_2	0.16546	0.546798	Methionine an	3.4.11.18	map	Metallopeptidase family M24
COJEPEMI_(	zitB_1	0.1652	0.684331	Zinc transporte	NA	0	Cation efflux family
COJEPEMI_(	COJEPE	0.16454	0.393225	hypothetical p	NA	0	SCP-2 sterol transfer family
COJEPEMI_(	COJEPE	0.16258	0.546227	hypothetical p	NA	0	NUDIX domain
COJEPEMI_(	COJEPE	0.16245	0.556038	hypothetical p	NA	0	Protein of unknown function (DUF1653)
COJEPEMI_(	COJEPE	0.16152	0.822084	hypothetical p	NA	radC	Belongs to the UPF0758 family
COJEPEMI_(	yhbO	0.16085	0.485363	Protein/nuclei	3.1.2.-	pfpI	DJ-1/PfpI family
COJEPEMI_(	eptA	0.16065	0.556146	Phosphoethan	2.7.-.-	eptA	Domain of unknown function (DUF1705)
COJEPEMI_(	COJEPE	0.16047	0.532587	hypothetical p	NA	0	Sigma 54 modulation protein / S30EA ribosomal protein
COJEPEMI_(	COJEPE	0.15996	0.5315	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.15994	0.696371	hypothetical p	NA	0	Protein of unknown function (DUF1275)
COJEPEMI_(	COJEPE	0.15821	NA	hypothetical p	NA	0	
COJEPEMI_(	yfcG_2	0.15773	0.552473	Disulfide-bond	1.8.4.-	gst7	Belongs to the GST superfamily
COJEPEMI_(	gpx1	0.15763	0.436873	Hydroperoxy fa	1.11.1.22	gpo	Belongs to the glutathione peroxidase family
COJEPEMI_(	greB	0.15741	0.583839	Transcription e	NA	greB	Necessary for efficient RNA polymerase transcription elongation past t
COJEPEMI_(	argD	0.15713	0.443668	Acetylornithin	2.6.1.11	argD	acetylornithine aminotransferase
COJEPEMI_(	COJEPE	0.15644	0.638774	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.15618	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ompR	0.15474	0.473878	Transcriptiona	NA	ompR	COG0745 Response regulators consisting of a CheY-like receiver domai
COJEPEMI_(	COJEPE	0.15438	0.654662	hypothetical p	NA	0	Carbonic anhydrase
COJEPEMI_(	scpB	0.15388	0.619722	Segregation a	NA	scpB	Participates in chromosomal partition during cell division. May act via t
COJEPEMI_(	macB	0.15361	0.573145	Macrolide exp	3.6.3.-	macB	Part of the tripartite efflux system MacAB-TolC. MacB is a non-canonic
COJEPEMI_(	tusE	0.15339	0.649237	Sulfurtransfer	2.8.1.-	tusE	Part of a sulfur-relay system
COJEPEMI_(	pncB2	0.15335	0.643179	Nicotinate phc	6.3.4.21	pncB	Catalyzes the synthesis of beta-nicotinate D- ribonucleotide from nicoti
COJEPEMI_(	COJEPE	0.15287	0.666482	putative Fe(2+	NA	yggX	Could be a mediator in iron transactions between iron acquisition and i
COJEPEMI_(	COJEPE	0.15253	0.870598	hypothetical p	NA	0	transcriptional regulator
COJEPEMI_(	COJEPE	0.15181	0.635859	hypothetical p	NA	lysM	LysM domain

COJEPEMI_(	paaK	0.15155	0.702952	Phenylacetate-	6.2.1.30	paaK	Catalyzes the activation of phenylacetic acid (PA) to phenylacetyl-CoA (
COJEPEMI_(	COJEPE	0.15127	0.583693	hypothetical p	NA	ytfL	Domain of unknown function DUF21
COJEPEMI_(	COJEPE	0.15079	0.728285	hypothetical p	NA	0	Phage lysozyme
COJEPEMI_(	COJEPE	0.15066	0.823774	hypothetical p	NA	0	Nitroreductase family
COJEPEMI_(	COJEPE	0.14847	0.65188	hypothetical p	NA	0	Tyrosine phosphatase family
COJEPEMI_(	COJEPE	0.14799	0.786348	hypothetical p	NA	0	Serine aminopeptidase, S33
COJEPEMI_(	exaE	0.14746	0.605978	Transcriptiona	NA	tcsR	Sigma-70, region 4
COJEPEMI_(	gltP_2	0.14743	0.60432	Proton/glutam	NA	gltP	Catalyzes the proton-dependent transport of glutamate and aspartate
COJEPEMI_(	COJEPE	0.14717	0.762285	hypothetical p	NA	0	KR domain
COJEPEMI_(	COJEPE	0.14666	0.844723	hypothetical p	NA	HA62_21	Amino acid synthesis
COJEPEMI_(	COJEPE	0.14652	0.667062	hypothetical p	NA	0	Cysteine-rich secretory protein family
COJEPEMI_(	ogt	0.14618	0.596572	Methylated-DI	2.1.1.63	ogt	Involved in the cellular defense against the biological effects of O6-me
COJEPEMI_(	mdlY	0.14544	0.664566	Mandelamide	3.5.1.86	iaaH	Amidase
COJEPEMI_(	COJEPE	0.14408	0.688948	Alpha-ketoglu	1.2.1.26	0	Aldehyde dehydrogenase family
COJEPEMI_(	COJEPE	0.14347	0.667277	hypothetical p	NA	pilZ	PilZ domain
COJEPEMI_(	COJEPE	0.14335	0.719937	hypothetical p	NA	0	
COJEPEMI_(	gutB	0.14194	0.728914	Sorbitol dehyd	1.1.1.-	adhB	Alcohol dehydrogenase GroES-like domain
COJEPEMI_(	COJEPE	0.14047	NA	hypothetical p	NA	0	GtrA-like protein
COJEPEMI_(	COJEPE	0.14025	0.775299	hypothetical p	NA	0	COG0697 Permeases of the drug metabolite transporter (DMT) superfa
COJEPEMI_(	tdh_2	0.14021	0.695928	L-threonine 3-	1.1.1.103	MA20_17	Alcohol dehydrogenase GroES-like domain
COJEPEMI_(	dhfrIII	0.13984	0.630854	Dihydrofolate	1.5.1.3	folA	Key enzyme in folate metabolism. Catalyzes an essential reaction for d
COJEPEMI_(	COJEPE	0.13955	0.794343	hypothetical p	NA	0	Protein of unknown function (DUF1295)
COJEPEMI_(	COJEPE	0.13737	0.859703	ISL3 family tra	NA	MA20_12	zinc-finger of transposase IS204/IS1001/IS1096/IS1165
COJEPEMI_(	COJEPE	0.13681	0.795818	hypothetical p	NA	MA20_14	E-Z type HEAT repeats
COJEPEMI_(	COJEPE	0.13651	0.649097	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2059)
COJEPEMI_(	ais	0.13607	0.871986	Aconitate isom	5.3.3.7	0	Bacterial extracellular solute-binding protein
COJEPEMI_(	COJEPE	0.13556	0.743265	hypothetical p	NA	0	
COJEPEMI_(	dld	0.13542	0.637831	Quinone-depe	1.1.5.12	dld	Catalyzes the oxidation of D-lactate to pyruvate
COJEPEMI_(	trpG	0.13537	0.625105	Anthranilate s	4.1.3.27	trpG	component II
COJEPEMI_(	garK	0.13498	0.720839	Glycerate 2-ki	2.7.1.165	glxK	Belongs to the glycerate kinase type-1 family

COJEPEMI_(	rpoZ	0.13423	0.630854	DNA-directed	2.7.7.6	rpoZ	Promotes RNA polymerase assembly. Latches the N- and C- terminal re
COJEPEMI_(	yghU	0.13415	0.617507	Disulfide-bond	1.8.4.-	yghU	Belongs to the GST superfamily
COJEPEMI_(	COJEPE	0.13317	0.775434	hypothetical p	NA	0	
COJEPEMI_(	rlmL	0.13307	0.673214	Ribosomal RN	NA	rlmL	Specifically methylates the guanine in position 2445 (m2G2445) and th
COJEPEMI_(	COJEPE	0.1327	0.694551	Putative 3-me	3.2.2.-	0	Methylpurine-DNA glycosylase (MPG)
COJEPEMI_(	tauB_1	0.13264	0.85451	Taurine impor	7.6.2.7	0	ATPases associated with a variety of cellular activities
COJEPEMI_(	lptD	0.13261	0.672034	LPS-assembly	NA	lptD	Together with LptE, is involved in the assembly of lipopolysaccharide (L
COJEPEMI_(	ydjA	0.13244	0.624975	Putative NAD(	1.-.-.-	0	Nitroreductase family
COJEPEMI_(	rluA_2	0.13128	0.643074	Dual-specificit	5.4.99.28	rluA	Pseudouridine synthase
COJEPEMI_(	phaC_2	0.13102	0.851734	Poly(3-hydroxy	2.3.1.-	phaC	alpha/beta hydrolase fold
COJEPEMI_(	folP_1	0.12884	0.644582	Dihydropteroa	2.5.1.15	folP	Catalyzes the condensation of para-aminobenzoate (pABA) with 6-hydr
COJEPEMI_(	wbpB	0.12868	0.694698	UDP-N-acetyl-	1.1.1.335	wbpB	Oxidoreductase family, C-terminal alpha/beta domain
COJEPEMI_(	COJEPE	0.12843	0.825599	hypothetical p	NA	yaiL	Uncharacterized protein conserved in bacteria (DUF2058)
COJEPEMI_(	sucD	0.12828	0.611692	Succinate--CoA	6.2.1.5	sucD	Succinyl-CoA synthetase functions in the citric acid cycle (TCA), couplin
COJEPEMI_(	yciO	0.12737	0.871986	putative prote	NA	yciO	Belongs to the SUA5 family
COJEPEMI_(	COJEPE	0.12697	0.661386	hypothetical p	NA	nadV	Nicotinate phosphoribosyltransferase (NAPRTase) family
COJEPEMI_(	proS	0.12625	0.673214	Proline--tRNA	6.1.1.15	proS	Catalyzes the attachment of proline to tRNA(Pro) in a two-step reactio
COJEPEMI_(	lepA	0.12522	0.613597	Elongation fac	3.6.5.-	lepA	Required for accurate and efficient protein synthesis under certain stre
COJEPEMI_(	thrB	0.12401	0.64881	Homoserine ki	2.7.1.39	thrB	Belongs to the pseudomonas-type ThrB family
COJEPEMI_(	COJEPE	0.12375	0.747269	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2147)
COJEPEMI_(	lldD	0.12328	0.707646	L-lactate dehy	1.1.-.-	lldD	Catalyzes the conversion of L-lactate to pyruvate. Is coupled to the resp
COJEPEMI_(	murJ	0.12314	0.694698	putative lipid I	NA	murJ	Involved in peptidoglycan biosynthesis. Transports lipid-linked peptidog
COJEPEMI_(	gatA_1	0.12286	0.732736	Glutamyl-tRN/	6.3.5.7	gatA	Allows the formation of correctly charged Gln-tRNA(Gln) through the t
COJEPEMI_(	gudP_2	0.12184	0.813041	putative gluca	NA	sauU	MFS/sugar transport protein
COJEPEMI_(	emrA_1	0.12122	0.700154	Colistin resista	NA	0	Barrel-sandwich domain of CusB or HlyD membrane-fusion
COJEPEMI_(	COJEPE	0.11985	0.777317	hypothetical p	NA	0	Putative MetA-pathway of phenol degradation
COJEPEMI_(	COJEPE	0.11892	0.733058	hypothetical p	NA	pilE	Type IV minor pilin ComP, DNA uptake sequence receptor
COJEPEMI_(	nudL	0.11874	0.684331	putative Nudix	3.6.1.-	nudL	COG0494 NTP pyrophosphohydrolases including oxidative damage repa
COJEPEMI_(	COJEPE	0.11858	0.836206	hypothetical p	NA	todE	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
COJEPEMI_(	COJEPE	0.11792	0.84409	hypothetical p	NA	0	

COJEPEMI_(	cidB_2	0.1175	0.807439	Holin-like prot	NA	lrgB	LrgB-like family
COJEPEMI_(	COJEPE	0.11581	0.696371	hypothetical p	NA	0	Attaches a formyl group to the free amino group of methionyl-tRNA(fM
COJEPEMI_(	COJEPE	0.11554	0.817198	hypothetical p	NA	ycsG	Natural resistance-associated macrophage protein
COJEPEMI_(	fldP_2	0.11541	0.853638	Flavodoxin Fld	NA	wrbA	Flavodoxin domain
COJEPEMI_(	ubiJ	0.11513	0.692296	Ubiquinone bi	NA	0	ubiquinone biosynthetic process from chorismate
COJEPEMI_(	COJEPE	0.11512	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ddc	0.11449	0.673214	L-2,4-diaminol	4.1.1.86	ddc	Pyridoxal-dependent decarboxylase conserved domain
COJEPEMI_(	cysG	0.11415	0.582037	Siroheme synt	NA	cysG	Multifunctional enzyme that catalyzes the SAM-dependent methylatior
COJEPEMI_(	COJEPE	0.11415	0.887127	hypothetical p	NA	0	
COJEPEMI_(	cobB	0.11403	0.715623	NAD-depende	2.3.1.286	cobB	NAD-dependent lysine deacetylase and desuccinylase that specifically r
COJEPEMI_(	COJEPE	0.11317	0.844723	hypothetical p	NA	0	Protein of unknown function (DUF817)
COJEPEMI_(	def_1	0.11278	0.695574	Peptide deforr	3.5.1.88	def	Removes the formyl group from the N-terminal Met of newly synthesiz
COJEPEMI_(	COJEPE	0.11184	0.64332	putative phosp	3.1.3.-	serB2	haloacid dehalogenase-like hydrolase
COJEPEMI_(	COJEPE	0.11182	0.778971	hypothetical p	NA	0	Membrane transport protein
COJEPEMI_(	rutF	0.11159	0.65859	FMN reductas	1.5.1.42	hpaC	Flavin reductase like domain
COJEPEMI_(	leuE_2	0.11133	0.755607	Leucine efflux	NA	MA20_22	LysE type translocator
COJEPEMI_(	COJEPE	0.111	NA	hypothetical p	NA	L	Phage head completion protein (GPL)
COJEPEMI_(	COJEPE	0.10912	0.659652	hypothetical p	NA	0	YcxB-like protein
COJEPEMI_(	yaaA	0.10862	0.64332	Peroxide stres	NA	yaaA	Belongs to the UPF0246 family
COJEPEMI_(	cusR_2	0.10861	0.666406	Transcriptiona	NA	irlR	Transcriptional regulatory protein, C terminal
COJEPEMI_(	COJEPE	0.1081	0.609512	hypothetical p	NA	yvdD	Belongs to the LOG family
COJEPEMI_(	betI_1	0.10785	0.785112	HTH-type trans	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	0.10739	0.711295	hypothetical p	NA	0	diguanylate cyclase
COJEPEMI_(	COJEPE	0.10601	0.681686	hypothetical p	NA	gspH	Pfam:N_methyl_2
COJEPEMI_(	yidD	0.105	0.810489	Putative mem	NA	yidD	Could be involved in insertion of integral membrane proteins into the m
COJEPEMI_(	czcA_2	0.1041	0.728285	Cobalt-zinc-ca	NA	czcA	Belongs to the resistance-nodulation-cell division (RND) (TC 2.A.6) fam
COJEPEMI_(	COJEPE	0.10304	0.743265	hypothetical p	NA	0	Ferric uptake regulator family
COJEPEMI_(	ettA	0.103	0.653803	Energy-depen	NA	yjjK	COG0488 ATPase components of ABC transporters with duplicated ATP
COJEPEMI_(	glpG	0.10287	0.822547	Rhomboid pro	3.4.21.10	0	Rhomboid family
COJEPEMI_(	COJEPE	0.10203	0.89882	hypothetical p	NA	0	

COJEPEMI_(	putP	0.10086	0.675625	Sodium/prolin	NA	putP	Belongs to the sodium solute symporter (SSF) (TC 2.A.21) family
COJEPEMI_(	COJEPE	0.09941	0.755459	hypothetical p	NA	hslJ	Domain of unknown function (DUF4377)
COJEPEMI_(	COJEPE	0.09919	0.719004	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.09894	0.867718	putative HTH-t	NA	argP	LysR substrate binding domain
COJEPEMI_(	COJEPE	0.09857	0.813353	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	aqpZ2	0.09856	0.762157	Aquaporin Z 2	NA	aqpZ	Channel that permits osmotically driven movement of water in both di
COJEPEMI_(	COJEPE	0.09832	NA	hypothetical p	NA	0	
COJEPEMI_(	rubB_2	0.09824	0.80363	Rubredoxin-N/	1.18.1.1	rubB	Pyridine nucleotide-disulphide oxidoreductase
COJEPEMI_(	COJEPE	0.09802	0.667818	hypothetical p	NA	0	Belongs to the UPF0149 family
COJEPEMI_(	COJEPE	0.09729	0.799012	hypothetical p	NA	0	Copper resistance protein B precursor (CopB)
COJEPEMI_(	ydiO	0.09721	0.741392	putative BsuM	2.1.1.37	hgiDIIM	C-5 cytosine-specific DNA methylase
COJEPEMI_(	COJEPE	0.09627	0.658955	hypothetical p	NA	0	Histidine phosphatase superfamily (branch 1)
COJEPEMI_(	rhaS_2	0.09551	0.748557	HTH-type trans	NA	0	AraC-type transcriptional regulator N-terminus
COJEPEMI_(	COJEPE	0.09508	0.750318	hypothetical p	NA	0	Nitroreductase family
COJEPEMI_(	COJEPE	0.09446	0.916519	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	hiuH_1	0.09325	NA	5-hydroxyisour	3.5.2.17	uraH	Belongs to the transthyretin family. 5-hydroxyisourate hydrolase subfar
COJEPEMI_(	ppsR	0.09096	0.727772	Phosphoenolpy	2.7.11.33	ydiA	Bifunctional serine threonine kinase and phosphorylase involved in the
COJEPEMI_(	ssuB_1	0.09085	0.876277	Aliphatic sulfo	3.6.3.-	ssuB	Part of the ABC transporter complex SsuABC involved in aliphatic sulfor
COJEPEMI_(	truB	0.09056	0.778028	tRNA pseudou	5.4.99.25	truB	Responsible for synthesis of pseudouridine from uracil- 55 in the psi G(
COJEPEMI_(	mshA_1	0.0897	0.728274	D-inositol-3-pl	2.4.1.250	0	Glycosyltransferase Family 4
COJEPEMI_(	COJEPE	0.08945	0.785112	hypothetical p	NA	rsbP	Sigma factor PP2C-like phosphatases
COJEPEMI_(	COJEPE	0.0894	0.750318	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.08833	0.733058	hypothetical p	NA	0	ThiS family
COJEPEMI_(	nlhH_2	0.08791	0.886028	Carboxylestera	3.1.1.1	0	Pfam:DUF2424
COJEPEMI_(	hisA	0.08773	0.768075	1-(5-phosphor	5.3.1.16	hisA	1-(5-phosphoribosyl)-5- (5-phosphoribosylamino)methylideneamino im
COJEPEMI_(	COJEPE	0.08734	0.882744	hypothetical p	NA	O	Phage capsid scaffolding protein (GPO) serine peptidase
COJEPEMI_(	ppc	0.08723	0.794343	Phosphoenolpy	4.1.1.31	ppc	Forms oxaloacetate, a four-carbon dicarboxylic acid source for the trica
COJEPEMI_(	trmD	0.08667	0.743265	tRNA (guanine	2.1.1.228	trmD	Belongs to the RNA methyltransferase TrmD family
COJEPEMI_(	kgtP_1	0.08652	0.771964	Alpha-ketoglut	NA	kgtP_1	Major facilitator Superfamily
COJEPEMI_(	lptE	0.08625	0.764407	LPS-assembly	NA	lptE	Together with LptD, is involved in the assembly of lipopolysaccharide (L

COJEPEMI_(	recB	0.08618	0.702952	RecBCD enzym	3.1.11.5	recB	A helicase nuclease that prepares dsDNA breaks (DSB) for recombinati
COJEPEMI_(	gbpR	0.086	0.819407	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	hcaB_4	0.0844	0.810513	3-phenylpropic	1.3.1.87	0	NAD dependent epimerase/dehydratase family
COJEPEMI_(	ppiC	0.08409	0.8267	Peptidyl-prolyl	5.2.1.8	ppiC	PPIC-type PPIASE domain
COJEPEMI_(	COJEPE	0.08389	0.743265	hypothetical p	NA	0	
COJEPEMI_(	yijE	0.08283	0.902646	putative cystin	NA	ydfC	EamA-like transporter family
COJEPEMI_(	loiP	0.08276	0.770554	Metalloprotea	3.4.24.-	Z012_09	Peptidase family M48
COJEPEMI_(	COJEPE	0.08238	0.721783	putative protei	NA	romA	Beta-lactamase superfamily domain
COJEPEMI_(	thiO	0.08192	0.780128	Glycine oxidas	1.4.3.19	thiO	FAD dependent oxidoreductase
COJEPEMI_(	kdsC	0.08106	0.814667	3-deoxy-D-ma	3.1.3.45	kdsC	Involved in the biosynthesis of lipopolysaccharides (LPSs). Catalyzes the
COJEPEMI_(	COJEPE	0.08102	0.848598	hypothetical p	NA	0	Putative inner membrane exporter, YdcZ
COJEPEMI_(	COJEPE	0.08096	0.799693	IS5 family trar	NA	ykgD	Cupin
COJEPEMI_(	pdxH	0.08052	0.731778	Pyridoxine/pyr	1.4.3.5	pdxH	Catalyzes the oxidation of either pyridoxine 5'- phosphate (PNP) or pyri
COJEPEMI_(	COJEPE	0.08004	0.888467	hypothetical p	NA	0	Domain of Unknown Function with PDB structure (DUF3861)
COJEPEMI_(	COJEPE	0.07981	0.861382	hypothetical p	NA	0	BrnA antitoxin of type II toxin-antitoxin system
COJEPEMI_(	COJEPE	0.0798	0.785614	hypothetical p	NA	gspG	general secretion pathway protein
COJEPEMI_(	COJEPE	0.0795	0.860819	hypothetical p	NA	0	Putative inner membrane exporter, YdcZ
COJEPEMI_(	benM_1	0.07878	0.863525	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	ribH	0.07876	0.813041	6,7-dimethyl-8	2.5.1.78	ribH	Catalyzes the formation of 6,7-dimethyl-8- ribityllumazine by condensa
COJEPEMI_(	COJEPE	0.07816	0.746595	hypothetical p	NA	pilY1	Tfp pilus assembly protein tip-associated adhesin PilY1
COJEPEMI_(	gshA	0.07793	0.787196	Glutamate--cy	6.3.2.2	gshA	Belongs to the glutamate--cysteine ligase type 1 family. Type 1 subfam
COJEPEMI_(	nanT_2	0.07776	0.868686	Sialic acid trar	NA	0	Major facilitator Superfamily
COJEPEMI_(	COJEPE	0.07771	0.8267	hypothetical p	NA	mdcH	WYL domain
COJEPEMI_(	pepN_1	0.07702	0.818516	Aminopeptida	3.4.11.2	0	ERAP1-like C-terminal domain
COJEPEMI_(	COJEPE	0.0769	0.860819	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	cspV	0.07597	0.734298	Cold shock pro	NA	0	'Cold-shock' DNA-binding domain
COJEPEMI_(	smc_1	0.07529	0.844723	Chromosome p	NA	sbcC	Putative exonuclease SbcCD, C subunit
COJEPEMI_(	COJEPE	0.07515	0.768991	hypothetical p	NA	MA20_41	Protein of unknown function (DUF815)
COJEPEMI_(	COJEPE	0.0746	0.821113	hypothetical p	NA	VY92_06	Belongs to the pirin family
COJEPEMI_(	ndmA	0.07429	0.927187	Methylxanthin	1.14.13.1	0	Rieske [2Fe-2S] domain

COJEPEMI_(	aroF_2	0.07282	0.761936	Phospho-2-deh	2.5.1.54	aroF	Stereospecific condensation of phosphoenolpyruvate (PEP) and D-eryth
COJEPEMI_(	COJEPE	0.07215	0.860819	5'-nucleotidas	3.1.3.5	gph	HAD-hyrolase-like
COJEPEMI_(	nimR_2	0.07069	0.870533	HTH-type trans	NA	0	AraC-like ligand binding domain
COJEPEMI_(	COJEPE	0.06996	0.821643	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.06969	0.787196	hypothetical p	NA	0	Belongs to the UPF0307 family
COJEPEMI_(	rsgA	0.0685	0.86351	Small ribosom	3.6.1.-	rsgA	One of several proteins that assist in the late maturation steps of the f
COJEPEMI_(	COJEPE	0.06829	0.93423	hypothetical p	NA	srpH	Bacterial transferase hexapeptide (six repeats)
COJEPEMI_(	lysA	0.06797	0.831705	Diaminopimel	4.1.1.20	lysA	Specifically catalyzes the decarboxylation of meso- diaminopimelate (r
COJEPEMI_(	COJEPE	0.06781	0.843746	hypothetical p	NA	0	transcriptional regulator
COJEPEMI_(	COJEPE	0.06679	0.904002	hypothetical p	NA	0	Mechanosensitive ion channel
COJEPEMI_(	COJEPE	0.06628	0.856329	hypothetical p	NA	miaE	tRNA-(MS[2]IO[6]A)-hydroxylase (MiaE)
COJEPEMI_(	COJEPE	0.06596	0.865062	hypothetical p	NA	0	Glutathione-dependent formaldehyde-activating enzyme
COJEPEMI_(	dmlA	0.06549	0.914672	D-malate deh	1.1.1.83	dmlA	Isocitrate/isopropylmalate dehydrogenase
COJEPEMI_(	fimA	0.06522	0.91734	Fimbrial prote	NA	ppdD	Pilin (bacterial filament)
COJEPEMI_(	COJEPE	0.06393	0.895555	hypothetical p	NA	0	Transglycosylase SLT domain
COJEPEMI_(	tatA	0.0639	0.9342	Sec-independe	NA	tatA	Part of the twin-arginine translocation (Tat) system that transports lar
COJEPEMI_(	COJEPE	0.06363	0.803345	hypothetical p	NA	0	Acid phosphatase homologues
COJEPEMI_(	scpA	0.06355	0.798823	Segregation a	NA	scpA	Participates in chromosomal partition during cell division. May act via t
COJEPEMI_(	ylil	0.06329	0.79626	Aldose sugar d	1.1.5.-	ylil	Glucose / Sorbosone dehydrogenase
COJEPEMI_(	yfcA	0.06317	0.885543	putative mem	NA	0	membrane transporter protein
COJEPEMI_(	COJEPE	0.06314	0.860819	hypothetical p	NA	0	Thioesterase-like superfamily
COJEPEMI_(	COJEPE	0.06142	0.887127	hypothetical p	NA	0	Activator of Hsp90 ATPase homolog 1-like protein
COJEPEMI_(	nepI	0.0604	0.962706	Purine ribonuc	NA	0	Major facilitator Superfamily
COJEPEMI_(	bicA_1	0.05921	0.841302	Bicarbonate tr	NA	0	STAS domain
COJEPEMI_(	COJEPE	0.05908	0.77569	hypothetical p	NA	0	Rhodanese Homology Domain
COJEPEMI_(	phaC_1	0.05904	0.895794	Poly(3-hydroxy	2.3.1.-	phaC	Poly-beta-hydroxybutyrate polymerase (PhaC) N-terminus
COJEPEMI_(	dltA	0.05857	0.855634	D-alanine--D-a	6.2.1.54	dhbF	AMP-binding enzyme
COJEPEMI_(	COJEPE	0.05842	0.84288	hypothetical p	NA	0	Sh3 type 3 domain protein
COJEPEMI_(	COJEPE	0.05805	0.92648	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.05804	0.914992	hypothetical p	NA	yraP	BON domain

COJEPEMI_(	ispH	0.05789	0.940791	4-hydroxy-3-m	1.17.7.4	ispH	Catalyzes the conversion of 1-hydroxy-2-methyl-2-(E)- butenyl 4-diphos
COJEPEMI_(	COJEPE	0.05788	0.872751	hypothetical p	NA	MA20_4	Protein of unknown function (DUF1285)
COJEPEMI_(	aceE	0.05717	0.83883	Pyruvate dehy	1.2.4.1	aceE	Component of the pyruvate dehydrogenase (PDH) complex, that catalyz
COJEPEMI_(	COJEPE	0.05663	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.05594	0.921295	hypothetical p	NA	rluA	COG0564 Pseudouridylate synthases, 23S RNA-specific
COJEPEMI_(	gatB	0.05593	0.830324	Aspartyl/gluta	6.3.5.-	gatB	Allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(
COJEPEMI_(	COJEPE	0.05564	0.835196	hypothetical p	NA	0	Membrane
COJEPEMI_(	pdxB	0.05557	0.865601	Erythronate-4-	1.1.1.290	pdxB	Catalyzes the oxidation of erythronate-4-phosphate to 3- hydroxy-2-oxo
COJEPEMI_(	rlmJ	0.05461	0.834274	Ribosomal RN	2.1.1.266	rlmJ	Specifically methylates the adenine in position 2030 of 23S rRNA
COJEPEMI_(	COJEPE	0.05388	0.967254	putative TonB-	NA	0	TonB-dependent receptor
COJEPEMI_(	clsA	0.05348	0.881924	Cardiolipin syn	2.7.8.-	0	PLD-like domain
COJEPEMI_(	COJEPE	0.05304	0.860504	hypothetical p	NA	0	Protein of unknown function (DUF3298)
COJEPEMI_(	COJEPE	0.05261	0.823774	hypothetical p	NA	0	EcsC protein family
COJEPEMI_(	COJEPE	0.05239	0.93423	hypothetical p	NA	0	diguanylate cyclase
COJEPEMI_(	COJEPE	0.05215	0.91166	hypothetical p	NA	0	Conserved TM helix
COJEPEMI_(	hcaT	0.05204	0.859305	putative 3-phe	NA	hcaT	Major facilitator Superfamily
COJEPEMI_(	COJEPE	0.05152	0.921295	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.05144	0.811979	hypothetical p	NA	0	SnoaL-like domain
COJEPEMI_(	COJEPE	0.0507	0.927574	hypothetical p	NA	0	MerR HTH family regulatory protein
COJEPEMI_(	hdfR_4	0.04999	0.870563	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	0.04956	0.860502	hypothetical p	NA	0	Thioesterase superfamily
COJEPEMI_(	dapA_4	0.04936	0.92106	4-hydroxy-tetr	4.3.3.7	dapAch4	Dihydrodipicolinate synthetase family
COJEPEMI_(	gshB	0.04933	0.834951	Glutathione sy	6.3.2.3	gshB	Belongs to the prokaryotic GSH synthase family
COJEPEMI_(	COJEPE	0.04836	0.934673	hypothetical p	NA	0	Phage-related minor tail protein
COJEPEMI_(	COJEPE	0.04649	0.909735	hypothetical p	NA	gspI	Type II secretion system (T2SS), protein I
COJEPEMI_(	COJEPE	0.04527	0.871968	hypothetical p	NA	0	
COJEPEMI_(	rsmA	0.04472	0.870563	Ribosomal RN	2.1.1.182	ksgA	Specifically dimethylates two adjacent adenosines (A1518 and A1519)
COJEPEMI_(	COJEPE	0.04416	0.935095	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.0417	0.906535	hypothetical p	NA	0	Sel1-like repeats.
COJEPEMI_(	yqaA	0.04135	0.923236	Inner membra	NA	yqaA	SNARE associated Golgi protein

COJEPEMI_(	COJEPE	0.04005	0.911596	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	0.03991	0.934673	hypothetical p	NA	0	Mu transposase, C-terminal
COJEPEMI_(	ptsP	0.03959	0.86525	Phosphoenolpy	2.7.3.9	ptsP	Belongs to the PEP-utilizing enzyme family
COJEPEMI_(	COJEPE	0.03778	0.965812	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.03615	0.860819	hypothetical p	NA	ftsK	Ftsk_gamma
COJEPEMI_(	dnaN	0.03482	0.901393	Beta sliding cl	NA	dnaN	Confers DNA tethering and processivity to DNA polymerases and other
COJEPEMI_(	ubiB_2	0.03428	0.93491	protein kinase	2.7.-.-	0	ABC1 family
COJEPEMI_(	COJEPE	0.03323	0.950307	hypothetical p	NA	0	
COJEPEMI_(	aidA_3	0.03322	0.92801	Quorum-quenc	NA	0	Acetyl xylan esterase (AXE1)
COJEPEMI_(	nfsB	0.03296	0.919043	Oxygen-insens	1.-.-.-	nfnB	nitroreductase
COJEPEMI_(	smpB	0.0327	0.886949	SsrA-binding p	NA	smpB	the 2 termini fold to resemble tRNA(Ala) and it encodes a tag peptide ,
COJEPEMI_(	COJEPE	0.03228	0.892647	hypothetical p	NA	ykuD	ErfK YbiS YcfS YnhG family protein
COJEPEMI_(	hemW	0.03101	0.959074	Heme chapero	NA	yggW	Involved in the biosynthesis of porphyrin-containing compound
COJEPEMI_(	COJEPE	0.0309	0.957485	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.02967	0.957355	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.02935	0.981416	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2239)
COJEPEMI_(	COJEPE	0.02874	0.909735	hypothetical p	NA	0	
COJEPEMI_(	mltB	0.02805	0.926892	Membrane-bo	4.2.2.-	mltB	Transglycosylase SLT domain
COJEPEMI_(	COJEPE	0.02782	0.929538	hypothetical p	NA	yegH	Transporter associated domain
COJEPEMI_(	rhtC_4	0.02748	0.971961	Threonine effl	NA	0	LysE type translocator
COJEPEMI_(	COJEPE	0.02724	0.970746	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.02703	0.970254	hypothetical p	NA	0	COG3209 Rhs family protein
COJEPEMI_(	tgnA	0.02449	0.963547	Flavin-depend	1.5.1.36	ntaB	Flavin reductase like domain
COJEPEMI_(	recG	0.02434	0.937941	ATP-dependen	3.6.4.12	recG	Critical role in recombination and DNA repair. Helps process Holliday ju
COJEPEMI_(	surA	0.02223	0.953296	Chaperone Sur	5.2.1.8	surA	Chaperone involved in the correct folding and assembly of outer memb
COJEPEMI_(	COJEPE	0.02195	0.971321	hypothetical p	NA	0	
COJEPEMI_(	glsA	0.02139	0.971321	Glutaminase	3.5.1.2	glsA	Belongs to the glutaminase family
COJEPEMI_(	COJEPE	0.02046	0.961203	putative HTH-t	NA	0	helix_turn_helix, arabinose operon control protein
COJEPEMI_(	COJEPE	0.01992	0.96528	hypothetical p	NA	0	Transcriptional regulator
COJEPEMI_(	COJEPE	0.01968	0.974953	putative prote	NA	yhiN	HI0933-like protein

COJEPEMI_(	gloB_2	0.01952	0.930201	Hydroxyacylglu	3.1.2.6	gloB	Thiolesterase that catalyzes the hydrolysis of S-D- lactoyl-glutathione t
COJEPEMI_(	clpS	0.01915	0.930913	ATP-dependen	NA	clpS	Involved in the modulation of the specificity of the ClpAP-mediated ATF
COJEPEMI_(	COJEPE	0.01816	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	syrM1	0.0176	0.965812	HTH-type trans	NA	0	Transcriptional regulator
COJEPEMI_(	uppP	0.01738	0.964441	Undecaprenyl-	3.6.1.27	uppP	Catalyzes the dephosphorylation of undecaprenyl diphosphate (UPP). C
COJEPEMI_(	COJEPE	0.01679	0.960678	hypothetical p	NA	0	ASCH domain
COJEPEMI_(	COJEPE	0.01664	0.935774	hypothetical p	NA	0	Lipopolysaccharide assembly protein A domain
COJEPEMI_(	leuO	0.01438	0.974953	HTH-type trans	NA	0	Bacterial regulatory helix-turn-helix protein, lysR family
COJEPEMI_(	acr3_2	0.01391	0.989398	Arsenical-resis	NA	arsB	Sodium Bile acid symporter family
COJEPEMI_(	COJEPE	0.01364	0.964297	5'-nucleotidas	3.1.3.5	idgB	HAD-hyrolase-like
COJEPEMI_(	metG	0.01314	0.972443	Methionine--tI	6.1.1.10	metG	Is required not only for elongation of protein synthesis but also for the i
COJEPEMI_(	COJEPE	0.01249	0.990695	hypothetical p	NA	0	
COJEPEMI_(	dmdC_4	0.01162	0.977706	3-methylmerc	1.3.8.-	0	Acyl-CoA dehydrogenase N terminal
COJEPEMI_(	COJEPE	0.0116	0.980652	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.00898	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.00878	0.986785	hypothetical p	NA	ychJ	SEC-C motif
COJEPEMI_(	prfB	0.00829	0.981507	Peptide chain	NA	prfB	Peptide chain release factor 2 directs the termination of translation in
COJEPEMI_(	COJEPE	0.00802	0.991855	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.00794	0.982716	hypothetical p	NA	ypfJ	Putative neutral zinc metallopeptidase
COJEPEMI_(	COJEPE	0.00772	0.992718	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.00705	0.993174	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.00675	0.981416	hypothetical p	NA	chrA	Chromate transporter
COJEPEMI_(	yejF	0.00617	0.986785	putative ABC t	NA	0	Belongs to the ABC transporter superfamily
COJEPEMI_(	murU	0.00593	0.985728	N-acetylmurar	2.7.7.99	rmlA	COG1208 Nucleoside-diphosphate-sugar pyrophosphorylase involved in
COJEPEMI_(	COJEPE	0.00551	0.985857	hypothetical p	NA	Z012_08	TPM domain
COJEPEMI_(	COJEPE	0.00543	0.984328	hypothetical p	NA	0	response to abiotic stimulus
COJEPEMI_(	COJEPE	0.00524	0.989345	hypothetical p	NA	0	Polyketide cyclase / dehydrase and lipid transport
COJEPEMI_(	COJEPE	0.00516	0.992581	hypothetical p	NA	0	Domain of unknown function (DUF4130
COJEPEMI_(	COJEPE	0.00503	0.985728	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	0.00467	0.990695	putative HTH-t	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term

COJEPEMI_(	COJEPE	0.00394	0.992718	hypothetical p	NA	0	PFAM ERF family protein
COJEPEMI_(	ackA	0.00392	0.986785	Acetate kinase	2.7.2.1	ackA	Catalyzes the formation of acetyl phosphate from acetate and ATP. Car
COJEPEMI_(	COJEPE	0.00365	0.995747	hypothetical p	NA	0	Putative 3TM holin, Phage_holin_3
COJEPEMI_(	thcD	0.00311	0.995401	Rhodocoxin re	1.18.1.-	0	Reductase C-terminal
COJEPEMI_(	mlaF	0.003	0.994623	Intermembran	3.6.3.-	mlaF	ATPases associated with a variety of cellular activities
COJEPEMI_(	rsmE_1	0.00233	0.9956	Ribosomal RN	2.1.1.193	rsmE1	Specifically methylates the N3 position of the uracil ring of uridine 149
COJEPEMI_(	COJEPE	0.00211	0.994099	hypothetical p	NA	0	Putative serine esterase (DUF676)
COJEPEMI_(	COJEPE	0.00209	0.994623	Adenine deam	3.5.4.2	add	Catalyzes the hydrolytic deamination of adenine to hypoxanthine. Plays
COJEPEMI_(	COJEPE	0.00162	0.995681	hypothetical p	NA	0	helix_turn_helix multiple antibiotic resistance protein
COJEPEMI_(	tusD	0.00057	0.998858	Sulfurtransfer	2.8.1.-	tusD	DsrE/DsrF-like family
COJEPEMI_(	COJEPE	0.00017	0.999088	hypothetical p	NA	PREP	Peptidase M16C associated
COJEPEMI_(	murG	-0.00125	0.995681	UDP-N-acetylg	2.4.1.227	murG	Cell wall formation. Catalyzes the transfer of a GlcNAc subunit on unde
COJEPEMI_(	cydB_1	-0.00125	0.998061	Cytochrome bo	7.1.1.7	cydB	oxidase, subunit
COJEPEMI_(	parC	-0.00159	0.995401	DNA topoisom	5.6.2.2	parC	Topoisomerase IV is essential for chromosome segregation. It relaxes s
COJEPEMI_(	tam	-0.00255	0.995681	Trans-aconitat	2.1.1.144	bioC	Converts the free carboxyl group of a malonyl-thioester to its methyl es
COJEPEMI_(	COJEPE	-0.00412	0.993099	Baeyer-Villige	1.14.13.-	0	flavoprotein involved in K transport
COJEPEMI_(	rplT	-0.00442	0.992634	50S ribosomal	NA	rplT	Binds directly to 23S ribosomal RNA and is necessary for the in vitro as
COJEPEMI_(	uctC_1	-0.00465	0.994099	Acetyl-CoA:oxa	2.8.3.19	caiB	CoA-transferase family III
COJEPEMI_(	calB_1	-0.00505	0.991495	Coniferyl aldeh	1.2.1.68	calB	belongs to the aldehyde dehydrogenase family
COJEPEMI_(	metI	-0.00544	0.993027	D-methionine	NA	metI	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-0.00591	NA	hypothetical p	NA	0	AraC-type transcriptional regulator N-terminus
COJEPEMI_(	proP_1	-0.00632	0.994078	Proline/betain	NA	proP	Sugar (and other) transporter
COJEPEMI_(	COJEPE	-0.0071	NA	hypothetical p	NA	0	Domain of unknown function (DUF3330)
COJEPEMI_(	COJEPE	-0.00994	0.970254	hypothetical p	NA	0	TPM domain
COJEPEMI_(	outO	-0.01012	0.980663	Type 4 prepilir	NA	pilD	Cleaves type-4 fimbrial leader sequence and methylates the N-termina
COJEPEMI_(	pncA	-0.01052	0.973521	Nicotinamidas	3.5.1.19	pncA	Isochorismatase family
COJEPEMI_(	rlpA	-0.01087	0.985728	Endolytic pept	4.2.2.-	rlpA	Lytic transglycosylase with a strong preference for naked glycan strand
COJEPEMI_(	bshA	-0.01102	0.970746	N-acetyl-alpha	2.4.1.-	0	Glycosyl transferases group 1
COJEPEMI_(	hfq	-0.01135	0.980663	RNA-binding p	NA	hfq	RNA chaperone that binds small regulatory RNA (sRNAs) and mRNAs t
COJEPEMI_(	dmlR_7	-0.01179	0.964441	HTH-type trans	NA	0	transcriptional regulator

COJEPEMI_(	yidC	-0.01254	0.971321	Membrane prc	NA	yidC	Required for the insertion and or proper folding and or complex format
COJEPEMI_(	COJEPE	-0.01378	0.985728	hypothetical p	NA	0	Parallel beta-helix repeats
COJEPEMI_(	mro	-0.01477	0.962812	Aldose 1-epim	5.1.3.3	galM	Converts alpha-aldose to the beta-anomer
COJEPEMI_(	blc_1	-0.01639	0.977984	Outer membra	NA	blc	Lipocalin-like domain
COJEPEMI_(	rplM	-0.01756	0.963716	50S ribosomal	NA	rplM	This protein is one of the early assembly proteins of the 50S ribosomal
COJEPEMI_(	plcN_1	-0.01796	0.976287	Non-hemolytic	3.1.4.3	plcN	Phosphoesterase family
COJEPEMI_(	epmA	-0.01802	0.955744	Elongation fac	6.3.1.-	epmA	tRNA synthetases class II (D, K and N)
COJEPEMI_(	rpoN	-0.02054	0.95664	RNA polymera	NA	rpoN	Sigma factors are initiation factors that promote the attachment of RN
COJEPEMI_(	folD	-0.02072	0.945041	Bifunctional p	NA	folD	Catalyzes the oxidation of 5,10- methylenetetrahydrofolate to 5,10-me
COJEPEMI_(	COJEPE	-0.02074	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.02096	0.927187	Iron-sulfur clus	NA	mrp	Binds and transfers iron-sulfur (Fe-S) clusters to target apoproteins. Ca
COJEPEMI_(	COJEPE	-0.02171	0.945413	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.02267	0.966909	hypothetical p	NA	0	DJ-1/PfpI family
COJEPEMI_(	acsA_2	-0.02334	0.951986	Acetyl-coenzyr	6.2.1.1	acsA	Catalyzes the conversion of acetate into acetyl-CoA (AcCoA), an essenti
COJEPEMI_(	COJEPE	-0.02369	0.955095	hypothetical p	NA	0	Endonuclease related to archaeal Holliday junction resolvase
COJEPEMI_(	sucC	-0.02386	0.925846	Succinate--Co/	6.2.1.5	sucC	Succinyl-CoA synthetase functions in the citric acid cycle (TCA), couplin
COJEPEMI_(	hemH	-0.02393	0.925466	Ferrochelatase	4.99.1.1	hemH	Catalyzes the ferrous insertion into protoporphyrin IX
COJEPEMI_(	COJEPE	-0.02401	0.970746	hypothetical p	NA	MA20_25	KR domain
COJEPEMI_(	moaA	-0.02497	0.935095	GTP 3',8-cycla	4.1.99.22	moaA	Catalyzes the cyclization of GTP to (8S)-3',8-cyclo-7,8- dihydroguanosin
COJEPEMI_(	COJEPE	-0.0254	0.963702	hypothetical p	NA	0	
COJEPEMI_(	trpB_2	-0.02546	0.914141	Tryptophan sy	4.2.1.20	trpB2	The beta subunit is responsible for the synthesis of L- tryptophan from
COJEPEMI_(	COJEPE	-0.02547	0.953296	hypothetical p	NA	0	Domain of unknown function (DUF4850)
COJEPEMI_(	COJEPE	-0.02567	0.962706	hypothetical p	NA	fadL	long-chain fatty acid transport protein
COJEPEMI_(	COJEPE	-0.02582	0.951177	hypothetical p	NA	0	hemolysin activation secretion protein
COJEPEMI_(	COJEPE	-0.02631	0.970772	hypothetical p	NA	ygiF	CYTH
COJEPEMI_(	ispF	-0.02653	0.927139	2-C-methyl-D-	4.6.1.12	ispF	Involved in the biosynthesis of isopentenyl diphosphate (IPP) and dimet
COJEPEMI_(	mtgA	-0.02667	0.945041	Biosynthetic p	2.4.1.129	mtgA	Peptidoglycan polymerase that catalyzes glycan chain elongation from
COJEPEMI_(	COJEPE	-0.02707	0.9133	Dihydrolipoylly	2.3.1.12	aceF	acetyltransferase component of pyruvate dehydrogenase complex
COJEPEMI_(	COJEPE	-0.02714	0.958294	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.02734	0.962706	hypothetical p	NA	0	

COJEPEMI_(	wax-dg	-0.02855	0.923236	O-acyltransfer	2.3.1.20	atfA1	Protein of unknown function (DUF1298)
COJEPEMI_(	polA	-0.02874	0.909735	DNA polymera	2.7.7.7	polA	In addition to polymerase activity, this DNA polymerase exhibits 5'-3' e
COJEPEMI_(	COJEPE	-0.02898	0.955953	hypothetical p	NA	eamA1	EamA-like transporter family
COJEPEMI_(	lolD	-0.02946	0.94157	Lipoprotein-re	3.6.3.-	lolD	Part of the ABC transporter complex LolCDE involved in the translocatio
COJEPEMI_(	pdxJ	-0.03021	0.923236	Pyridoxine 5'-p	2.6.99.2	pdxJ	Catalyzes the complicated ring closure reaction between the two acycli
COJEPEMI_(	dapA_2	-0.03182	0.920341	4-hydroxy-tetr	4.3.3.7	dapA	Catalyzes the condensation of (S)-aspartate-beta- semialdehyde (S)-AS
COJEPEMI_(	soxR	-0.03183	0.969782	Redox-sensitiv	NA	soxR	helix_turn_helix, mercury resistance
COJEPEMI_(	ftsY	-0.03212	0.919043	Signal recogni	NA	ftsY	Involved in targeting and insertion of nascent membrane proteins into
COJEPEMI_(	COJEPE	-0.03262	0.903586	putative prote	NA	aarF	ABC1 family
COJEPEMI_(	rcsC_4	-0.03279	0.961803	Sensor histidir	2.7.13.3	chpA	Signal transducing histidine kinase, homodimeric domain
COJEPEMI_(	COJEPE	-0.03312	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.03318	0.920284	hypothetical p	NA	0	
COJEPEMI_(	hcaR_1	-0.03338	0.939937	Hca operon tra	NA	0	LysR substrate binding domain
COJEPEMI_(	mmgC_	-0.03347	0.952404	Acyl-CoA dehy	1.3.99.-	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	nlpD	-0.03378	0.903881	Murein hydrol	NA	nlpD	Peptidase family M23
COJEPEMI_(	COJEPE	-0.03432	0.945413	hypothetical p	NA	gpD	Phage late control gene D protein (GPD)
COJEPEMI_(	COJEPE	-0.03628	0.875729	putative HTH-t	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	COJEPE	-0.03685	0.865601	hypothetical p	NA	0	CorA-like Mg2+ transporter protein
COJEPEMI_(	COJEPE	-0.03751	0.889911	putative meta	3.-.-.-	blh	Metallo-beta-lactamase superfamily
COJEPEMI_(	COJEPE	-0.03896	0.894143	Tn3 family tra	NA	MA20_18	Lytic murein transglycosylase
COJEPEMI_(	pilT_1	-0.0397	0.9133	Twitching mot	NA	pilT	twitching motility protein
COJEPEMI_(	COJEPE	-0.04007	NA	Single-strande	NA	0	Single-strand binding protein family
COJEPEMI_(	gltB	-0.04023	0.89837	Glutamate syr	1.4.1.13	gltB	Glutamate synthase central domain
COJEPEMI_(	cnbA	-0.04073	0.882744	Chloronitrober	1.7.1.16	pnbA	Nitroreductase family
COJEPEMI_(	argJ	-0.04075	0.870563	Arginine biosy	NA	argJ	Catalyzes two activities which are involved in the cyclic version of argin
COJEPEMI_(	fadA_2	-0.04087	0.898974	3-ketoacyl-CoA	2.3.1.16	fadA	Catalyzes the final step of fatty acid oxidation in which acetyl-CoA is re
COJEPEMI_(	COJEPE	-0.042	0.904264	hypothetical p	NA	0	Glutathione-dependent formaldehyde-activating enzyme
COJEPEMI_(	srpG	-0.04284	0.839657	Cysteine synth	2.5.1.47	cysK	Belongs to the cysteine synthase cystathionine beta- synthase family
COJEPEMI_(	ydhP_2	-0.04297	0.90669	Inner membra	NA	araJ	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-0.04447	0.922163	hypothetical p	NA	ybdF	YjbR

COJEPEMI_(	COJEPE	-0.0445	0.865062	hypothetical p	NA	0	
COJEPEMI_(	ompW	-0.0445	0.961109	Outer membra	NA	ompW	OmpW family
COJEPEMI_(	COJEPE	-0.04464	0.879734	hypothetical p	NA	0	Acyl-ACP thioesterase
COJEPEMI_(	COJEPE	-0.04524	0.886108	hypothetical p	NA	yebS	Paraquat-inducible protein A
COJEPEMI_(	COJEPE	-0.04644	0.9133	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	rnd_2	-0.04668	0.846255	Ribonuclease I	3.1.13.5	rnd	HRDC domain
COJEPEMI_(	hxlR_2	-0.04734	0.894729	HTH-type trans	NA	0	HxlR-like helix-turn-helix
COJEPEMI_(	add	-0.04761	0.88085	Adenosine dea	3.5.4.4	add	Adenosine/AMP deaminase
COJEPEMI_(	pitA_2	-0.04826	0.887127	Low-affinity in	NA	pitA	Phosphate transporter family
COJEPEMI_(	yciB	-0.04885	0.887237	Intracellular se	NA	ispZ	probably involved in intracellular septation
COJEPEMI_(	COJEPE	-0.04899	0.902599	hypothetical p	NA	0	Ribonuclease toxin, BrnT, of type II toxin-antitoxin system
COJEPEMI_(	wbpE	-0.04902	0.894143	UDP-2-acetam	2.6.1.98	wbpE	Belongs to the DegT DnrJ EryC1 family
COJEPEMI_(	naiP_1	-0.05061	0.863721	Putative niacir	NA	naiP	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-0.05062	0.884713	hypothetical p	NA	0	RDD family
COJEPEMI_(	yafJ	-0.05081	0.805082	Putative glutar	2.4.2.-	yafJ	glutamine amidotransferase
COJEPEMI_(	pgaA	-0.05088	0.914992	Poly-beta-1,6-	NA	hmsH	Exports the biofilm adhesin polysaccharide poly-beta- 1,6-N-acetyl-D-g
COJEPEMI_(	COJEPE	-0.05188	0.855831	hypothetical p	NA	gst	Glutathione S-transferase, N-terminal domain
COJEPEMI_(	bicA_2	-0.05224	0.873784	Bicarbonate tr	NA	0	STAS domain
COJEPEMI_(	nlhH_1	-0.05458	0.847986	Carboxylestera	3.1.1.1	estA	Steryl acetyl hydrolase
COJEPEMI_(	COJEPE	-0.05619	0.817198	Epimerase fan	NA	sulA	Domain of unknown function (DUF1731)
COJEPEMI_(	greA	-0.05678	0.818516	Transcription e	NA	greA	Necessary for efficient RNA polymerase transcription elongation past t
COJEPEMI_(	sthA	-0.05701	0.832669	Soluble pyridir	1.6.1.1	sthA	Soluble pyridine nucleotide transhydrogenase
COJEPEMI_(	recF_1	-0.05723	0.849744	DNA replicatio	NA	recF	it is required for DNA replication and normal SOS inducibility. RecF bin
COJEPEMI_(	COJEPE	-0.0577	0.818177	putative prote	NA	yrbA	Belongs to the BolA IbaG family
COJEPEMI_(	COJEPE	-0.05793	0.820449	hypothetical p	NA	0	COG3209 Rhs family protein
COJEPEMI_(	COJEPE	-0.05886	0.851734	hypothetical p	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	yddE_2	-0.05924	0.862047	putative isome	5.1.-.-	0	Proline racemase
COJEPEMI_(	COJEPE	-0.05967	0.881891	hypothetical p	NA	Z012_04	Protein of unknown function (DUF3298)
COJEPEMI_(	COJEPE	-0.06028	NA	hypothetical p	NA	0	
COJEPEMI_(	gph	-0.06125	0.829141	Phosphoglycol	3.1.3.18	gph	HAD-hyrolase-like

COJEPEMI_(	cpnA	-0.06152	0.925234	Cyclopentanol	1.1.1.163	pldh-t	KR domain
COJEPEMI_(	kbp	-0.06199	0.8321	Potassium bin	NA	ygaU	BON domain
COJEPEMI_(	COJEPE	-0.06213	0.822084	hypothetical p	NA	0	Outer membrane protein transport protein (OMPP1/FadL/TodX)
COJEPEMI_(	dmlR_2	-0.06233	0.848976	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	hdfR_3	-0.06253	0.921367	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	pstB	-0.06285	0.862147	Phosphate imp	7.3.2.1	pstB	Part of the ABC transporter complex PstSACB involved in phosphate imp
COJEPEMI_(	COJEPE	-0.06309	0.89901	hypothetical p	NA	0	TnsA endonuclease N terminal
COJEPEMI_(	COJEPE	-0.0632	0.905299	hypothetical p	NA	acpT	4'-phosphopantetheinyl transferase superfamily
COJEPEMI_(	COJEPE	-0.06372	0.925068	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	gsiA	-0.06454	0.881891	Glutathione im	7.4.2.10	gsiA	Belongs to the ABC transporter superfamily
COJEPEMI_(	glpD	-0.06528	0.830784	Aerobic glycer	1.1.5.3	glpD	C-terminal domain of alpha-glycerophosphate oxidase
COJEPEMI_(	trmL	-0.06529	0.820449	tRNA (cytidine	2.1.1.207	trmL	Methylates the ribose at the nucleotide 34 wobble position in the two l
COJEPEMI_(	COJEPE	-0.06571	0.786348	Single-strande	NA	ssb	Plays an important role in DNA replication, recombination and repair. B
COJEPEMI_(	mexB_1	-0.06641	0.761936	Multidrug resi	NA	acrB	AcrB/AcrD/AcrF family
COJEPEMI_(	thrC	-0.06673	0.853805	Threonine synt	4.2.3.1	thrC	Catalyzes the gamma-elimination of phosphate from L- phosphohomos
COJEPEMI_(	yffB	-0.06683	0.891187	Protein YffB	NA	yffB	Belongs to the ArsC family
COJEPEMI_(	ubiC	-0.06693	0.865726	Chorismate py	4.1.3.40	ubiC	Removes the pyruvyl group from chorismate, with concomitant aromat
COJEPEMI_(	pgrR_2	-0.06808	0.84409	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	ampG	-0.06821	0.881891	Anhydromurop	NA	0	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-0.06821	0.871537	hypothetical p	NA	0	
COJEPEMI_(	rarA	-0.06826	0.817301	Replication-as	NA	rarA	COG2256 ATPase related to the helicase subunit of the Holliday junctio
COJEPEMI_(	COJEPE	-0.06975	0.750318	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.07024	NA	hypothetical p	NA	0	Protein of unknown function (DUF1656)
COJEPEMI_(	COJEPE	-0.07033	0.895541	hypothetical p	NA	0	Domain of unknown function (DUF4442)
COJEPEMI_(	moaC	-0.07171	0.807467	Cyclic pyranop	NA	moaC	Catalyzes the conversion of (8S)-3',8-cyclo-7,8- dihydroguanosine 5'-trip
COJEPEMI_(	COJEPE	-0.07187	0.854229	hypothetical p	NA	ureJ	HupE / UreJ protein
COJEPEMI_(	allS	-0.07195	0.853167	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	cat1	-0.07219	0.823068	Succinyl-CoA:c	2.8.3.-	cat1	acetyl-CoA hydrolase
COJEPEMI_(	COJEPE	-0.07234	0.84524	hypothetical p	NA	0	Psort location Cytoplasmic, score 8.96
COJEPEMI_(	COJEPE	-0.07238	0.761936	hypothetical p	NA	0	Fels-1 Prophage Protein-like

COJEPEMI_(	ahr	-0.07304	0.844723	Aldehyde redu	1.1.1.2	yjgB	Alcohol dehydrogenase GroES-like domain
COJEPEMI_(	COJEPE	-0.07475	0.895555	hypothetical p	NA	0	Sulphur transport
COJEPEMI_(	gabR_1	-0.07483	0.926386	HTH-type trans	NA	0	helix_turn_helix gluconate operon transcriptional repressor
COJEPEMI_(	frmA	-0.07525	0.865062	S-(hydroxymet	1.1.1.284	adhC	Belongs to the zinc-containing alcohol dehydrogenase family. Class-III s
COJEPEMI_(	COJEPE	-0.07576	0.761369	hypothetical p	NA	0	Transcriptional regulator
COJEPEMI_(	COJEPE	-0.07803	0.777911	putative HTH-t	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	COJEPE	-0.07823	0.873725	hypothetical p	NA	0	N-acetylmuramidase
COJEPEMI_(	COJEPE	-0.07967	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.08057	0.82869	Hydroxycinnan	4.1.2.41	ech	Belongs to the enoyl-CoA hydratase isomerase family
COJEPEMI_(	sutR_1	-0.08057	0.887127	HTH-type trans	NA	sinR	Cro/C1-type HTH DNA-binding domain
COJEPEMI_(	mrkD_2	-0.08131	0.87851	Fimbria adhes	NA	0	Fimbrial protein
COJEPEMI_(	bioD1	-0.08191	0.840075	ATP-dependen	6.3.3.3	bioD	Catalyzes a mechanistically unusual reaction, the ATP- dependent inser
COJEPEMI_(	ispA	-0.08202	0.750346	Farnesyl dipho	2.5.1.10	ispA	Belongs to the FPP GGPP synthase family
COJEPEMI_(	COJEPE	-0.08328	0.724463	Nitronate mor	1.13.12.-	0	Nitronate monooxygenase
COJEPEMI_(	COJEPE	-0.08349	0.747624	hypothetical p	NA	pbpG	Belongs to the peptidase S11 family
COJEPEMI_(	nuoN	-0.08447	0.792459	NADH-quinone	7.1.1.-	nuoN	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) c
COJEPEMI_(	COJEPE	-0.08519	0.914992	hypothetical p	NA	0	Zinc-dependent metalloprotease
COJEPEMI_(	czcS	-0.08529	0.788433	Sensor protein	2.7.13.3	irlS	Member of a two-component regulatory system
COJEPEMI_(	COJEPE	-0.08584	0.8321	hypothetical p	NA	0	Forkhead associated domain
COJEPEMI_(	COJEPE	-0.08584	0.664771	hypothetical p	NA	yegP	Domain of unknown function (DUF1508)
COJEPEMI_(	COJEPE	-0.08636	0.822547	hypothetical p	NA	comE	Prokaryotic N-terminal methylation motif
COJEPEMI_(	yqgF	-0.08653	0.725658	Putative pre-1	3.1.-.-	yqgF	Could be a nuclease involved in processing of the 5'-end of pre-16S rRN
COJEPEMI_(	ilvI	-0.08731	0.775299	Acetolactate s	2.2.1.6	ilvI	acetolactate synthase
COJEPEMI_(	fabG_5	-0.08732	0.747269	3-oxoacyl-[acy	1.1.1.100	fabG	KR domain
COJEPEMI_(	glmM	-0.08818	0.727777	Phosphoglucos	5.4.2.10	glmM	Catalyzes the conversion of glucosamine-6-phosphate to glucosamine-1
COJEPEMI_(	yjdF	-0.08836	0.847826	Inner membra	NA	yjdF	Predicted membrane protein (DUF2238)
COJEPEMI_(	ompA	-0.08926	0.857312	Outer membra	NA	0	OmpA family
COJEPEMI_(	ubiB_1	-0.09051	0.865062	protein kinase	2.7.-.-	0	ABC1 family
COJEPEMI_(	mdtA_2	-0.09193	0.762922	Multidrug resi	NA	nolF	Belongs to the membrane fusion protein (MFP) (TC 8.A.1) family
COJEPEMI_(	crt	-0.09221	0.813353	Short-chain-er	4.2.1.150	0	Belongs to the enoyl-CoA hydratase isomerase family

COJEPEMI_(	pgaB	-0.09268	0.760655	Poly-beta-1,6-	3.5.1.-	pgaB	Hypothetical glycosyl hydrolase family 13
COJEPEMI_(	COJEPE	-0.09376	0.904002	hypothetical p	NA	0	
COJEPEMI_(	yceD	-0.09422	0.604422	Large ribosom	NA	yceD	Uncharacterized ACR, COG1399
COJEPEMI_(	COJEPE	-0.09453	0.836061	hypothetical p	NA	puuE	Polysaccharide deacetylase
COJEPEMI_(	spoT	-0.09527	0.666449	Bifunctional (p	NA	spoT	HD domain
COJEPEMI_(	COJEPE	-0.09545	0.863721	hypothetical p	NA	0	
COJEPEMI_(	ahpF_2	-0.09574	0.74579	Alkyl hydroper	1.8.1.-	ahpF	Alkyl hydroperoxide reductase
COJEPEMI_(	abaQ	-0.09615	0.838051	Quinolone resi	NA	IV02_106	COG0477 Permeases of the major facilitator superfamily
COJEPEMI_(	yfhL	-0.09663	0.925768	Ferredoxin Yfh	NA	yfhL	4Fe-4S dicluster domain
COJEPEMI_(	lpxC	-0.0967	0.792916	UDP-3-O-acyl-	3.5.1.108	lpxC	Catalyzes the hydrolysis of UDP-3-O-myristoyl-N- acetylglucosamine to
COJEPEMI_(	COJEPE	-0.09699	0.813817	hypothetical p	NA	0	Sugar (and other) transporter
COJEPEMI_(	fkpB	-0.09714	0.775236	FKBP-type 16 k	5.2.1.8	fkpB	Peptidyl-prolyl cis-trans
COJEPEMI_(	rseP	-0.09715	0.6872	Regulator of s	3.4.24.-	rseP	zinc metalloprotease
COJEPEMI_(	trpB_1	-0.0972	0.764423	Tryptophan sy	4.2.1.20	trpB	The beta subunit is responsible for the synthesis of L- tryptophan from
COJEPEMI_(	actP_1	-0.09755	0.778028	Cation/acetate	NA	actP	Belongs to the sodium solute symporter (SSF) (TC 2.A.21) family
COJEPEMI_(	rnr	-0.09809	0.684331	Ribonuclease I	3.1.13.1	rnr	3'-5' exoribonuclease that releases 5'-nucleoside monophosphates and
COJEPEMI_(	COJEPE	-0.09867	0.80719	hypothetical p	NA	0	Domian of unknown function (DUF4951)
COJEPEMI_(	COJEPE	-0.099	0.761369	hypothetical p	NA	0	NUDIX domain
COJEPEMI_(	COJEPE	-0.09913	0.915713	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.09919	0.729311	hypothetical p	NA	0	D-alanyl-D-alanine carboxypeptidase
COJEPEMI_(	recO	-0.09966	0.769175	DNA repair pro	NA	recO	Belongs to the RecO family
COJEPEMI_(	COJEPE	-0.09969	NA	hypothetical p	NA	0	Evidence 3 Function proposed based on presence of conserved amino a
COJEPEMI_(	fabG_4	-0.10027	0.838051	3-oxoacyl-[acy	1.1.1.100	IV02_097	KR domain
COJEPEMI_(	COJEPE	-0.10067	0.790556	hypothetical p	NA	0	
COJEPEMI_(	mltF_2	-0.10107	0.78362	Membrane-bo	4.2.2.-	mltF	Transglycosylase SLT domain
COJEPEMI_(	COJEPE	-0.10184	0.887237	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ftsN	-0.10284	0.602943	Cell division pr	NA	ftsN	Sporulation related domain
COJEPEMI_(	COJEPE	-0.10364	0.799693	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.10376	0.556895	Putative trans	NA	perM	AI-2E family transporter
COJEPEMI_(	COJEPE	-0.10384	0.909735	hypothetical p	NA	#N/A	#N/A

COJEPEMI_(	dddP	-0.10441	0.794343	Dimethlysulfo	4.4.1.3	dddP	Creatinase/Prolidase N-terminal domain
COJEPEMI_(	tynA	-0.10495	0.778388	Primary amine	1.4.3.21	tynA	Copper amine oxidase, enzyme domain
COJEPEMI_(	COJEPE	-0.1068	0.882744	hypothetical p	NA	0	outer membrane porin, OprD family
COJEPEMI_(	yybR_1	-0.10728	0.817283	putative HTH-t	NA	0	HxlR-like helix-turn-helix
COJEPEMI_(	yceI	-0.10737	0.634383	Protein YceI	NA	0	YceI-like domain
COJEPEMI_(	COJEPE	-0.10787	0.637195	hypothetical p	NA	yaiW	Protein of unknown function (DUF1615)
COJEPEMI_(	argF	-0.10906	0.822547	Ornithine carb	2.1.3.3	argF	Reversibly catalyzes the transfer of the carbamoyl group from carbamc
COJEPEMI_(	glmS	-0.10942	0.737749	Glutamine--fr	2.6.1.16	glmS	Catalyzes the first step in hexosamine metabolism, converting fructose
COJEPEMI_(	sucA	-0.11197	0.750318	2-oxoglutarate	1.2.4.2	sucA	COG0567 2-oxoglutarate dehydrogenase complex, dehydrogenase (E1)
COJEPEMI_(	COJEPE	-0.11203	0.761936	hypothetical p	NA	alkB	2OG-Fe(II) oxygenase superfamily
COJEPEMI_(	COJEPE	-0.11257	0.804022	hypothetical p	NA	ycaP	Protein of unknown function (DUF421)
COJEPEMI_(	COJEPE	-0.11395	0.857365	hypothetical p	NA	IV02_12(	AI-2E family transporter
COJEPEMI_(	serS	-0.11519	0.542946	Serine--tRNA l	6.1.1.11	serS	Catalyzes the attachment of serine to tRNA(Ser). Is also able to aminoa
COJEPEMI_(	COJEPE	-0.11563	0.599741	hypothetical p	NA	pssA	Belongs to the CDP-alcohol phosphatidyltransferase class-I family
COJEPEMI_(	xcpX	-0.11615	0.682642	Type II secreti	NA	gspK	Type II secretion system (T2SS), protein K
COJEPEMI_(	COJEPE	-0.11646	NA	hypothetical p	NA	Z012_11!	Uncharacterized protein conserved in bacteria (DUF2184)
COJEPEMI_(	czcD_2	-0.11656	0.649097	Metal cation e	NA	czcD	Cation efflux family
COJEPEMI_(	dnaG	-0.11752	0.673836	DNA primase	2.7.7.-	dnaG	RNA polymerase that catalyzes the synthesis of short RNA molecules u
COJEPEMI_(	COJEPE	-0.11758	0.711163	hypothetical p	NA	0	Acetyltransferase (GNAT) domain
COJEPEMI_(	hin_2	-0.1179	0.764229	DNA-invertase	NA	0	Resolvase, N terminal domain
COJEPEMI_(	pap	-0.11819	0.702952	Polyphosphate	2.7.4.-	pap	Polyphosphate kinase 2 (PPK2)
COJEPEMI_(	COJEPE	-0.11819	0.659652	hypothetical p	NA	0	Protein of unknown function (DUF2804)
COJEPEMI_(	COJEPE	-0.11885	0.841029	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.11916	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	lapB	-0.12055	0.511652	Lipopolysacch	NA	pilF	Tetratricopeptide repeat
COJEPEMI_(	csy3	-0.12061	0.625862	CRISPR-associ	NA	csy3	CRISPR-associated protein (Cas_Csy3)
COJEPEMI_(	ureD	-0.12072	0.831933	Urease access	NA	ureD	Required for maturation of urease via the functional incorporation of th
COJEPEMI_(	xerD	-0.12081	0.671689	Tyrosine recon	NA	xerD	recombinase XerD
COJEPEMI_(	COJEPE	-0.12094	0.694578	hypothetical p	NA	0	Zinc-dependent metalloprotease
COJEPEMI_(	yejE	-0.12094	0.783167	Inner membra	NA	yejE	Binding-protein-dependent transport system inner membrane compone

COJEPEMI_(	mrcB	-0.12119	0.689816	Penicillin-bind	NA	mrcB	Cell wall formation. Synthesis of cross-linked peptidoglycan from the li
COJEPEMI_(	rnhA	-0.12136	0.704743	Ribonuclease I	3.1.26.4	dnaQ	Endonuclease that specifically degrades the RNA of RNA- DNA hybrids
COJEPEMI_(	COJEPE	-0.12155	0.770554	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.1232	0.726147	hypothetical p	NA	0	
COJEPEMI_(	sucB	-0.12335	0.702216	Dihydrolipoylly	2.3.1.61	sucB	The 2-oxoglutarate dehydrogenase complex catalyzes the overall conve
COJEPEMI_(	suhB	-0.12377	0.610865	Inositol-1-mor	3.1.3.25	suhB	Inositol monophosphatase
COJEPEMI_(	COJEPE	-0.124	NA	hypothetical p	NA	0	transcriptional regulator
COJEPEMI_(	COJEPE	-0.12455	0.70968	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2236)
COJEPEMI_(	adk	-0.12495	0.526943	Adenylate kina	2.7.4.3	adk	Catalyzes the reversible transfer of the terminal phosphate group betw
COJEPEMI_(	COJEPE	-0.12594	0.656633	hypothetical p	NA	0	Beta-lactamase enzyme family
COJEPEMI_(	COJEPE	-0.12597	0.705537	hypothetical p	NA	0	hydrolase of the alpha beta-hydrolase fold
COJEPEMI_(	dsbC_1	-0.1282	0.842195	putative thiol:(	NA	dsbC	Required for disulfide bond formation in some periplasmic proteins. Ac
COJEPEMI_(	COJEPE	-0.12904	0.726837	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	nusB	-0.12916	0.690915	Transcription a	NA	nusB	Involved in transcription antitermination. Required for transcription of r
COJEPEMI_(	ppx	-0.12938	0.573145	Exopolyphosph	3.6.1.11	gppA	Belongs to the GppA Ppx family
COJEPEMI_(	rapA	-0.12973	0.6498	RNA polymera	3.6.4.-	rapA	Transcription regulator that activates transcription by stimulating RNA
COJEPEMI_(	trpD_2	-0.12986	0.753988	Anthranilate p	2.4.2.18	ybiB	Glycosyl transferase family, helical bundle domain
COJEPEMI_(	COJEPE	-0.13019	0.728274	hypothetical p	NA	0	Transcriptional regulator
COJEPEMI_(	yciV	-0.13171	0.703217	5'-3' exoribonu	3.1.13.-	trpH	DNA polymerase alpha chain like domain
COJEPEMI_(	icd_1	-0.13288	0.567865	Isocitrate dehy	1.1.1.42	icd	Isocitrate dehydrogenase
COJEPEMI_(	glmU	-0.13308	0.6765	Bifunctional pr	NA	glmU	Catalyzes the last two sequential reactions in the de novo biosynthetic
COJEPEMI_(	mreB	-0.13357	0.632977	Cell shape-det	NA	mreB	Rod shape-determining protein MreB
COJEPEMI_(	xseA	-0.13403	0.704743	Exodeoxyribon	3.1.11.6	xseA	Bidirectionally degrades single-stranded DNA into large acid-insoluble (
COJEPEMI_(	gltC_2	-0.13419	0.729311	HTH-type trans	NA	ywbI	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.13564	0.605978	hypothetical p	NA	xdhA	CO dehydrogenase flavoprotein C-terminal domain
COJEPEMI_(	sufS	-0.13681	0.783167	Cysteine desul	4.4.1.16	csdB	Cys/Met metabolism PLP-dependent enzyme
COJEPEMI_(	fabR_2	-0.13686	0.712477	HTH-type trans	NA	fabR	Bacterial regulatory proteins, tetR family
COJEPEMI_(	dadA_2	-0.13755	0.65859	D-amino acid (	1.4.99.-	dadA3	FAD dependent oxidoreductase
COJEPEMI_(	astB	-0.13833	0.563924	N-succinylargi	3.5.3.23	astB	Catalyzes the hydrolysis of N(2)-succinylarginine into N(2)-succinylornit
COJEPEMI_(	esiB_1	-0.13851	0.768075	Secretory imm	NA	#N/A	#N/A

COJEPEMI_(	trmJ	-0.13945	0.732507	tRNA (cytidine	2.1.1.-	trmJ	Catalyzes the formation of 2'O-methylated cytidine (Cm32) or 2'O-met
COJEPEMI_(	COJEPE	-0.14125	0.737038	Mono(2-hydro	3.1.1.102	hcaG	Tannase and feruloyl esterase
COJEPEMI_(	degQ	-0.14185	0.622893	Periplasmic pH	3.4.21.10	mucD	Belongs to the peptidase S1C family
COJEPEMI_(	recD2	-0.14196	0.544175	ATP-dependen	3.6.4.12	pif1	Helix-turn-helix domain
COJEPEMI_(	COJEPE	-0.1423	0.698905	hypothetical p	NA	0	Type II secretion system (T2SS), protein N
COJEPEMI_(	mdtA_1	-0.1424	0.623978	Multidrug resi	NA	0	Belongs to the membrane fusion protein (MFP) (TC 8.A.1) family
COJEPEMI_(	COJEPE	-0.14296	0.801192	hypothetical p	NA	0	Part of the outer membrane protein assembly complex, which is involv
COJEPEMI_(	hcaR_3	-0.14304	0.761499	Hca operon tra	NA	0	Transcriptional regulator
COJEPEMI_(	COJEPE	-0.1438	0.707899	hypothetical p	NA	0	pathogenesis
COJEPEMI_(	glnK	-0.14431	0.625571	Nitrogen regul	NA	glnK	Belongs to the P(II) protein family
COJEPEMI_(	COJEPE	-0.14472	0.831705	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.14483	0.644582	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ydcO_1	-0.1454	0.843746	Inner membra	NA	ydcO	Benzoate membrane transport protein
COJEPEMI_(	parE	-0.14561	0.60824	DNA topoisom	5.6.2.2	parE	Topoisomerase IV is essential for chromosome segregation. It relaxes s
COJEPEMI_(	calB_2	-0.14594	0.726616	Coniferyl aldeh	1.2.1.68	calB	belongs to the aldehyde dehydrogenase family
COJEPEMI_(	purT	-0.14623	0.653497	Formate-depe	2.1.2.-	purT	Involved in the de novo purine biosynthesis. Catalyzes the transfer of fo
COJEPEMI_(	ung	-0.14669	0.457807	Uracil-DNA gly	3.2.2.27	ung	Excises uracil residues from the DNA which can arise as a result of mis
COJEPEMI_(	COJEPE	-0.14761	0.552473	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.14831	0.673214	hypothetical p	NA	0	
COJEPEMI_(	gltT	-0.1485	0.721217	Proton/sodium	NA	gltT	Belongs to the dicarboxylate amino acid cation symporter (DAACS) (TC
COJEPEMI_(	czcO	-0.14945	0.574366	putative oxido	1.-.-.-	0	Flavin-binding monooxygenase-like
COJEPEMI_(	COJEPE	-0.15114	0.692209	hypothetical p	NA	olsB	Acetyltransferase (GNAT) domain
COJEPEMI_(	der	-0.15122	0.68618	GTPase Der	NA	der	GTPase that plays an essential role in the late steps of ribosome bioge
COJEPEMI_(	plsB	-0.15192	0.476922	Glycerol-3-phc	2.3.1.15	plsB	Belongs to the GPAT DAPAT family
COJEPEMI_(	COJEPE	-0.15334	0.621461	hypothetical p	NA	0	Methyltransferase domain
COJEPEMI_(	accA1_1	-0.15343	0.564074	Acetyl-/propio	NA	atuF	Biotin carboxylase C-terminal domain
COJEPEMI_(	pilT_2	-0.15375	0.737749	Twitching mot	NA	pilU	Type II/IV secretion system protein
COJEPEMI_(	epsE	-0.15441	0.696658	Type II secreti	NA	gspE	Type II secretory pathway, ATPase PulE Tfp pilus assembly pathway, AT
COJEPEMI_(	COJEPE	-0.15549	0.673214	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	recF_2	-0.15597	0.702952	DNA replicatio	NA	0	AAA ATPase domain

COJEPEMI_(	qseB_2	-0.15612	0.662952	Transcriptiona	NA	qseB2	Transcriptional regulatory protein, C terminal
COJEPEMI_(	COJEPE	-0.1563	0.68227	hypothetical p	NA	MA20_19	Virulence activator alpha C-term
COJEPEMI_(	lnt	-0.15637	0.648013	Apolipoproteir	2.3.1.269	lnt	Transfers the fatty acyl group on membrane lipoproteins
COJEPEMI_(	gpmI	-0.15708	0.396004	2,3-bisphosph	5.4.2.12	gpmI	Catalyzes the interconversion of 2-phosphoglycerate and 3-phosphoglyc
COJEPEMI_(	COJEPE	-0.15745	0.855789	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	nudC_2	-0.15909	0.501805	NADH pyropho	3.6.1.22	nudC_1	Nudix N-terminal
COJEPEMI_(	COJEPE	-0.15938	NA	hypothetical p	NA	0	Uncharacterized conserved protein (DUF2280)
COJEPEMI_(	COJEPE	-0.15995	0.567575	hypothetical p	NA	0	Lysine exporter LysO
COJEPEMI_(	COJEPE	-0.16033	0.737038	hypothetical p	NA	0	SMI1 / KNR4 family
COJEPEMI_(	lysS	-0.16059	0.612159	Lysine--tRNA l	6.1.1.6	lysS	Belongs to the class-II aminoacyl-tRNA synthetase family
COJEPEMI_(	COJEPE	-0.16059	0.711163	4-hydroxyproli	5.1.1.8	0	Proline racemase
COJEPEMI_(	cycA_1	-0.16139	0.664412	D-serine/D-ala	NA	cycA	Amino acid permease
COJEPEMI_(	COJEPE	-0.16142	NA	hypothetical p	NA	desC	Fatty acid desaturase
COJEPEMI_(	sttH	-0.16207	0.728412	Streptothricin	3.5.2.19	yddQ	Isochorismatase family
COJEPEMI_(	hemA	-0.16212	0.589521	Glutamyl-tRN/	1.2.1.70	hemA	Catalyzes the NADPH-dependent reduction of glutamyl- tRNA(Glu) to g
COJEPEMI_(	rcsC_3	-0.16251	0.452128	Sensor histidir	2.7.13.3	baeS	HAMP (Histidine kinases, Adenylyl cyclases, Methyl binding proteins, PH
COJEPEMI_(	COJEPE	-0.16347	NA	hypothetical p	NA	0	transcriptional regulator
COJEPEMI_(	emrK	-0.16379	0.711163	putative multi	NA	emrA	HlyD membrane-fusion protein of T1SS
COJEPEMI_(	ppk_2	-0.16389	0.606165	Polyphosphate	2.7.4.1	ppk	Catalyzes the reversible transfer of the terminal phosphate of ATP to fo
COJEPEMI_(	rhtA_1	-0.16464	0.56861	Threonine/hor	NA	rhtA	EamA-like transporter family
COJEPEMI_(	glxR_1	-0.16503	0.636546	2-hydroxy-3-o>	1.1.1.60	glxR	Ketopantoate reductase PanE/ApbA
COJEPEMI_(	COJEPE	-0.16625	0.563138	hypothetical p	NA	0	NADPH-dependent FMN reductase
COJEPEMI_(	ywrO	-0.16692	0.763191	General stress	1.6.99.-	0	Flavodoxin-like fold
COJEPEMI_(	COJEPE	-0.16757	0.57289	hypothetical p	NA	0	
COJEPEMI_(	bbsG	-0.16768	0.560342	(R)-benzylsucc	1.3.8.3	HA62_10	acyl-CoA dehydrogenase
COJEPEMI_(	COJEPE	-0.16795	0.498002	hypothetical p	NA	0	START domain
COJEPEMI_(	COJEPE	-0.16968	0.374864	hypothetical p	NA	ecnB	Entericidin EcnA/B family
COJEPEMI_(	COJEPE	-0.16969	0.80687	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.1709	NA	hypothetical p	NA	0	
COJEPEMI_(	mnmA	-0.17095	0.606165	tRNA-specific	2.8.1.13	mnmA	Catalyzes the 2-thiolation of uridine at the wobble position (U34) of tR

COJEPEMI_(	COJEPE	-0.17132	0.559388	hypothetical p	NA	0	Belongs to the UPF0145 family
COJEPEMI_(	cyoD	-0.17149	0.550086	Cytochrome bc	NA	cyoD	Prokaryotic Cytochrome C oxidase subunit IV
COJEPEMI_(	pdhR	-0.17234	0.523486	Pyruvate dehy	NA	0	FCD
COJEPEMI_(	tag	-0.17324	0.589521	DNA-3-methyl	3.2.2.20	tag	Methyladenine glycosylase
COJEPEMI_(	COJEPE	-0.17382	NA	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	minC	-0.17402	0.483434	Septum site-d	NA	minC	Cell division inhibitor that blocks the formation of polar Z ring septums.
COJEPEMI_(	COJEPE	-0.17457	0.571383	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.17553	0.689816	hypothetical p	NA	carAa	Rieske [2Fe-2S] domain
COJEPEMI_(	ppsA	-0.17581	0.393225	Phosphoenolpy	2.7.9.2	ppsA	Catalyzes the phosphorylation of pyruvate to phosphoenolpyruvate
COJEPEMI_(	COJEPE	-0.17647	0.722528	hypothetical p	NA	ydeK	EamA-like transporter family
COJEPEMI_(	COJEPE	-0.17653	0.737038	hypothetical p	NA	dprA	nucleotide-binding protein involved in DNA uptake
COJEPEMI_(	COJEPE	-0.17724	0.660627	hypothetical p	NA	gspJ	general secretion pathway protein
COJEPEMI_(	COJEPE	-0.17936	0.718673	hypothetical p	NA	yfcM	Elongation factor P hydroxylase
COJEPEMI_(	cysA_2	-0.18058	0.682642	Sulfate/thiosu	7.3.2.3	modC	ABC transporter
COJEPEMI_(	emrY	-0.18169	0.68786	putative multi	NA	0	Major Facilitator Superfamily
COJEPEMI_(	ycfH_1	-0.18171	0.43878	putative meta	3.1.-.-	ycfH	TatD related DNase
COJEPEMI_(	gcvH	-0.18198	0.478101	Glycine cleava	NA	gcvH	The glycine cleavage system catalyzes the degradation of glycine. The I
COJEPEMI_(	COJEPE	-0.18367	0.617923	hypothetical p	NA	MA20_3	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-0.18421	0.64332	hypothetical p	NA	modE	Bacterial regulatory helix-turn-helix protein, lysR family
COJEPEMI_(	kdpD	-0.18478	0.360799	Sensor protein	2.7.13.3	kdpD	PhoQ Sensor
COJEPEMI_(	tas	-0.18597	0.70089	Protein tas	NA	tas	Aldo/keto reductase family
COJEPEMI_(	COJEPE	-0.18626	0.704743	hypothetical p	NA	metL	Homoserine dehydrogenase
COJEPEMI_(	yjcH	-0.18643	0.61734	Inner membra	NA	yjcH	Protein of unknown function, DUF485
COJEPEMI_(	COJEPE	-0.1866	0.378528	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.18836	0.516901	hypothetical p	NA	0	Bacterial protein of unknown function (Gcw_chp)
COJEPEMI_(	pucD	-0.18846	0.540305	putative xanth	1.17.1.4	xdhB	Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead doma
COJEPEMI_(	purU	-0.18846	0.440826	Formyltetrahy	3.5.1.10	purU	Catalyzes the hydrolysis of 10-formyltetrahydrofolate (formyl-FH4) to f
COJEPEMI_(	rcsC_1	-0.18852	0.384864	Sensor histidir	2.7.13.3	0	PhoQ Sensor
COJEPEMI_(	COJEPE	-0.18892	NA	4-sulfomucon	3.1.1.92	0	Amidohydrolase
COJEPEMI_(	COJEPE	-0.18929	0.559388	hypothetical p	NA	0	

COJEPEMI_(	rcsC_8	-0.19001	0.56861	Sensor histidir	2.7.13.3	barA	PhoQ Sensor
COJEPEMI_(	COJEPE	-0.19094	0.56861	hypothetical p	NA	xdhC	XdhC and CoxI family
COJEPEMI_(	topA_2	-0.19129	NA	DNA topoisom	5.6.2.1	0	Releases the supercoiling and torsional tension of DNA, which is introd
COJEPEMI_(	emrB_2	-0.19156	0.526982	Multidrug exp	NA	emrB	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-0.19167	NA	IS4 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	COJEPE	-0.19237	0.793626	hypothetical p	NA	0	
COJEPEMI_(	pgsA	-0.19239	0.387915	CDP-diacylglyc	2.7.8.5	pgsA	Belongs to the CDP-alcohol phosphatidyltransferase class-I family
COJEPEMI_(	COJEPE	-0.19293	0.804022	hypothetical p	NA	hopJ	HopJ type III effector protein
COJEPEMI_(	thyA	-0.19299	0.376547	Thymidylate s	2.1.1.45	thyA	Catalyzes the reductive methylation of 2'-deoxyuridine- 5'-monophosph
COJEPEMI_(	COJEPE	-0.19345	0.528456	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.19355	0.468724	hypothetical p	NA	holB	DNA polymerase III
COJEPEMI_(	yedI	-0.19405	0.672734	Inner membra	NA	yedI	Protein of unknown function (DUF808)
COJEPEMI_(	COJEPE	-0.19464	0.470431	hypothetical p	NA	vanR	FCD
COJEPEMI_(	hcnC	-0.19507	0.673214	Hydrogen cyan	1.4.99.5	0	FAD dependent oxidoreductase
COJEPEMI_(	COJEPE	-0.19548	0.328233	hypothetical p	NA	0	Domain of unknown function (DUF4760)
COJEPEMI_(	hflX	-0.19654	0.364967	GTPase HflX	NA	hflX	GTPase that associates with the 50S ribosomal subunit and may have a
COJEPEMI_(	dmlR_9	-0.19687	0.729311	HTH-type trans	NA	Z012_10(	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.19749	0.541842	IS256 family tr	NA	0	Transposase, Mutator family
COJEPEMI_(	rimP	-0.19911	0.409515	Ribosome mat	NA	rimP	Required for maturation of 30S ribosomal subunits
COJEPEMI_(	COJEPE	-0.20066	0.454251	hypothetical p	NA	0	
COJEPEMI_(	prc	-0.20089	0.250955	Tail-specific p	3.4.21.10	prc	Belongs to the peptidase S41A family
COJEPEMI_(	coaX	-0.20095	0.578722	Type III pantot	2.7.1.33	coaX	Catalyzes the phosphorylation of pantothenate (Pan), the first step in C
COJEPEMI_(	waaA	-0.20107	0.519487	3-deoxy-D-ma	2.4.99.12	kdtA	3-Deoxy-D-manno-octulosonic-acid transferase (kdotransferase)
COJEPEMI_(	lrp_4	-0.2011	0.64332	Leucine-respo	NA	0	helix_turn_helix ASNC type
COJEPEMI_(	COJEPE	-0.20111	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.2015	0.45701	hypothetical p	NA	yraR	Nucleoside-diphosphate-sugar epimerases
COJEPEMI_(	COJEPE	-0.20187	0.778135	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.20221	0.551103	hypothetical p	NA	0	
COJEPEMI_(	ybjJ	-0.20536	0.418808	Inner membra	NA	0	Major Facilitator Superfamily
COJEPEMI_(	ephD	-0.20627	0.42186	putative oxido	1.-.-.-	0	Alpha/beta hydrolase family

COJEPEMI_(	prpF	-0.20641	0.31243	2-methyl-acon	5.3.3.-	prpF	PrpF protein
COJEPEMI_(	ureC	-0.20651	0.535845	Urease subuni	3.5.1.5	ureC	Belongs to the metallo-dependent hydrolases superfamily. Urease alph
COJEPEMI_(	aroK	-0.20726	0.295738	Shikimate kina	2.7.1.71	aroK	Catalyzes the specific phosphorylation of the 3-hydroxyl group of shikim
COJEPEMI_(	cobP	-0.20763	0.611692	Bifunctional a	2.7.1.156	cobU	Catalyzes ATP-dependent phosphorylation of adenosylcobinamide and a
COJEPEMI_(	gmk	-0.20811	0.494994	Guanylate kina	2.7.4.8	gmk	Essential for recycling GMP and indirectly, cGMP
COJEPEMI_(	COJEPE	-0.20823	NA	hypothetical p	NA	0	Putative inner membrane exporter, YdcZ
COJEPEMI_(	COJEPE	-0.2084	0.402832	hypothetical p	NA	yhbS	Acetyltransferase (GNAT) domain
COJEPEMI_(	cyoC	-0.20845	0.499722	Cytochrome bc	NA	cyoC	Cytochrome c oxidase subunit III
COJEPEMI_(	COJEPE	-0.20904	0.648837	hypothetical p	NA	0	NMT1-like family
COJEPEMI_(	tmk	-0.20948	0.426063	Thymidylate ki	2.7.4.9	tmk	Phosphorylation of dTMP to form dTDP in both de novo and salvage pat
COJEPEMI_(	rsmH	-0.20949	0.395654	Ribosomal RN	2.1.1.199	rsmH	Specifically methylates the N4 position of cytidine in position 1402 (C1
COJEPEMI_(	lipR_2	-0.20964	0.792862	Putative acety	3.1.1.-	0	Steryl acetyl hydrolase
COJEPEMI_(	mscS	-0.20999	0.448431	Small-conduct	NA	0	Mechanosensitive ion channel
COJEPEMI_(	ybaL	-0.21094	0.319706	Putative catior	NA	ybaL	Belongs to the monovalent cation proton antiporter 2 (CPA2) transporte
COJEPEMI_(	COJEPE	-0.21179	0.726616	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.21182	0.498859	Acetyltransfer	2.3.1.-	0	Acetyltransferase (GNAT) domain
COJEPEMI_(	mltF_1	-0.21235	0.429458	Membrane-bo	4.2.2.-	0	Transglycosylase SLT domain
COJEPEMI_(	csy2	-0.21376	0.625498	CRISPR-associ	NA	csy2	CRISPR-associated protein (Cas_Csy2)
COJEPEMI_(	edd	-0.21408	0.433806	Phosphoglucor	4.2.1.12	edd	Belongs to the IlvD Edd family
COJEPEMI_(	COJEPE	-0.21438	0.323179	hypothetical p	NA	0	STAS domain
COJEPEMI_(	kefC_2	-0.21721	0.53321	Glutathione-re	NA	kefB	Belongs to the monovalent cation proton antiporter 2 (CPA2) transporte
COJEPEMI_(	COJEPE	-0.2184	0.452773	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2237)
COJEPEMI_(	yhcR	-0.2186	0.650711	Endonuclease	3.1.31.-	yhcR	5'-nucleotidase, C-terminal domain
COJEPEMI_(	COJEPE	-0.21903	0.405477	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.21956	0.614259	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	cysA_1	-0.21961	0.658955	Sulfate/thiosu	7.3.2.3	cysA	Part of the ABC transporter complex CysAWTP involved in sulfate thiosu
COJEPEMI_(	rhaS_7	-0.22025	0.293241	HTH-type trans	NA	0	AraC-like ligand binding domain
COJEPEMI_(	aroC	-0.22042	0.447166	Chorismate sy	4.2.3.5	aroC	Catalyzes the anti-1,4-elimination of the C-3 phosphate and the C-6 pro
COJEPEMI_(	COJEPE	-0.22086	0.451093	hypothetical p	NA	mltD	COG0741 Soluble lytic murein transglycosylase and related regulatory p
COJEPEMI_(	oprM_2	-0.22089	0.435655	Outer membra	NA	oprM	Outer membrane efflux protein

COJEPEMI_(	rsmG	-0.22142	0.424631	Ribosomal RN	2.1.1.170	rsmG	Specifically methylates the N7 position of guanine in position 527 of 16
COJEPEMI_(	COJEPE	-0.22145	0.635772	hypothetical p	NA	0	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-0.22296	NA	hypothetical p	NA	0	Branched-chain amino acid transport protein (AzlD)
COJEPEMI_(	COJEPE	-0.22323	0.589521	Baeyer-Villige	1.14.13.-	0	Flavin-binding monooxygenase-like
COJEPEMI_(	pgaC_2	-0.22325	0.421289	Poly-beta-1,6-	2.4.1.-	pgaC	Glycosyl transferase family 21
COJEPEMI_(	COJEPE	-0.2233	0.775434	hypothetical p	NA	0	COG0790 FOG TPR repeat, SEL1 subfamily
COJEPEMI_(	COJEPE	-0.22446	0.646975	hypothetical p	NA	0	YGGT family
COJEPEMI_(	COJEPE	-0.22509	0.649111	hypothetical p	NA	0	
COJEPEMI_(	betS	-0.22636	0.363583	Glycine betain	NA	0	Belongs to the BCCT transporter (TC 2.A.15) family
COJEPEMI_(	dmlR_1	-0.22785	0.665652	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.2279	NA	hypothetical p	NA	gpX	Phage Tail Protein X
COJEPEMI_(	COJEPE	-0.22857	0.672734	hypothetical p	NA	0	Membrane transport protein
COJEPEMI_(	alsT	-0.22868	0.43878	Amino-acid ca	NA	agcS	Sodium:alanine symporter family
COJEPEMI_(	COJEPE	-0.22896	0.256691	hypothetical p	NA	0	Glutathione S-transferase, C-terminal domain
COJEPEMI_(	cntA	-0.22936	0.656081	Carnitine mon	1.14.13.2	yeaW	Ring hydroxylating alpha subunit (catalytic domain)
COJEPEMI_(	COJEPE	-0.22943	0.631315	Extracellular s	3.4.21.-	0	Belongs to the peptidase S8 family
COJEPEMI_(	acrB	-0.2302	0.533582	Multidrug effl	NA	0	MMPL family
COJEPEMI_(	yddE_1	-0.2311	0.37425	putative isome	5.1.-.-	yddE_3	Phenazine biosynthesis-like protein
COJEPEMI_(	metC	-0.23115	0.404619	Cystathionine	4.4.1.13	metC	Cys/Met metabolism PLP-dependent enzyme
COJEPEMI_(	ffh	-0.2313	0.339482	Signal recogni	NA	ffh	Involved in targeting and insertion of nascent membrane proteins into
COJEPEMI_(	COJEPE	-0.23304	0.367503	hypothetical p	NA	0	Glycosyl transferases group 1
COJEPEMI_(	COJEPE	-0.23305	0.359354	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.23318	0.485363	hypothetical p	NA	0	Protein of unknown function (DUF1275)
COJEPEMI_(	aroP_2	-0.23334	0.454251	Aromatic amir	NA	pheP	Amino acid permease
COJEPEMI_(	COJEPE	-0.23405	0.599741	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.23752	0.692296	hypothetical p	NA	0	
COJEPEMI_(	recJ	-0.2386	0.33427	Single-strande	3.1.-.-	recJ	single-stranded-DNA-specific exonuclease RecJ
COJEPEMI_(	COJEPE	-0.23908	0.464176	hypothetical p	NA	0	Glycosyl hydrolases family 25
COJEPEMI_(	tolQ_3	-0.23953	0.515658	Tol-Pal system	NA	exbB2	MotA/TolQ/ExbB proton channel family
COJEPEMI_(	cobO	-0.23996	0.498424	Cobalamin ade	2.5.1.-	yvqK	Cobalamin adenosyltransferase

COJEPEMI_(	COJEPE	-0.24002	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	pxpA	-0.24043	0.481241	5-oxoprolinase	3.5.2.9	ybgL	Belongs to the UPF0271 (lamB) family
COJEPEMI_(	COJEPE	-0.24085	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.24209	0.399906	hypothetical p	NA	0	
COJEPEMI_(	yfeX_1	-0.24219	0.360594	Dye-decolorizi	1.11.1.-	0	Dyp-type peroxidase family
COJEPEMI_(	COJEPE	-0.24236	0.509651	hypothetical p	NA	0	Thioesterase-like superfamily
COJEPEMI_(	clpA	-0.24278	0.218178	ATP-dependen	NA	clpA	ATP-dependent Clp protease ATP-binding subunit
COJEPEMI_(	COJEPE	-0.24325	0.389383	hypothetical p	NA	0	Rossmann-like domain
COJEPEMI_(	btuB_2	-0.24345	0.426063	Vitamin B12 t	NA	btuB	TonB dependent receptor
COJEPEMI_(	COJEPE	-0.24532	0.345498	hypothetical p	NA	0	N-terminal half of MaoC dehydratase
COJEPEMI_(	exoA	-0.24542	0.451213	Exodeoxyribon	3.1.11.2	exoA	Endonuclease/Exonuclease/phosphatase family
COJEPEMI_(	COJEPE	-0.24566	0.380233	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.24571	0.630854	hypothetical p	NA	0	M61 glycyl aminopeptidase
COJEPEMI_(	COJEPE	-0.24622	0.567828	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.24628	0.422246	RNA-binding p	NA	yhbY	RNA-binding protein containing KH domain, possibly ribosomal protein
COJEPEMI_(	qseC_2	-0.24725	0.454306	Sensor protein	2.7.13.3	pmrB	His Kinase A (phosphoacceptor) domain
COJEPEMI_(	COJEPE	-0.24753	0.65282	hypothetical p	NA	0	hemolysin activation secretion protein
COJEPEMI_(	COJEPE	-0.24852	0.399906	hypothetical p	NA	MA20_24	Uncharacterised protein family (UPF0093)
COJEPEMI_(	COJEPE	-0.24884	0.822547	hypothetical p	NA	0	
COJEPEMI_(	fis	-0.24893	0.363583	DNA-binding p	NA	fis	Activates ribosomal RNA transcription. Plays a direct role in upstream a
COJEPEMI_(	lpxL_2	-0.25064	0.236218	Lipid A biosynt	2.3.1.241	lpxL	Catalyzes the transfer of laurate from lauroyl-acyl carrier protein (ACP)
COJEPEMI_(	COJEPE	-0.25137	0.480846	hypothetical p	NA	0	Peptidase family M23
COJEPEMI_(	COJEPE	-0.25194	0.236344	hypothetical p	NA	0	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
COJEPEMI_(	COJEPE	-0.25232	0.288386	hypothetical p	NA	0	
COJEPEMI_(	def_2	-0.25232	0.674353	Peptide deforr	3.5.1.88	def2	Removes the formyl group from the N-terminal Met of newly synthesiz
COJEPEMI_(	COJEPE	-0.25279	0.728285	hypothetical p	NA	FII	Phage tail tube protein FII
COJEPEMI_(	COJEPE	-0.25368	NA	hypothetical p	NA	V	Type VI secretion system, phage-baseplate injector
COJEPEMI_(	COJEPE	-0.25432	0.335867	hypothetical p	NA	MA20_43	pathogenesis
COJEPEMI_(	hcnB	-0.25477	0.454551	Hydrogen cyan	1.4.99.5	ooxA	Thi4 family
COJEPEMI_(	COJEPE	-0.25479	0.732318	hypothetical p	NA	0	Domain of unknown function (DUF4265)

COJEPEMI_(	gstB_1	-0.25489	0.567828	Glutathione S-	2.5.1.18	gst	Belongs to the GST superfamily
COJEPEMI_(	astC_1	-0.25528	0.326297	Succinylornithi	2.6.1.81	argD	acetylornithine aminotransferase
COJEPEMI_(	atpC	-0.25539	0.376547	ATP synthase (	NA	atpC	Produces ATP from ADP in the presence of a proton gradient across the
COJEPEMI_(	pgrR_3	-0.25575	0.466009	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.25594	0.339482	hypothetical p	NA	0	Outer membrane efflux protein
COJEPEMI_(	lspA_1	-0.25686	0.254307	Lipoprotein sig	3.4.23.36	lspA	This protein specifically catalyzes the removal of signal peptides from p
COJEPEMI_(	COJEPE	-0.25686	0.430249	6-deoxy-6-sulf	3.1.1.99	0	SMP-30/Gluconolaconase/LRE-like region
COJEPEMI_(	COJEPE	-0.25808	0.679437	hypothetical p	NA	S	Phage virion morphogenesis family
COJEPEMI_(	COJEPE	-0.25813	0.481414	hypothetical p	NA	M	Phage small terminase subunit
COJEPEMI_(	COJEPE	-0.25962	0.367438	hypothetical p	NA	0	Tfp pilus assembly protein FimV
COJEPEMI_(	COJEPE	-0.25988	0.621988	hypothetical p	NA	0	NMT1-like family
COJEPEMI_(	COJEPE	-0.26045	0.388356	hypothetical p	NA	0	Selenoprotein, putative
COJEPEMI_(	COJEPE	-0.26138	0.331984	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	glnQ_1	-0.26233	0.389161	Glutamine tra	NA	gltL	ABC transporter
COJEPEMI_(	alaA	-0.26309	0.38404	Glutamate-pyr	2.6.1.2	alaA	Aminotransferase
COJEPEMI_(	ilvH	-0.26341	0.393841	Acetolactate s	2.2.1.6	ilvH	Acetolactate synthase small
COJEPEMI_(	COJEPE	-0.26355	0.489303	hypothetical p	NA	0	Pfam Methyltransferase
COJEPEMI_(	amgK	-0.26404	0.393463	N-acetylmurar	2.7.1.221	MA20_24	Phosphotransferase enzyme family
COJEPEMI_(	ligA	-0.26448	0.306507	DNA ligase	6.5.1.2	ligA	DNA ligase that catalyzes the formation of phosphodiester linkages bet
COJEPEMI_(	COJEPE	-0.26479	0.385244	hypothetical p	NA	0	Domain of unknown function (DUF3336)
COJEPEMI_(	COJEPE	-0.26485	0.371302	hypothetical p	NA	MA20_41	Protein of unknown function (DUF815)
COJEPEMI_(	COJEPE	-0.26708	0.497948	hypothetical p	NA	0	Putative diguanylate phosphodiesterase
COJEPEMI_(	prmB	-0.26714	0.376547	50S ribosomal	2.1.1.298	prmB	Specifically methylates the 50S ribosomal protein L3 on a specific gluta
COJEPEMI_(	COJEPE	-0.26725	NA	hypothetical p	NA	0	transcriptional regulator
COJEPEMI_(	COJEPE	-0.26747	0.31282	hypothetical p	NA	0	Activator of cell division through the inhibition of FtsZ GTPase activity,
COJEPEMI_(	COJEPE	-0.2675	0.574844	hypothetical p	NA	0	fatty acid desaturase
COJEPEMI_(	pcpD	-0.26763	0.705345	Tetrachlorober	1.1.1.404	vanB	2Fe-2S iron-sulfur cluster binding domain
COJEPEMI_(	aptA	-0.26929	0.502615	Apulose-4-pho	2.2.1.-	tktB	Transketolase, thiamine diphosphate binding domain
COJEPEMI_(	nimR_1	-0.27033	0.645256	HTH-type trans	NA	0	helix_turn_helix, arabinose operon control protein
COJEPEMI_(	ybaK	-0.27083	0.723535	Cys-tRNA(Pro)	4.2.-.-	ybaK	Belongs to the prolyl-tRNA editing family. YbaK EbsC subfamily

COJEPEMI_(	neo	-0.27095	0.360189	Aminoglycosid	2.7.1.95	0	Phosphotransferase enzyme family
COJEPEMI_(	aspA	-0.27096	0.635254	Aspartate amr	4.3.1.1	aspA	Fumarase C C-terminus
COJEPEMI_(	pyrH	-0.27097	0.311679	Uridylate kina	2.7.4.22	pyrH	Catalyzes the reversible phosphorylation of UMP to UDP
COJEPEMI_(	xerC_4	-0.27121	0.690439	Tyrosine recon	NA	rci	Phage integrase family
COJEPEMI_(	trmO	-0.27131	0.372796	tRNA (adenine	2.1.1.-	yaeB	Uncharacterised protein family UPF0066
COJEPEMI_(	cmpR_1	-0.27191	0.274251	HTH-type trans	NA	yeiE	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.27205	0.230928	Putative cytoki	3.2.2.-	VM57_08	Belongs to the LOG family
COJEPEMI_(	COJEPE	-0.2726	0.684331	hypothetical p	NA	0	
COJEPEMI_(	dusB	-0.27276	0.242503	tRNA-dihydrou	1.3.1.-	dusB	Catalyzes the synthesis of 5,6-dihydrouridine (D), a modified base foun
COJEPEMI_(	COJEPE	-0.27296	NA	hypothetical p	NA	0	
COJEPEMI_(	ydgI	-0.27407	0.559388	Putative argini	NA	ydgI	Amino acid permease
COJEPEMI_(	COJEPE	-0.2752	0.240601	hypothetical p	NA	bplE	Glycosyl transferase 4-like domain
COJEPEMI_(	folP_2	-0.27531	0.404605	Dihydropteroa	2.5.1.15	folP	Catalyzes the condensation of para-aminobenzoate (pABA) with 6-hydr
COJEPEMI_(	rhaS_4	-0.27558	0.410107	HTH-type trans	NA	0	AraC-like ligand binding domain
COJEPEMI_(	COJEPE	-0.27767	0.324556	hypothetical p	NA	impA	ImpA, N-terminal, type VI secretion system
COJEPEMI_(	pobR	-0.27789	0.40842	p-hydroxybenz	NA	pcaU	helix_turn_helix isocitrate lyase regulation
COJEPEMI_(	fur	-0.27858	0.138036	Ferric uptake r	NA	fur	Belongs to the Fur family
COJEPEMI_(	leuB	-0.2795	0.483434	3-isopropylma	1.1.1.85	leuB	Catalyzes the oxidation of 3-carboxy-2-hydroxy-4- methylpentanoate (3
COJEPEMI_(	COJEPE	-0.27981	0.657036	hypothetical p	NA	0	Protein of unknown function (DUF3465)
COJEPEMI_(	COJEPE	-0.28003	0.203597	hypothetical p	NA	yjiN	Protein of unknown function (DUF445)
COJEPEMI_(	fabR_1	-0.28037	0.222064	HTH-type trans	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	-0.28052	0.314719	hypothetical p	NA	rluE	Belongs to the pseudouridine synthase RsuA family
COJEPEMI_(	pilQ	-0.28185	0.43878	Type IV pilus b	NA	pilQ	Secretin and TonB N terminus short domain
COJEPEMI_(	COJEPE	-0.28191	0.799012	putative TonB-	NA	irp	Outer membrane receptor proteins mostly Fe transport
COJEPEMI_(	COJEPE	-0.28239	0.478101	hypothetical p	NA	0	
COJEPEMI_(	yjiE	-0.2825	0.222398	HTH-type trans	NA	IV02_243	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.28268	0.387185	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	glpK	-0.28279	0.36698	Glycerol kinas	2.7.1.30	glpK	Key enzyme in the regulation of glycerol uptake and metabolism. Catal
COJEPEMI_(	apxIB	-0.28304	0.361437	Toxin RTX-I tra	NA	cvaB	Peptidase C39 family
COJEPEMI_(	rodZ	-0.28345	0.176549	Cytoskeleton p	NA	0	Domain of unknown function (DUF4115)

COJEPEMI_(	recN	-0.28394	0.129532	DNA repair pro	NA	recN	May be involved in recombinational repair of damaged DNA
COJEPEMI_(	glaR	-0.28397	0.564074	HTH-type trans	NA	0	FCD domain
COJEPEMI_(	COJEPE	-0.28453	0.275829	hypothetical p	NA	pepQ	C-terminal region of peptidase_M24
COJEPEMI_(	COJEPE	-0.28506	NA	IS4 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	maeB	-0.28515	0.26415	NADP-depend	1.1.1.40	maeB	Malic enzyme, NAD binding domain
COJEPEMI_(	COJEPE	-0.28555	0.629654	hypothetical p	NA	0	integron gene cassette protein
COJEPEMI_(	menH_1	-0.28615	0.27087	2-succinyl-6-hy	4.2.99.20	0	Alpha/beta hydrolase family
COJEPEMI_(	COJEPE	-0.28634	0.707315	hypothetical p	NA	0	
COJEPEMI_(	sstT	-0.28774	0.306012	Serine/threoni	NA	sstT	Involved in the import of serine and threonine into the cell, with the co
COJEPEMI_(	dnaB_1	-0.28779	0.450359	Replicative DN	3.6.4.12	0	DnaB-like helicase N terminal domain
COJEPEMI_(	COJEPE	-0.28866	0.322923	hypothetical p	NA	yaiI	Belongs to the UPF0178 family
COJEPEMI_(	COJEPE	-0.28935	0.121275	Glycine betain	NA	betT	Belongs to the BCCT transporter (TC 2.A.15) family
COJEPEMI_(	yejB	-0.28946	0.290909	Inner membra	NA	yejB	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-0.29024	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.2903	0.176256	hypothetical p	NA	desC	Fatty acid desaturase
COJEPEMI_(	atsA	-0.29166	0.432668	Arylsulfatase	3.1.6.1	atsA	Sulfatase
COJEPEMI_(	COJEPE	-0.29166	0.361376	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2147)
COJEPEMI_(	COJEPE	-0.29291	0.347335	hypothetical p	NA	0	Domain of unknown function (DUF4258)
COJEPEMI_(	oxyR	-0.29398	0.320877	Hydrogen pero	NA	oxyR	Transcriptional regulator
COJEPEMI_(	tktA	-0.29414	0.10843	Transketolase	2.2.1.1	tktA	Catalyzes the transfer of a two-carbon ketol group from a ketose donor
COJEPEMI_(	tusA_1	-0.29479	0.240762	Sulfur carrier p	NA	0	Belongs to the sulfur carrier protein TusA family
COJEPEMI_(	COJEPE	-0.29597	0.373095	hypothetical p	NA	ybgK	Allophanate hydrolase subunit 2
COJEPEMI_(	COJEPE	-0.29672	0.499722	hypothetical p	NA	insB4	cog cog1662
COJEPEMI_(	ilvA	-0.29743	0.156566	L-threonine de	4.3.1.19	ilvA	Catalyzes the anaerobic formation of alpha-ketobutyrate and ammonia
COJEPEMI_(	COJEPE	-0.29849	0.372913	hypothetical p	NA	cyaB	Adenylyl- / guanylyl cyclase, catalytic domain
COJEPEMI_(	btuB_1	-0.29899	0.47411	Vitamin B12 tr	NA	oprC	TonB dependent receptor
COJEPEMI_(	COJEPE	-0.2998	0.499605	hypothetical p	NA	0	deoxyhypusine monooxygenase activity
COJEPEMI_(	hom	-0.3011	0.320085	Homoserine de	1.1.1.3	hom	homoserine dehydrogenase
COJEPEMI_(	COJEPE	-0.30129	0.43878	hypothetical p	NA	0	PgaD-like protein
COJEPEMI_(	selO	-0.302	0.241618	Protein adenyl	2.7.7.-	0	Uncharacterized ACR, YdiU/UPF0061 family

COJEPEMI_(	cysQ	-0.30244	0.360799	3'(2'),5'-bisph(	3.1.3.7	cysQ	Inositol monophosphatase family
COJEPEMI_(	rpsI	-0.30304	0.263484	30S ribosomal	NA	rpsI	Belongs to the universal ribosomal protein uS9 family
COJEPEMI_(	yddG_2	-0.30362	0.275955	Aromatic amir	NA	yddG	EamA-like transporter family
COJEPEMI_(	COJEPE	-0.30388	0.454784	hypothetical p	NA	0	protein conserved in bacteria
COJEPEMI_(	COJEPE	-0.30414	0.433823	hypothetical p	NA	0	Phage portal protein
COJEPEMI_(	recD	-0.30434	0.348919	RecBCD enzyr	3.1.11.5	recD	A helicase nuclease that prepares dsDNA breaks (DSB) for recombinati
COJEPEMI_(	COJEPE	-0.30523	0.352919	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.30595	0.599741	hypothetical p	NA	0	
COJEPEMI_(	nudJ	-0.30639	0.281368	Phosphatase N	3.6.1.-	nudJ	Belongs to the Nudix hydrolase family. NudJ subfamily
COJEPEMI_(	sspA	-0.30703	0.360799	Stringent starv	NA	sspA	starvation protein A
COJEPEMI_(	atoC	-0.30728	0.167645	Regulatory prc	NA	pilR	Sigma-54 interaction domain
COJEPEMI_(	cinA_2	-0.3073	0.234762	Putative comp	NA	0	Belongs to the CinA family
COJEPEMI_(	rng	-0.30785	0.307355	Ribonuclease (	3.1.26.-	cafA	Ribonuclease E/G family
COJEPEMI_(	ureE	-0.30887	0.389525	Urease access	NA	ureE	Involved in urease metallocenter assembly. Binds nickel. Probably funct
COJEPEMI_(	COJEPE	-0.30982	0.331196	hypothetical p	NA	0	AAA domain
COJEPEMI_(	COJEPE	-0.31119	0.166496	hypothetical p	NA	0	Belongs to the RNase T2 family
COJEPEMI_(	dctA_1	-0.31299	0.123923	Aerobic C4-dic	NA	dctA	Responsible for the transport of dicarboxylates such as succinate, fuma
COJEPEMI_(	COJEPE	-0.31389	0.654434	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	aptB	-0.31472	0.528298	Apulose-4-pho	2.2.1.-	tktB	Transketolase, pyrimidine binding domain
COJEPEMI_(	argT	-0.31533	0.48147	Lysine/arginin	NA	argT	Bacterial periplasmic substrate-binding proteins
COJEPEMI_(	COJEPE	-0.316	0.533035	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.31606	0.330164	hypothetical p	NA	0	Protein of unknown function DUF262
COJEPEMI_(	cas3	-0.3161	0.128912	CRISPR-associ	3.1.-.-	cas3	CRISPR-associated helicase, Cas3
COJEPEMI_(	rnhB	-0.31612	0.389383	Ribonuclease I	3.1.26.4	rnhB	Endonuclease that specifically degrades the RNA of RNA- DNA hybrids
COJEPEMI_(	cueR	-0.31694	0.38404	HTH-type trans	NA	soxR_2	helix_turn_helix, mercury resistance
COJEPEMI_(	gacA	-0.31694	0.330096	Response regu	NA	uvrY	response regulator
COJEPEMI_(	ampC_1	-0.32028	0.439865	Beta-lactamas	3.5.2.6	ampC	Beta-lactamase
COJEPEMI_(	COJEPE	-0.32036	0.611692	hypothetical p	NA	metQ3	NLPA lipoprotein
COJEPEMI_(	astD	-0.32152	0.236668	N-succinylglut	1.2.1.71	astD	Catalyzes the NAD-dependent reduction of succinylglutamate semialde
COJEPEMI_(	COJEPE	-0.32158	0.137717	hypothetical p	NA	plsC	Acyltransferase

COJEPEMI_(	COJEPE	-0.32184	0.455869	hypothetical p	NA	0	
COJEPEMI_(	fsr	-0.32238	0.349923	Fosmidomycin	NA	fsr	Major Facilitator Superfamily
COJEPEMI_(	lpxL_1	-0.32255	0.599741	Lipid A biosynt	2.3.1.241	htrB	Bacterial lipid A biosynthesis acyltransferase
COJEPEMI_(	carB_2	-0.32307	0.248898	Carbamoyl-ph	NA	bccA	Biotin carboxylase, N-terminal domain
COJEPEMI_(	dcyD	-0.32341	0.374864	D-cysteine des	4.4.1.15	dcyD	Pyridoxal-phosphate dependent enzyme
COJEPEMI_(	COJEPE	-0.32497	0.539092	hypothetical p	NA	comF	competence protein
COJEPEMI_(	yfeX_2	-0.32565	0.208791	Dye-decolorizi	1.11.1.-	yfeX	Dyp-type peroxidase family
COJEPEMI_(	COJEPE	-0.32602	0.313609	hypothetical p	NA	wlaX	3'-5' exonuclease related to the exonuclease domain of PolB
COJEPEMI_(	cvaA	-0.32651	0.366834	Colicin V secre	NA	raxA	HlyD membrane-fusion protein of T1SS
COJEPEMI_(	rnfH	-0.32684	0.247787	Protein RnfH	NA	0	Belongs to the UPF0125 (RnfH) family
COJEPEMI_(	COJEPE	-0.32743	0.502615	hypothetical p	NA	N	Phage major capsid protein, P2 family
COJEPEMI_(	COJEPE	-0.32842	0.557742	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	lpdG	-0.32913	0.18861	Dihydrolipoyl c	1.8.1.4	odhL	COG1249 Pyruvate 2-oxoglutarate dehydrogenase complex, dihydrolipo
COJEPEMI_(	mscL	-0.32973	0.237816	Large-conduct	NA	mscL	Channel that opens in response to stretch forces in the membrane lipid
COJEPEMI_(	COJEPE	-0.33003	0.364995	hypothetical p	NA	0	
COJEPEMI_(	ribA	-0.33134	0.245429	GTP cyclohydr	3.5.4.25	ribA	Catalyzes the conversion of GTP to 2,5-diamino-6- ribosylamino-4(3H)-
COJEPEMI_(	bioA	-0.33151	0.207477	Adenosylmeth	2.6.1.62	bioA	Catalyzes the transfer of the alpha-amino group from S- adenosyl-L-me
COJEPEMI_(	lcdH	-0.332	0.171038	L-carnitine del	1.1.1.108	0	3-hydroxyacyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	nagZ	-0.33203	0.274388	Beta-hexosam	3.2.1.52	nagZ	Plays a role in peptidoglycan recycling by cleaving the terminal beta-1,4
COJEPEMI_(	COJEPE	-0.33396	0.258668	hypothetical p	NA	chiG	Mycolic acid cyclopropane synthetase
COJEPEMI_(	lolB	-0.3341	0.281012	Outer-membra	NA	lolB	Plays a critical role in the incorporation of lipoproteins in the outer mer
COJEPEMI_(	lysP	-0.33422	0.313391	Lysine-specific	NA	lysP	Amino acid permease
COJEPEMI_(	COJEPE	-0.33515	0.404262	hypothetical p	NA	0	Acetyltransferase (GNAT) domain
COJEPEMI_(	prtR	-0.33519	0.331379	HTH-type trans	NA	CI	Helix-turn-helix XRE-family like proteins
COJEPEMI_(	COJEPE	-0.33541	0.431068	hypothetical p	NA	0	
COJEPEMI_(	clsC_2	-0.33543	0.143474	Cardiolipin syn	2.7.8.-	0	Phospholipase D
COJEPEMI_(	COJEPE	-0.33652	0.124958	hypothetical p	NA	0	Tetratricopeptide repeat
COJEPEMI_(	mrcA	-0.33694	0.178334	Penicillin-bind	NA	mrcA	penicillin-binding protein
COJEPEMI_(	COJEPE	-0.33703	0.183809	hypothetical p	NA	0	
COJEPEMI_(	mraY	-0.33753	0.141525	Phospho-N-ac	2.7.8.13	mraY	First step of the lipid cycle reactions in the biosynthesis of the cell wall

COJEPEMI_(	alc	-0.33856	0.241614	allantoicase	3.5.3.4	alc	Belongs to the allantoicase family
COJEPEMI_(	COJEPE	-0.3386	0.353905	hypothetical p	NA	0	alpha beta
COJEPEMI_(	pcrA_2	-0.3387	0.154221	ATP-dependen	3.6.4.12	rep	UvrD-like helicase C-terminal domain
COJEPEMI_(	dacA	-0.33879	0.324556	D-alanyl-D-ala	3.4.16.4	dacA	Belongs to the peptidase S11 family
COJEPEMI_(	COJEPE	-0.33923	0.226106	hypothetical p	NA	0	Zonular occludens toxin (Zot)
COJEPEMI_(	abaF_2	-0.33925	0.515834	Fosfomycin re	NA	0	Sugar (and other) transporter
COJEPEMI_(	silP	-0.33954	0.032552	Silver exportin	7.2.2.15	copF	P-type ATPase
COJEPEMI_(	hyi	-0.33965	0.478101	Hydroxypyruva	5.3.1.22	hyi	Belongs to the hyi family
COJEPEMI_(	ilvC	-0.34017	0.270197	Ketol-acid red	1.1.1.86	ilvC	Involved in the biosynthesis of branched-chain amino acids (BCAA). Cat
COJEPEMI_(	prmA	-0.34064	0.078138	Ribosomal pro	2.1.1.-	prmA	Methylates ribosomal protein L11
COJEPEMI_(	COJEPE	-0.3407	0.740212	hypothetical p	NA	0	4-amino-4-deoxy-alpha-L-arabinopyranosyl undecaprenyl phosphate bic
COJEPEMI_(	COJEPE	-0.34219	0.293438	hypothetical p	NA	0	Effector of murein hydrolase LrgA
COJEPEMI_(	COJEPE	-0.34225	0.404178	hypothetical p	NA	sfp	Belongs to the P-Pant transferase superfamily
COJEPEMI_(	cysW	-0.34228	0.619035	Sulfate transp	NA	cysW	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-0.34342	0.280116	hypothetical p	NA	ybgC-2	Acyl-ACP thioesterase
COJEPEMI_(	yhdE	-0.3441	0.339075	dTTP/UTP pyro	3.6.1.9	maf	Maf-like protein
COJEPEMI_(	COJEPE	-0.34451	0.562113	hypothetical p	NA	0	Domain of unknown function (DUF4844)
COJEPEMI_(	rlmH	-0.34459	0.267546	Ribosomal RN	2.1.1.177	rlmH	Specifically methylates the pseudouridine at position 1915 (m3Psi1915
COJEPEMI_(	leuE_1	-0.34479	0.2037	Leucine efflux	NA	leuE	LysE type translocator
COJEPEMI_(	cydB_2	-0.34489	0.286622	Cytochrome bo	7.1.1.7	cioB	Cytochrome bd terminal oxidase subunit II
COJEPEMI_(	COJEPE	-0.3452	0.360799	hypothetical p	NA	0	
COJEPEMI_(	pyrC	-0.34531	0.207924	Dihydroorotase	3.5.2.3	pyrC	Catalyzes the reversible cyclization of carbamoyl aspartate to dihydroo
COJEPEMI_(	dgkA	-0.34548	0.249235	Diacylglycerol	2.7.1.107	dgkA	Recycling of diacylglycerol produced during the turnover of membrane
COJEPEMI_(	COJEPE	-0.34559	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.3457	0.466096	hypothetical p	NA	0	Toprim-like
COJEPEMI_(	COJEPE	-0.3457	0.249505	hypothetical p	NA	0	
COJEPEMI_(	cobT	-0.34638	0.263021	Nicotinate-nuc	2.4.2.21	cobT	Catalyzes the synthesis of alpha-ribazole-5'-phosphate from nicotinate
COJEPEMI_(	nadE	-0.34664	0.067578	Glutamine-dep	6.3.5.1	nadE	Catalyzes the ATP-dependent amidation of deamido-NAD to form NAD
COJEPEMI_(	baeR	-0.34728	0.180794	Transcriptiona	NA	baeR	Transcriptional regulatory protein, C terminal
COJEPEMI_(	COJEPE	-0.34731	0.291801	hypothetical p	NA	0	Belongs to the 'phage' integrase family

COJEPEMI_(	gabD_2	-0.3476	0.470431	Succinate-sem	1.2.1.79	gabD	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat
COJEPEMI_(	COJEPE	-0.34803	0.124958	hypothetical p	NA	0	
COJEPEMI_(	lrp_3	-0.34861	0.265197	Leucine-respo	NA	lrp2	helix_turn_helix ASNC type
COJEPEMI_(	COJEPE	-0.34879	0.38817	hypothetical p	NA	0	Domain of unknown function (DUF1330)
COJEPEMI_(	dusA	-0.34889	0.253054	tRNA-dihydrou	1.3.1.-	dusA	Catalyzes the synthesis of 5,6-dihydrouridine (D), a modified base foun
COJEPEMI_(	rhtA_2	-0.3493	0.25335	Threonine/hor	NA	rhtA	EamA-like transporter family
COJEPEMI_(	recC	-0.35018	0.127798	RecBCD enzym	3.1.11.5	recC	A helicase nuclease that prepares dsDNA breaks (DSB) for recombinati
COJEPEMI_(	COJEPE	-0.35099	0.541958	hypothetical p	NA	0	Polysaccharide biosynthesis protein
COJEPEMI_(	epsF_1	-0.35299	0.112982	Type II secreti	NA	gspF	general secretion pathway protein
COJEPEMI_(	COJEPE	-0.35307	0.111963	hypothetical p	NA	phaI	Poly(hydroxyalcanoate) granule associated protein (phasin)
COJEPEMI_(	yngG	-0.35323	0.167845	Hydroxymethy	4.1.3.4	0	Hydroxymethylglutaryl-CoA lyase
COJEPEMI_(	COJEPE	-0.35344	0.585129	Putative unive	NA	uspA	Universal stress protein family
COJEPEMI_(	mlaE	-0.35354	0.114161	Intermembran	NA	mlaE	Permease MlaE
COJEPEMI_(	COJEPE	-0.35451	0.666105	hypothetical p	NA	arsR	helix_turn_helix, Arsenical Resistance Operon Repressor
COJEPEMI_(	alaS	-0.35531	0.2367	Alanine--tRNA	6.1.1.7	alaS	Catalyzes the attachment of alanine to tRNA(Ala) in a two-step reactio
COJEPEMI_(	COJEPE	-0.35599	0.318794	hypothetical p	NA	0	2OG-Fe(II) oxygenase superfamily
COJEPEMI_(	cyoB	-0.35615	0.283467	Cytochrome bo	7.1.1.3	cyoB	Belongs to the heme-copper respiratory oxidase family
COJEPEMI_(	pheT	-0.35626	0.12977	Phenylalanine-	6.1.1.20	pheT	Belongs to the phenylalanyl-tRNA synthetase beta subunit family. Type
COJEPEMI_(	COJEPE	-0.35634	0.188247	Beta-lactamas	3.5.2.6	bla	Penicillin binding protein transpeptidase domain
COJEPEMI_(	yebC	-0.35683	0.098594	putative trans	NA	yebC	transcriptional regulatory protein
COJEPEMI_(	priA	-0.3583	0.256854	Primosomal pr	3.6.4.-	priA	Involved in the restart of stalled replication forks. Recognizes and binds
COJEPEMI_(	COJEPE	-0.35933	0.198677	hypothetical p	NA	0	
COJEPEMI_(	yfdE	-0.36046	0.247622	Acetyl-CoA:oxa	2.8.3.19	0	CoA-transferase family III
COJEPEMI_(	COJEPE	-0.36059	0.427719	hypothetical p	NA	exoX	3'-5' exonuclease activity on single or double-strand DNA
COJEPEMI_(	COJEPE	-0.36144	0.233174	hypothetical p	NA	0	WYL domain
COJEPEMI_(	bepA_2	-0.36374	0.273002	Beta-barrel as	3.4.-.-	MA20_42	COG0457 FOG TPR repeat
COJEPEMI_(	dxr	-0.36442	0.21885	1-deoxy-D-xylu	1.1.1.267	dxr	Catalyzes the NADP-dependent rearrangement and reduction of 1-deox
COJEPEMI_(	COJEPE	-0.36446	0.299256	hypothetical p	NA	0	
COJEPEMI_(	prmC	-0.36471	0.323472	Release factor	2.1.1.297	prmC	Methylates the class 1 translation termination release factors RF1 PrfA
COJEPEMI_(	COJEPE	-0.36609	0.107859	hypothetical p	NA	0	Domain of unknown function (DUF4105)

COJEPEMI_(	kefF_2	-0.36651	0.693069	Glutathione-re	1.6.5.2	0	Flavodoxin-like fold
COJEPEMI_(	oppA	-0.36656	0.291623	Oligopeptide-b	NA	0	Bacterial extracellular solute-binding proteins, family 5 Middle
COJEPEMI_(	purC	-0.36673	0.167795	Phosphoribosy	6.3.2.6	purC	Belongs to the SAICAR synthetase family
COJEPEMI_(	zipA	-0.36677	0.062165	Cell division pr	NA	zipA	Essential cell division protein that stabilizes the FtsZ protofilaments by
COJEPEMI_(	xcpQ	-0.36739	0.078516	Secretin XcpQ	NA	gspD	Bacterial type II and III secretion system protein
COJEPEMI_(	COJEPE	-0.36753	0.054562	hypothetical p	NA	feoA	FeoA
COJEPEMI_(	COJEPE	-0.36844	0.619035	hypothetical p	NA	0	GDYXXLXY protein
COJEPEMI_(	putA	-0.37062	0.088568	Bifunctional pr	NA	putA	Oxidizes proline to glutamate for use as a carbon and nitrogen source
COJEPEMI_(	ruvC	-0.37078	0.245429	Crossover junc	3.1.22.4	ruvC	Nuclease that resolves Holliday junction intermediates in genetic recon
COJEPEMI_(	dctA_2	-0.3709	0.222086	C4-dicarboxyla	NA	dctA	Responsible for the transport of dicarboxylates such as succinate, fuma
COJEPEMI_(	COJEPE	-0.37097	0.429846	hypothetical p	NA	0	Glutathione-dependent formaldehyde-activating enzyme
COJEPEMI_(	COJEPE	-0.3717	NA	hypothetical p	NA	0	
COJEPEMI_(	norG_4	-0.37312	0.316355	HTH-type trans	NA	ydcR	helix_turn_helix gluconate operon transcriptional repressor
COJEPEMI_(	COJEPE	-0.37359	0.087403	hypothetical p	NA	0	TniQ
COJEPEMI_(	COJEPE	-0.37432	0.329679	hypothetical p	NA	tnpA	Tn3 transposase DDE domain
COJEPEMI_(	fabZ	-0.3744	0.094554	3-hydroxyacyl-	4.2.1.59	fabZ	Involved in unsaturated fatty acids biosynthesis. Catalyzes the dehydrat
COJEPEMI_(	aprE	-0.37548	0.295273	Subtilisin E	3.4.21.62	0	Subtilase family
COJEPEMI_(	cusS	-0.376	0.135262	Sensor histidir	2.7.13.3	copS	PhoQ Sensor
COJEPEMI_(	COJEPE	-0.37671	0.093617	Putative 4-hyd	4.1.3.17	rraA	Catalyzes the aldol cleavage of 4-hydroxy-4-methyl-2- oxoglutarate (HM
COJEPEMI_(	murD	-0.37697	0.061377	UDP-N-acetylr	6.3.2.9	murD	Cell wall formation. Catalyzes the addition of glutamate to the nucleoti
COJEPEMI_(	COJEPE	-0.37792	0.411352	hypothetical p	NA	pilB	Type II secretory pathway, ATPase PulE Tfp pilus assembly pathway, AT
COJEPEMI_(	COJEPE	-0.37952	0.540169	hypothetical p	NA	0	
COJEPEMI_(	ileS	-0.38001	0.135155	Isoleucine--tRI	6.1.1.5	ileS	amino acids such as valine, to avoid such errors it has two additional di
COJEPEMI_(	uvrB_2	-0.38104	0.029452	UvrABC systen	NA	0	Type III restriction protein res subunit
COJEPEMI_(	cyoA	-0.38122	0.260012	Cytochrome bc	NA	cyoA	COX Aromatic Rich Motif
COJEPEMI_(	hcaR_2	-0.38177	0.467323	Hca operon tra	NA	ynfL	LysR substrate binding domain
COJEPEMI_(	gyrB	-0.38223	0.027644	DNA gyrase su	5.6.2.2	gyrB	A type II topoisomerase that negatively supercoils closed circular doubl
COJEPEMI_(	srpA	-0.38293	0.053596	Catalase-relat	1.11.1.-	srpA	Has an organic peroxide-dependent peroxidase activity
COJEPEMI_(	fhuA	-0.38336	0.114236	Ferrichrome o	NA	0	TonB dependent receptor
COJEPEMI_(	hisM	-0.3836	0.349923	Histidine trans	NA	hisM	Binding-protein-dependent transport system inner membrane compone

COJEPEMI_(	citN	-0.38398	0.335752	Citrate transpo	NA	citN	Citrate transporter
COJEPEMI_(	bioF	-0.38443	0.135319	8-amino-7-oxo	2.3.1.47	bioF	8-amino-7-oxononanoate synthase
COJEPEMI_(	COJEPE	-0.38475	NA	hypothetical p	NA	0	
COJEPEMI_(	rhaS_3	-0.38572	0.073886	HTH-type trans	NA	rhaR	AraC-like ligand binding domain
COJEPEMI_(	COJEPE	-0.3862	0.436856	hypothetical p	NA	0	
COJEPEMI_(	mepA	-0.38748	0.107734	Multidrug expo	NA	0	MatE
COJEPEMI_(	COJEPE	-0.38766	0.121275	hypothetical p	NA	vacJ	MlaA lipoprotein
COJEPEMI_(	COJEPE	-0.38881	0.279328	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.38906	0.111064	hypothetical p	NA	0	Domain of Unknown Function (DUF1543)
COJEPEMI_(	COJEPE	-0.38978	0.43878	hypothetical p	NA	0	PgaD-like protein
COJEPEMI_(	COJEPE	-0.39044	0.597652	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.3915	0.273464	hypothetical p	NA	0	Endonuclease/Exonuclease/phosphatase family
COJEPEMI_(	COJEPE	-0.39251	0.461101	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.39307	0.213228	hypothetical p	NA	0	Domain of unknown function
COJEPEMI_(	COJEPE	-0.39339	0.213228	hypothetical p	NA	wza	Polysaccharide biosynthesis/export protein
COJEPEMI_(	phrB	-0.39369	0.21258	Deoxyribodipyr	4.1.99.3	phrB	DNA photolyase
COJEPEMI_(	COJEPE	-0.39442	0.360594	hypothetical p	NA	nucH	Lamin Tail Domain
COJEPEMI_(	ureF	-0.40037	0.271525	Urease access	NA	ureF	Required for maturation of urease via the functional incorporation of th
COJEPEMI_(	smtB	-0.40069	0.252027	Succinyl-CoA--	2.8.3.22	0	CoA-transferase family III
COJEPEMI_(	ahcY	-0.40089	0.274251	Adenosylhomo	3.3.1.1	ahcY	May play a key role in the regulation of the intracellular concentration o
COJEPEMI_(	COJEPE	-0.40109	0.226477	O-acetyl-L-hor	2.5.1.-	metY	Cys/Met metabolism PLP-dependent enzyme
COJEPEMI_(	cntO_1	-0.40127	0.702216	Metal-pseudo	NA	0	TonB dependent receptor
COJEPEMI_(	COJEPE	-0.40189	0.040406	hypothetical p	NA	0	NAD-dependent DNA ligase
COJEPEMI_(	rhtC_1	-0.40291	0.333683	Threonine efflu	NA	0	LysE type translocator
COJEPEMI_(	COJEPE	-0.40315	0.024723	hypothetical p	NA	iorA	Pyruvate ferredoxin/flavodoxin oxidoreductase
COJEPEMI_(	dmdC_1	-0.40389	0.334254	3-methylmerca	1.3.8.-	0	acyl-CoA dehydrogenase
COJEPEMI_(	sfnC_1	-0.40403	0.281368	putative FMNH	1.14.14.-	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	COJEPE	-0.40473	0.104527	hypothetical p	NA	0	
COJEPEMI_(	metK	-0.40491	0.175098	S-adenosylme	2.5.1.6	metK	Catalyzes the formation of S-adenosylmethionine (AdoMet) from meth
COJEPEMI_(	oprB_1	-0.40573	0.028272	Porin B	NA	oprB	Carbohydrate-selective porin, OprB family

COJEPEMI_(	COJEPE	-0.40618	0.071408	putative HTH-t	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	COJEPE	-0.40683	0.198341	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	pheS	-0.4094	0.100745	Phenylalanine-	6.1.1.20	pheS	Belongs to the class-II aminoacyl-tRNA synthetase family. Phe-tRNA sy
COJEPEMI_(	COJEPE	-0.41118	0.2037	hypothetical p	NA	appC	N-terminal TM domain of oligopeptide transport permease C
COJEPEMI_(	COJEPE	-0.41125	0.186459	hypothetical p	NA	0	
COJEPEMI_(	ugpQ	-0.41142	0.213649	Glycerophosph	3.1.4.46	0	Glycerophosphoryl diester phosphodiesterase family
COJEPEMI_(	eda	-0.4123	0.114092	KHG/KDPG ald	NA	eda	KDPG and KHG aldolase
COJEPEMI_(	ghrB	-0.41245	0.036807	Glyoxylate/hyc	1.1.1.79	ghrB	Belongs to the D-isomer specific 2-hydroxyacid dehydrogenase family
COJEPEMI_(	anmK	-0.41271	0.121612	Anhydro-N-ace	2.7.1.170	anmK	Catalyzes the specific phosphorylation of 1,6-anhydro-N- acetylmurami
COJEPEMI_(	COJEPE	-0.41322	0.151802	hypothetical p	NA	0	Gram-negative-bacterium-type cell outer membrane assembly
COJEPEMI_(	COJEPE	-0.4149	0.443368	hypothetical p	NA	0	Protein of unknown function (DUF4236)
COJEPEMI_(	COJEPE	-0.41548	0.461623	hypothetical p	NA	0	Small Multidrug Resistance protein
COJEPEMI_(	virS_1	-0.41574	0.26527	HTH-type trans	NA	0	helix_turn_helix, arabinose operon control protein
COJEPEMI_(	fabG_3	-0.41609	0.563006	3-oxoacyl-[acy	1.1.1.100	0	KR domain
COJEPEMI_(	gabR_3	-0.41651	0.320292	HTH-type trans	NA	0	helix_turn_helix gluconate operon transcriptional repressor
COJEPEMI_(	gltP_1	-0.41736	0.032659	Proton/glutam	NA	gltP	Catalyzes the proton-dependent transport of glutamate and aspartate
COJEPEMI_(	COJEPE	-0.41813	0.310867	Putative hydro	4.2.1.-	0	Belongs to the D-glutamate cyclase family
COJEPEMI_(	COJEPE	-0.41843	0.516577	hypothetical p	NA	pilV	type IV pilus modification protein PilV
COJEPEMI_(	hyuE	-0.41871	0.603173	Hydantoin race	5.1.99.5	hyuE	Asp/Glu/Hydantoin racemase
COJEPEMI_(	dmdC_3	-0.41907	0.105006	3-methylmerc	1.3.8.-	0	acyl-CoA dehydrogenase
COJEPEMI_(	gpsA	-0.41919	0.093373	Glycerol-3-phc	1.1.1.94	gpsA	Glycerol-3-phosphate dehydrogenase
COJEPEMI_(	COJEPE	-0.41967	0.360189	hypothetical p	NA	0	Exhibits S-adenosyl-L-methionine-dependent methyltransferase activity
COJEPEMI_(	COJEPE	-0.42073	0.22559	hypothetical p	NA	0	Outer membrane efflux protein
COJEPEMI_(	COJEPE	-0.4213	0.183201	hypothetical p	NA	0	MarC family integral membrane protein
COJEPEMI_(	yrdA_3	-0.42197	0.068589	Protein YrdA	NA	dapH	Hexapeptide repeat of succinyl-transferase
COJEPEMI_(	COJEPE	-0.42264	0.599276	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.42369	0.229372	hypothetical p	NA	0	Metallo-beta-lactamase superfamily
COJEPEMI_(	COJEPE	-0.42385	0.399906	hypothetical p	NA	0	Bacterial transcriptional regulator
COJEPEMI_(	COJEPE	-0.42409	0.247944	hypothetical p	NA	sspB	stringent starvation protein B
COJEPEMI_(	COQ3_1	-0.42412	0.188807	Ubiquinone bi	2.1.1.222	cfa	Mycolic acid cyclopropane synthetase

COJEPEMI_(	cpo	-0.42471	0.054014	Non-heme chl	1.11.1.10	cpo	Serine aminopeptidase, S33
COJEPEMI_(	COJEPE	-0.42669	0.433909	hypothetical p	NA	0	
COJEPEMI_(	ydeP	-0.42695	0.068132	Protein YdeP	NA	ydeP	Belongs to the prokaryotic molybdopterin-containing oxidoreductase fa
COJEPEMI_(	atpB	-0.42746	0.192005	ATP synthase s	NA	atpB	it plays a direct role in the translocation of protons across the membra
COJEPEMI_(	COJEPE	-0.42901	0.073309	hypothetical p	NA	0	
COJEPEMI_(	tsaQ1_1	-0.42925	0.378564	HTH-type trans	NA	0	helix_turn_helix isocitrate lyase regulation
COJEPEMI_(	rarD	-0.43059	0.35786	Protein RarD	NA	rarD	EamA-like transporter family
COJEPEMI_(	bamA_1	-0.43083	0.027343	Outer membra	NA	bamA	Part of the outer membrane protein assembly complex, which is involv
COJEPEMI_(	pepP	-0.43088	0.062709	Xaa-Pro amino	3.4.11.9	pepP	Belongs to the peptidase M24B family
COJEPEMI_(	COJEPE	-0.43176	0.431068	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.43278	0.231661	putative prote	NA	gph	Haloacid dehalogenase-like hydrolase
COJEPEMI_(	COJEPE	-0.4329	0.42953	hypothetical p	NA	0	TonB C terminal
COJEPEMI_(	COJEPE	-0.43341	0.071351	hypothetical p	NA	TLL0138	Uncharacterized protein conserved in bacteria (DUF2062)
COJEPEMI_(	rcsC_6	-0.43535	0.25335	Sensor histidir	2.7.13.3	MA20_23	helix_turn_helix, Lux Regulon
COJEPEMI_(	COJEPE	-0.43585	0.195589	hypothetical p	NA	0	hemolysin activation secretion protein
COJEPEMI_(	gdhA_2	-0.43602	0.130064	NADP-specific	1.4.1.4	gdhA	Belongs to the Glu Leu Phe Val dehydrogenases family
COJEPEMI_(	COJEPE	-0.43626	NA	hypothetical p	NA	0	2Fe-2S iron-sulfur cluster binding domain
COJEPEMI_(	phoR	-0.43634	0.024933	Phosphate reg	2.7.13.3	phoR	Histidine kinase
COJEPEMI_(	COJEPE	-0.43703	0.123923	Baeyer-Villige	1.14.13.-	0	Flavin-binding monooxygenase-like
COJEPEMI_(	ispG	-0.43844	0.165054	4-hydroxy-3-m	1.17.7.3	ispG	Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-2,4cPP) into
COJEPEMI_(	iscX	-0.43865	0.060105	Protein IscX	NA	iscX	Fe-S assembly protein IscX
COJEPEMI_(	COJEPE	-0.43888	0.452086	IS21 family tra	NA	0	IstB-like ATP binding protein
COJEPEMI_(	dauR	-0.43954	0.306636	Transcriptiona	NA	0	YheO-like PAS domain
COJEPEMI_(	budC_1	-0.43968	0.37266	Diacetyl reduc	1.1.1.304	budC	COG1028 Dehydrogenases with different specificities (related to short-
COJEPEMI_(	sutR_3	-0.43995	0.46034	HTH-type trans	NA	0	Helix-turn-helix domain
COJEPEMI_(	copA_1	-0.43995	0.032418	Copper resista	NA	copA	Multicopper oxidase
COJEPEMI_(	mutM	-0.44186	0.469094	Formamidopyr	3.2.2.23	fpg	Involved in base excision repair of DNA damaged by oxidation or by mu
COJEPEMI_(	COJEPE	-0.44214	0.511652	hypothetical p	NA	0	Glycosyl hydrolase 108
COJEPEMI_(	moaE1	-0.44218	0.043024	Molybdopterin	2.8.1.12	moaE	Molybdopterin converting factor, large subunit
COJEPEMI_(	nudF	-0.4422	0.220104	ADP-ribose py	3.6.1.13	nudF	NUDIX domain

COJEPEMI_(	rsmB	-0.44274	0.066107	Ribosomal RN	2.1.1.176	sun	Specifically methylates the cytosine at position 967 (m5C967) of 16S rR
COJEPEMI_(	rne	-0.44331	0.217617	Ribonuclease I	3.1.26.12	rne	Endoribonuclease that plays a central role in RNA processing and decay
COJEPEMI_(	bamB	-0.44342	0.07727	Outer membra	NA	bamB	Part of the outer membrane protein assembly complex, which is involv
COJEPEMI_(	murC	-0.44411	0.146239	UDP-N-acetylr	6.3.2.8	murC	Belongs to the MurCDEF family
COJEPEMI_(	ftsQ	-0.44411	0.010921	Cell division pr	NA	ftsQ	Essential cell division protein. May link together the upstream cell divis
COJEPEMI_(	COJEPE	-0.44449	0.283467	hypothetical p	NA	gpR	P2 phage tail completion protein R (GpR)
COJEPEMI_(	COJEPE	-0.44454	0.493126	putative prote	NA	HA62_21	Bacterial extracellular solute-binding protein
COJEPEMI_(	mrpF	-0.44487	0.232725	Na(+)/H(+) an	NA	phaF	Multiple resistance and pH regulation protein F (MrpF / PhaF)
COJEPEMI_(	glnG	-0.44511	0.066866	DNA-binding t	NA	glnG	response regulator
COJEPEMI_(	prfA	-0.44518	0.062735	Peptide chain	NA	prfA	Peptide chain release factor 1 directs the termination of translation in
COJEPEMI_(	intA	-0.4456	0.191261	Prophage inte	NA	0	Pfam:DUF4102
COJEPEMI_(	pdhD	-0.44603	0.376817	Dihydrolipoyl c	1.8.1.4	0	Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
COJEPEMI_(	argH	-0.44617	0.193522	Argininosuccin	4.3.2.1	argH	argininosuccinate lyase
COJEPEMI_(	COJEPE	-0.44643	0.049494	hypothetical p	NA	0	
COJEPEMI_(	comEC	-0.44662	0.454732	ComE operon p	NA	ycaI	Competence protein ComEC
COJEPEMI_(	COJEPE	-0.44674	0.177796	hypothetical p	NA	0	FCD domain
COJEPEMI_(	COJEPE	-0.4468	0.161194	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.44686	0.261702	hypothetical p	NA	0	Domain of unknown function (DUF4882)
COJEPEMI_(	smc_2	-0.44743	0.082038	Chromosome p	NA	smc	Required for chromosome condensation and partitioning
COJEPEMI_(	COJEPE	-0.44882	0.167811	hypothetical p	NA	holC	DNA polymerase III, chi subunit
COJEPEMI_(	rsmC	-0.44926	0.18476	Ribosomal RN	2.1.1.172	rsmC	Specifically methylates the guanine in position 1207 of 16S rRNA in the
COJEPEMI_(	COJEPE	-0.44943	0.085296	hypothetical p	NA	impJ	Bacterial Type VI secretion, VC_A0110, EvfL, ImpJ, VasE
COJEPEMI_(	COJEPE	-0.4502	0.156071	hypothetical p	NA	0	Metallo-beta-lactamase superfamily
COJEPEMI_(	zapE	-0.45103	0.004129	Cell division pr	NA	zapE	Reduces the stability of FtsZ polymers in the presence of ATP
COJEPEMI_(	COJEPE	-0.4513	0.449132	hypothetical p	NA	0	Protein of unknown function (DUF805)
COJEPEMI_(	ubiB_3	-0.45159	0.09764	putative prote	2.7.-.-	ubiB	ABC1 family
COJEPEMI_(	cidB_1	-0.45203	0.159088	Holin-like prot	NA	lrgB	LrgB-like family
COJEPEMI_(	COJEPE	-0.45219	0.046078	hypothetical p	NA	0	Protein of unknown function (DUF1294)
COJEPEMI_(	smf-1_	-0.45349	0.698905	Major fimbrial	NA	0	Type-1 fimbrial protein, A
COJEPEMI_(	betA	-0.45446	0.141582	Oxygen-depen	1.1.99.1	betA	Involved in the biosynthesis of the osmoprotectant glycine betaine. Cat

COJEPEMI_(	phnO	-0.4555	0.087851	Aminoalkylphc	2.3.1.280	phnO	Acetyltransferase (GNAT) domain
COJEPEMI_(	sdaA	-0.4564	0.118811	L-serine dehyd	4.3.1.17	sdaA	Serine dehydratase beta chain
COJEPEMI_(	COJEPE	-0.4581	0.597942	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.45903	0.589521	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.45913	0.612655	hypothetical p	NA	0	Branched-chain amino acid transport protein (AzlD)
COJEPEMI_(	COJEPE	-0.45917	0.645285	hypothetical p	NA	0	von willebrand factor, type A
COJEPEMI_(	nicP_2	-0.45977	0.287907	Porin-like prot	NA	0	outer membrane porin, OprD family
COJEPEMI_(	COJEPE	-0.46001	0.047349	Alpha-ketoglut	1.2.1.26	aldH	Aldehyde dehydrogenase family
COJEPEMI_(	COJEPE	-0.46002	0.23907	hypothetical p	NA	0	DnaJ molecular chaperone homology domain
COJEPEMI_(	rfnT	-0.46057	0.231383	Riboflavin trar	NA	0	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-0.46242	0.174737	hypothetical p	NA	0	Chromate transporter
COJEPEMI_(	COJEPE	-0.46247	0.48147	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	qseC_1	-0.46287	0.058437	Sensor protein	2.7.13.3	qseC	His Kinase A (phosphoacceptor) domain
COJEPEMI_(	metZ	-0.4632	0.040052	O-succinylhom	2.5.1.-	metZ	Catalyzes the formation of L-homocysteine from O- succinyl-L-homoser
COJEPEMI_(	yccS_2	-0.46382	0.068589	Inner membra	NA	yccS	FUSC-like inner membrane protein yccS
COJEPEMI_(	pal_2	-0.46399	0.034504	Peptidoglycan-	NA	0	OmpA family
COJEPEMI_(	COJEPE	-0.46452	0.12719	putative meta	3.-.-.-	0	Metallo-beta-lactamase superfamily
COJEPEMI_(	COJEPE	-0.46488	0.389525	hypothetical p	NA	0	Uncharacterised protein family (UPF0227)
COJEPEMI_(	COJEPE	-0.46546	0.057287	hypothetical p	NA	0	Gamma-glutamyl cyclotransferase, AIG2-like
COJEPEMI_(	COJEPE	-0.4663	0.027663	hypothetical p	NA	0	Glutathione S-transferase, N-terminal domain
COJEPEMI_(	hiuH_2	-0.4671	0.385244	5-hydroxyisour	3.5.2.17	yedX	Transthyretin
COJEPEMI_(	pcrA_1	-0.46748	0.013928	ATP-dependen	3.6.4.12	0	UvrD-like helicase C-terminal domain
COJEPEMI_(	lldP	-0.46798	0.560342	L-lactate perm	NA	lldP	L-lactate permease
COJEPEMI_(	COJEPE	-0.46843	NA	hypothetical p	NA	paaI	Thioesterase superfamily
COJEPEMI_(	garD	-0.47226	0.210684	Galactarate de	4.2.1.42	garD	D-galactarate dehydratase / Altronate hydrolase, C terminus
COJEPEMI_(	yahB	-0.47256	0.348051	putative HTH-t	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.47294	0.508986	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.47306	0.347276	hypothetical p	NA	yigE	Phosphodiester glycosidase
COJEPEMI_(	COJEPE	-0.47319	0.066579	hypothetical p	NA	0	Rhomboid family
COJEPEMI_(	COJEPE	-0.47506	0.100504	hypothetical p	NA	0	FCD

COJEPEMI_(	perB	-0.47519	0.078444	GDP-perosami	2.3.1.227	0	maltose O-acetyltransferase activity
COJEPEMI_(	COJEPE	-0.47541	0.293614	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	fadA_1	-0.47616	0.168969	Putative acyltr	2.3.1.-	fadA	Belongs to the thiolase family
COJEPEMI_(	tilS	-0.47624	0.061171	tRNA(Ile)-lysic	6.3.4.19	tilS	Ligates lysine onto the cytidine present at position 34 of the AUA codor
COJEPEMI_(	atpD1	-0.47664	0.10724	ATP synthase s	7.1.2.2	atpD	Produces ATP from ADP in the presence of a proton gradient across the
COJEPEMI_(	rlmB_2	-0.4776	0.043815	23S rRNA (gua	2.1.1.185	rlmB	Specifically methylates the ribose of guanosine 2251 in 23S rRNA
COJEPEMI_(	COJEPE	-0.47792	0.509807	hypothetical p	NA	BP3797	EamA-like transporter family
COJEPEMI_(	COJEPE	-0.47798	0.163019	hypothetical p	NA	0	Belongs to the peptidase S1B family
COJEPEMI_(	COJEPE	-0.47871	0.388286	hypothetical p	NA	0	Domain of unknown function (DUF4105)
COJEPEMI_(	COJEPE	-0.47901	0.019897	putative oxido	1.-.-.-	0	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	COJEPE	-0.48042	0.121431	hypothetical p	NA	0	Bacterial protein of unknown function (DUF885)
COJEPEMI_(	yhgF	-0.48082	0.079903	Protein YhgF	NA	yhgF	Tex-like protein N-terminal domain
COJEPEMI_(	kdpA	-0.48143	0.245429	Potassium-tra	NA	kdpA	Part of the high-affinity ATP-driven potassium transport (or Kdp) syster
COJEPEMI_(	gloB_1	-0.48208	0.028212	Hydroxyacylglu	3.1.2.6	ytnP	Metallo-beta-lactamase superfamily
COJEPEMI_(	COJEPE	-0.48281	0.414287	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.4829	0.042476	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.48335	0.18318	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.48472	0.088958	hypothetical p	NA	hpcD	5-carboxymethyl-2-hydroxymuconate isomerase
COJEPEMI_(	COJEPE	-0.48518	0.116009	hypothetical p	NA	0	
COJEPEMI_(	sfnC_3	-0.48608	0.460798	putative FMNH	1.14.14.-	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	leuS	-0.48743	0.128829	Leucine--tRNA	6.1.1.4	leuS	Belongs to the class-I aminoacyl-tRNA synthetase family
COJEPEMI_(	cpoB	-0.48862	0.091808	Cell division cc	NA	cpoB	TolA binding protein trimerisation
COJEPEMI_(	COJEPE	-0.49042	0.338491	Alpha-ketoglut	1.2.1.26	0	Aldehyde dehydrogenase family
COJEPEMI_(	cynR_2	-0.49099	0.100239	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	glnS	-0.49136	0.053798	Glutamine--tR	6.1.1.18	glnS	tRNA synthetases class I (E and Q), anti-codon binding domain
COJEPEMI_(	COJEPE	-0.49182	0.022144	hypothetical p	NA	0	
COJEPEMI_(	etfB	-0.49308	0.044131	Electron transf	NA	etfB	Electron transfer flavoprotein
COJEPEMI_(	qseB_1	-0.4934	0.025013	Transcriptiona	NA	qseB	Transcriptional regulatory protein, C terminal
COJEPEMI_(	folB	-0.4937	0.157531	Dihydroneopte	4.1.2.25	folB	Catalyzes the conversion of 7,8-dihydroneopterin to 6- hydroxymethyl-7
COJEPEMI_(	ycgM	-0.49381	0.066327	putative prote	NA	ycgM	Fumarylacetoacetate (FAA) hydrolase family

COJEPEMI_(	aat	-0.49722	0.058219	Leucyl/phenyla	2.3.2.6	aat	Functions in the N-end rule pathway of protein degradation where it cc
COJEPEMI_(	ssuC_2	-0.49783	0.275172	Putative aliph	NA	0	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-0.4981	0.197139	hypothetical p	NA	0	Endonuclease/Exonuclease/phosphatase family
COJEPEMI_(	etfA	-0.49884	0.070789	Electron transf	NA	etfA	Electron transfer flavoprotein
COJEPEMI_(	btsR	-0.50051	0.075588	Transcriptiona	NA	algR	LytTr DNA-binding domain
COJEPEMI_(	COJEPE	-0.50063	0.189902	hypothetical p	NA	0	
COJEPEMI_(	argS	-0.50137	0.043472	Arginine--tRN/	6.1.1.19	argS	Arginyl-tRNA synthetase
COJEPEMI_(	COJEPE	-0.50165	0.141912	Acetyltransfer	2.3.1.-	yjcF	Acetyltransferase (GNAT) domain
COJEPEMI_(	nicP_1	-0.50205	0.295556	Porin-like prot	NA	0	outer membrane porin, OprD family
COJEPEMI_(	dmlR_6	-0.50427	0.042687	HTH-type trans	NA	VL23_16	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.50451	0.2234	hypothetical p	NA	ywfM	EamA-like transporter family
COJEPEMI_(	COJEPE	-0.50513	0.003977	hypothetical p	NA	Z012_09	Belongs to the sodium neurotransmitter symporter (SNF) (TC 2.A.22) fa
COJEPEMI_(	lrp_7	-0.50655	0.171138	Leucine-respo	NA	0	helix_turn_helix ASNC type
COJEPEMI_(	COJEPE	-0.50837	0.590104	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	lplT	-0.50875	0.054014	Lysophospholi	NA	lplT	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-0.50981	0.208467	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.5105	0.478101	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.51115	0.112933	hypothetical p	NA	0	Major facilitator superfamily
COJEPEMI_(	COJEPE	-0.51125	0.076763	hypothetical p	NA	0	Bacterial capsule synthesis protein PGA_cap
COJEPEMI_(	yciI	-0.51145	0.151802	Protein YciI	NA	yciI	YCII-related domain
COJEPEMI_(	linX	-0.5117	0.64332	2,5-dichloro-2,	1.1.1.-	0	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	COJEPE	-0.51192	0.004962	putative prote	NA	Z012_06	Tautomerase enzyme
COJEPEMI_(	COJEPE	-0.51206	0.217051	hypothetical p	NA	0	
COJEPEMI_(	yjdJ	-0.51388	0.45639	putative prote	NA	yjdJ	GCN5-related N-acetyl-transferase
COJEPEMI_(	ampD	-0.51396	0.044076	1,6-anhydro-N	3.5.1.28	ampD	Ami_2
COJEPEMI_(	COJEPE	-0.51412	0.037879	hypothetical p	NA	cydA	Ubiquinol Oxidase
COJEPEMI_(	nicT	-0.51425	0.209161	Putative meta	NA	0	COG0477 Permeases of the major facilitator superfamily
COJEPEMI_(	COJEPE	-0.51473	0.085121	hypothetical p	NA	0	Protein of unknown function (DUF805)
COJEPEMI_(	COJEPE	-0.51546	0.132661	hypothetical p	NA	Z012_03	Bacterial low temperature requirement A protein (LtrA)
COJEPEMI_(	COJEPE	-0.51607	0.01553	hypothetical p	NA	0	L,D-transpeptidase catalytic domain

COJEPEMI_(	xerC_2	-0.5163	0.017053	Tyrosine recon	NA	xerC	Belongs to the 'phage' integrase family. XerC subfamily
COJEPEMI_(	azoR1	-0.51666	0.178878	FMN-depende	1.7.1.17	azoR	Catalyzes the reductive cleavage of azo bond in aromatic azo compoun
COJEPEMI_(	puuB_3	-0.51877	0.070415	Gamma-gluta	1.4.3.-	0	FAD dependent oxidoreductase
COJEPEMI_(	adh1	-0.51911	0.004281	Long-chain-alc	1.1.1.192	dhaT	Iron-containing alcohol dehydrogenase
COJEPEMI_(	decR_2	-0.51929	0.454551	DNA-binding t	NA	lrp_2	Lrp/AsnC ligand binding domain
COJEPEMI_(	hisS	-0.52017	0.003214	Histidine--tRN	6.1.1.21	hisS	histidyl-tRNA synthetase
COJEPEMI_(	COJEPE	-0.52041	0.164282	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.52046	0.543836	hypothetical p	NA	0	Transcriptional regulator
COJEPEMI_(	COJEPE	-0.52095	0.331379	hypothetical p	NA	0	Permease for cytosine/purines, uracil, thiamine, allantoin
COJEPEMI_(	yqjF	-0.52112	0.275901	Inner membra	NA	yqjF	DoxX
COJEPEMI_(	COJEPE	-0.5229	0.233368	hypothetical p	NA	0	Motif C-terminal to PAS motifs (likely to contribute to PAS structural do
COJEPEMI_(	COJEPE	-0.52351	0.316385	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.52377	0.26527	hypothetical p	NA	0	
COJEPEMI_(	dnaE	-0.52534	0.079462	DNA polymera	2.7.7.7	dnaE	DNA polymerase
COJEPEMI_(	cstA	-0.52538	0.063496	Peptide transp	NA	cstA	Carbon starvation protein
COJEPEMI_(	COJEPE	-0.52563	0.046882	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ybeY	-0.52571	0.085881	Endoribonucle	3.1.-.-	ybeY	Single strand-specific metallo-endoribonuclease involved in late-stage
COJEPEMI_(	COJEPE	-0.52608	NA	hypothetical p	NA	0	Tail E family protein
COJEPEMI_(	blc_2	-0.52674	0.452773	Outer membra	NA	blc	Lipocalin-like domain
COJEPEMI_(	COJEPE	-0.52749	0.062864	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2094)
COJEPEMI_(	rhaS_8	-0.52767	0.079758	HTH-type trans	NA	0	PAS fold
COJEPEMI_(	queF	-0.5283	0.041891	NADPH-depen	1.7.1.13	queF	Catalyzes the NADPH-dependent reduction of 7-cyano-7- deazaguanine
COJEPEMI_(	lpxD	-0.52847	0.007665	UDP-3-O-acylg	2.3.1.-	lpxD	Catalyzes the N-acylation of UDP-3-O-acylglucosamine using 3-hydroxy
COJEPEMI_(	aaeB	-0.52997	0.189193	p-hydroxybenz	NA	0	Fusaric acid resistance protein family
COJEPEMI_(	phoU	-0.53031	0.010513	Phosphate-spe	NA	phoU	Plays a role in the regulation of phosphate uptake
COJEPEMI_(	czcR	-0.53036	0.011985	Transcriptiona	NA	irlR	Transcriptional regulatory protein, C terminal
COJEPEMI_(	ssuA_3	-0.53043	0.21466	Putative alipha	NA	0	NMT1-like family
COJEPEMI_(	mneA	-0.53096	0.062102	Putative mang	NA	IV02_135	Uncharacterized protein family UPF0016
COJEPEMI_(	COJEPE	-0.53189	0.029942	hypothetical p	NA	0	GDSL-like Lipase/Acylhydrolase family
COJEPEMI_(	COJEPE	-0.53195	0.057701	hypothetical p	NA	0	Glycosyl transferases group 1

COJEPEMI_(	mhpC	-0.53395	0.537533	2-hydroxy-6-o	3.7.1.14	0	Alpha/beta hydrolase family
COJEPEMI_(	COJEPE	-0.53577	0.088081	hypothetical p	NA	0	PFAM Glycosyl transferase, group 1
COJEPEMI_(	htpX_2	-0.5363	0.021829	Protease HtpX	3.4.24.-	htpX	Peptidase family M48
COJEPEMI_(	COJEPE	-0.53754	0.606413	hypothetical p	NA	0	Lecithin retinol acyltransferase
COJEPEMI_(	COJEPE	-0.53854	0.393237	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.53907	0.045331	hypothetical p	NA	0	PepSY-associated TM region
COJEPEMI_(	paaX	-0.53946	0.077588	Transcriptiona	NA	paaX	PaaX-like protein
COJEPEMI_(	amtB_2	-0.54033	0.032552	Ammonia cha	NA	amtB	Ammonium Transporter Family
COJEPEMI_(	cat_2	-0.54195	0.051439	Chloramphenic	2.3.1.28	0	This enzyme is an effector of chloramphenicol resistance in bacteria
COJEPEMI_(	ubiH	-0.54207	0.002847	2-octaprenyl-6	1.14.13.-	ubiH	FAD binding domain
COJEPEMI_(	rhdA	-0.54332	0.120899	Thiosulfate su	2.8.1.1	rhdA	Rhodanese Homology Domain
COJEPEMI_(	COJEPE	-0.54372	0.13279	hypothetical p	NA	0	Domain of unknown function (DUF4845)
COJEPEMI_(	COJEPE	-0.54373	0.422246	hypothetical p	NA	0	Dicarboxylate carrier protein MatC N-terminus
COJEPEMI_(	COJEPE	-0.54388	0.068937	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.54426	0.002409	hypothetical p	NA	0	Secretory lipase
COJEPEMI_(	COJEPE	-0.54764	0.536969	hypothetical p	NA	azlC	AzlC protein
COJEPEMI_(	argC	-0.54942	0.006509	N-acetyl-gamr	1.2.1.38	argC	Catalyzes the NADPH-dependent reduction of N-acetyl-5- glutamyl pho
COJEPEMI_(	cynR_1	-0.55055	0.172278	HTH-type trans	NA	mdcR	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.55061	0.071498	hypothetical p	NA	0	
COJEPEMI_(	glnQ_2	-0.55077	0.272748	Glutamine tra	NA	glnQ	AAA domain, putative AbiEii toxin, Type IV TA system
COJEPEMI_(	psd	-0.55091	0.190941	Phosphatidylse	4.1.1.65	psd	Belongs to the phosphatidylserine decarboxylase family. PSD-B subfam
COJEPEMI_(	metXS	-0.55115	0.04194	Homoserine O	2.3.1.46	metX	Transfers a succinyl group from succinyl-CoA to L- homoserine, forming
COJEPEMI_(	craA	-0.55162	0.094554	Chloramphenic	NA	cmr	Major facilitator Superfamily
COJEPEMI_(	pgi	-0.55316	0.389246	Glucose-6-pho	5.3.1.9	pgi	Belongs to the GPI family
COJEPEMI_(	COJEPE	-0.55341	0.46864	hypothetical p	NA	0	
COJEPEMI_(	phnR	-0.55358	0.08946	Putative trans	NA	0	UTRA
COJEPEMI_(	COJEPE	-0.5554	0.145077	hypothetical p	NA	0	helix_turn_helix, Lux Regulon
COJEPEMI_(	feaR	-0.55608	0.144406	Transcriptiona	NA	feaR	AraC-binding-like domain
COJEPEMI_(	COJEPE	-0.5567	0.573145	hypothetical p	NA	tetR7	Bacterial regulatory proteins, tetR family
COJEPEMI_(	cusR_1	-0.55924	0.040656	Transcriptiona	NA	0	Transcriptional regulatory protein, C terminal

COJEPEMI_(	epmB	-0.55968	0.167858	L-lysine 2,3-an	5.4.3.-	epmB	4Fe-4S single cluster domain
COJEPEMI_(	COJEPE	-0.56241	0.319051	hypothetical p	NA	0	
COJEPEMI_(	mmgC_	-0.56285	0.002963	Acyl-CoA dehy	1.3.99.-	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	COJEPE	-0.56371	0.016766	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.56419	0.20376	hypothetical p	NA	0	PAAR motif
COJEPEMI_(	COJEPE	-0.56513	0.291808	hypothetical p	NA	0	DNA (cytosine-5-)-methyltransferase activity
COJEPEMI_(	COJEPE	-0.56666	0.028551	hypothetical p	NA	0	
COJEPEMI_(	znuA	-0.56768	0.394425	High-affinity z	NA	sitA	Zinc-uptake complex component A periplasmic
COJEPEMI_(	COJEPE	-0.56795	0.00681	hypothetical p	NA	0	Forms passive diffusion pores that allow small molecular weight hydro
COJEPEMI_(	pcaF_3	-0.56944	0.168591	Beta-ketoadip	2.3.1.174	dcaF	Belongs to the thiolase family
COJEPEMI_(	COJEPE	-0.57047	0.090265	NADH dehydro	1.6.-.-	0	Pyridine nucleotide-disulphide oxidoreductase
COJEPEMI_(	htrE_1	-0.57095	0.133913	Outer membra	NA	mrkC	usher protein
COJEPEMI_(	COJEPE	-0.57129	0.173865	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	-0.57136	0.105062	hypothetical p	NA	0	Tetratricopeptide repeat
COJEPEMI_(	rsuA	-0.57168	0.000296	Ribosomal sm	5.4.99.19	rsuA	Belongs to the pseudouridine synthase RsuA family
COJEPEMI_(	COJEPE	-0.57238	0.034504	hypothetical p	NA	0	transcriptional regulator
COJEPEMI_(	paiB	-0.57309	0.226912	Protease synth	NA	paiB	Putative FMN-binding domain
COJEPEMI_(	gltR_1	-0.57315	0.133808	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.57398	0.295678	hypothetical p	NA	0	
COJEPEMI_(	galE_1	-0.57509	0.263021	UDP-glucose 4	5.1.3.2	galE	UDP-glucose 4-epimerase
COJEPEMI_(	COJEPE	-0.57544	0.117038	hypothetical p	NA	sndH	Glucose / Sorbosone dehydrogenase
COJEPEMI_(	glxR_2	-0.57617	0.060799	2-hydroxy-3-ox	1.1.1.60	0	NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase
COJEPEMI_(	COJEPE	-0.57625	0.11968	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.57711	0.010909	hypothetical p	NA	0	ABC-type transport auxiliary lipoprotein component
COJEPEMI_(	COJEPE	-0.58011	0.059868	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	rdmC	-0.58119	0.108306	Aclacinomycin	3.1.1.95	estB	Serine aminopeptidase, S33
COJEPEMI_(	tetA_1	-0.58126	0.106217	Tetracycline re	NA	tetA	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-0.58181	0.023188	hypothetical p	NA	0	Protein of unknown function (DUF4256)
COJEPEMI_(	sasA_2	-0.58216	0.002483	Adaptive-resp	2.7.-.-	rstB	PhoQ Sensor
COJEPEMI_(	dmlR_1	-0.58485	0.067393	HTH-type trans	NA	0	LysR substrate binding domain

COJEPEMI_(	dtpT	-0.58559	0.141673	Di-/tripeptide	NA	dtpT	POT family
COJEPEMI_(	ybdL	-0.58609	0.000596	Methionine an	2.6.1.88	ybdL	Cys/Met metabolism PLP-dependent enzyme
COJEPEMI_(	fadJ_2	-0.58663	0.058268	Fatty acid oxid	NA	fadJ	Belongs to the enoyl-CoA hydratase isomerase family
COJEPEMI_(	tyrB	-0.58717	0.069716	Aromatic-ami	2.6.1.57	tyrB	Aminotransferase class I and II
COJEPEMI_(	COJEPE	-0.58795	0.521219	hypothetical p	NA	0	Putative phage holin
COJEPEMI_(	COJEPE	-0.58822	0.331288	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.58824	0.004907	GTP cyclohydr	NA	ybgI	NIF3 (NGG1p interacting factor 3)
COJEPEMI_(	lip1	-0.58889	0.013619	Lipase 1	3.1.1.3	0	Serine aminopeptidase, S33
COJEPEMI_(	mobA	-0.59004	0.078444	Molybdenum c	2.7.7.77	mobA	Transfers a GMP moiety from GTP to Mo-molybdopterin (Mo- MPT) co
COJEPEMI_(	COJEPE	-0.59014	0.020233	hypothetical p	NA	ats	Acetyltransferase (GNAT) domain
COJEPEMI_(	COJEPE	-0.5963	0.169705	putative 5-deh	4.2.1.41	kdgD	Belongs to the DapA family
COJEPEMI_(	COJEPE	-0.5973	0.000342	Aspartate kina	2.7.2.4	lysC	Belongs to the aspartokinase family
COJEPEMI_(	metQ_1	-0.59761	0.027413	Methionine-bi	NA	0	NLPA lipoprotein
COJEPEMI_(	dmlR_8	-0.59806	0.083022	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	vdh	-0.5981	0.03517	Vanillin dehyd	1.2.1.67	vdh	belongs to the aldehyde dehydrogenase family
COJEPEMI_(	cpdA_1	-0.59903	0.333204	3',5'-cyclic ade	3.1.4.53	yaeI	Calcineurin-like phosphoesterase superfamily domain
COJEPEMI_(	epsL	-0.59939	0.001055	putative sugar	2.-.-.-	pglC	Bacterial sugar transferase
COJEPEMI_(	serC	-0.59941	0.108056	Phosphoserine	2.6.1.52	serC	Catalyzes the reversible conversion of 3- phosphohydroxypyruvate to ph
COJEPEMI_(	COJEPE	-0.5998	0.004106	hypothetical p	NA	0	MAPEG family
COJEPEMI_(	COJEPE	-0.60103	0.061348	hypothetical p	NA	0	Protein of unknown function (DUF1232)
COJEPEMI_(	COJEPE	-0.60103	0.064786	hypothetical p	NA	0	Protein of unknown function (DUF1449)
COJEPEMI_(	COJEPE	-0.60131	0.456673	hypothetical p	NA	0	Protein of unknown function (DUF962)
COJEPEMI_(	asnC	-0.60142	0.055832	Regulatory prc	NA	0	DeoR-like helix-turn-helix domain
COJEPEMI_(	cybC	-0.60182	0.000191	Soluble cytoch	NA	cybC	Cytochrome b562
COJEPEMI_(	COJEPE	-0.60381	NA	hypothetical p	NA	0	
COJEPEMI_(	aes	-0.60462	0.021718	Acetyl esteras	3.1.1.-	0	Carboxylesterase family
COJEPEMI_(	COJEPE	-0.60771	0.023852	hypothetical p	NA	0	Belongs to the UPF0145 family
COJEPEMI_(	COJEPE	-0.60777	0.24966	putative prote	NA	MA20_32	Circularly permuted ATP-grasp type 2
COJEPEMI_(	epd	-0.60816	0.008584	D-erythrose-4-	1.2.1.72	gap	Belongs to the glyceraldehyde-3-phosphate dehydrogenase family
COJEPEMI_(	COJEPE	-0.60922	0.065057	hypothetical p	NA	mreD	rod shape-determining protein MreD

COJEPEMI_(	gltS	-0.60983	0.002811	Sodium/glutar	NA	gltS	Catalyzes the sodium-dependent transport of glutamate
COJEPEMI_(	proP_2	-0.6104	0.065904	Proline/betain	NA	cjaB	Major facilitator superfamily
COJEPEMI_(	COJEPE	-0.61074	0.0142	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.61156	0.06248	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	gltC_1	-0.61375	0.01644	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	atpA	-0.61387	0.048673	ATP synthase s	7.1.2.2	atpA	Produces ATP from ADP in the presence of a proton gradient across the
COJEPEMI_(	COJEPE	-0.61458	0.050333	hypothetical p	NA	rbn	UPF0761 membrane protein
COJEPEMI_(	COJEPE	-0.61459	0.067599	hypothetical p	NA	ygdD	Protein of unknown function (DUF423)
COJEPEMI_(	COJEPE	-0.61468	0.027791	Baeyer-Villige	1.14.13.-	0	Flavin-binding monooxygenase-like
COJEPEMI_(	COJEPE	-0.61524	0.104022	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.61647	0.155381	hypothetical p	NA	0	Tyrosine phosphatase family
COJEPEMI_(	COJEPE	-0.61648	0.081157	hypothetical p	NA	0	
COJEPEMI_(	mip	-0.61674	0.020905	Outer membra	5.2.1.8	fklB	peptidyl-prolyl cis-trans isomerase
COJEPEMI_(	rcsC_5	-0.61814	0.024163	Sensor histidir	2.7.13.3	baeS	PhoQ Sensor
COJEPEMI_(	COJEPE	-0.61849	0.024141	hypothetical p	NA	phaD	Bacterial transcriptional repressor
COJEPEMI_(	nhaP	-0.61876	0.147166	Na(+)/H(+) an	NA	0	Sodium/hydrogen exchanger family
COJEPEMI_(	COJEPE	-0.61905	0.387035	hypothetical p	NA	ydaF_1	Acetyltransferase (GNAT) domain
COJEPEMI_(	COJEPE	-0.61947	0.05624	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.62058	0.007381	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.6214	0.041891	hypothetical p	NA	0	PaaX-like protein C-terminal domain
COJEPEMI_(	queC_2	-0.62183	0.292711	7-cyano-7-dea	6.3.4.20	0	Queuosine biosynthesis protein QueC
COJEPEMI_(	COJEPE	-0.62278	0.245798	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	bfr_1	-0.62329	0.560342	Bacterioferriti	1.16.3.1	bfr	Iron-storage protein, whose ferroxidase center binds Fe(2) ions, oxidiz
COJEPEMI_(	COJEPE	-0.62512	0.47072	hypothetical p	NA	0	
COJEPEMI_(	csy1	-0.62543	0.040656	CRISPR-associ	NA	csy1	CRISPR-associated protein (Cas_Csy1)
COJEPEMI_(	hbpA	-0.62594	0.065265	Heme-binding	NA	hbpA	Bacterial extracellular solute-binding proteins, family 5 Middle
COJEPEMI_(	COJEPE	-0.62624	0.168591	hypothetical p	NA	MA20_03	Esterase-like activity of phytase
COJEPEMI_(	COJEPE	-0.62675	0.131739	hypothetical p	NA	0	PAP2 (Acid phosphatase) superfamily protein
COJEPEMI_(	paaF_2	-0.62766	0.222064	2,3-dehydroad	4.2.1.17	dcaE	Enoyl-CoA hydratase/isomerase
COJEPEMI_(	atpH	-0.62787	0.058964	ATP synthase s	NA	atpH	F(1)F(0) ATP synthase produces ATP from ADP in the presence of a pro

COJEPEMI_(	czcA_1	-0.62953	0.014011	Cobalt-zinc-ca	NA	0	Belongs to the resistance-nodulation-cell division (RND) (TC 2.A.6) fam
COJEPEMI_(	COJEPE	-0.63066	0.430249	hypothetical p	NA	0	Putative general bacterial porin
COJEPEMI_(	lptG	-0.6324	0.008182	Lipopolysaccha	NA	lptG	Predicted permease YjgP/YjgQ family
COJEPEMI_(	emrA_3	-0.63321	0.070297	Colistin resista	NA	emrA	Barrel-sandwich domain of CusB or HlyD membrane-fusion
COJEPEMI_(	COJEPE	-0.63371	0.01133	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.63583	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.63646	0.002717	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.63723	0.132285	hypothetical p	NA	0	Tfp pilus assembly protein FimV
COJEPEMI_(	COJEPE	-0.6375	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.63801	NA	hypothetical p	NA	0	Prokaryotic dksA/traR C4-type zinc finger
COJEPEMI_(	COJEPE	-0.64001	0.144812	hypothetical p	NA	0	
COJEPEMI_(	gyrA	-0.64253	8.24E-06	DNA gyrase su	5.6.2.2	gyrA	A type II topoisomerase that negatively supercoils closed circular doubl
COJEPEMI_(	COJEPE	-0.64288	0.377762	hypothetical p	NA	0	
COJEPEMI_(	mmpI	-0.6437	0.331379	Major membra	NA	srpI	- Catabolite gene activator and regulatory subunit of cAMP-dependent
COJEPEMI_(	COJEPE	-0.64399	0.029329	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.64448	0.049501	hypothetical p	NA	0	
COJEPEMI_(	lrp_2	-0.64483	0.088568	Leucine-respo	NA	0	Lrp/AsnC ligand binding domain
COJEPEMI_(	COJEPE	-0.6454	0.394468	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	secF	-0.6462	0.023009	Protein translc	NA	secF	Part of the Sec protein translocase complex. Interacts with the SecYEG
COJEPEMI_(	soj	-0.64653	0.001045	Sporulation ini	3.6.-.-	parA	4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family
COJEPEMI_(	yadH	-0.64665	0.016768	Inner membra	NA	yadH	Transport permease protein
COJEPEMI_(	COJEPE	-0.64811	0.045276	hypothetical p	NA	yneE	Bestrophin, RFP-TM, chloride channel
COJEPEMI_(	COJEPE	-0.64886	0.178296	hypothetical p	NA	yeaO	Protein of unknown function, DUF488
COJEPEMI_(	COJEPE	-0.6492	0.065381	hypothetical p	NA	0	Carboxymuconolactone decarboxylase family
COJEPEMI_(	hisI	-0.64926	0.006502	Histidine biosy	3.5.4.19	hisI	belongs to the PRA-CH family
COJEPEMI_(	COJEPE	-0.64961	0.076689	hypothetical p	NA	0	
COJEPEMI_(	hpt	-0.65027	0.029443	Hypoxanthine	2.4.2.8	hpt	Belongs to the purine pyrimidine phosphoribosyltransferase family
COJEPEMI_(	COJEPE	-0.6504	0.304088	hypothetical p	NA	Z012_00(	
COJEPEMI_(	hcaB_1	-0.65091	0.000735	3-phenylpropic	1.3.1.87	0	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	COJEPE	-0.65188	0.226886	hypothetical p	NA	wblG	Glycosyl transferases group 1

COJEPEMI_(	lacC	-0.65197	0.014264	Tagatose-6-ph	2.7.1.144	fruK	Belongs to the carbohydrate kinase PfkB family
COJEPEMI_(	ddl_1	-0.65373	0.002862	D-alanine--D-a	6.3.2.4	ddl	Belongs to the D-alanine--D-alanine ligase family
COJEPEMI_(	COJEPE	-0.6556	0.007819	hypothetical p	NA	0	Domain of unknown function (DUF4442)
COJEPEMI_(	COJEPE	-0.65587	0.027669	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	ktrB	-0.65592	0.009099	Ktr system pot	NA	ktrB	potassium uptake protein, TrkH
COJEPEMI_(	COJEPE	-0.65601	0.001823	hypothetical p	NA	yjgR	Bacterial protein of unknown function (DUF853)
COJEPEMI_(	COJEPE	-0.65718	0.018633	hypothetical p	NA	0	Bacterial transcriptional regulator
COJEPEMI_(	COJEPE	-0.65794	0.003903	hypothetical p	NA	0	Phosphotransferase enzyme family
COJEPEMI_(	COJEPE	-0.65825	0.006356	putative CtpA-	3.4.21.-	ctp	tail specific protease
COJEPEMI_(	gltR_3	-0.66003	0.017674	HTH-type trans	NA	MA20_16	LysR substrate binding domain
COJEPEMI_(	COJEPE	-0.66008	0.034137	hypothetical p	NA	0	Lysine methyltransferase
COJEPEMI_(	accA_1	-0.66168	0.044158	Acetyl-coenzyr	2.1.3.15	atuC	Carboxyl transferase domain
COJEPEMI_(	ampC_1	-0.66177	0.003209	Beta-lactamas	3.5.2.6	ampC	Beta-lactamase
COJEPEMI_(	COJEPE	-0.6622	0.096737	hypothetical p	NA	0	Peptidase C39 family
COJEPEMI_(	COJEPE	-0.66242	0.209648	hypothetical p	NA	0	
COJEPEMI_(	hisQ	-0.66248	0.258668	Histidine trans	NA	hisQ	COG4215 ABC-type arginine transport system, permease component
COJEPEMI_(	betT1	-0.66385	0.00694	Osmo-indeper	NA	betT	BCCT, betaine/carnitine/choline family transporter
COJEPEMI_(	yceF	-0.66404	0.022935	7-methyl-GTP	3.6.1.-	yceF	Maf-like protein
COJEPEMI_(	COJEPE	-0.66428	0.019504	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.66498	0.001068	hypothetical p	NA	0	PGAP1-like protein
COJEPEMI_(	COJEPE	-0.66559	0.013216	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.66589	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.6665	0.014381	hypothetical p	NA	0	EamA-like transporter family
COJEPEMI_(	cidA	-0.66706	0.33061	Holin-like prot	NA	cidA	LrgA family
COJEPEMI_(	envZ	-0.66738	0.003878	Osmolarity sei	2.7.13.3	envZ	PhoQ Sensor
COJEPEMI_(	COJEPE	-0.6675	0.307086	hypothetical p	NA	0	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-0.66767	0.006647	N-acetyldiami	3.5.1.47	0	Peptidase dimerisation domain
COJEPEMI_(	gstB_2	-0.66767	0.00196	Glutathione S-	2.5.1.18	yliJ	Glutathione S-transferase, N-terminal domain
COJEPEMI_(	lpxB	-0.66828	0.000199	Lipid-A-disacc	2.4.1.182	lpxB	Condensation of UDP-2,3-diacylglucosamine and 2,3- diacylglucosamin
COJEPEMI_(	ohrB	-0.67005	0.303912	Organic hydro	NA	ohr	OsmC-like protein

COJEPEMI_(	hflD	-0.67075	0.009078	High frequenc	NA	hflD	Protein of unknown function (DUF489)
COJEPEMI_(	COJEPE	-0.67197	NA	IS5 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	galU	-0.6735	0.497824	UTP--glucose-	2.7.7.9	galU	UTP-glucose-1-phosphate uridylyltransferase
COJEPEMI_(	COJEPE	-0.67352	0.077741	hypothetical p	NA	0	
COJEPEMI_(	rnd_1	-0.67491	0.05816	Ribonuclease I	3.1.13.5	0	3'-5' exonuclease
COJEPEMI_(	sasA_3	-0.67617	0.02373	Adaptive-resp	2.7.-.-	pilS	PAS domain
COJEPEMI_(	COJEPE	-0.67756	0.009229	hypothetical p	NA	pqiA	Paraquat-inducible protein A
COJEPEMI_(	fpr_1	-0.67822	0.073535	Ferredoxin--N	1.18.1.2	fpr	Oxidoreductase FAD-binding domain
COJEPEMI_(	epsF_2	-0.67904	0.01553	Type II secreti	NA	pilC	Type II secretion system (T2SS), protein F
COJEPEMI_(	pqqE	-0.67979	0.061377	PqqA peptide	1.21.98.4	pqqE	Iron-sulfur cluster-binding domain
COJEPEMI_(	COJEPE	-0.68033	0.520103	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.6811	0.033331	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.68383	0.547768	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.6845	0.001668	hypothetical p	NA	0	diguanylate cyclase
COJEPEMI_(	COJEPE	-0.68667	0.002337	hypothetical p	NA	0	phosphohistidine phosphatase
COJEPEMI_(	pheP	-0.68696	0.020233	Phenylalanine-	NA	0	Amino acid permease
COJEPEMI_(	trmA	-0.68704	0.032659	tRNA/tmRNA	2.1.1.-	trmA	Dual-specificity methyltransferase that catalyzes the formation of 5-m
COJEPEMI_(	yadG	-0.68744	0.000559	putative ABC t	NA	yadG	AAA domain, putative AbiEii toxin, Type IV TA system
COJEPEMI_(	COJEPE	-0.68803	0.171866	hypothetical p	NA	0	Domain of unknown function (DUF1853)
COJEPEMI_(	esiB_2	-0.68902	5.16E-06	Secretory imm	NA	0	Sel1-like repeats.
COJEPEMI_(	ssuR	-0.68958	0.023045	HTH-type trans	NA	cbl	Transcriptional regulator
COJEPEMI_(	sauU	-0.69023	0.007759	putative sulfo	NA	0	Sugar (and other) transporter
COJEPEMI_(	ftsI	-0.69079	0.000632	Peptidoglycan	3.4.16.4	ftsI	Catalyzes cross-linking of the peptidoglycan cell wall at the division sep
COJEPEMI_(	slmA	-0.69098	0.003292	Nucleoid occlu	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	-0.69146	0.332011	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	yfcG_1	-0.69153	0.357019	Disulfide-bond	1.8.4.-	gst5	Glutathione S-transferase, C-terminal domain
COJEPEMI_(	maeA	-0.69251	0.021792	NAD-depende	1.1.1.38	maeA	malate dehydrogenase (decarboxylating) (NAD+) activity
COJEPEMI_(	lrp_6	-0.6941	0.008956	Leucine-respo	NA	putR	AsnC-type helix-turn-helix domain
COJEPEMI_(	proC_2	-0.6946	2.32E-05	Pyrroline-5-ca	1.5.1.2	proC	Catalyzes the reduction of 1-pyrroline-5-carboxylate (PCA) to L-proline
COJEPEMI_(	COJEPE	-0.69485	0.245054	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2314)

COJEPEMI_(	eno	-0.69515	0.004856	Enolase	4.2.1.11	eno	Catalyzes the reversible conversion of 2- phosphoglycerate into phosph
COJEPEMI_(	COJEPE	-0.69587	0.003141	hypothetical p	NA	0	
COJEPEMI_(	hisG	-0.69761	0.000682	ATP phosphori	2.4.2.17	hisG	Catalyzes the condensation of ATP and 5-phosphoribose 1- diphosphate
COJEPEMI_(	ftsW	-0.6983	0.000334	putative peptic	2.4.1.129	ftsW	Peptidoglycan polymerase that is essential for cell division
COJEPEMI_(	norM_2	-0.6984	0.019271	Multidrug resi	NA	mdtK	MatE
COJEPEMI_(	menE	-0.69868	0.057701	2-succinylbenz	6.2.1.26	fcs	AMP-binding enzyme
COJEPEMI_(	ftsA_1	-0.69985	0.001696	Cell division pr	NA	ftsA	Cell division protein that is involved in the assembly of the Z ring. May
COJEPEMI_(	COJEPE	-0.70052	5.42E-05	hypothetical p	NA	0	protein conserved in bacteria
COJEPEMI_(	paaH_1	-0.70071	0.100366	3-hydroxyadip	1.1.1.-	dcaH	3-hydroxyacyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	atpE	-0.70084	0.07014	ATP synthase s	NA	atpE	F(1)F(0) ATP synthase produces ATP from ADP in the presence of a pro
COJEPEMI_(	bioH	-0.70192	0.004949	Pimeloyl-[acyl	3.1.1.85	bioH	hydrolases or acyltransferases (alpha beta hydrolase superfamily)
COJEPEMI_(	yeiR	-0.70319	0.005808	Zinc-binding G	3.6.-.-	yeiR	CobW/HypB/UreG, nucleotide-binding domain
COJEPEMI_(	proB	-0.7035	4.29E-05	Glutamate 5-k	2.7.2.11	proB	Catalyzes the transfer of a phosphate group to glutamate to form L-glu
COJEPEMI_(	COJEPE	-0.70388	0.002534	hypothetical p	NA	0	Domain of unknown function (DUF4112)
COJEPEMI_(	COJEPE	-0.70425	0.009856	hypothetical p	NA	0	Secretory lipase
COJEPEMI_(	sasA_1	-0.70426	0.004429	Adaptive-resp	2.7.-.-	colS	His Kinase A (phosphoacceptor) domain
COJEPEMI_(	recR	-0.70459	0.000325	Recombinatio	NA	recR	May play a role in DNA repair. It seems to be involved in an RecBC-inde
COJEPEMI_(	COJEPE	-0.70466	0.000781	hypothetical p	NA	0	OsmC-like protein
COJEPEMI_(	COJEPE	-0.70508	0.032081	putative HTH-t	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	COJEPE	-0.70616	0.064892	hypothetical p	NA	guaA_1	Glutamine amidotransferase class-I
COJEPEMI_(	COJEPE	-0.7064	0.060785	hypothetical p	NA	acdP	Membrane dipeptidase (Peptidase family M19)
COJEPEMI_(	dsbC_2	-0.70692	0.185878	putative thiol:	NA	dsbC	Required for disulfide bond formation in some periplasmic proteins. Ac
COJEPEMI_(	COJEPE	-0.7071	0.00423	hypothetical p	NA	0	Type II secretion system protein C
COJEPEMI_(	parB	-0.70753	0.000509	putative chron	NA	parB	Belongs to the ParB family
COJEPEMI_(	COJEPE	-0.70758	0.021401	hypothetical p	NA	0	
COJEPEMI_(	psiE	-0.70793	0.017348	Protein PsiE	NA	psiE	Phosphate-starvation-inducible E
COJEPEMI_(	thiL	-0.70831	0.014902	Thiamine-mor	2.7.4.16	thiL	Catalyzes the ATP-dependent phosphorylation of thiamine- monophosp
COJEPEMI_(	COJEPE	-0.70836	0.074921	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ppiD	-0.71093	0.000874	Peptidyl-prolyl	5.2.1.8	ppiD	Peptidylprolyl isomerase
COJEPEMI_(	naiP_2	-0.71094	0.216453	Putative niacir	NA	0	Uncharacterised MFS-type transporter YbfB

COJEPEMI_(	decR_1	-0.71104	0.130286	DNA-binding t	NA	0	helix_turn_helix ASNC type
COJEPEMI_(	lpxA	-0.71152	1.23E-05	Acyl-[acyl-carr	2.3.1.129	lpxA	Involved in the biosynthesis of lipid A, a phosphorylated glycolipid that a
COJEPEMI_(	COJEPE	-0.71184	0.123805	hypothetical p	NA	P	Terminase RNaseH-like domain
COJEPEMI_(	COJEPE	-0.71236	0.105505	hypothetical p	NA	0	Belongs to the purine-cytosine permease (2.A.39) family
COJEPEMI_(	COJEPE	-0.71376	0.028787	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.71387	0.088162	putative signa	NA	0	Putative diguanylate phosphodiesterase
COJEPEMI_(	cysS	-0.71389	0.009679	Cysteine--tRN/	6.1.1.16	cysS	Belongs to the class-I aminoacyl-tRNA synthetase family
COJEPEMI_(	ptk	-0.7147	0.004234	Tyrosine-prote	2.7.10.-	wzc	G-rich domain on putative tyrosine kinase
COJEPEMI_(	virS_2	-0.71537	0.014039	HTH-type trans	NA	0	Arabinose-binding domain of AraC transcription regulator, N-term
COJEPEMI_(	COJEPE	-0.71682	0.011054	hypothetical p	NA	0	
COJEPEMI_(	sfnG	-0.71712	0.279829	FMNH(2)-depe	1.14.14.3	sfnG	Luciferase-like monooxygenase
COJEPEMI_(	yceJ_1	-0.71723	0.026487	Cytochrome b5	NA	cybB	Cytochrome b/b6/petB
COJEPEMI_(	COJEPE	-0.7178	0.006692	hypothetical p	NA	0	
COJEPEMI_(	rlmA	-0.71846	0.003209	23S rRNA (gua	2.1.1.187	rrmA	Methyltransferase domain
COJEPEMI_(	rpoC	-0.71854	0.000699	DNA-directed	2.7.7.6	rpoC	DNA-dependent RNA polymerase catalyzes the transcription of DNA int
COJEPEMI_(	pepA	-0.7198	0.006672	cytosol amino	3.4.11.10	pepA	Presumably involved in the processing and regular turnover of intracellu
COJEPEMI_(	COJEPE	-0.721	0.019152	hypothetical p	NA	dotU1	Type VI secretion system protein DotU
COJEPEMI_(	COJEPE	-0.72208	0.016226	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	purD	-0.7224	0.000206	Phosphoribosy	6.3.4.13	purD	Belongs to the GARS family
COJEPEMI_(	orn	-0.72254	0.026114	Oligoribonucle	3.1.-.-	orn	3'-to-5' exoribonuclease specific for small oligoribonucleotides
COJEPEMI_(	ssuC_1	-0.72266	0.382353	Putative aliph	NA	ssuC	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	mltG	-0.7229	0.018514	Endolytic mure	4.2.2.-	mltG	Functions as a peptidoglycan terminase that cleaves nascent peptidogly
COJEPEMI_(	sbmA	-0.72383	0.00724	Peptide antibi	NA	sbmA	SbmA/BacA-like family
COJEPEMI_(	COJEPE	-0.72426	5.28E-05	hypothetical p	NA	0	Putative MetA-pathway of phenol degradation
COJEPEMI_(	pqqC	-0.72579	0.009773	Pyrroloquinolir	1.3.3.11	pqqC	Ring cyclization and eight-electron oxidation of 3a-(2- amino-2-carboxy
COJEPEMI_(	rpsO	-0.7261	0.005299	30S ribosomal	NA	rpsO	Forms an intersubunit bridge (bridge B4) with the 23S rRNA of the 50S
COJEPEMI_(	yajC	-0.72626	0.006515	Sec translocon	NA	yajC	Preprotein translocase subunit YajC
COJEPEMI_(	prlC_2	-0.72681	0.040406	Oligopeptidase	3.4.24.70	prlC	Peptidase family M3
COJEPEMI_(	COJEPE	-0.72848	0.336133	hypothetical p	NA	azlC	AzlC protein
COJEPEMI_(	COJEPE	-0.7286	3.21E-05	hypothetical p	NA	0	diguanylate cyclase

COJEPEMI_(	COJEPE	-0.72962	0.003367	hypothetical p	NA	yajQ	Belongs to the UPF0234 family
COJEPEMI_(	kefF_1	-0.72974	0.193206	Glutathione-re	1.6.5.2	0	Flavodoxin-like fold
COJEPEMI_(	cat_1	-0.73166	0.019149	Chloramphenic	2.3.1.28	0	Hexapeptide repeat of succinyl-transferase
COJEPEMI_(	tal	-0.73192	0.272694	Transaldolase	2.2.1.2	tal	Transaldolase is important for the balance of metabolites in the pentos
COJEPEMI_(	gudD	-0.73241	0.000861	Glucarate deh	4.2.1.40	gudD	Mandelate racemase / muconate lactonizing enzyme, C-terminal doma
COJEPEMI_(	thadh	-0.73301	0.037997	L-threo-3-hydr	4.3.1.16	srr	Pyridoxal-phosphate dependent enzyme
COJEPEMI_(	COJEPE	-0.73349	0.230275	hypothetical p	NA	pglF	RmlD substrate binding domain
COJEPEMI_(	aroB	-0.73484	0.000169	3-dehydroquin	4.2.3.4	aroB	Catalyzes the conversion of 3-deoxy-D-arabino- heptulosonate 7-phospl
COJEPEMI_(	ppk_1	-0.7352	9.70E-06	Polyphosphate	2.7.4.1	ppk	Catalyzes the reversible transfer of the terminal phosphate of ATP to fo
COJEPEMI_(	COJEPE	-0.73575	NA	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	-0.73597	0.000738	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	-0.7372	0.034582	hypothetical p	NA	0	thiamine diphosphate biosynthetic process
COJEPEMI_(	COJEPE	-0.73839	0.065386	hypothetical p	NA	0	
COJEPEMI_(	pta	-0.73928	0.000964	Phosphate ace	2.3.1.8	pta	belongs to the CobB CobQ family
COJEPEMI_(	COJEPE	-0.73944	0.002976	hypothetical p	NA	0	
COJEPEMI_(	lon_1	-0.73949	0.000609	Lon protease	3.4.21.53	0	Belongs to the peptidase S16 family
COJEPEMI_(	COJEPE	-0.73982	0.011801	hypothetical p	NA	0	Phosphoglycerate mutase family
COJEPEMI_(	COJEPE	-0.74049	0.373095	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.74123	0.203776	hypothetical p	NA	0	Methyltransferase domain
COJEPEMI_(	COJEPE	-0.74182	0.169244	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.74241	0.236429	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.74314	0.006026	hypothetical p	NA	0	
COJEPEMI_(	atpF	-0.74415	0.028139	ATP synthase s	NA	atpF	Component of the F(0) channel, it forms part of the peripheral stalk, lir
COJEPEMI_(	pcpR	-0.74459	0.000124	PCP degradati	NA	0	LysR substrate binding domain
COJEPEMI_(	ycfH_2	-0.74566	0.001279	putative meta	3.1.-.-	0	TatD related DNase
COJEPEMI_(	COJEPE	-0.7463	0.189902	hypothetical p	NA	0	-acetyltransferase
COJEPEMI_(	COJEPE	-0.74636	0.48147	IS21 family tra	NA	0	Integrase core domain
COJEPEMI_(	plaP	-0.74701	0.015285	Low-affinity p	NA	yeeF	Amino acid permease
COJEPEMI_(	COJEPE	-0.74813	0.00915	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	rlmB_1	-0.75404	0.000345	23S rRNA (gua	2.1.1.185	spoU	SpoU rRNA Methylase family

COJEPEMI_(	pcaK_2	-0.75473	0.011419	4-hydroxybenz	NA	pcaK	Uncharacterised MFS-type transporter YbfB
COJEPEMI_(	oprM_1	-0.75516	4.27E-05	Outer membra	NA	oprM	Outer membrane efflux protein
COJEPEMI_(	COJEPE	-0.75546	0.001627	hypothetical p	NA	0	Protein of unknown function (DUF445)
COJEPEMI_(	pspB	-0.75631	0.164832	Putative phosp	3.1.3.3	cobC	Phosphoglycerate mutase family
COJEPEMI_(	COJEPE	-0.75686	0.12743	hypothetical p	NA	0	
COJEPEMI_(	fruA	-0.76022	0.000747	PTS system fru	NA	fruA	Phosphotransferase system, EIIC
COJEPEMI_(	ycaC_3	-0.76072	0.006672	putative hydro	4.-.-.-	ycaC	Isochorismatase family
COJEPEMI_(	dmoA_	-0.767	0.316118	Dimethyl-sulfi	1.14.13.1	0	Luciferase-like monooxygenase
COJEPEMI_(	rep_2	-0.76768	0.009417	ATP-dependen	3.6.4.12	0	DNA helicase
COJEPEMI_(	COJEPE	-0.76782	0.000106	hypothetical p	NA	0	TRAP-type C4-dicarboxylate transport system periplasmic component
COJEPEMI_(	sfnC_2	-0.76819	0.118807	putative FMNH	1.14.14.-	soxC	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	ohrR	-0.76899	0.105486	Organic hydrop	NA	ohrR	helix_turn_helix multiple antibiotic resistance protein
COJEPEMI_(	birA	-0.77011	0.023936	Bifunctional lig	6.3.4.15	birA	Biotin/lipoate A/B protein ligase family
COJEPEMI_(	COJEPE	-0.77043	NA	hypothetical p	NA	0	Ogr/Delta-like zinc finger
COJEPEMI_(	metF	-0.77107	0.022969	5,10-methylen	1.5.1.20	metF	Methylenetetrahydrofolate reductase
COJEPEMI_(	COJEPE	-0.77185	0.000104	hypothetical p	NA	0	
COJEPEMI_(	atpG	-0.77307	0.006754	ATP synthase g	NA	atpG	Produces ATP from ADP in the presence of a proton gradient across the
COJEPEMI_(	COJEPE	-0.77404	5.42E-05	hypothetical p	NA	0	DUF218 domain
COJEPEMI_(	hda	-0.7758	0.000169	DnaA regulato	NA	hda	Belongs to the DnaA family
COJEPEMI_(	COJEPE	-0.77724	0.263021	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.77825	0.000159	hypothetical p	NA	0	Mitochondrial fission ELM1
COJEPEMI_(	COJEPE	-0.77835	NA	hypothetical p	NA	0	
COJEPEMI_(	mmgC_	-0.77998	0.0362	Acyl-CoA dehy	1.3.99.-	fadE	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	per	-0.78122	0.049225	GDP-perosami	2.6.1.102	btrR	Belongs to the DegT DnrJ EryC1 family
COJEPEMI_(	clpP	-0.78237	5.04E-05	ATP-dependen	3.4.21.92	clpP	Cleaves peptides in various proteins in a process that requires ATP hydr
COJEPEMI_(	pcaU	-0.78278	0.028139	Pca operon reg	NA	pcaU	helix_turn_helix isocitrate lyase regulation
COJEPEMI_(	COJEPE	-0.78421	NA	hypothetical p	NA	0	Protein of unknown function (DUF2726)
COJEPEMI_(	COJEPE	-0.78522	NA	hypothetical p	NA	0	Phage protein (N4 Gp49/phage Sf6 gene 66) family
COJEPEMI_(	arnT	-0.78625	0.26204	Undecaprenyl	2.4.2.43	arnT	Dolichyl-phosphate-mannose-protein mannosyltransferase
COJEPEMI_(	COJEPE	-0.78757	0.003243	hypothetical p	NA	cspC	Excalibur calcium-binding domain

COJEPEMI_(	COJEPE	-0.78942	0.00052	Long-chain-fat	6.2.1.3	MA20_2(	AMP-binding enzyme C-terminal domain
COJEPEMI_(	COJEPE	-0.79045	0.042309	putative ribosc	1.14.11.-	ycfD	A domain family that is part of the cupin metalloenzyme superfamily.
COJEPEMI_(	COJEPE	-0.79048	0.065157	hypothetical p	NA	0	
COJEPEMI_(	bacC_2	-0.79097	0.208575	Dihydroantica	1.1.1.385	0	Enoyl-(Acyl carrier protein) reductase
COJEPEMI_(	COJEPE	-0.79137	0.19348	hypothetical p	NA	0	
COJEPEMI_(	alx	-0.7938	0.027598	Putative mem	NA	alx	Integral membrane protein TerC family
COJEPEMI_(	uao	-0.79632	NA	Uric acid degr	NA	uraD	OHCU decarboxylase
COJEPEMI_(	COJEPE	-0.79854	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.79865	0.010937	hypothetical p	NA	Z012_09(	Na H antiporter
COJEPEMI_(	norM_1	-0.79913	0.226486	Multidrug resi	NA	norM	MatE
COJEPEMI_(	COJEPE	-0.79987	0.111012	hypothetical p	NA	yneF	diguanylate cyclase
COJEPEMI_(	COJEPE	-0.80076	NA	IS4 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	COJEPE	-0.80177	0.231865	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.80198	0.000878	hypothetical p	NA	0	Protein of unknown function (DUF2846)
COJEPEMI_(	COJEPE	-0.80262	0.056111	hypothetical p	NA	tcuB	TIGRFAM CitB domain protein
COJEPEMI_(	COJEPE	-0.80337	0.054263	hypothetical p	NA	0	LysE type translocator
COJEPEMI_(	COJEPE	-0.80374	0.063197	hypothetical p	NA	0	VirC1 protein
COJEPEMI_(	dmlR_4	-0.80648	0.003955	HTH-type trans	NA	0	Transcriptional regulator
COJEPEMI_(	lepB	-0.80708	0.000237	Signal peptida	3.4.21.89	lepB	Belongs to the peptidase S26 family
COJEPEMI_(	glnL	-0.80777	0.000259	Sensory histidi	2.7.13.3	glnL	PAS domain
COJEPEMI_(	mreC	-0.80986	0.0014	Cell shape-det	NA	mreC	Involved in formation and maintenance of cell shape
COJEPEMI_(	COJEPE	-0.81222	0.011678	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.81399	0.049325	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.81485	0.036132	hypothetical p	NA	0	Pfam:DUF955
COJEPEMI_(	mhpT	-0.8168	0.017236	3-(3-hydroxy-p	NA	mhpT	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-0.81748	0.256247	hypothetical p	NA	0	Domain of unknown function (DUF1833)
COJEPEMI_(	hmp	-0.818	0.462821	Flavohemopro	1.14.12.1	hmp	Globin
COJEPEMI_(	COJEPE	-0.81916	0.218936	hypothetical p	NA	0	Domain of unknown function (DUF4442)
COJEPEMI_(	COJEPE	-0.81959	NA	hypothetical p	NA	0	
COJEPEMI_(	ktrA	-0.82014	0.001577	Ktr system pot	NA	ktrA	TrkA-N domain

COJEPEMI_(	iutA_2	-0.82152	0.000306	Ferric aerobac	NA	0	TonB dependent receptor
COJEPEMI_(	ftsL	-0.82218	0.000632	Cell division pr	NA	ftsL	Essential cell division protein. May link together the upstream cell divis
COJEPEMI_(	COJEPE	-0.8225	0.046882	hypothetical p	NA	fimT	Type II transport protein GspH
COJEPEMI_(	COJEPE	-0.82287	5.10E-05	hypothetical p	NA	pilJ	Methyl-accepting chemotaxis-like domains (chemotaxis sensory transd
COJEPEMI_(	COJEPE	-0.82289	0.228531	hypothetical p	NA	0	Transcriptional regulator
COJEPEMI_(	kdsA	-0.82294	0.009551	2-dehydro-3-d	2.5.1.55	kdsA	Belongs to the KdsA family
COJEPEMI_(	COJEPE	-0.82361	5.92E-05	hypothetical p	NA	icmF	Type VI secretion protein IcmF C-terminal
COJEPEMI_(	COJEPE	-0.82383	0.265197	hypothetical p	NA	0	Parallel beta-helix repeats
COJEPEMI_(	COJEPE	-0.82453	0.278596	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.82487	NA	IS4 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	COJEPE	-0.82575	0.096214	hypothetical p	NA	0	
COJEPEMI_(	soxC_2	-0.8261	0.182439	Dibenzothioph	NA	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	aroA	-0.82648	5.32E-05	3-phosphoshik	2.5.1.19	aroA	Catalyzes the transfer of the enolpyruvyl moiety of phosphoenolpyruvat
COJEPEMI_(	fhuE_1	-0.828	0.001024	FhuE receptor	NA	0	TonB dependent receptor
COJEPEMI_(	quiC	-0.8294	0.018685	3-dehydroshiki	4.2.1.118	quiC	Periplasmic copper-binding protein (NosD)
COJEPEMI_(	pqqD	-0.82942	0.016663	PqqA binding p	NA	pqqD	Coenzyme PQQ synthesis protein D (PqqD)
COJEPEMI_(	COQ5_1	-0.83274	0.019271	2-methoxy-6-p	2.1.1.163	0	Methyltransferase domain
COJEPEMI_(	gdhB_2	-0.83603	0.000198	Quinoprotein g	1.1.5.2	gdhB	Glucose / Sorbosone dehydrogenase
COJEPEMI_(	COJEPE	-0.83807	0.05169	hypothetical p	NA	0	
COJEPEMI_(	murA	-0.83848	1.05E-05	UDP-N-acetylg	2.5.1.7	murA	Belongs to the EPSP synthase family. MurA subfamily
COJEPEMI_(	gntK	-0.83972	0.001998	Thermoresista	2.7.1.12	gntK	AAA domain
COJEPEMI_(	minD	-0.8408	0.001448	Septum site-d	NA	minD	Belongs to the ParA family
COJEPEMI_(	obg	-0.84174	0.002682	GTPase Obg	3.6.5.-	obg	An essential GTPase which binds GTP, GDP and possibly (p)ppGpp with
COJEPEMI_(	COJEPE	-0.84252	8.12E-07	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.84332	3.25E-06	Putative multi	3.6.3.-	vcaM	ABC transporter
COJEPEMI_(	fadE	-0.84555	0.018325	Acyl-coenzyme	1.3.8.7	fadE	Domain of unknown function (DUF1974)
COJEPEMI_(	ycgL	-0.84631	0.000726	Protein YcgL	NA	ycgL	YcgL domain
COJEPEMI_(	caiD	-0.84633	4.38E-06	Carnitinyl-CoA	4.2.1.149	0	Enoyl-CoA hydratase
COJEPEMI_(	RBKS	-0.8469	7.33E-05	Ribokinase	2.7.1.15	pfkB	pfkB family carbohydrate kinase
COJEPEMI_(	cpdA_4	-0.84708	0.006576	3',5'-cyclic ade	3.1.4.53	cpdA	Hydrolyzes cAMP to 5'-AMP. Plays an important regulatory role in modu

COJEPEMI_(	glyQ	-0.84789	0.000991	Glycine--tRNA	6.1.1.14	glyQ	glycyl-tRNA synthetase, alpha subunit
COJEPEMI_(	COJEPE	-0.85039	0.054037	hypothetical p	NA	impH	overlaps another CDS with the same product name
COJEPEMI_(	COJEPE	-0.85057	6.49E-06	hypothetical p	NA	yfgM	Tetratricopeptide repeat-like domain
COJEPEMI_(	rpoB	-0.85218	2.08E-05	DNA-directed	2.7.7.6	rpoB	DNA-dependent RNA polymerase catalyzes the transcription of DNA int
COJEPEMI_(	COJEPE	-0.85445	0.000233	putative signa	NA	0	Putative diguanylate phosphodiesterase
COJEPEMI_(	COJEPE	-0.85474	0.020547	hypothetical p	NA	pstA	Phosphate transport system permease
COJEPEMI_(	lptF	-0.85501	0.000145	Lipopolysaccha	NA	lptF	Predicted permease YjgP/YjgQ family
COJEPEMI_(	rhtA_3	-0.856	0.222573	Threonine/hor	NA	rhtA	EamA-like transporter family
COJEPEMI_(	COJEPE	-0.85933	0.05816	hypothetical p	NA	0	
COJEPEMI_(	fosB	-0.85993	0.165148	Metallothiol tr	2.5.1.-	0	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
COJEPEMI_(	COJEPE	-0.86278	0.045331	hypothetical p	NA	0	Flavodoxin
COJEPEMI_(	prsE	-0.8628	0.000819	Type I secretio	NA	0	HlyD membrane-fusion protein of T1SS
COJEPEMI_(	comM_	-0.86317	0.004219	Competence p	NA	comM	Magnesium chelatase, subunit ChlI
COJEPEMI_(	kynU	-0.86449	0.004036	Kynureninase	3.7.1.3	kynU	Catalyzes the cleavage of L-kynurenine (L-Kyn) and L-3- hydroxykynuren
COJEPEMI_(	COJEPE	-0.8653	0.000131	Putative phosp	3.1.1.32	pldA	Phospholipase
COJEPEMI_(	COJEPE	-0.86622	0.183035	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.86787	0.105195	hypothetical p	NA	0	Acetyltransferase (GNAT) domain
COJEPEMI_(	COJEPE	-0.86897	0.110008	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-0.87367	1.83E-07	hypothetical p	NA	0	
COJEPEMI_(	minE	-0.87492	0.000195	Cell division to	NA	minE	Prevents the cell division inhibition by proteins MinC and MinD at interr
COJEPEMI_(	yrdA_2	-0.87631	0.029942	Protein YrdA	NA	paaY	Bacterial transferase hexapeptide (six repeats)
COJEPEMI_(	murE	-0.87647	2.11E-05	UDP-N-acetylr	6.3.2.13	murE	Catalyzes the addition of meso-diaminopimelic acid to the nucleotide p
COJEPEMI_(	ruvB_2	-0.87754	0.002219	Holliday juncti	3.6.4.12	dnaX	DNA polymerase III is a complex, multichain enzyme responsible for m
COJEPEMI_(	COJEPE	-0.87762	2.25E-06	Beta-ketodeca	2.3.1.207	fabH	synthase III
COJEPEMI_(	surE_2	-0.88146	0.085881	5'/3'-nucleotic	3.1.3.5	0	Survival protein SurE
COJEPEMI_(	COJEPE	-0.88238	0.005101	hypothetical p	NA	atuA	Pfam:DUF1446
COJEPEMI_(	COJEPE	-0.88484	0.065381	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.88815	0.160346	hypothetical p	NA	0	Uncharacterized protein conserved in bacteria (DUF2247)
COJEPEMI_(	ftsB	-0.88856	4.13E-05	Cell division pr	NA	ftsB	Essential cell division protein. May link together the upstream cell divis
COJEPEMI_(	COJEPE	-0.89074	0.043815	Alpha-ketoglut	1.2.1.26	0	Aldehyde dehydrogenase family

COJEPEMI_(	COJEPE	-0.89118	0.17157	hypothetical p	NA	0	
COJEPEMI_(	proP_3	-0.89159	0.054358	Proline/betain	NA	citA	Sugar (and other) transporter
COJEPEMI_(	COJEPE	-0.89207	NA	hypothetical p	NA	0	Uncharacterized conserved protein (DUF2280)
COJEPEMI_(	COJEPE	-0.89228	0.192425	hypothetical p	NA	0	Hep Hag repeat protein
COJEPEMI_(	lipR_1	-0.89288	0.00603	Putative acety	3.1.1.-	est	Steryl acetyl hydrolase
COJEPEMI_(	ttr	-0.89374	0.212608	Acetyltransfer	2.3.1.-	ttr	Acetyltransferase (GNAT) domain
COJEPEMI_(	aroP_1	-0.89391	0.175426	Aromatic amir	NA	aroP	Amino acid permease
COJEPEMI_(	COJEPE	-0.89394	0.01332	hypothetical p	NA	tolA	Gram-negative bacterial TonB protein C-terminal
COJEPEMI_(	glnH_2	-0.89479	0.048324	ABC transporte	NA	cjaA	Bacterial periplasmic substrate-binding proteins
COJEPEMI_(	nagL	-0.89594	0.147332	Maleylpyruvat	5.2.1.4	maiA	Glutathione S-transferase, N-terminal domain
COJEPEMI_(	moeA	-0.89677	0.000234	Molybdopterin	2.10.1.1	moeA	Probable molybdopterin binding domain
COJEPEMI_(	COJEPE	-0.89714	0.001457	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.90092	0.02683	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	mnhE1	-0.90118	0.004292	Na(+)/H(+) an	NA	phaE	Na+/H+ ion antiporter subunit
COJEPEMI_(	COJEPE	-0.90303	0.217008	hypothetical p	NA	MA20_23	EamA-like transporter family
COJEPEMI_(	COJEPE	-0.90513	NA	hypothetical p	NA	0	transcriptional regulator
COJEPEMI_(	hcaR_4	-0.90802	0.198461	Hca operon tra	NA	0	LysR substrate binding domain
COJEPEMI_(	hisD	-0.90823	1.69E-05	Histidinol dehy	1.1.1.23	hisD	Catalyzes the sequential NAD-dependent oxidations of L- histidinol to L
COJEPEMI_(	COJEPE	-0.90964	2.78E-05	hypothetical p	NA	0	Protein similar to CwfJ C-terminus 1
COJEPEMI_(	gsiC	-0.91191	0.002506	Glutathione tr	NA	0	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	ycgJ	-0.91249	NA	putative meth	2.1.1.-	yafE	DREV methyltransferase
COJEPEMI_(	thlA_1	-0.91565	1.23E-06	Acetyl-CoA ace	2.3.1.9	bamN	Belongs to the thiolase family
COJEPEMI_(	COJEPE	-0.91974	0.013978	hypothetical p	NA	0	protein conserved in bacteria
COJEPEMI_(	thiE_2	-0.92144	0.012385	Thiamine-phos	2.5.1.3	0	Belongs to the Nudix hydrolase family
COJEPEMI_(	miaB	-0.92269	0.000667	tRNA-2-methy	2.8.4.3	miaB	Catalyzes the methylthiolation of N6- (dimethylallyl)adenosine (i(6)A),
COJEPEMI_(	btuE	-0.92304	5.08E-06	Thioredoxin/gl	1.11.1.15	btuE	Glutathione peroxidase
COJEPEMI_(	COJEPE	-0.92655	5.86E-07	hypothetical p	NA	0	MaoC like domain
COJEPEMI_(	COJEPE	-0.92777	0.007293	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.93014	4.92E-07	hypothetical p	NA	0	
COJEPEMI_(	gpFI	-0.93061	NA	Putative proph	NA	fI	Phage tail sheath protein subtilisin-like domain

COJEPEMI_(	hisC	-0.93164	0.000959	Histidinol-phos	2.6.1.9	hisC	Belongs to the class-II pyridoxal-phosphate-dependent aminotransferas
COJEPEMI_(	ves	-0.9317	0.095672	Protein Ves	NA	hutD	HutD
COJEPEMI_(	COJEPE	-0.93198	4.98E-06	hypothetical p	NA	0	
COJEPEMI_(	yjjV	-0.93343	0.005341	putative meta	3.1.-.-	yjjV	TatD related DNase
COJEPEMI_(	thiG	-0.93384	9.85E-05	Thiazole synth	2.8.1.10	thiG	Catalyzes the rearrangement of 1-deoxy-D-xylulose 5- phosphate (DXP)
COJEPEMI_(	murF	-0.93403	0.001136	UDP-N-acetylr	6.3.2.10	murF	Involved in cell wall formation. Catalyzes the final step in the synthesis
COJEPEMI_(	prs2	-0.93432	0.102139	Putative ribose	2.7.6.1	0	Phosphoribosyl transferase domain
COJEPEMI_(	hdfR_1	-0.93452	0.008521	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	ftsA_2	-0.93498	0.005883	Cell division pr	NA	pilM	Type IV pilus assembly protein PilM;
COJEPEMI_(	ttuB_1	-0.93618	0.064241	Putative tartra	NA	0	Major facilitator superfamily
COJEPEMI_(	COJEPE	-0.9367	0.13279	hypothetical p	NA	0	
COJEPEMI_(	mdtC	-0.93679	1.23E-05	Multidrug resi	NA	nolG	Belongs to the resistance-nodulation-cell division (RND) (TC 2.A.6) fam
COJEPEMI_(	COJEPE	-0.93794	0.193551	hypothetical p	NA	0	helix_turn_helix, arabinose operon control protein
COJEPEMI_(	btuD	-0.93822	0.065766	Vitamin B12 ir	7.6.2.8	0	ATPases associated with a variety of cellular activities
COJEPEMI_(	COJEPE	-0.93842	5.32E-05	hypothetical p	NA	ycaQ	Winged helix DNA-binding domain
COJEPEMI_(	menH_	-0.94029	0.006012	2-succinyl-6-hy	4.2.99.20	0	alpha/beta hydrolase fold
COJEPEMI_(	dhaT_1	-0.94134	0.000253	1,3-propanedi	1.1.1.202	0	Iron-containing alcohol dehydrogenase
COJEPEMI_(	menH_	-0.94194	0.002309	2-succinyl-6-hy	4.2.99.20	pldB	Serine aminopeptidase, S33
COJEPEMI_(	COJEPE	-0.94201	1.19E-09	Outer membra	NA	omp	Belongs to the ompA family
COJEPEMI_(	ptp	-0.94225	7.00E-06	Low molecular	3.1.3.48	ptp	Belongs to the low molecular weight phosphotyrosine protein phospha
COJEPEMI_(	COJEPE	-0.94288	8.24E-05	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.94468	0.360799	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.94569	0.002138	hypothetical p	NA	0	Domain of unknown function (DUF4154)
COJEPEMI_(	rluC	-0.94634	0.000424	Ribosomal larg	5.4.99.24	rluC	Responsible for synthesis of pseudouridine from uracil
COJEPEMI_(	tsaQ1_	-0.95148	0.002699	HTH-type trans	NA	dcaR	helix_turn_helix isocitrate lyase regulation
COJEPEMI_(	COJEPE	-0.95653	0.000198	hypothetical p	NA	yqfA	Haemolysin-III related
COJEPEMI_(	pgl	-0.95774	0.000596	6-phosphogluc	3.1.1.31	pggL	Lactonase, 7-bladed beta-propeller
COJEPEMI_(	ggt	-0.95785	0.000232	Glutathione hy	3.4.19.13	ggt	Gamma-glutamyltranspeptidase
COJEPEMI_(	gapN	-0.95803	4.76E-07	NADP-depend	1.2.1.9	gapN	Aldehyde dehydrogenase family
COJEPEMI_(	COJEPE	-0.9595	2.05E-06	hypothetical p	NA	MA20_01	VWA domain containing CoxE-like protein

COJEPEMI_(	COJEPE	-0.96342	2.31E-06	hypothetical p	NA	metI	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-0.96348	0.208884	hypothetical p	NA	0	of the drug metabolite transporter (DMT) superfamily
COJEPEMI_(	acsA_1	-0.9648	3.95E-06	Acetyl-coenzyr	6.2.1.1	acs-2	AMP-binding enzyme C-terminal domain
COJEPEMI_(	COJEPE	-0.96488	0.204565	hypothetical p	NA	0	Belongs to the 'phage' integrase family
COJEPEMI_(	COJEPE	-0.96499	0.001956	hypothetical p	NA	0	
COJEPEMI_(	gntT	-0.96516	0.000102	High-affinity g	NA	gntT	GntP family permease
COJEPEMI_(	bepA_1	-0.96524	3.19E-06	Beta-barrel as	3.4.-.-	bepA	Functions as both a chaperone and a metalloprotease. Maintains the ir
COJEPEMI_(	COJEPE	-0.96579	0.12743	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	ndhB	-0.96592	9.58E-08	NAD(P)H-quin	7.1.1.-	nha	Domain related to MnhB subunit of Na+/H+ antiporter
COJEPEMI_(	rnt	-0.96964	0.001062	Ribonuclease T	3.1.13.-	rnt	Trims short 3' overhangs of a variety of RNA species, leaving a one or t
COJEPEMI_(	COJEPE	-0.97052	0.000212	Long-chain-fat	6.2.1.3	0	AMP-binding enzyme C-terminal domain
COJEPEMI_(	COJEPE	-0.97053	0.033441	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	secD	-0.97135	6.43E-05	Protein translc	NA	secD	Part of the Sec protein translocase complex. Interacts with the SecYEG
COJEPEMI_(	ygeA	-0.97138	0.001024	L-aspartate/gl	5.1.1.13	ygeA	Asp/Glu/Hydantoin racemase
COJEPEMI_(	COJEPE	-0.97667	1.17E-05	hypothetical p	NA	0	Leucine carboxyl methyltransferase
COJEPEMI_(	COJEPE	-0.97946	0.369599	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-0.98059	0.001511	hypothetical p	NA	0	
COJEPEMI_(	quiA	-0.98319	0.000131	Quinate/shikir	1.1.5.8	quiA	PQQ-like domain
COJEPEMI_(	COJEPE	-0.98657	4.84E-06	hypothetical p	NA	0	
COJEPEMI_(	glnP	-0.9877	0.231492	putative glutar	NA	0	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	oprD	-0.98935	5.53E-05	Porin D	3.4.21.-	oprQ	outer membrane porin, OprD family
COJEPEMI_(	fatA_1	-0.99245	1.38E-06	Ferric-anguiba	NA	bauA	TonB-dependent Receptor Plug Domain
COJEPEMI_(	COJEPE	-0.99472	0.059016	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	exbD_4	-0.99481	0.000131	Biopolymer tra	NA	exbD	Biopolymer transport protein
COJEPEMI_(	COJEPE	-0.99599	0.036389	hypothetical p	NA	0	Predicted metal-dependent hydrolase
COJEPEMI_(	COJEPE	-0.99777	0.212491	hypothetical p	NA	0	
COJEPEMI_(	mmuM	-1.00069	0.065759	Homocysteine	2.1.1.10	mmuM	Homocysteine S-methyltransferase
COJEPEMI_(	COJEPE	-1.00193	1.96E-05	hypothetical p	NA	pstC	probably responsible for the translocation of the substrate across the m
COJEPEMI_(	COJEPE	-1.00233	0.006346	hypothetical p	NA	0	Initiator Replication protein
COJEPEMI_(	metR	-1.00319	7.67E-05	HTH-type trans	NA	metR	Transcriptional regulator

COJEPEMI_(	ycaC_1	-1.00339	1.20E-10	putative hydro	4.-.-.-	ycaC	Isochorismatase family
COJEPEMI_(	mnmC	-1.00618	0.000518	tRNA 5-methy	NA	mnmC	Catalyzes the last two steps in the biosynthesis of 5- methylaminometl
COJEPEMI_(	COJEPE	-1.00623	NA	IS4 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	COJEPE	-1.00633	0.299221	hypothetical p	NA	Z012_10	Protein of unknown function (DUF541)
COJEPEMI_(	gcvA_2	-1.00999	0.035312	Glycine cleava	NA	phnR	LysR substrate binding domain
COJEPEMI_(	dnaA	-1.01065	3.78E-07	Chromosomal	NA	dnaA	it binds specifically double-stranded DNA at a 9 bp consensus (dnaA bo
COJEPEMI_(	COJEPE	-1.01172	5.10E-11	hypothetical p	NA	pqqL	Belongs to the peptidase M16 family
COJEPEMI_(	COJEPE	-1.01316	0.000497	Putative low m	3.1.3.48	ptpA	Belongs to the low molecular weight phosphotyrosine protein phospha
COJEPEMI_(	arnC	-1.01359	7.07E-07	Undecaprenyl-	2.4.2.53	0	Glycosyl transferase family 21
COJEPEMI_(	COJEPE	-1.01514	1.28E-06	hypothetical p	NA	ytfN	TamB, inner membrane protein subunit of TAM complex
COJEPEMI_(	soxC_1	-1.01643	0.156071	Dibenzothioph	NA	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	COJEPE	-1.01836	2.70E-05	hypothetical p	NA	yejA	Bacterial extracellular solute-binding proteins, family 5 Middle
COJEPEMI_(	COJEPE	-1.01896	NA	hypothetical p	NA	0	adenylate kinase activity
COJEPEMI_(	ubiI	-1.01914	1.12E-05	2-octaprenylph	1.14.13.2	visC	Squalene epoxidase
COJEPEMI_(	yhfA	-1.02116	5.81E-06	Protein YhfA	NA	yhfA	OsmC-like protein
COJEPEMI_(	glnE	-1.02167	2.07E-06	Bifunctional gl	NA	glnE	Involved in the regulation of glutamine synthetase GlnA, a key enzyme
COJEPEMI_(	cyoE	-1.02204	0.010529	Protoheme IX	2.5.1.141	cyoE	Converts heme B (protoheme IX) to heme O by substitution of the vinyl
COJEPEMI_(	COJEPE	-1.02357	0.004361	hypothetical p	NA	yedA	EamA-like transporter family
COJEPEMI_(	mmgC_	-1.02366	8.07E-06	Acyl-CoA dehy	1.3.99.-	fadFx	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	COJEPE	-1.02752	0.116455	hypothetical p	NA	fahA	Fumarylacetoacetase N-terminal
COJEPEMI_(	COJEPE	-1.02787	9.65E-05	hypothetical p	NA	0	
COJEPEMI_(	bamA_	-1.03067	1.23E-07	Outer membra	NA	ytfM	Surface antigen
COJEPEMI_(	COJEPE	-1.03518	0.001145	hypothetical p	NA	0	COG1585 Membrane protein implicated in regulation of membrane pro
COJEPEMI_(	murB	-1.03774	6.35E-05	UDP-N-acetyle	1.3.1.98	murB	Cell wall formation
COJEPEMI_(	COJEPE	-1.03838	2.12E-12	hypothetical p	NA	0	Protein of unknown function (DUF2726)
COJEPEMI_(	COJEPE	-1.04191	9.45E-07	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.04316	0.091252	hypothetical p	NA	0	Antioxidant protein with alkyl hydroperoxidase activity. Required for the
COJEPEMI_(	COJEPE	-1.04411	2.56E-06	hypothetical p	NA	xcpY	Involved in a type II secretion system (T2SS, formerly general secretion
COJEPEMI_(	oprB_2	-1.04446	0.000376	Porin B	NA	oprB	Carbohydrate-selective porin, OprB family
COJEPEMI_(	tgt	-1.04449	0.000324	Queuine tRNA	2.4.2.29	tgt	Catalyzes the base-exchange of a guanine (G) residue with the queuine

COJEPEMI_(	acnB	-1.04516	4.45E-11	Aconitate hydr	4.2.1.3	acnB	Belongs to the aconitase IPM isomerase family
COJEPEMI_(	tauD	-1.04678	0.309173	Alpha-ketoglut	1.14.11.1	tauD	Taurine catabolism dioxygenase TauD, TfdA family
COJEPEMI_(	COJEPE	-1.04772	5.27E-05	hypothetical p	NA	0	Beta-lactamase
COJEPEMI_(	yccS_1	-1.05006	0.013661	Inner membra	NA	yccS	FUSC-like inner membrane protein yccS
COJEPEMI_(	COJEPE	-1.0505	0.276307	hypothetical p	NA	0	
COJEPEMI_(	aroQ	-1.05926	6.73E-05	3-dehydroquin	4.2.1.10	aroQ	Catalyzes a trans-dehydration via an enolate intermediate
COJEPEMI_(	perR	-1.06171	0.007422	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	gdhB_1	-1.06367	1.91E-12	Quinoprotein g	1.1.5.2	gdhB	Glucose / Sorbosone dehydrogenase
COJEPEMI_(	COJEPE	-1.06435	NA	hypothetical p	NA	0	
COJEPEMI_(	kefC_1	-1.06544	2.30E-08	Glutathione-re	NA	kefB	Belongs to the monovalent cation proton antiporter 2 (CPA2) transporte
COJEPEMI_(	COJEPE	-1.06619	0.006631	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.06823	0.043195	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.07137	0.07727	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.07473	NA	hypothetical p	NA	0	
COJEPEMI_(	dedA_2	-1.077	0.266324	Protein DedA	NA	dedA	SNARE associated Golgi protein
COJEPEMI_(	COJEPE	-1.07701	1.24E-07	hypothetical p	NA	0	Polysaccharide deacetylase
COJEPEMI_(	cntO_4	-1.07705	7.94E-09	Metal-pseudop	NA	0	TonB dependent receptor
COJEPEMI_(	COJEPE	-1.07871	0.00262	hypothetical p	NA	0	self proteolysis
COJEPEMI_(	psaB	-1.07887	0.005489	Photosystem I	1.97.1.12	yfiB	Belongs to the ompA family
COJEPEMI_(	COJEPE	-1.08045	0.000167	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.08077	0.00024	hypothetical p	NA	0	Protein of unknown function (DUF3015)
COJEPEMI_(	COJEPE	-1.08325	0.004135	putative prote	NA	comEA	Helix-hairpin-helix motif
COJEPEMI_(	COJEPE	-1.08372	0.027663	hypothetical p	NA	pilN	Fimbrial assembly protein (PilN)
COJEPEMI_(	vfr	-1.08417	0.000107	Cyclic AMP rec	NA	crp	helix_turn_helix, cAMP Regulatory protein
COJEPEMI_(	COJEPE	-1.08504	NA	hypothetical p	NA	ssb	Single-strand binding protein family
COJEPEMI_(	COJEPE	-1.08539	1.93E-07	hypothetical p	NA	mdtN_2	Biotin-lipoyl like
COJEPEMI_(	cpdA_2	-1.08837	6.58E-06	3',5'-cyclic ade	3.1.4.53	cpdA	Calcineurin-like phosphoesterase superfamily domain
COJEPEMI_(	hdfR_5	-1.09259	5.62E-05	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	-1.09329	0.001081	hypothetical p	NA	impB	Type VI secretion system, VipA, VC_A0107 or Hcp2
COJEPEMI_(	echA8_	-1.0938	0.005619	putative enoyl	4.2.1.17	atuE	Belongs to the enoyl-CoA hydratase isomerase family

COJEPEMI_(	COJEPE	-1.0964	2.05E-06	hypothetical p	NA	0	long-chain fatty acid transport protein
COJEPEMI_(	ispU	-1.09907	1.44E-05	Ditrans,polycis	2.5.1.31	uppS	Catalyzes the sequential condensation of isopentenyl diphosphate (IPP)
COJEPEMI_(	ssuD	-1.10423	0.167845	Alkanesulfona	1.14.14.5	ssuD	Catalyzes the desulfonation of aliphatic sulfonates
COJEPEMI_(	COJEPE	-1.10636	0.02181	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.10755	0.000704	hypothetical p	NA	dsbC	Required for disulfide bond formation in some periplasmic proteins. Ac
COJEPEMI_(	ydiK	-1.11221	1.14E-05	Putative trans	NA	0	AI-2E family transporter
COJEPEMI_(	ynfM	-1.11398	0.022072	Inner membra	NA	ynfM	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-1.1147	0.002077	hypothetical p	NA	basI	4'-phosphopantetheinyl transferase superfamily
COJEPEMI_(	COJEPE	-1.11621	5.81E-06	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.11825	3.22E-08	hypothetical p	NA	0	Domain of unknown function (DUF4468) with TBP-like fold
COJEPEMI_(	COJEPE	-1.12101	0.000932	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.1254	0.009608	hypothetical p	NA	pilP	Pilus assembly protein, PilP
COJEPEMI_(	COJEPE	-1.12782	8.29E-05	hypothetical p	NA	0	
COJEPEMI_(	dadA_1	-1.1285	3.91E-06	D-amino acid	1.4.99.-	dadA3	FAD dependent oxidoreductase
COJEPEMI_(	COJEPE	-1.13441	3.61E-05	hypothetical p	NA	0	
COJEPEMI_(	csrA	-1.13773	4.71E-11	Translational r	NA	csrA	Could accelerate the degradation of some genes transcripts potentially
COJEPEMI_(	COJEPE	-1.14	0.098078	putative HTH-t	NA	0	helix_turn_helix, arabinose operon control protein
COJEPEMI_(	dnaB_2	-1.14124	0.002748	Replicative DN	3.6.4.12	0	DnaB-like helicase N terminal domain
COJEPEMI_(	COJEPE	-1.14144	0.003802	hypothetical p	NA	0	DnaD domain protein
COJEPEMI_(	COJEPE	-1.14609	0.03097	hypothetical p	NA	0	OmpW family
COJEPEMI_(	glcC	-1.14722	0.01722	Glc operon tra	NA	0	transcriptional
COJEPEMI_(	COJEPE	-1.14838	0.041196	hypothetical p	NA	0	GrpB protein
COJEPEMI_(	COJEPE	-1.14863	NA	hypothetical p	NA	MA20_14	4Fe-4S binding domain
COJEPEMI_(	COJEPE	-1.1491	0.036845	hypothetical p	NA	0	Protein conserved in bacteria
COJEPEMI_(	COJEPE	-1.15374	0.123056	hypothetical p	NA	0	acetoacetate decarboxylase
COJEPEMI_(	lgrE	-1.15704	0.000312	Linear gramici	1.1.-.-	basH	Thioesterase domain
COJEPEMI_(	dapL	-1.15753	2.33E-07	LL-diaminopim	2.6.1.83	dapC	Aminotransferase class I and II
COJEPEMI_(	COJEPE	-1.15829	0.000932	hypothetical p	NA	0	LemA family
COJEPEMI_(	eriC	-1.15945	0.063509	Chloride/fluori	NA	eriC	Voltage gated chloride channel
COJEPEMI_(	racE	-1.15969	0.019224	Glutamate rac	5.1.1.3	murI	Provides the (R)-glutamate required for cell wall biosynthesis

COJEPEMI_(	COJEPE	-1.16175	5.48E-08	hypothetical p	NA	0	
COJEPEMI_(	mtlD	-1.162	1.52E-07	Mannitol-1-ph	1.1.1.17	0	Haloacid dehalogenase-like hydrolase
COJEPEMI_(	glcB	-1.16629	5.73E-14	Malate syntha	2.3.3.9	glcB	Involved in the glycolate utilization. Catalyzes the condensation and sul
COJEPEMI_(	COJEPE	-1.16904	0.004307	hypothetical p	NA	gspE	Type II secretion system (T2SS), protein E, N-terminal domain
COJEPEMI_(	gudP_1	-1.16971	1.03E-05	putative gluca	NA	0	Major Facilitator Superfamily
COJEPEMI_(	ybiV	-1.17059	0.001139	Sugar phospha	3.1.3.23	supH	Sucrose-6F-phosphate phosphohydrolase
COJEPEMI_(	pknD	-1.17374	0.004578	Serine/threoni	2.7.11.1	0	Protein tyrosine kinase
COJEPEMI_(	COJEPE	-1.17866	4.72E-07	hypothetical p	NA	fruB	Phosphoenolpyruvate-dependent sugar phosphotransferase system, EII
COJEPEMI_(	mmsB	-1.17941	5.99E-08	3-hydroxyisobu	1.1.1.31	mmsB	Belongs to the 3-hydroxyisobutyrate dehydrogenase family
COJEPEMI_(	COJEPE	-1.18081	0.000978	hypothetical p	NA	pilO	Pilus assembly protein, PilO
COJEPEMI_(	COJEPE	-1.18108	0.228531	hypothetical p	NA	0	
COJEPEMI_(	mqo	-1.18318	1.42E-09	Malate:quinon	1.1.5.4	mqo	Malate:quinone oxidoreductase (Mqo)
COJEPEMI_(	COJEPE	-1.18393	7.03E-10	hypothetical p	NA	0	
COJEPEMI_(	holA	-1.18846	0.000601	DNA polymera	2.7.7.7	holA	DNA polymerase III, delta subunit
COJEPEMI_(	dgcN	-1.18949	0.000476	Diguanylate cy	2.7.7.65	yfiN	Periplasmic sensor domain
COJEPEMI_(	COJEPE	-1.19053	0.123724	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.19132	2.26E-06	hypothetical p	NA	0	Protein of unknown function DUF45
COJEPEMI_(	COJEPE	-1.19192	2.15E-05	hypothetical p	NA	0	beta-ketoacyl-acyl-carrier-protein synthase II activity
COJEPEMI_(	ppiA	-1.1985	0.001408	Peptidyl-prolyl	5.2.1.8	ppiA	PPIases accelerate the folding of proteins. It catalyzes the cis-trans isor
COJEPEMI_(	desA3_	-1.19968	7.20E-06	NADPH-depen	1.14.19.-	desA3	Fatty acid desaturase
COJEPEMI_(	rho	-1.20107	4.47E-07	Transcription t	3.6.4.-	rho	Facilitates transcription termination by a mechanism that involves Rho
COJEPEMI_(	COJEPE	-1.20408	0.085529	hypothetical p	NA	0	Pfam Transposase IS66
COJEPEMI_(	COJEPE	-1.2094	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.2098	0.000145	hypothetical p	NA	0	
COJEPEMI_(	fumC	-1.21041	3.22E-11	Fumarate hydı	4.2.1.2	fumC	Involved in the TCA cycle. Catalyzes the stereospecific interconversion c
COJEPEMI_(	dmlR_1	-1.21057	0.001267	HTH-type trans	NA	0	Transcriptional regulator
COJEPEMI_(	COJEPE	-1.21068	6.68E-11	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.21419	3.75E-05	hypothetical p	NA	pilI	Two component signalling adaptor domain
COJEPEMI_(	ssuA_2	-1.21517	0.153467	Putative aliph	NA	ssuA	ABC transporter, phosphonate, periplasmic substrate-binding protein
COJEPEMI_(	acnD	-1.22174	0.000604	2-methylcitrat	4.2.1.117	acnD	Catalyzes the isomerization of citrate to isocitrate via cis-aconitate

COJEPEMI_(	aspS	-1.22389	0.001823	Aspartate--tRI	6.1.1.23	aspS	Aspartyl-tRNA synthetase with relaxed tRNA specificity since it is able
COJEPEMI_(	ttuB_2	-1.22531	0.000984	Putative tartra	NA	0	COG0477 Permeases of the major facilitator superfamily
COJEPEMI_(	rlhA	-1.22552	0.20928	23S rRNA 5-hy	NA	yegQ	Peptidase family U32
COJEPEMI_(	prpB	-1.22602	0.000428	2-methylisocit	4.1.3.30	prpB	Catalyzes the thermodynamically favored C-C bond cleavage of (2R,3S)-
COJEPEMI_(	gntR	-1.23108	5.98E-05	putative D-xyl	NA	prpR	FCD
COJEPEMI_(	COJEPE	-1.23511	2.11E-06	hypothetical p	NA	0	
COJEPEMI_(	glyS	-1.23605	2.88E-05	Glycine--tRNA	6.1.1.14	glyS	Glycyl-tRNA synthetase beta subunit
COJEPEMI_(	COJEPE	-1.23646	0.040406	hypothetical p	NA	0	Domain of unknown function (DUF4055)
COJEPEMI_(	COJEPE	-1.24155	7.45E-05	hypothetical p	NA	0	ABC-2 family transporter protein
COJEPEMI_(	COJEPE	-1.24296	0.012804	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	fadH_1	-1.24465	0.000986	putative 2,4-di	1.3.1.34	atuB	KR domain
COJEPEMI_(	pitA_1	-1.25044	0.005362	L-methionine s	2.3.1.-	yncA	Acetyltransferase (GNAT) domain
COJEPEMI_(	COJEPE	-1.2534	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	pleD	-1.25549	1.94E-05	Response regu	NA	pilH	Response regulator receiver domain
COJEPEMI_(	COJEPE	-1.25967	0.017707	hypothetical p	NA	0	Phage Mu protein F like protein
COJEPEMI_(	COJEPE	-1.25975	0.004106	hypothetical p	NA	0	
COJEPEMI_(	gltC_3	-1.26034	5.62E-06	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	-1.26275	0.103848	hypothetical p	NA	0	Zonular occludens toxin (Zot)
COJEPEMI_(	pcaK_5	-1.26288	0.00035	4-hydroxybenz	NA	vanK	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-1.26375	4.81E-06	hypothetical p	NA	0	Domain of unknown function (DUF4339)
COJEPEMI_(	pqiB	-1.26465	1.50E-08	Intermembran	NA	pqiB	MlaD protein
COJEPEMI_(	mutS	-1.2653	1.34E-09	DNA mismatcl	NA	mutS	that it carries out the mismatch recognition step. This protein has a we
COJEPEMI_(	COJEPE	-1.26553	0.010513	hypothetical p	NA	0	
COJEPEMI_(	pcaG	-1.26584	0.008473	Protocatechua	1.13.11.3	pcaG	Dioxygenase
COJEPEMI_(	purB	-1.26688	8.51E-09	Adenylosuccin	4.3.2.2	purB	Belongs to the lyase 1 family. Adenylosuccinate lyase subfamily
COJEPEMI_(	COJEPE	-1.26808	1.41E-06	hypothetical p	NA	0	Tripartite ATP-independent periplasmic transporter, DctM component
COJEPEMI_(	COJEPE	-1.2689	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.27074	4.12E-05	hypothetical p	NA	0	
COJEPEMI_(	iscR_1	-1.27243	0.000419	HTH-type trans	NA	0	Transcriptional regulator
COJEPEMI_(	sdsA	-1.27298	1.19E-05	All-trans-nona	2.5.1.84	ispB	Belongs to the FPP GGPP synthase family

COJEPEMI_(	mmsA	-1.27408	5.68E-07	Methylmalona	1.2.1.27	mmsA	Aldehyde dehydrogenase family
COJEPEMI_(	COJEPE	-1.27742	0.006103	hypothetical p	NA	0	
COJEPEMI_(	tauA	-1.27923	0.192005	Taurine-bindin	NA	tauA	Substrate binding domain of ABC-type glycine betaine transport system
COJEPEMI_(	dadA1	-1.27927	2.72E-08	D-amino acid (	1.4.99.-	dadA	Oxidative deamination of D-amino acids
COJEPEMI_(	coaE	-1.28075	0.000798	Dephospho-Co	2.7.1.24	coaE	Catalyzes the phosphorylation of the 3'-hydroxyl group of dephosphoco
COJEPEMI_(	COJEPE	-1.28342	1.05E-14	hypothetical p	NA	0	Arc-like DNA binding domain
COJEPEMI_(	COJEPE	-1.28918	0.177796	hypothetical p	NA	0	Cupin superfamily protein
COJEPEMI_(	aroF_1	-1.28943	3.32E-09	Phospho-2-deh	2.5.1.54	aroF	Stereospecific condensation of phosphoenolpyruvate (PEP) and D-eryth
COJEPEMI_(	gltJ	-1.29114	3.80E-07	Glutamate/as	NA	gltJ	Binding-protein-dependent transport system inner membrane compon
COJEPEMI_(	yadV_1	-1.29576	0.094505	putative fimbr	NA	cupB4	Pili assembly chaperone PapD, C-terminal domain
COJEPEMI_(	pcaJ_3	-1.29899	0.000396	3-oxoadipate (	2.8.3.6	pcaJ	3-oxoadipate CoA-transferase activity
COJEPEMI_(	COJEPE	-1.29973	3.86E-19	hypothetical p	NA	VP2647	Predicted membrane protein (DUF2061)
COJEPEMI_(	COJEPE	-1.29986	3.62E-07	hypothetical p	NA	ycnE	Antibiotic biosynthesis monooxygenase
COJEPEMI_(	cmpR_1	-1.30107	0.001153	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	COJEPE	-1.30213	0.021667	hypothetical p	NA	dcaP	Forms passive diffusion pores that allow small molecular weight hydro
COJEPEMI_(	COJEPE	-1.30351	0.176656	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	mmgC_	-1.30614	0.000972	Acyl-CoA dehy	1.3.99.-	atuD	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	queE	-1.30632	2.06E-07	7-carboxy-7-de	4.3.99.3	queE	Catalyzes the complex heterocyclic radical-mediated conversion of 6-ca
COJEPEMI_(	COJEPE	-1.30651	0.072628	hypothetical p	NA	msuE	Flavodoxin-like fold
COJEPEMI_(	COJEPE	-1.30684	1.15E-10	hypothetical p	NA	yoaF	Domain of unknown function (DUF333)
COJEPEMI_(	pfeA	-1.30865	1.27E-14	Ferric enterob	NA	fepA	TonB dependent receptor
COJEPEMI_(	pyrG	-1.30986	1.31E-08	CTP synthase	6.3.4.2	pyrG	Catalyzes the ATP-dependent amination of UTP to CTP with either L-glu
COJEPEMI_(	COJEPE	-1.30996	6.65E-09	hypothetical p	NA	0	
COJEPEMI_(	fhuE_2	-1.31305	1.81E-07	FhuE receptor	NA	fpvA1	TonB dependent receptor
COJEPEMI_(	lip	-1.3134	0.000984	Triacylglycerol	3.1.1.3	lip	alpha/beta hydrolase fold
COJEPEMI_(	COJEPE	-1.31602	1.24E-05	hypothetical p	NA	vasA	overlaps another CDS with the same product name
COJEPEMI_(	gltK	-1.32215	8.94E-08	Glutamate/as	NA	gltK	Binding-protein-dependent transport system inner membrane compon
COJEPEMI_(	COJEPE	-1.3271	0.008305	hypothetical p	NA	0	Terminase RNaseH-like domain
COJEPEMI_(	COJEPE	-1.33092	0.193522	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.33298	0.003296	hypothetical p	NA	0	

COJEPEMI_(	glnH_1	-1.3369	0.000179	ABC transporte	NA	cjaA	Bacterial extracellular solute-binding proteins, family 3
COJEPEMI_(	COJEPE	-1.33906	0.055969	hypothetical p	NA	0	Protein of unknown function (DUF2799)
COJEPEMI_(	COJEPE	-1.34034	0.02683	hypothetical p	NA	0	
COJEPEMI_(	betT2	-1.34588	4.11E-08	Osmo-depend	NA	betT	Belongs to the BCCT transporter (TC 2.A.15) family
COJEPEMI_(	adeP	-1.34616	2.28E-15	Adenine perm	NA	purP	Permease family
COJEPEMI_(	recE	-1.34621	0.049364	Exodeoxyribon	3.1.11.-	0	PDDEXK-like domain of unknown function (DUF3799)
COJEPEMI_(	araC_2	-1.34662	0.002896	L-arabonate de	4.2.1.25	ilvD1	Dehydratase family
COJEPEMI_(	ytrE	-1.34717	4.84E-06	ABC transporte	NA	ybbA	ABC transporter
COJEPEMI_(	COJEPE	-1.34823	5.29E-09	hypothetical p	NA	0	Secretory lipase
COJEPEMI_(	COJEPE	-1.35254	5.34E-10	hypothetical p	NA	gstA	Glutathione S-transferase
COJEPEMI_(	COJEPE	-1.35843	0.000254	hypothetical p	NA	0	Type II secretion system (T2SS), protein M
COJEPEMI_(	accB	-1.36094	1.17E-06	Biotin carboxy	NA	accB	first, biotin carboxylase catalyzes the carboxylation of the carrier protei
COJEPEMI_(	COJEPE	-1.36685	0.001091	hypothetical p	NA	0	Domain of unknown function (DUF4105)
COJEPEMI_(	norR	-1.37274	1.11E-06	Anaerobic nitr	NA	0	Sigma-54 interaction domain
COJEPEMI_(	phoP	-1.37865	8.86E-05	Alkaline phosp	NA	pilG	Response regulator receiver domain
COJEPEMI_(	ssuC_3	-1.38433	0.127369	Putative alipha	NA	tauC	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	COJEPE	-1.3866	1.10E-10	hypothetical p	NA	0	Bacterial regulatory proteins, tetR family
COJEPEMI_(	kdpE	-1.3926	0.003977	KDP operon tra	NA	kdpE	Transcriptional regulatory protein, C terminal
COJEPEMI_(	metXA	-1.3945	6.89E-12	Bifunctional m	NA	metW	Methionine biosynthesis protein MetW
COJEPEMI_(	ispD	-1.40227	1.63E-09	2-C-methyl-D-	2.7.7.60	ispD	Catalyzes the formation of 4-diphosphocytidyl-2-C- methyl-D-erythritol
COJEPEMI_(	COJEPE	-1.40813	0.170756	IS4 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	budC_2	-1.41329	0.00134	Diacetyl reduc	1.1.1.304	ephD	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	COJEPE	-1.41509	6.41E-05	hypothetical p	NA	0	Bacterial transcriptional repressor C-terminal
COJEPEMI_(	dmdC_1	-1.41699	3.38E-08	3-methylmerca	1.3.8.-	acdA	acyl-CoA dehydrogenase
COJEPEMI_(	COJEPE	-1.41805	1.33E-12	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	glnD	-1.41969	1.03E-10	Bifunctional ur	NA	glnD	Modifies, by uridylylation and deuridylylation, the PII regulatory protein
COJEPEMI_(	lpxP	-1.42118	9.01E-16	Lipid A biosynt	2.3.1.242	lpxL	Catalyzes the transfer of laurate from lauroyl-acyl carrier protein (ACP)
COJEPEMI_(	COJEPE	-1.42592	7.71E-06	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.42731	9.57E-09	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.42793	3.75E-08	hypothetical p	NA	chrA	Chromate transporter

COJEPEMI_(	thlA_2	-1.42998	2.29E-07	Acetyl-CoA ace	2.3.1.9	bamN	Belongs to the thiolase family
COJEPEMI_(	COJEPE	-1.43121	NA	hypothetical p	NA	0	
COJEPEMI_(	dmlR_3	-1.43493	2.48E-11	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	sacA	-1.43619	0.000267	UDP-N-acetylg	5.1.3.14	wecB	Belongs to the UDP-N-acetylglucosamine 2-epimerase family
COJEPEMI_(	COJEPE	-1.44081	0.15852	hypothetical p	NA	Z012_05	Membrane
COJEPEMI_(	COJEPE	-1.44399	1.44E-09	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.44577	3.71E-08	hypothetical p	NA	gcr	Site-specific recombinase
COJEPEMI_(	ycaC_2	-1.44616	1.83E-10	putative hydro	4.-.-.-	0	Isochorismatase family
COJEPEMI_(	COJEPE	-1.45016	2.32E-05	hypothetical p	NA	0	Protein of unknown function (DUF3426)
COJEPEMI_(	COJEPE	-1.45798	5.16E-06	hypothetical p	NA	evpB	Type VI secretion protein, EvpB/VC_A0108, tail sheath
COJEPEMI_(	glnM	-1.4593	0.063602	putative glutar	NA	papP	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	purA	-1.45951	1.64E-18	Adenylosuccin	6.3.4.4	purA	Plays an important role in the de novo pathway of purine nucleotide bio
COJEPEMI_(	COJEPE	-1.46185	3.60E-07	hypothetical p	NA	lgtF	COG0463 Glycosyltransferases involved in cell wall biogenesis
COJEPEMI_(	hdfR_2	-1.46626	7.75E-06	HTH-type trans	NA	0	LysR substrate binding domain
COJEPEMI_(	echA8_	-1.46945	2.47E-14	putative enoyl	4.2.1.17	fadB1	Belongs to the enoyl-CoA hydratase isomerase family
COJEPEMI_(	COJEPE	-1.47309	NA	hypothetical p	NA	folP	Catalyzes the condensation of para-aminobenzoate (pABA) with 6-hydr
COJEPEMI_(	hchA_1	-1.47401	8.28E-09	Protein/nuclei	3.1.2.-	hchA	DJ-1/PfpI family
COJEPEMI_(	hcp1	-1.47432	9.24E-08	Protein hcp1	NA	0	Type VI secretion system effector, Hcp
COJEPEMI_(	tadA	-1.47854	1.14E-09	tRNA-specific	3.5.4.33	tadA	Catalyzes the deamination of adenosine to inosine at the wobble positi
COJEPEMI_(	accC	-1.47885	2.95E-06	Biotin carboxy	6.3.4.14	accC	Biotin carboxylase
COJEPEMI_(	COJEPE	-1.48826	7.28E-12	hypothetical p	NA	0	D-alanine [D-alanyl carrier protein] ligase activity
COJEPEMI_(	COJEPE	-1.49265	7.34E-06	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	dsbD	-1.49556	1.81E-12	Thiol:disulfide	1.8.1.8	dsbD	Thiol disulfide interchange protein
COJEPEMI_(	COJEPE	-1.49849	1.72E-08	hypothetical p	NA	ynfA	Uncharacterised BCR, YnfA/UPF0060 family
COJEPEMI_(	fadD	-1.49951	4.60E-11	Long-chain-fat	6.2.1.3	fadD	COG0318 Acyl-CoA synthetases (AMP-forming) AMP-acid ligases II
COJEPEMI_(	kstR2	-1.5076	0.001688	HTH-type trans	NA	pfiT	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	-1.51287	0.134176	hypothetical p	NA	0	Serine hydrolase
COJEPEMI_(	COJEPE	-1.51349	1.83E-07	hypothetical p	NA	besA	Putative esterase
COJEPEMI_(	pnp	-1.51547	6.56E-12	Polyribonucleo	2.7.7.8	pnp	Involved in mRNA degradation. Catalyzes the phosphorolysis of single-s
COJEPEMI_(	icd_2	-1.51591	3.69E-11	Isocitrate deh	1.1.1.42	icd	Isocitrate/isopropylmalate dehydrogenase

COJEPEMI_(	purH	-1.51641	2.90E-10	Bifunctional p	NA	purH	Bifunctional purine biosynthesis protein PurH
COJEPEMI_(	ltxB	-1.51783	1.84E-09	Leukotoxin exp	7.4.2.5	0	ABC transporter transmembrane region
COJEPEMI_(	COJEPE	-1.52015	2.34E-05	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.52254	6.50E-15	hypothetical p	NA	cdsA	Belongs to the CDS family
COJEPEMI_(	tauB_2	-1.52601	0.097663	Taurine impor	7.6.2.7	tauB	Part of the ABC transporter complex TauABC involved in taurine import
COJEPEMI_(	COJEPE	-1.52688	0.031567	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.52749	0.02521	hypothetical p	NA	tonB3	Gram-negative bacterial TonB protein C-terminal
COJEPEMI_(	feoB	-1.52939	2.13E-31	Fe(2+) transpc	NA	feoB	Ferrous iron transport protein B
COJEPEMI_(	COJEPE	-1.52965	0.038818	hypothetical p	NA	yraN	Belongs to the UPF0102 family
COJEPEMI_(	lpxH	-1.54221	0.000163	UDP-2,3-diacy	3.6.1.54	lpxH	Hydrolyzes the pyrophosphate bond of UDP-2,3- diacylglucosamine to y
COJEPEMI_(	COJEPE	-1.54654	0.000277	hypothetical p	NA	0	Bacteriophage replication protein O
COJEPEMI_(	COJEPE	-1.549	0.02893	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.55021	2.22E-06	hypothetical p	NA	ompH	Outer membrane protein (OmpH-like)
COJEPEMI_(	cmr	-1.55168	1.77E-07	HTH-type trans	NA	0	Cyclic nucleotide-monophosphate binding domain
COJEPEMI_(	hpf	-1.55768	5.54E-09	Ribosome hibe	NA	hpf	Sigma 54 modulation protein / S30EA ribosomal protein
COJEPEMI_(	COJEPE	-1.56215	6.42E-15	Isocitrate lyas	4.1.3.1	aceA	Isocitrate lyase
COJEPEMI_(	COJEPE	-1.56335	7.60E-05	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	gcd	-1.56815	3.47E-12	Quinoprotein g	1.1.5.2	gcd	PQQ-like domain
COJEPEMI_(	COJEPE	-1.57008	0.000361	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.57156	0.018014	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.57337	1.80E-07	hypothetical p	NA	0	membrane transporter protein
COJEPEMI_(	COJEPE	-1.57464	0.105505	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	mrpD	-1.57508	1.92E-09	Na(+)/H(+) an	NA	phaD	Proton-conducting membrane transporter
COJEPEMI_(	pcaI_3	-1.57864	0.000135	3-oxoadipate (	2.8.3.6	pcaI	3-oxoadipate CoA-transferase activity
COJEPEMI_(	qmcA	-1.58133	1.99E-07	Protein QmcA	NA	qmcA	prohibitin homologues
COJEPEMI_(	COJEPE	-1.58576	0.011985	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.5858	0.00307	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.59281	0.000747	hypothetical p	NA	0	
COJEPEMI_(	fimW	-1.59306	3.01E-05	Cyclic-di-GMP	NA	0	
COJEPEMI_(	COJEPE	-1.59334	1.48E-07	hypothetical p	NA	hcaR	helix_turn_helix multiple antibiotic resistance protein

COJEPEMI_(	COJEPE	-1.59408	1.74E-09	hypothetical p	NA	MA20_01	AAA domain (Cdc48 subfamily)
COJEPEMI_(	metN_1	-1.59463	8.29E-21	Methionine im	3.6.3.-	metN	Part of the ABC transporter complex MetNIQ involved in methionine im
COJEPEMI_(	mexA	-1.59508	2.59E-05	Multidrug resi	NA	acrE	Barrel-sandwich domain of CusB or HlyD membrane-fusion
COJEPEMI_(	ssuA_1	-1.59822	0.028139	Putative alpha	NA	ssuA	ABC transporter substrate-binding protein
COJEPEMI_(	COJEPE	-1.60239	1.51E-06	hypothetical p	NA	0	Histidine kinase
COJEPEMI_(	rutC	-1.60423	1.01E-06	Putative amin	1.-.-.-	0	Endoribonuclease L-PSP
COJEPEMI_(	COJEPE	-1.60627	0.000249	hypothetical p	NA	0	2'-5' RNA ligase superfamily
COJEPEMI_(	COJEPE	-1.60812	4.79E-18	hypothetical p	NA	0	Sel1-like repeats.
COJEPEMI_(	COJEPE	-1.61352	0.032918	Putative ester	3.1.-.-	0	Thioesterase-like superfamily
COJEPEMI_(	COJEPE	-1.61776	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.61877	2.16E-09	hypothetical p	NA	0	
COJEPEMI_(	hupB	-1.62278	3.90E-17	DNA-binding p	NA	hupB	Histone-like DNA-binding protein which is capable of wrapping DNA to
COJEPEMI_(	COJEPE	-1.62726	1.92E-05	hypothetical p	NA	madM	Malonate/sodium symporter MadM subunit
COJEPEMI_(	COJEPE	-1.63575	0.036941	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	rsmE_2	-1.64165	1.50E-06	Ribosomal RN	2.1.1.193	rsmE	Specifically methylates the N3 position of the uracil ring of uridine 149
COJEPEMI_(	cycA_4	-1.64961	7.92E-11	D-serine/D-ala	NA	cycA	Amino acid permease
COJEPEMI_(	sbp_2	-1.65051	0.09455	Sulfate-bindin	NA	sbp	sulfate ABC transporter
COJEPEMI_(	COJEPE	-1.65281	5.90E-05	hypothetical p	NA	0	
COJEPEMI_(	tolQ_4	-1.65647	9.68E-09	Tol-Pal system	NA	0	MotA TolQ ExbB proton channel
COJEPEMI_(	cspG_1	-1.65973	4.57E-17	Cold shock-like	NA	cspA	'Cold-shock' DNA-binding domain
COJEPEMI_(	hisZ	-1.66496	6.56E-13	ATP phosphori	NA	hisZ	Required for the first step of histidine biosynthesis. May allow the feed
COJEPEMI_(	COJEPE	-1.67273	0.008682	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-1.67738	6.16E-09	3-hydroxylami	5.4.4.3	glnA	glutamine synthetase
COJEPEMI_(	COJEPE	-1.68099	1.58E-05	hypothetical p	NA	MA20_14	Fumarylacetoacetate (FAA) hydrolase family
COJEPEMI_(	hutG	-1.68413	0.005319	Formimidoylgl	3.5.3.8	hutG	Catalyzes the conversion of N-formimidoyl-L-glutamate to L-glutamate
COJEPEMI_(	COJEPE	-1.71528	0.00022	hypothetical p	NA	cobZ	FAD dependent oxidoreductase
COJEPEMI_(	COJEPE	-1.71693	0.012017	hypothetical p	NA	0	Uncharacterized conserved protein (DUF2280)
COJEPEMI_(	COJEPE	-1.72451	0.076134	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.72741	0.05862	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	mnhC1	-1.72742	1.29E-07	Na(+)/H(+) an	NA	phaC	NADH-ubiquinone/plastoquinone oxidoreductase chain 4L

COJEPEMI_(	COJEPE	-1.72923	0.037879	hypothetical p	NA	0	
COJEPEMI_(	pqqB	-1.74545	3.64E-14	Coenzyme PQ(	NA	pqqB	May be involved in the transport of PQQ or its precursor to the periplas
COJEPEMI_(	COJEPE	-1.74919	1.19E-07	NADPH oxidor	1.-.-.-	0	Ferric reductase NAD binding domain
COJEPEMI_(	COJEPE	-1.75584	0.003194	Dihydrolipoyl c	1.8.1.4	0	Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
COJEPEMI_(	fdhD	-1.75705	1.94E-08	Sulfur carrier p	NA	fdhD	Required for formate dehydrogenase (FDH) activity. Acts as a sulfur car
COJEPEMI_(	cycA_3	-1.75902	2.12E-11	D-serine/D-ala	NA	cycA	Amino acid permease
COJEPEMI_(	cmpR_3	-1.76427	1.07E-11	HTH-type trans	NA	cmpR_1	Transcriptional regulator
COJEPEMI_(	COJEPE	-1.77088	2.86E-14	hypothetical p	NA	0	Acid phosphatase homologues
COJEPEMI_(	nicP_3	-1.77544	4.78E-05	Porin-like prot	NA	0	outer membrane porin, OprD family
COJEPEMI_(	ilvE	-1.77725	6.61E-12	Branched-chai	2.6.1.42	ilvE	Belongs to the class-IV pyridoxal-phosphate-dependent aminotransfera
COJEPEMI_(	pcaK_3	-1.77772	0.00025	4-hydroxybenz	NA	pcaK	Major facilitator Superfamily
COJEPEMI_(	brnQ	-1.77883	4.77E-09	Branched-chai	NA	brnQ	Component of the transport system for branched-chain amino acids
COJEPEMI_(	COJEPE	-1.78554	1.32E-14	hypothetical p	NA	0	Domain of unknown function (DUF1852)
COJEPEMI_(	COJEPE	-1.80498	0.043119	Tn3 family tra	NA	0	Domain of unknown function (DUF4158)
COJEPEMI_(	COJEPE	-1.80889	5.10E-06	hypothetical p	NA	ybbP	FtsX-like permease family
COJEPEMI_(	COJEPE	-1.82602	NA	hypothetical p	NA	gpW	Gene 25-like lysozyme
COJEPEMI_(	cycA_2	-1.82964	8.08E-06	D-serine/D-ala	NA	cycA	Amino acid permease
COJEPEMI_(	xecA1	-1.83018	6.19E-18	2-hydroxyprop	4.4.1.23	metE	Cobalamin-independent synthase, Catalytic domain
COJEPEMI_(	COJEPE	-1.83102	5.65E-05	hypothetical p	NA	0	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (HPPK)
COJEPEMI_(	COJEPE	-1.8401	1.02E-08	hypothetical p	NA	0	Acetyltransferase (GNAT) domain
COJEPEMI_(	COJEPE	-1.84152	2.69E-07	hypothetical p	NA	0	Gene 25-like lysozyme
COJEPEMI_(	dadX	-1.85152	6.02E-09	Alanine racem	5.1.1.1	alr	Catalyzes the interconversion of L-alanine and D- alanine. May also act
COJEPEMI_(	COJEPE	-1.86521	NA	hypothetical p	NA	0	
COJEPEMI_(	kgtP_2	-1.87883	4.37E-07	Alpha-ketoglut	NA	kgtP	Sugar (and other) transporter
COJEPEMI_(	yhjE	-1.89327	2.54E-11	Inner membra	NA	yhjE	Sugar (and other) transporter
COJEPEMI_(	prpC	-1.89888	1.98E-07	2-methylcitrat	2.3.3.5	prpC	Belongs to the citrate synthase family
COJEPEMI_(	COJEPE	-1.90605	0.001155	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.92779	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-1.95232	0.00792	hypothetical p	NA	rhtC	LysE type translocator
COJEPEMI_(	fadJ_1	-1.95659	3.22E-31	Fatty acid oxid	5.1.2.3	0	Enoyl-CoA hydratase/isomerase

COJEPEMI_(	lipA_2	-1.96867	0.001008	Lipoyl synthas(	2.8.1.8	lipA	Catalyzes the radical-mediated insertion of two sulfur atoms into the C
COJEPEMI_(	metQ_3	-1.97974	3.57E-12	putative D-me	NA	0	NLPA lipoprotein
COJEPEMI_(	COJEPE	-2.0173	NA	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	hin_1	-2.03706	NA	DNA-invertase	NA	0	DNA invertase
COJEPEMI_(	COJEPE	-2.04047	2.15E-05	hypothetical p	NA	nlpD_1	Peptidase family M23
COJEPEMI_(	COJEPE	-2.07355	4.26E-06	hypothetical p	NA	pcaC	Carboxymuconolactone decarboxylase family
COJEPEMI_(	COJEPE	-2.07696	NA	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-2.09448	0.003364	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	COJEPE	-2.11513	0.016149	hypothetical p	NA	0	
COJEPEMI_(	pcaH	-2.12374	2.01E-06	Protocatechua	1.13.11.3	pcaH	Protocatechuate 3,4-dioxygenase beta subunit N terminal
COJEPEMI_(	COJEPE	-2.13373	8.55E-28	hypothetical p	NA	0	Putative diguanylate phosphodiesterase
COJEPEMI_(	COJEPE	-2.13508	0.021159	hypothetical p	NA	0	
COJEPEMI_(	cysT	-2.14214	0.00898	Sulfate transp	NA	cysT	Binding-protein-dependent transport system inner membrane compone
COJEPEMI_(	mmgC_	-2.16116	1.16E-12	Acyl-CoA dehy	1.3.99.-	yngJ	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	COJEPE	-2.17674	NA	IS4 family trar	NA	0	Transposase DDE domain
COJEPEMI_(	cntO_2	-2.2295	2.20E-19	Metal-pseudo	NA	0	TonB dependent receptor
COJEPEMI_(	COJEPE	-2.23805	0.003578	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	denD	-2.24128	9.72E-10	D-erythronate	1.1.1.410	0	Male sterility protein
COJEPEMI_(	COJEPE	-2.25855	7.96E-11	hypothetical p	NA	mdcE	Malonate decarboxylase gamma subunit (MdcE)
COJEPEMI_(	COJEPE	-2.28927	3.37E-08	hypothetical p	NA	0	Secretin and TonB N terminus short domain
COJEPEMI_(	hutI	-2.29104	0.000429	Imidazolonepr	3.5.2.7	hutI	Amidohydrolase family
COJEPEMI_(	mexB_1	-2.29391	6.79E-17	Multidrug resi	NA	acrB	efflux pump
COJEPEMI_(	abaF_1	-2.30311	2.25E-24	Fosfomycin re	NA	0	Sugar (and other) transporter
COJEPEMI_(	COJEPE	-2.30938	2.23E-14	hypothetical p	NA	hmuP	Hemin uptake protein hemP
COJEPEMI_(	COJEPE	-2.31037	0.001738	hypothetical p	NA	MA20_42	Thioesterase-like superfamily
COJEPEMI_(	bdhA	-2.31666	6.03E-12	D-beta-hydrox	1.1.1.30	bdhA	KR domain
COJEPEMI_(	COJEPE	-2.34467	1.16E-18	hypothetical p	NA	0	Pfam:Methyltransf_6
COJEPEMI_(	fabD_1	-2.34763	7.85E-10	Malonyl CoA-a	2.3.1.39	mdcH	Acyl transferase domain
COJEPEMI_(	acrA	-2.36626	2.30E-20	Multidrug effl	NA	acrA	Belongs to the membrane fusion protein (MFP) (TC 8.A.1) family
COJEPEMI_(	COJEPE	-2.39958	1.57E-07	hypothetical p	NA	0	

COJEPEMI_(	atoE	-2.40558	3.05E-18	Putative short-	NA	atoE	Short chain fatty acid transporter
COJEPEMI_(	yjhB_1	-2.41375	1.24E-18	Putative meta	NA	dcaK	Major facilitator Superfamily
COJEPEMI_(	COJEPE	-2.45167	2.66E-10	hypothetical p	NA	madL	Malonate transporter MadL subunit
COJEPEMI_(	COJEPE	-2.4668	3.68E-11	hypothetical p	NA	VPA0159	Domain of unknown function (DUF4198)
COJEPEMI_(	COJEPE	-2.47379	1.17E-07	hypothetical p	NA	0	Forms passive diffusion pores that allow small molecular weight hydro
COJEPEMI_(	COJEPE	-2.47392	0.00162	hypothetical p	NA	0	
COJEPEMI_(	styD	-2.49104	1.28E-08	Phenylacetald	1.2.1.39	0	Aldehyde dehydrogenase family
COJEPEMI_(	lifO	-2.51191	5.27E-08	Lipase chaperc	NA	lifO	May be involved in the folding of the extracellular lipase during its pass
COJEPEMI_(	pdhC	-2.53877	2.15E-05	Dihydrolipoylly	2.3.1.12	pdhC	2-oxoacid dehydrogenases acyltransferase (catalytic domain)
COJEPEMI_(	quiB	-2.58717	7.62E-08	Catabolic 3-de	4.2.1.10	aroD	Involved in the third step of the chorismate pathway, which leads to th
COJEPEMI_(	mmgC_	-2.60003	3.15E-08	Acyl-CoA dehy	1.3.99.-	hcaD	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	COJEPE	-2.61783	2.76E-27	hypothetical p	NA	0	COG2610 H gluconate symporter and related permeases
COJEPEMI_(	deaD	-2.6421	2.46E-23	ATP-dependen	3.6.4.13	rhlE-1	Belongs to the DEAD box helicase family
COJEPEMI_(	COJEPE	-2.67259	5.36E-06	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-2.69113	1.66E-17	hypothetical p	NA	0	
COJEPEMI_(	hutH	-2.71464	0.000946	Histidine amm	4.3.1.3	hutH	histidine ammonia-lyase activity
COJEPEMI_(	iucD_2	-2.72514	2.32E-26	L-lysine N6-m	1.14.13.5	0	L-lysine 6-monooxygenase (NADPH-requiring)
COJEPEMI_(	iucA	-2.734	1.73E-33	N(2)-citryl-N(6	6.3.2.38	iucA	IucA / IucC family
COJEPEMI_(	COJEPE	-2.73979	0.000308	hypothetical p	NA	0	Protein of unknown function (DUF3237)
COJEPEMI_(	scmP	-2.74318	1.27E-05	N-acetylcystei	3.5.1.-	amaA	Peptidase dimerisation domain
COJEPEMI_(	COJEPE	-2.75579	2.71E-06	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	proY	-2.76907	1.30E-05	Proline-specifi	NA	proY	Amino acid permease
COJEPEMI_(	aroP_3	-2.82118	1.41E-16	Aromatic amir	NA	aroP	Amino acid permease
COJEPEMI_(	pcaB	-2.82395	5.99E-11	3-carboxy-cis,c	5.5.1.2	pcaB	Adenylosuccinate lyase C-terminus
COJEPEMI_(	COJEPE	-2.8707	1.35E-05	hypothetical p	NA	fcy21	Permease for cytosine/purines, uracil, thiamine, allantoin
COJEPEMI_(	dhbA	-2.89239	2.79E-42	2,3-dihydro-2,3	1.3.1.28	entA	Enoyl-(Acyl carrier protein) reductase
COJEPEMI_(	nagR_1	-2.89464	1.32E-07	HTH-type trans	NA	hutC	UTRA
COJEPEMI_(	madC	-2.89785	9.50E-20	Malonyl-S-ACP	2.1.3.10	mdcD	Carboxyl transferase domain
COJEPEMI_(	COJEPE	-2.92687	2.12E-24	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-2.94726	7.40E-06	hypothetical p	NA	0	

COJEPEMI_(	COJEPE	-2.96504	1.40E-08	hypothetical p	NA	0	
COJEPEMI_(	COJEPE	-2.97041	2.07E-06	hypothetical p	NA	0	
COJEPEMI_(	catD_1	-3.01778	1.51E-10	3-oxoadipate e	3.1.1.24	pcaD	Ndr family
COJEPEMI_(	COJEPE	-3.03577	3.51E-06	hypothetical p	NA	0	
COJEPEMI_(	hutU	-3.04598	0.000207	Urocanate hyd	4.2.1.49	hutU	Catalyzes the conversion of urocanate to 4-imidazolone- 5-propionate
COJEPEMI_(	citG	-3.06368	1.71E-17	2-(5''-triphosp	2.4.2.52	mdcB	Involved in the formation of 2-(5''-phosphoribosyl)-3'- dephosphocoenz
COJEPEMI_(	mdcG	-3.06533	7.40E-21	Phosphoribosy	2.7.7.66	mdcG	Phosphoribosyl-dephospho-CoA transferase MdcG
COJEPEMI_(	ipdC	-3.10475	1.70E-12	Indole-3-pyruv	4.1.1.74	ipdC	Thiamine pyrophosphate enzyme, central domain
COJEPEMI_(	pcaK_1	-3.11968	1.37E-12	4-hydroxybenz	NA	pcaK	Uncharacterised MFS-type transporter YbfB
COJEPEMI_(	vibB	-3.14021	5.17E-40	Vibriobactin-s	3.3.2.1	entB	Isochorismatase family
COJEPEMI_(	pcaF_1	-3.19364	2.47E-14	Beta-ketoadip	2.3.1.174	pcaF	Belongs to the thiolase family
COJEPEMI_(	COJEPE	-3.19954	1.21E-09	hypothetical p	NA	0	
COJEPEMI_(	acoB	-3.21102	1.04E-07	Acetoin:2,6-di	1.1.1.-	acoB	Transketolase, C-terminal domain
COJEPEMI_(	farB	-3.34796	1.61E-35	Fatty acid resi	NA	lmrB	Sugar (and other) transporter
COJEPEMI_(	COJEPE	-3.36411	6.91E-38	hypothetical p	NA	0	PepSY-associated TM region
COJEPEMI_(	COJEPE	-3.37965	5.43E-16	hypothetical p	NA	0	Siderophore biosynthesis protein domain
COJEPEMI_(	mdcC	-3.41729	4.24E-17	Malonate dec	NA	mdcC	Subunit of malonate decarboxylase, it is an acyl carrier protein to whicl
COJEPEMI_(	pcaJ_1	-3.41844	2.79E-14	3-oxoadipate (	2.8.3.6	pcaJ	3-oxoadipate CoA-transferase activity
COJEPEMI_(	madA	-3.44508	5.05E-19	Acetyl-S-ACP:r	2.3.1.187	mdcA	Malonate decarboxylase, alpha subunit, transporter
COJEPEMI_(	angR	-3.50973	4.64E-58	Anguibactin sy	NA	0	AMP-binding enzyme C-terminal domain
COJEPEMI_(	scoB	-3.51567	4.28E-33	putative succir	2.8.3.5	atoA	Coenzyme A transferase
COJEPEMI_(	COJEPE	-3.52834	1.95E-08	hypothetical p	NA	0	
COJEPEMI_(	fecI	-3.57831	7.62E-18	putative RNA p	NA	0	ECF sigma factor
COJEPEMI_(	COJEPE	-3.59311	3.09E-139	hypothetical p	NA	0	Condensation domain
COJEPEMI_(	COJEPE	-3.62757	1.96E-17	hypothetical p	NA	0	FecR protein
COJEPEMI_(	COJEPE	-3.67521	8.70E-38	hypothetical p	NA	0	Siderophore-interacting FAD-binding domain
COJEPEMI_(	thiC	-3.68787	4.07E-47	Phosphomethy	4.1.99.17	thiC	Catalyzes the synthesis of the hydroxymethylpyrimidine phosphate (HM
COJEPEMI_(	COJEPE	-3.73697	6.66E-10	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	scoA	-3.83718	8.73E-43	putative succir	2.8.3.5	lpsI	Coenzyme A transferase
COJEPEMI_(	astC_2	-3.91834	1.39E-43	Succinylornithi	2.6.1.81	argD	acetylornithine aminotransferase

COJEPEMI_(	pcaI_1	-3.99805	2.23E-21	3-oxoadipate (	2.8.3.6	pcaI	3-oxoadipate CoA-transferase activity
COJEPEMI_(	acoA	-4.04244	4.46E-11	Acetoin:2,6-di(	1.1.1.-	acoA	Dehydrogenase E1 component
COJEPEMI_(	sbnF	-4.0804	2.22E-54	2-[(L-alanin-3-	6.3.2.55	0	IucA / IucC family
COJEPEMI_(	COJEPE	-4.09074	1.14E-58	putative ABC t	NA	0	ABC transporter transmembrane region
COJEPEMI_(	lagD	-4.09218	3.68E-51	Lactococcin-G-	3.4.22.-	0	ABC transporter transmembrane region
COJEPEMI_(	COJEPE	-4.10367	3.24E-06	hypothetical p	NA	0	
COJEPEMI_(	cmoA	-4.15678	2.26E-22	Carboxy-S-ade	2.1.3.-	cmoA	Methyltransferase domain
COJEPEMI_(	iucD_1	-4.17592	2.81E-76	L-lysine N6-m(	1.14.13.5	basC	L-lysine 6-monooxygenase (NADPH-requiring)
COJEPEMI_(	COJEPE	-4.28272	4.28E-53	hypothetical p	NA	0	FhuF 2Fe-2S C-terminal domain
COJEPEMI_(	COJEPE	-4.41097	1.34E-81	hypothetical p	NA	0	IucA / IucC family
COJEPEMI_(	mmgC_	-4.44926	3.11E-42	Acyl-CoA dehy(	1.3.99.-	0	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	fadD3	-4.52947	4.56E-26	3-[(3aS,4S,7aS	6.2.1.41	acsf	AMP-binding enzyme C-terminal domain
COJEPEMI_(	COJEPE	-4.53574	3.15E-29	TPR repeat-co(	NA	0	Protein of unknown function (DUF560)
COJEPEMI_(	fatB	-4.60696	1.35E-68	Ferric-anguiba	NA	fatB	Periplasmic binding protein
COJEPEMI_(	COJEPE	-4.67137	7.92E-29	hypothetical p	NA	0	Gram-negative bacterial TonB protein C-terminal
COJEPEMI_(	COJEPE	-4.69162	1.11E-28	hypothetical p	NA	0	membrane
COJEPEMI_(	COJEPE	-4.79765	3.49E-45	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	rhtB_3	-4.83287	1.08E-119	Homoserine/h	NA	0	LysE type translocator
COJEPEMI_(	yclP	-4.8399	1.43E-62	Petrobactin im	7.2.2.-	vctC	ABC transporter
COJEPEMI_(	astA_2	-4.86554	4.15E-62	Arginine N-suc	2.3.1.109	astA	Arginine N-succinyltransferase beta subunit
COJEPEMI_(	accA1_	-4.88424	1.11E-30	Acetyl-/propio	NA	mccA	Biotin carboxylase C-terminal domain
COJEPEMI_(	COJEPE	-4.88615	4.31E-83	hypothetical p	NA	0	Pfam:NRPS
COJEPEMI_(	dpgD	-4.89028	2.42E-27	Enoyl-CoA-hyd	4.2.1.17	paaG5	Belongs to the enoyl-CoA hydratase isomerase family
COJEPEMI_(	COJEPE	-5.01017	1.36E-20	hypothetical p	NA	#N/A	#N/A
COJEPEMI_(	pigA	-5.04633	1.22E-38	Heme oxygena	1.14.99.5	hemO	Heme oxygenase
COJEPEMI_(	hdc	-5.23018	8.25E-148	Histidine deca	4.1.1.22	hdc	Pyridoxal-dependent decarboxylase conserved domain
COJEPEMI_(	betI_2	-5.24635	1.04E-31	HTH-type trans	NA	MA20_03	Bacterial regulatory proteins, tetR family
COJEPEMI_(	COJEPE	-5.27016	5.69E-32	Methylmalony	2.1.3.1	mccB	Carboxyl transferase domain
COJEPEMI_(	COJEPE	-5.30875	9.82E-76	putative oxido	1.-.-.-	0	Belongs to the short-chain dehydrogenases reductases (SDR) family
COJEPEMI_(	liuE	-5.33724	1.94E-33	3-hydroxy-3-is(	4.1.3.26	mvaB	HMGL-like

COJEPEMI_(	COJEPE	-5.40808	1.47E-55	hypothetical p	NA	0	C-lobe and N-lobe beta barrels of Tf-binding protein B
COJEPEMI_(	fatD	-5.43113	9.15E-68	Ferric-anguiba	NA	bauD	Belongs to the binding-protein-dependent transport system permease
COJEPEMI_(	acsA_3	-5.47594	1.89E-91	Acetyl-coenzyr	6.2.1.1	acs-2	AMP-binding enzyme C-terminal domain
COJEPEMI_(	mmgC_	-5.71374	1.67E-34	Acyl-CoA dehy	1.3.99.-	ivd	Acyl-CoA dehydrogenase, C-terminal domain
COJEPEMI_(	entE	-5.71748	3.25E-149	Enterobactin s	6.3.2.14	entE	AMP-binding enzyme C-terminal domain
COJEPEMI_(	entC	-5.81366	1.86E-65	Isochorismate	5.4.4.2	entC	chorismate binding enzyme
COJEPEMI_(	fatC	-5.8181	7.36E-60	Ferric-anguiba	NA	bauC	Belongs to the binding-protein-dependent transport system permease
COJEPEMI_(	entB	-6.42527	1.72E-169	Enterobactin s	6.3.2.14	entB	Isochorismatase family
COJEPEMI_(	argO	-6.51604	7.65E-86	Arginine expor	NA	lysE	LysE type translocator

activity of the latter

se family
completing the reaction cycle. Several rounds of ATP-dependent interactions between DnaJ, DnaK and GrpE are required for fully efficient folding.
preventing the aggregation of stress-denatured proteins, in association with DnaK and GrpE. It is the nucleotide exchange factor for DnaK and ma

uce beta-alanine

f unfolded polypeptides generated under stress conditions

lown, to xanthosine 5'-monophosphate (XMP), so it can be reused for RNA or DNA synthesis

, where it nucleates assembly of the head domain of the 30S subunit. Is located at the subunit interface close to the decoding center, probably bloc

9) in 23S rRNA

-dihydroxy-2-butanone 4-phosphate

tion and ATP hydrolysis and functions as a proton pump across the membrane

e, and is involved in E site tRNA release

ith GTP-bound translation factors

l and glutathione, to S-lactoylglutathione

lADPH and glutathione reductase. Reduces low molecular weight disulfides and proteins

ng and oxidatively damaged proteins from irreversible aggregation. Plays an important role in the bacterial defense system toward oxidative stress

slation elongation. During this step, the ribosome changes from the pre-translocational (PRE) to the post- translocational (POST) state as the newl

enters, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples

:omycin

f the cell cytoplasm. It is a molecular chaperone that binds to a subset of precursor proteins, maintaining them in a translocation-competent state

end of the 23S rRNA, where it nucleates assembly of the 50S subunit
DNA lesions. UvrC both incises the 5' and 3' sides of the lesion. The N-terminal half is responsible for the 3' incision and the C-terminal half is resp

-end of 16S ribosomal RNA

ɔunit in a nucleotide-independent manner
ehalose

oxidoreductase subfamily

ins that surrounds the polypeptide exit tunnel on the outside of the ribosome. Forms the main docking site for trigger factor binding to the riboson

enters, to quinones in the respiratory chain
ibly P site tRNAs

lA polymerase to specific initiation sites and are then released. This sigma factor is the primary sigma factor during exponential growth

the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransfera

ıinal cysteine of membrane lipoproteins
ɔosomal RNA

ibosome, positioning it for translation
DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 UvrA and 2 UvrB subunits scans DNA fo
enters, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples

tunnel on the outside of the subunit, while an extended beta-hairpin is found that lines the wall of the exit tunnel in the center of the 70S riboson

yrophosphate (PRPP) and glutamine
on

here it forms part of the central protuberance

ethyl-2-oxobutanoate (2-oxoisovalerate) to form 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate)

-ribosyl-1-pyrophosphate (PRPP) via the transfer of pyrophosphoryl group from ATP to 1-hydroxyl of ribose-5-phosphate (Rib-5-P)

ion of the ribosome with GTP-bound translation factors

) in tRNA

S rRNA, where it helps stabilize the platform of the 30S subunit

ich are toxic to biological systems

ith GTP-bound translation factors. Is thus essential for accurate translation
L-aspartate to iminoaspartate
enters, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples

D subunit (chain G)

d in the D-loop of most tRNAs, via the reduction of the C5-C6 double bond in target uridines. Specifically modifies U16 in tRNAs

luster coordination is flexible as the role of this complex is to build and then hand off Fe-S clusters
assic translation factor GTPase family. CysN NodQ subfamily

enters, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples

osynthetic pathway. Catalyzes the ATP-dependent conversion of formylglycinamide ribonucleotide (FGAR) and glutamine to yield formylglycinamid

central domain where it helps coordinate assembly of the platform of the 30S subunit

n of mutant and abnormal proteins as well as certain short-lived regulatory proteins. Required for cellular homeostasis and for survival from DNA

ructure. It is located near the subunit interface in the base of the L7 L12 stalk, and near the tRNA binding site of the peptidyltransferase center

alyzes the reversible oxidation of betaine aldehyde to the corresponding acid

ransfer this cluster to apoproteins, and thereby intervenes in the maturation of Fe S proteins. Could also act as a scaffold chaperone for damaged I
Stabilizes the binding of IF-2 and IF-3 on the 30S subunit to which N-formylmethionyl-tRNA(fMet) subsequently binds. Helps modulate mRNA sel

enters, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples

action with DNA. Acts by binding directly to the C-terminal domain of GyrB, which probably disrupts DNA binding by the gyrase

rsion of dihydroxyacetone phosphate (DHAP) to D-glyceraldehyde-3-phosphate (G3P)

ase domains

at position 37 (t(6)A37) in tRNAs that read codons beginning with adenine. Is involved in the transfer of the threonylcarbamoyl moiety of threonyl

ane to the outer membrane. Only forms a complex with a lipoprotein if the residue after the N-terminal Cys is not an aspartate (The Asp acts as a
ment of the 5S RNA into the large ribosomal subunit, where it forms part of the central protuberance

preprotein conducting channel. Has a central role in coupling the hydrolysis of ATP to the transfer of proteins into and across the cell membrane, s
so be responsible for determining the conformation of the 16S rRNA at the A site

formation of the head with respect to the body

de (L-ASA) by the reductive dephosphorylation of L- aspartyl-4-phosphate

amily

lmalate, via the formation of 2-isopropylmaleate

tion 37 in tRNAs that read codons beginning with uridine, leading to the formation of N6-(dimethylallyl)adenosine (i(6)A)

op off the ribosome during protein synthesis

alyzes the reversible oxidation of betaine aldehyde to the corresponding acid

s dependent on ATP binding by UvrB and probably causes local melting of the DNA helix, facilitating insertion of UvrB beta-hairpin between the DN

tein L14 (rplN), blocking formation of intersubunit bridge B8. Prevents association of the 30S and 50S ribosomal subunits and the formation of func

lmalate, via the formation of 2-isopropylmaleate

of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP)

ase domains
A to produce the mature 5'-terminus. It can also cleave other RNA substrates such as 4.5S RNA. The protein component plays an auxiliary but esse

enters, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples

ibosome
nps together the 2 halves of SecY. May contact the channel plug during translocation

o the A-site of ribosomes during protein biosynthesis

onuclease activity. Probably involved in tRNA maturation, by removing a 3'-trailer from precursor tRNA

site. By recycling D-aminoacyl-tRNA to D-amino acids and free tRNA molecules, this enzyme counteracts the toxicity associated with the formatic

ent of the 5S RNA into the large ribosomal subunit, where it forms part of the central protuberance. In the 70S ribosome it contacts protein S13 of

e (PEP), the rate-limiting step in the metabolic pathway that produces glucose from lactate and other precursors derived from the citric acid cycle

ecovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE

utside of the subunit

s of 2Fe2S cluster formation and transfer are observed, suggesting that IscA acts catalytically. Recruits intracellular free iron so as to provide iron

stem and loop of transfer RNAs

ediator of the stringent response that coordinates a variety of cellular activities in response to changes in nutritional abundance

curs when 3 or more consecutive Pro residues or the sequence PPG is present in a protein, possibly by augmenting the peptidyl transferase activity

e (RNAP). Required for negative regulation of rRNA expression and positive regulation of several amino acid biosynthesis promoters. Also required

en-III to yield coproporphyrinogen-III

finity binding and energy dependent uptake into the periplasmic space of specific substrates. It could act to transduce energy from the cytoplasmi

synthesis of deoxyribonucleotides from the corresponding ribonucleotides

n, which catalyzes the hydrolysis of ATP coupled with the electrogenic transport of potassium into the cytoplasm. This subunit acts as a catalytic cl
ng proteins. Seems to help targeting proteins to be folded toward HscA
ediator of the stringent response that coordinates a variety of cellular activities in response to changes in nutritional abundance
ds to the corresponding amines. Requires NADH, but not NADPH, as an electron donor for its activity

prenyl-3-methyl-6-methoxy-1,4-benzoquinol resulting in the formation of 2-nonaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4- benzoquinol

DP to GTP. It remains bound to the aminoacyl-tRNA.EF- Tu.GTP complex up to the GTP hydrolysis stage on the ribosome

ɔ-phosphate

(N5-CAIR) to 4-carboxy-5-aminoimidazole ribonucleotide (CAIR)

se family. PhnW subfamily

e RNA helices of the 16S rRNA. Forms part of the Shine-Dalgarno cleft in the 70S ribosome

nded DNA and acts in a progressive fashion along the DNA in the 3' to 5' direction

lition of a carboxymethylaminomethyl (cmnm) group at the wobble position (U34) of certain tRNAs, forming tRNA- cmnm(5)s(2)U34

ich is a hypermodified base found in the wobble positions of tRNA(Asp), tRNA(Asn), tRNA(His) and tRNA(Tyr)

philic materials across the outer membrane
ich are toxic to biological systems

l thiamine biosynthesis family 1

f ATP and the subsequent transfer of glutamate onto a tRNA(Asp). Glutamate is transferred on the 2-amino-5-(4,5- dihydroxy-2-cyclopenten-1-yl) ı

-(3-hydroxydodecanoyl)-L-HSL (3-hydroxy-C(12)-HSL or OH-dDHL)

elices of the 16S rRNA. In the 70S ribosome it contacts the 23S rRNA (bridge B1a) and protein L5 of the 50S subunit (bridge B1b), connecting the 2

reonine (HTP) into 2-amino-3-oxo-4- (phosphohydroxy)butyric acid which spontaneously decarboxylates to form 3-amino-2-oxopropyl phosphate (A

ıe immediate precursor of thymidine nucleotides and it decreases the intracellular concentration of dUTP so that uracil cannot be incorporated int

een 70S ribosomes and their 50S and 30S subunits in favor of the free subunits, thus enhancing the availability of 30S subunits on which protein sy

actor)

eotide (AIR) and HCO(3)(-) to N5- carboxyaminoimidazole ribonucleotide (N5-CAIR)

ed in assembly and insertion of beta-barrel proteins into the outer membrane

ts by oxidizing the DsbA protein

ge folded proteins containing a characteristic twin-arginine motif in their signal peptide across membranes. Together with TatB, TatC is part of a r

where it nucleates assembly of the body of the 30S subunit
ahydrofolate (THF) serving as the one-carbon carrier. This reaction serves as the major source of one-carbon groups required for the biosynthesis o

0S ribosomal subunit, possibly for assembly of the head region. Probably interacts with S19. Essential for efficient processing of 16S rRNA. May be

2.A.23) family

midine moiety of thiamine compounds, a reaction that is part of a thiamine salvage pathway

nthesis of aromatic amino acids. Catalyzes the reversible NADPH linked reduction of 3-dehydroshikimate (DHSA) to yield shikimate (SA)

ɔiquinone biosynthetic pathway

'-phosphate (XMP), the first committed and rate- limiting step in the de novo synthesis of guanine nucleotides, and therefore plays an important r

ɛ protease to specific substrates. Can perform chaperone functions in the absence of ClpP

8

protein S12
Protects formylmethionyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30S ribosomal subunits. Also involved in the hydrolys
ı of a sulfur atom into dethiobiotin via a radical- based mechanism

ımerization of proline imidic peptide bonds in oligopeptides

ase activity. The DNA N-glycosylase activity releases various damaged pyrimidines from DNA by cleaving the N- glycosidic bond, leaving an AP (apu

10-methylenetetrahydrofolate is transferred onto alpha-ketoisovalerate to form ketopantoate
ed in assembly and insertion of beta-barrel proteins into the outer membrane

alyzes the reversible oxidation of betaine aldehyde to the corresponding acid

pendent reaction via a pantoyl-adenylate intermediate

mutagenesis. Copies undamaged DNA at stalled replication forks, which arise in vivo from mismatched or misaligned primer ends. These misalign

termination of protein biosynthesis. May increase the efficiency of translation by recycling ribosomes from one round of translation to another

philic materials across the outer membrane

riety of metabolic reactions

to RNA using the four ribonucleoside triphosphates as substrates

l thiamine biosynthesis family 2

le exchange. Plays a role in 16S rRNA processing and 30S ribosomal subunit biogenesis and possibly also in cell cycle regulation and energy metab

uence in tRNAs without using a nucleic acid template. Adds these three nucleotides in the order of C, C, and A to the tRNA nucleotide-73, using CTF

n III

e nrd genes and operons by binding to NrdR- boxes
e into 5-amino-6-(ribosylamino)-2,4(1h,3h)- pyrimidinedione 5'-phosphate
tetrahydrodipicolinate

hosphate to form quinolinate

ction glutamate is first activated by ATP to form Glu-AMP and then transferred to the acceptor end of tRNA(Glu)

-6 and C-8 positions of the octanoyl moiety bound to the lipoyl domains of lipoate-dependent enzymes, thereby converting the octanoylated doma

ranslocation of LPS from the inner membrane to the outer membrane. May form a bridge between the inner membrane and the outer membrane

te to 5-phospho-ribosyl-glycinamide (GAR), producing 5-phospho-ribosyl-N-formylglycinamide (FGAR) and tetrahydrofolate

es them by dioxygen to Fe(3), and participates in the subsequent Fe(3) oxide mineral core formation within the central cavity of the protein comp

sts of two halves formed by TMs 1-5 and 6-10. These two domains form a lateral gate at the front which open onto the bilayer between TMs 2 and
ane pre-uroporphyrinogen in several discrete steps

Fe-S cluster assembly, tRNA modification or cofactor biosynthesis. Catalyzes the removal of elemental sulfur atoms from cysteine to produce alan
proteins. Has a low intrinsic ATPase activity which is markedly stimulated by HscB
nd glutamate. The HisH subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to HisF for the synthesis o

2.A.23) family

2'-O position of the ribose in the fully assembled 50S ribosomal subunit

unctional core of the 30S ribosomal subunit. Associates with free 30S ribosomal subunits (but not with 30S subunits that are part of 70S ribosome
The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediat

NA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs.

lectron acceptor

mily

ucture in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination. Ru

P) to meso-diaminoheptanedioate (meso- DAP), a precursor of L-lysine and an essential component of the bacterial peptidoglycan

prolipoproteins

ich is a hypermodified base found in the wobble positions of tRNA(Asp), tRNA(Asn), tRNA(His) and tRNA(Tyr)

nomethyl group of 7-deazaguanine (preQ1-tRNA) to give epoxyqueuosine (oQ-tRNA)

may play a role in the structure and function of the aminoacyl-tRNA binding site

at position 37 (t(6)A37) in tRNAs that read codons beginning with adenine. Catalyzes the conversion of L-threonine, HCO(3)(-) CO(2) and ATP to gi

er editing activity that hydrolyzes mischarged Thr-tRNA(Val) in a tRNA-dependent manner
ate lyase

ter. This process requires GTP hydrolysis, probably effectuated by UreG
o uridine 5'-monophosphate (UMP)

l phosphate to indole and glyceraldehyde 3- phosphate

bunit Na H antiporter, MnhA subunit
nport. Responsible for energy coupling to the transport system

synthesis of deoxyribonucleotides from the corresponding ribonucleotides

biotin carboxylase catalyzes the carboxylation of biotin on its carrier protein (BCCP) and then the CO(2) group is transferred by the carboxyltransfe

ninopimelate by linking it to UDP-N- acetylmuramate

d system which includes mercuric reductase. MerA protein is responsible for volatilizing mercury as Hg(0)

proteins (some contain LysM invasin domains)
nd glutamate. The HisF subunit catalyzes the cyclization activity that produces IGP and AICAR from PRFAR using the ammonia provided by the HisH

phosphate ions

tion L-threonine is first activated by ATP to form Thr-AMP and then transferred to the acceptor end of tRNA(Thr)

hosphate (PRPP) to UMP and diphosphate

', and is a key enzyme in the biosynthesis of NADP. Catalyzes specifically the phosphorylation on 2'-hydroxyl of the adenosine moiety of NAD to yiel

'ldisaccharide 1-phosphate intermediate (termed DS-1- P) to form tetraacyldisaccharide 1,4'-bis-phosphate (lipid IVA)

its toxicity

.-phosphate and the respective free bases. Can use uridine, adenosine, guanosine, cytidine, thymidine, inosine and xanthosine as substrates. Also c

on other amino acids

n carboxylase (BC) catalyzes the carboxylation of biotin on its carrier protein (BCCP) and then the CO(2) group is transferred by the transcarboxylas
ate (PGP) to phosphatidylglycerol (PG)

toplasmic and membrane proteins. Plays a role in the quality control of integral membrane proteins

ial lipopolysaccharide in Gram-negative bacteria

ly synthesized protein in an open conformation. Functions as a peptidyl-prolyl cis-trans isomerase

NA transcript to yield the immediate precursors to the large and small rRNAs (23S and 16S). Processes some mRNAs, and tRNAs when they are er
(DMKH2) to menaquinol (MKH2) and the conversion of 2-polyprenyl-6-methoxy-1,4-benzoquinol (DDMQH2) to 2- polyprenyl-3-methyl-6-methoxy-1

ans polyprenyl group. Mediates the second step in the final reaction sequence of ubiquinone-8 (UQ-8) biosynthesis, which is the condensation of th

(CDG) to 7-cyano-7-deazaguanine (preQ(0))

n, which catalyzes the hydrolysis of ATP coupled with the electrogenic transport of potassium into the cytoplasm. This subunit is responsible for er
ent ATPase activity and unwinds double-stranded RNA

se activity

-terminal PDZ domain

ıily

/lcobalamin (Ado-cobalamin). Also synthesizes adenosylcobalamin 5'-phosphate from adenosylcobinamide-GDP and alpha-ribazole 5'-phosphate

:en inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins to methionine

ucture in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination. Ru

se RNAs for decay. Plays a significant role in the global control of gene expression, through influencing the rate of transcript degradation, and in th

osition of lipid A, a bioactive component of lipopolysaccharide (LPS), thereby releasing the primary fatty acyl moiety

ose 1-diphosphate to orotate, leading to the formation of orotidine monophosphate (OMP)

se family

assembled 30S particle

dihydroxy-2-butanone 4-phosphate
ns containing an N-terminal aspartate or glutamate

alyzes the reversible oxidation of betaine aldehyde to the corresponding acid

ı adaptive immune system that provides protection against mobile genetic elements (viruses, transposable elements and conjugative plasmids). C

ıediates, plays a role in repairing DNA breaks. Stimulates the branch migration of RecA-mediated strand transfer reactions, allowing the 3' invadir

eine, yielding dephospho-CoA (dPCoA) and pyrophosphate

›synthetic process

Met). The formyl group appears to play a dual role in the initiator identity of N-formylmethionyl-tRNA by promoting its recognition by IF2 and preve

esponsible for energy coupling to the transport system

cysteine is conjugated to 4'-phosphopantothenate to form 4-phosphopantothenoylcysteine, in the latter compound is decarboxylated to form 4'-pl

alyzes the reversible oxidation of betaine aldehyde to the corresponding acid

RNA, to form 2-thiocytidine (s(2)C32). The sulfur atoms are provided by the cysteine cysteine desulfurase (IscS) system
uced during the DNA replication and transcription, by transiently cleaving and rejoining one strand of the DNA duplex. Introduces a single-strand br

nethyl (cmnm) group at the wobble position (U34) of certain tRNAs, forming tRNA-cmnm(5)s(2)U34

cific DNA-binding protein that functions in genetic recombination as well as in transcriptional and translational control

łZ-P) and 2-methyl-4-amino-5-hydroxymethyl pyrimidine pyrophosphate (HMP-PP) to form thiamine monophosphate (TMP)

se-1-pyrophosphate (PRPP) to anthranilate to yield N-(5'-phosphoribosyl)-anthranilate (PRA)

ge folded proteins containing a characteristic twin-arginine motif in their signal peptide across membranes. Together with TatC, TatB is part of a r

nosphates

amily

t and for biogenesis of the outer membrane. Transmembrane domains (TMD) form a pore in the inner membrane and the ATP-binding domain (N

nily

forming succinate and LL-2,6- diaminoheptanedioate (DAP), an intermediate involved in the bacterial biosynthesis of lysine and meso-diaminopim

n 16S rRNA

rboxylation of propionate groups of rings A and B of coproporphyrinogen-III to yield the vinyl groups in protoporphyrinogen-IX

sition 2 of adenine 37 in tRNAs

alyzes the reversible oxidation of betaine aldehyde to the corresponding acid

o the A-site of ribosomes during protein biosynthesis

sites for ATP binding, DNA binding, and interaction with DnaC protein, primase, and other prepriming proteins

ı replication and are intermediates in certain DNA recombination reactions. The complex acts as a 3'- 5' double strand exonuclease that can open h

from the 5'-end of triphosphorylated RNA, leading to a more labile monophosphorylated state that can stimulate subsequent ribonuclease cleavag

omeostasis

ı of gene expression, nucleoid organization and DNA protection

cids via beta-oxidation cycle. Catalyzes the formation of 3-oxoacyl-CoA from enoyl-CoA via L-3-hydroxyacyl-CoA. It can also use D-3-hydroxyacyl-CoA

late mRNA with a short Shine-Dalgarno (SD) purine-rich sequence

ain

on tyrosine is first activated by ATP to form Tyr- AMP and then transferred to the acceptor end of tRNA(Tyr)
alyzes the reversible oxidation of betaine aldehyde to the corresponding acid

eptation

orms of NAD(P)HX and the dehydration of the S-form of NAD(P)HX at the expense of ADP, which is converted to AMP. This allows the repair of both

RNAP) stalled at DNA lesions. Mediates ATP-dependent release of RNAP and its truncated transcript from the DNA, and recruitment of nucleotide

ulates activities of RF-1 and RF-2. It binds guanine nucleotides and has strong preference for UGA stop codons. It may interact directly with the rib
tanoyl-acyl-carrier-protein onto the lipoyl domains of lipoate-dependent enzymes. Lipoyl-ACP can also act as a substrate although octanoyl-ACP is l

ed for dam-dependent methyl-directed DNA mismatch repair. May act as a molecular matchmaker , a protein that promotes the formation of a sta

into L-glutamate 5-semialdehyde and phosphate. The product spontaneously undergoes cyclization to form 1-pyrroline-5- carboxylate

hesis of anthranilate, an intermediate in the biosynthesis of L-tryptophan. In the first step, the glutamine- binding beta subunit (TrpG) of anthranil

cific DNA-binding protein that functions in genetic recombination as well as in transcriptional and translational control
tes to their monophosphate derivatives, with a high preference for the non-canonical purine nucleotides XTP (xanthosine triphosphate), dITP (deox

ring) at the future cell division site. The regulation of the ring assembly controls the timing and the location of cell division. One of the functions of

n and a winged-helix DNA-binding domain

-hydroxyethylthiazole (THZ)
Gln) through the transamidation of misacylated Asp- tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or g

emplate-encoded arresting sites. The arresting sites in DNA have the property of trapping a certain fraction of elongating RNA polymerases that p

n and a winged-helix DNA-binding domain

he formation of a condensin-like complex containing Smc and ScpA that pull DNA away from mid-cell into both cell halves
al ABC transporter that contains transmembrane domains (TMD), which form a pore in the inner membrane, and an ATP-binding domain (NBD), w

nate and 5-phospho-D-ribose 1-phosphate at the expense of ATP
ron-requiring processes, such as synthesis and or repair of Fe-S clusters in biosynthetic enzymes

PA-CoA)

thylguanine (O6-MeG) and O4-methylthymine (O4-MeT) in DNA. Repairs the methylated nucleobase in DNA by stoichiometrically transferring the

ımily

e novo glycine and purine synthesis, and for DNA precursor synthesis

egions of the beta' subunit thereby facilitating its interaction with the beta and alpha subunits

ıe guanine in position 2069 (m7G2069) of 23S rRNA

.PS) at the surface of the outer membrane

oxymethyl-7,8-dihydropterin diphosphate (DHPt-PP) to form 7,8-dihydropteroate (H2Pte), the immediate precursor of folate derivatives

g the hydrolysis of succinyl-CoA to the synthesis of either ATP or GTP and thus represents the only step of substrate-level phosphorylation in the TC

n proline is first activated by ATP to form Pro- AMP and then transferred to the acceptor end of tRNA(Pro). As ProRS can inadvertently accommoda
ss conditions. May act as a fidelity factor of the translation reaction, by catalyzing a one-codon backward translocation of tRNAs on improperly tra

ıiratory chain
lycan precursors from the inner to the outer leaflet of the cytoplasmic membrane
ransamidation of misacylated Glu-tRNA(Gln) in organisms which lack glutaminyl-tRNA synthetase. The reaction takes place in the presence of glu

ir enzymes

Met). The formyl group appears to play a dual role in the initiator identity of N-formylmethionyl-tRNA by promoting its recognition by IF2 and preve

ns of uroporphyrinogen III at position C-2 and C-7 to form precorrin-2 via precorrin-1. Then it catalyzes the NAD- dependent ring dehydrogenation of

removes acetyl and succinyl groups on target proteins. Modulates the activities of several proteins which are inactive in their acylated form

ted proteins. Requires at least a dipeptide for an efficient rate of reaction. N-terminal L-methionine is a prerequisite for activity but the enzyme ha

membrane
ily

ase domains

rections. It is involved in the osmoregulation and in the maintenance of cell turgor during volume expansion in rapidly growing cells. It mediates ra

mily
regulation of the phosphoenolpyruvate synthase (PEPS) by catalyzing its phosphorylation dephosphorylation
nates import. Responsible for energy coupling to the transport system
C loop of transfer RNAs

idazole-4-carboxamide isomerase

rboxylic acid cycle

LPS) at the surface of the outer membrane. Required for the proper assembly of LptD. Binds LPS and may serve as the LPS recognition site at the o

onal DNA repair. Binds to DSBs and unwinds DNA via a highly rapid and processive ATP-dependent bidirectional helicase activity. Unwinds dsDNA u

e hydrolysis of 3-deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) to 3-deoxy-D-manno-octulosonate (KDO) and inorganic phosphate

doxamine 5'-phosphate (PMP) into pyridoxal 5'-phosphate (PLP)

tion of 5-amino-6-(D- ribitylamino)uracil with 3,4-dihydroxy-2-butanone 4-phosphate. This is the penultimate step in the biosynthesis of riboflavin

nily

rose-4-phosphate (E4P) giving rise to 3-deoxy-D- arabino-heptulosonate-7-phosphate (DAHP)

unctional core of the 30S ribosomal subunit. Helps release RbfA from mature subunits. May play a role in the assembly of ribosomal proteins into

neso-DAP) to L-lysine

ge folded proteins containing a characteristic twin-arginine motif in their signal peptide across membranes. TatA could form the protein-conductir

:he formation of a condensin-like complex containing Smc and ScpB that pull DNA away from mid-cell into both cell halves

phate (HMBPP) into a mixture of isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP). Acts in the terminal step of the DOXP MEI

es the overall conversion of pyruvate to acetyl-CoA and CO(2)

Gln) through the transamidation of misacylated Asp- tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or g

-4-phosphonooxybutanoate

in the loop of a conserved hairpin near the 3'-end of 16S rRNA in the 30S particle. May play a critical role in biogenesis of 30S subunits

proteins. Acts as a clamp, forming a ring around DNA (a reaction catalyzed by the clamp-loading complex) which diffuses in an ATP-independent r

, a short internal open reading frame. During trans-translation Ala- aminoacylated tmRNA acts like a tRNA, entering the A-site of stalled ribosome

nction intermediates to mature products by catalyzing branch migration. Has a DNA unwinding activity characteristic of a DNA helicase with a 3'- t
rane proteins. Recognizes specific patterns of aromatic residues and the orientation of their side chains, which are found more frequently in integ

o form glutathione and D-lactic acid
ᵖ-dependent protein degradation

onfers resistance to bacitracin

initiation of all mRNA translation through initiator tRNA(fMet) aminoacylation

response to the peptide chain termination codons UGA and UAA

lipopolysaccharide biosynthesis translation initiation factor 2B, gamma epsilon subunits (eIF-2Bgamma eIF-2Bepsilon)

ı also catalyze the reverse reaction

8 (m3U1498) in 16S rRNA. Acts on the fully assembled 30S ribosomal subunit

an important role in the purine salvage pathway and in nitrogen catabolism

ecaprenyl-pyrophosphoryl-MurNAc-pentapeptide (lipid intermediate I) to form undecaprenyl-pyrophosphoryl-MurNAc- (pentapeptide)GlcNAc (lipid

supercoiled DNA. Performs the decatenation events required during the replication of a circular DNA molecule
ster by transfer of a methyl group from S-adenosyl- L-methionine (SAM). It allows to synthesize pimeloyl-ACP via the fatty acid synthetic pathway

sembly process of the 50S ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit

ent

l (generally Phe) residue

s that lack stem peptides

o facilitate mRNA translational regulation in response to envelope stress, environmental stress and changes in metabolite concentrations. Also bi

ion of integral membrane proteins into the membrane. Involved in integration of membrane proteins that insert both dependently and independer

subunit, although it is not seen to bind rRNA by itself. It is important during the early stages of 50S assembly

lA polymerase to specific initiation sites and are then released
thenyltetrahydrofolate and then the hydrolysis of 5,10-methenyltetrahydrofolate to 10- formyltetrahydrofolate

ın hydrolyze ATP

al intermediate at the junction of anabolic and catabolic pathways. AcsA undergoes a two-step reaction. In the first half reaction, AcsA combines

g the hydrolysis of succinyl-CoA to the synthesis of either ATP or GTP and thus represents the only step of substrate-level phosphorylation in the TC

e 5'-triphosphate

indole and L-serine

:hylallyl diphosphate (DMAPP), two major building blocks of isoprenoid compounds. Catalyzes the conversion of 4- diphosphocytidyl-2-C-methyl-D-e
lipid-linked precursors

xonuclease activity

ın of lipoproteins, in an ATP-dependent manner
ic compounds 1-deoxy-D-xylulose-5-phosphate (DXP) and 3-amino-2-oxopropyl phosphate (1-amino-acetone-3-phosphate or AAP) to form pyridoxir
SA and pyruvate to 4-hydroxy- tetrahydrodipicolinate (HTPA)

the cytoplasmic membrane. Acts as a receptor for the complex formed by the signal recognition particle (SRP) and the ribosome-nascent chain (RI

ıine biosynthesis the synthesis of N- acetylglutamate from glutamate and acetyl-CoA as the acetyl donor, and of ornithine by transacetylation betw
leased and the CoA ester of a fatty acid two carbons shorter is formed

lucosamine (PGA) across the outer membrane. The PGA transported seems to be partially N-deacetylated since N- deacetylation of PGA by PgaB i

emplate-encoded arresting sites. The arresting sites in DNA have the property of trapping a certain fraction of elongating RNA polymerases that p

ds preferentially to single-stranded, linear DNA. It also seems to bind ATP

port. Responsible for energy coupling to the transport system

leucyl isoacceptors tRNA(Leu)(CmAA) and tRNA(Leu)(cmnm5UmAA). Catalyzes the methyl transfer from S- adenosyl-L-methionine to the 2'-OH of
inds to ssDNA and to an array of partner proteins to recruit them to their sites of action during DNA metabolism

erine and the beta-addition of water to produce L- threonine

ization of the ring, to provide 4- hydroxybenzoate (4HB) for the ubiquinone pathway

n resolvase

phosphate to cyclic pyranopterin monophosphate (cPMP)

ɜubfamily

ˈtion of CO2 between the N7 and N8 nitrogen atoms of 7,8-diaminopelargonic acid (DAPA) to form an ureido ring

enters, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples

lA

1-phosphate

form UDP-3-O-myristoylglucosamine and acetate, the committed step in lipid A biosynthesis

indole and L-serine

is involved in maturation of structured RNAs

cid motif, structural feature or limited homology

›yl phosphate (CP) to the N(epsilon) atom of ornithine (ORN) to produce L-citrulline
-6P into glucosamine-6P using glutamine as a nitrogen source
component, and related enzymes

acylate tRNA(Sec) with serine, to form the misacylated tRNA L-seryl-tRNA(Sec), which will be further converted into selenocysteinyl-tRNA(Sec)

ısed as primers for DNA polymerase during DNA replication

ıe urease nickel metallocenter

ent

pid intermediates. The enzyme has a penicillin-insensitive transglycosylase N-terminal domain (formation of linear glycan strands) and a penicillir

rsion of 2-oxoglutarate to succinyl-CoA and CO(2)

een ATP and AMP. Plays an important role in cellular energy homeostasis and in adenine nucleotide metabolism

ts by transferring its disulfide bond to other proteins and is reduced in the process

ribosomal RNA (rRNA) genes. Binds specifically to the boxA antiterminator sequence of the ribosomal RNA (rrn) operons

polymerase (RNAP) recycling in case of stress conditions such as supercoiled DNA or high salt concentrations. Probably acts by releasing the RNAF

pathway for UDP-N-acetylglucosamine (UDP- GlcNAc). The C-terminal domain catalyzes the transfer of acetyl group from acetyl coenzyme A to gl

oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides

hine, ammonia and CO(2)

hylated uridine (Um32) at position 32 in tRNA

ed in assembly and insertion of beta-barrel proteins into the outer membrane

supercoiled DNA. Performs the decatenation events required during the replication of a circular DNA molecule

rmate to 5-phospho-ribosyl-glycinamide (GAR), producing 5-phospho-ribosyl-N-formylglycinamide (FGAR). Formate is provided by PurU via hydrol
incorporation of dUMP residues by DNA polymerase or due to deamination of cytosine

2.A.23) family

nesis

Pase PilB

cerate

lutamate 1-semialdehyde (GSA)
nosphatases) domain

orm a long-chain polyphosphate (polyP)

NA, leading to the formation of s(2)U34

. Rapidly oscillates between the poles of the cell to destabilize FtsZ filaments that have formed before they mature into polar Z rings. Prevents Fts

H protein shuttles the methylamine group of glycine from the P protein to the T protein
ent

ain
ormate and tetrahydrofolate (FH4)

uced during the DNA replication and transcription, by transiently cleaving and rejoining one strand of the DNA duplex. Introduces a single-strand br

ıate (dUMP) to 2'-deoxythymidine-5'-monophosphate (dTMP) while utilizing 5,10-methylenetetrahydrofolate (mTHF) as the methyl donor and redu

ı role during protein synthesis or ribosome biogenesis

oA biosynthesis

ıa subunit family
ıic acid using ATP as a cosubstrate
addition of GMP to adenosylcobinamide phosphate

:hways of dTTP synthesis
402) of 16S rRNA

er (TC 2.A.37) family

er (TC 2.A.37) family

ılfate import. Responsible for energy coupling to the transport system

)R hydrogen from 5-enolpyruvylshikimate-3-phosphate (EPSP) to yield chorismate, which is the branch point compound that serves as the starting s
proteins (some contain LysM invasin domains)

ɔS rRNA
ɛnt

the cytoplasmic membrane. Binds to the hydrophobic signal sequence of the ribosome-nascent chain (RNC) as it emerges from the ribosomes. The

activation of rRNA promoters
to Kdo(2)-lipid IV(A) to form Kdo(2)- (lauroyl)-lipid IV(A)

ed proteins. Requires at least a dipeptide for an efficient rate of reaction. N-terminal L-methionine is a prerequisite for activity but the enzyme ha

membrane

prolipoproteins

tween 5'-phosphoryl and 3'-hydroxyl groups in double-stranded DNA using NAD as a coenzyme and as the energy source for the reaction. It is esse

mine residue

therefore promoting FtsZ assembly into bundles of protofilaments necessary for the formation of the division Z ring. It is recruited early at mid-ce

d in the D-loop of most tRNAs, via the reduction of the C5-C6 double bond in target uridines

·oxymethyl-7,8-dihydropterin diphosphate (DHPt-PP) to form 7,8-dihydropteroate (H2Pte), the immediate precursor of folate derivatives

-isopropylmalate) to 3-carboxy-4-methyl-2- oxopentanoate. The product decarboxylates to 4-methyl-2 oxopentanoate

yzes the phosphorylation of glycerol to yield sn- glycerol 3-phosphate

ncomitant import of sodium (symport system)

ent

to an aldose acceptor, via a covalent intermediate with the cofactor thiamine pyrophosphate

from threonine in a two-step reaction. The first step involved a dehydration of threonine and a production of enamine intermediates (aminocroto

onal DNA repair. Binds to DSBs and unwinds DNA via a highly rapid and processive ATP-dependent bidirectional helicase activity. Unwinds dsDNA

tions as a nickel donor during metallocenter assembly

rate, and malate across the membrane

hyde into succinylglutamate

amide dehydrogenase (E3) component, and related enzymes
l bilayer. May participate in the regulation of osmotic pressure changes within the cell

pyrimidinone 5'-phosphate (DARP), formate and pyrophosphate
ethionine (SAM) to 7-keto-8-aminopelargonic acid (KAPA) to form 7,8-diaminopelargonic acid (DAPA). It is the only animotransferase known to uti

4-linked N-acetylglucosamine (GlcNAc) from peptide-linked peptidoglycan fragments, giving rise to free GlcNAc, anhydro-N-acetylmuramic acid ar

mbrane after they are released by the LolA protein

peptidoglycan

alyzes an alkyl-migration followed by a ketol- acid reduction of (S)-2-acetolactate (S2AL) to yield (R)-2,3- dihydroxy-isovalerate. In the isomerase r

osynthetic process

ent

) in 23S rRNA

rotate
phospholipid

mononucleotide (NAMN) and 5,6- dimethylbenzimidazole (DMB)
. Uses L-glutamine as a nitrogen source

alyzes the reversible oxidation of betaine aldehyde to the corresponding acid

d in the D-loop of most tRNAs, via the reduction of the C5-C6 double bond in target uridines. Specifically modifies U20 and U20a in tRNAs

onal DNA repair. Binds to DSBs and unwinds DNA via a highly rapid and processive ATP-dependent bidirectional helicase activity. Unwinds dsDNA u

n alanine is first activated by ATP to form Ala- AMP and then transferred to the acceptor end of tRNA(Ala). Also edits incorrectly charged Ser-tRNA

1 subfamily

the arrested nascent DNA chain at stalled replication forks. It can open the DNA duplex, via its helicase activity, and promote assembly of the prir

y-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythritol 4-phosphate (MEP)

and RF2 PrfB on the glutamine residue of the universally conserved GGQ motif

cross-linking them and that serves as a cytoplasmic membrane anchor for the Z ring. Also required for the recruitment to the septal ring of downs

nbination. Cleaves the cruciform structure in supercoiled DNA by nicking to strands with the same polarity at sites symmetrically opposed at the ju
ırate, and malate across the membrane

:ion of short chain beta-hydroxyacyl-ACPs and long chain saturated and unsaturated beta-hydroxyacyl-ACPs

/IG) into 2 molecules of pyruvate. Also contains a secondary oxaloacetate (OAA) decarboxylase activity due to the common pyruvate enolate transi
ide precursor UDP-N-acetylmuramoyl-L-alanine (UMA)
TPase PilB

istinct tRNA(Ile)-dependent editing activities. One activity is designated as 'pretransfer' editing and involves the hydrolysis of activated Val-AMP. T

e-stranded (ds) DNA in an ATP-dependent manner to modulate DNA topology and maintain chromosomes in an underwound state. Negative supe

ent

ıe urease nickel metallocenter

of adenosylhomocysteine

ıionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrc

nthetase alpha subunit type 1 subfamily

c acid (anhMurNAc) with the simultaneous cleavage of the 1,6-anhydro ring, generating MurNAc-6-P. Is required for the utilization of anhMurNAc

y

mily
ne

ed in assembly and insertion of beta-barrel proteins into the outer membrane

1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate

chain alcohol dehydrogenases)

tagenic agents. Acts as DNA glycosylase that recognizes and removes damaged bases. Has a preference for oxidized purines, such as 7,8-dihydro-8

RNA
. Required for the maturation of 5S and 16S rRNAs and the majority of tRNAs. Also involved in the degradation of most mRNAs
ed in assembly and insertion of beta-barrel proteins into the outer membrane

ion proteins, which are predominantly cytoplasmic, with the downstream cell division proteins, which are predominantly periplasmic. May control

response to the peptide chain termination codons UAG and UAA

30S particle

alyzes the oxidation of choline to betaine aldehyde and betaine aldehyde to glycine betaine at the same rate

rine (OSHS) and hydrogen sulfide

n-specific tRNA(Ile) that contains the anticodon CAU, in an ATP-dependent manner. Cytidine is converted to lysidine, thus changing the amino acid
membrane. The catalytic sites are hosted primarily by the beta subunits

n, which catalyzes the hydrolysis of ATP coupled with the electrogenic transport of potassium into the cytoplasm. This subunit binds and transport

',8-dihydropterin

ɔnjugates Leu, Phe and, less efficiently, Met from aminoacyl-tRNAs to the N-termini of proteins containing an N-terminal arginine or lysine
ɛnt

ɜmily

ds to the corresponding amines. Requires NADH, but not NADPH, as an electron donor for its activity

omain)

70S ribosome quality control and in maturation of the 3' terminus of the 16S rRNA

(preQ0) to 7-aminomethyl-7-deazaguanine (preQ1)
acyl-ACP as the acyl donor. Is involved in the biosynthesis of lipid A, a phosphorylated glycolipid that anchors the lipopolysaccharide to the outer m

sphate to yield N-acetyl-L-glutamate 5-semialdehyde

ily. Prokaryotic type I sub-subfamily
; succinyl-L-homoserine

ophilic materials across the outer membrane

factor (Moco or molybdenum cofactor) to form Mo- molybdopterin guanine dinucleotide (Mo-MGD) cofactor

ıosphoserine and of 3-hydroxy-2-oxo-4- phosphonooxybutanoate to phosphohydroxythreonine

membrane. The alpha chain is a regulatory subunit

es them by dioxygen to Fe(3), and participates in the subsequent Fe(3) oxide mineral core formation within the central cavity of the protein comp

ton or sodium gradient. F-type ATPases consist of two structural domains, F(1) containing the extramembraneous catalytic core and F(0) containir

ily

e-stranded (ds) DNA in an ATP-dependent manner to modulate DNA topology and maintain chromosomes in an underwound state. Negative super

protein

preprotein conducting channel. SecDF uses the proton motive force (PMF) to complete protein translocation after the ATP-dependent function of S

ent

e-1-phosphate to form lipid A disaccharide, a precursor of lipid A, a phosphorylated glycolipid that anchors the lipopolysaccharide to the outer mer

ethyluridine at position 54 (m5U54) in all tRNAs, and that of position 341 (m5U341) in tmRNA (transfer-mRNA)

ɔtum

oenolpyruvate. It is essential for the degradation of carbohydrates via glycolysis

e to form N'-(5'-phosphoribosyl)-ATP (PR-ATP). Has a crucial role in the pathway because the rate of histidine biosynthesis seems to be controlled

serve as a membrane anchor for the Z ring

ton or sodium gradient. F-type ATPases consist of two structural domains, F(1) containing the extramembraneous catalytic core and F(0) containir

ıtamate 5-phosphate

ependent recombinational process of DNA repair. It may act with RecF and RecO

:ts by transferring its disulfide bond to other proteins and is reduced in the process

hate (TMP) to form thiamine-pyrophosphate (TPP), the active form of vitamin B1

anchors the lipopolysaccharide to the outer membrane of the cell

to RNA using the four ribonucleoside triphosphates as substrates
ular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides

ent
ycan strands endolytically to terminate their elongation

ethyl)-4,5-dioxo-4,5,6,7,8,9-hexahydroquinoline- 7,9-dicarboxylic-acid to PQQ
subunit in the ribosome

se-phosphate pathway
ain

nate (DAHP) to dehydroquinate (DHQ)
orm a long-chain polyphosphate (polyP)

aking F(1) to F(0)

membrane. The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex

olysis. Has a chymotrypsin-like activity. Plays a major role in the degradation of misfolded proteins

ion proteins, which are predominantly cytoplasmic, with the downstream cell division proteins, which are predominantly periplasmic

ucer).

e (PEP) to the 5-hydroxyl of shikimate-3- phosphate (S3P) to produce enolpyruvyl shikimate-3-phosphate and inorganic phosphate

moderate affinity, with high nucleotide exchange rates and a fairly low GTP hydrolysis rate. Plays a role in control of the cell cycle, stress respons

ulating the intracellular concentration of cAMP, thereby influencing cAMP-dependent processes

to RNA using the four ribonucleoside triphosphates as substrates

ine (L-3OHKyn) into anthranilic acid (AA) and 3- hydroxyanthranilic acid (3-OHAA), respectively

nal division sites while permitting inhibition at polar sites. This ensures cell division at the proper site by restricting the formation of a division sept

precursor UDP-N-acetylmuramoyl-L-alanyl-D-glutamate (UMAG) in the biosynthesis of bacterial cell-wall peptidoglycan
ost of the replicative synthesis in bacteria. This DNA polymerase also exhibits 3' to 5' exonuclease activity

ion proteins, which are predominantly cytoplasmic, with the downstream cell division proteins, which are predominantly periplasmic

-histidinaldehyde and then to L-histidine

ent

leading to the formation of 2- methylthio-N6-(dimethylallyl)adenosine (ms(2)i(6)A) at position 37 in tRNAs that read codons beginning with uridir

se family. Histidinol-phosphate aminotransferase subfamily

to produce the thiazole phosphate moiety of thiamine. Sulfur is provided by the thiocarboxylate moiety of the carrier protein ThiS. In vitro, sulfur c
of UDP-N-acetylmuramoyl-pentapeptide, the precursor of murein

ily

tase family

ent

ıtegrity of the outer membrane by promoting either the assembly or the elimination of outer membrane proteins, depending on their folding state

wo nucleotide 3' overhang. Responsible for the end-turnover of tRNA specifically removes the terminal AMP residue from uncharged tRNA (tRNA-

preprotein conducting channel. SecDF uses the proton motive force (PMF) to complete protein translocation after the ATP-dependent function of S

ent

ıembrane

ıyl-2-thiouridine (mnm(5)s(2)U) at the wobble position (U34) in tRNA. Catalyzes the FAD-dependent demodification of cmnm(5)s(2)U34 to nm(5)

x) 5'-TTATC CA A CA A-3'. DnaA binds to ATP and to acidic phospholipids

tase family

in the process to assimilate ammonia. When cellular nitrogen levels are high, the C-terminal adenylyl transferase (AT) inactivates GlnA by covaler
group on carbon 2 of heme B porphyrin ring with a hydroxyethyl farnesyl side group

ɔtease activity

e reduction of the AhpC active site cysteine residues and for the regeneration of the AhpC enzyme activity
pathway, GSP) for the export of proteins

ɛ precursor 7-aminomethyl-7-deazaguanine (PreQ1) at position 34 (anticodon wobble position) in tRNAs with GU(N) anticodons (tRNA-Asp, -Asn, -

er (TC 2.A.37) family

with (2E,6E)-farnesyl diphosphate (E,E-FPP) to yield (2Z,6Z,10Z,14Z,18Z,22Z,26Z,30Z,34E,38E)-undecaprenyl diphosphate (di-trans,octa-cis-UPP).

ts by transferring its disulfide bond to other proteins and is reduced in the process

through selective RNA binding

ɔsequent hydrolysis of acetyl-coenzyme A (acetyl-CoA) and glyoxylate to form malate and CoA

A 2

merization of proline imidic peptide bonds in oligopeptides

binding to the nascent RNA, activation of Rho's RNA-dependent ATPase activity, and release of the mRNA from the DNA template

ɔf fumarate to L-malate

to aspartylate not only its cognate tRNA(Asp) but also tRNA(Asn). Reaction proceeds in two steps L-aspartate is first activated by ATP to form Asp

-2-methylisocitrate to yield pyruvate and succinate

eak ATPase activity

n

enzyme A to form coenzyme A

rose-4-phosphate (E4P) giving rise to 3-deoxy-D- arabino-heptulosonate-7-phosphate (DAHP)
ent

philic materials across the outer membrane

rboxy-5,6,7,8-tetrahydropterin (CPH4) to 7- carboxy-7-deazaguanine (CDG), a step common to the biosynthetic pathways of all 7-deazapurine-cont

utamine or ammonia as the source of nitrogen. Regulates intracellular CTP levels through interactions with the four ribonucleotide triphosphates

ent

n and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA

ent

from CTP and 2-C-methyl-D-erythritol 4- phosphate (MEP)

s (GlnB and homologs), in response to the nitrogen status of the cell that GlnD senses through the glutamine level. Under low glutamine levels, ca
to Kdo(2)-lipid IV(A) to form Kdo(2)- (lauroyl)-lipid IV(A)

ent
osynthesis. Catalyzes the first committed step in the biosynthesis of AMP from IMP

oxymethyl-7,8-dihydropterin diphosphate (DHPt-PP) to form 7,8-dihydropteroate (H2Pte), the immediate precursor of folate derivatives

on 34 of tRNA(Arg2)

stranded polyribonucleotides processively in the 3'- to 5'-direction

. Responsible for energy coupling to the transport system

ield 2,3-diacylglucosamine 1-phosphate (lipid X) and UMP by catalyzing the attack of water at the alpha-P atom. Involved in the biosynthesis of lip

ıport. Responsible for energy coupling to the transport system

stabilize it, and thus to prevent its denaturation under extreme environmental conditions

8 (m3U1498) in 16S rRNA. Acts on the fully assembled 30S ribosomal subunit

dback regulation of ATP phosphoribosyltransferase activity by histidine

and formamide

m

rrier protein that transfers sulfur from IscS to the molybdenum cofactor prior to its insertion into FDH

ıse family

on other amino acids

:-6 and C-8 positions of the octanoyl moiety bound to the lipoyl domains of lipoate-dependent enzymes, thereby converting the octanoylated doma

ent

›philic materials across the outer membrane

›age through the periplasm

e biosynthesis of aromatic amino acids. Catalyzes the cis-dehydration of 3-dehydroquinate (DHQ) and introduces the first double bond of the arom

yme-A, the prosthetic group of the acyl-carrier protein of the malonate decarboxylase

ɲ acetyl and malonyl thioester residues are bound via a 2'-(5''-phosphoribosyl)-3'-dephospho-CoA prosthetic group and turn over during the catalyti

IP-P) moiety of thiamine from aminoimidazole ribotide (AIR) in a radical S-adenosyl-L-methionine (SAM)-dependent reaction

family. FecCD subfamily

family. FecCD subfamily

Also involved, together with DnaK and GrpE, in the DNA replication of plasmids through activation of initiation proteins
y function as a thermosensor. Unfolded proteins bind initially to DnaJ

cks exit of the E-site tRNA

s

y formed A-site-bound peptidyl-tRNA and P-site-bound deacylated tRNA move to the P and E sites, respectively. Catalyzes the coordinated movem

the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membr

. It also specifically binds to its receptor SecA

onsible for the 5' incision

ne

ase activity

r abnormalities. When the presence of a lesion has been verified by UvrB, the UvrA molecules dissociate
the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membr

ne

the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membr

the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membr

line ribonucleotide (FGAM) and glutamate

damage and developmental changes induced by stress. Degrades polypeptides processively to yield small peptide fragments that are 5 to 10 amir

Fe S proteins

ection, yielding the 30S pre- initiation complex (PIC). Upon addition of the 50S ribosomal subunit IF-1, IF-2 and IF-3 are released leaving the matur

the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membr

carbamoyl-AMP (TC-AMP) to the N6 group of A37, together with TsaE and TsaB. TsaD likely plays a direct catalytic role in this reaction

targeting signal to indicate that the lipoprotein should stay in the inner membrane)

serving both as a receptor for the preprotein-SecB complex and as an ATP-driven molecular motor driving the stepwise translocation of polypeptide

NA strands. Then UvrB probes one DNA strand for the presence of a lesion. If a lesion is found the UvrA subunits dissociate and the UvrB-DNA preir

ctional ribosomes, thus repressing translation

ntial role in vivo by binding to the 5'-leader sequence and broadening the substrate specificity of the ribozyme

the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membr

ɔn of D-aminoacyl-tRNA entities in vivo and helps enforce protein L-homochirality

the 30S subunit (bridge B1b), connecting the 2 subunits

for the assembly of transient iron-sulfur cluster in IscU in the presence of IscS, L-cysteine and the thioredoxin reductase system

ı of the ribosome. Modification of Lys-34 is required for alleviation

l for regulation of fis expression

c membrane to specific energy- requiring processes in the outer membrane, resulting in the release into the periplasm of ligands bound by these c

haperone that increases the ATP- binding affinity of the ATP-hydrolyzing subunit KdpB by the formation of a transient KdpB KdpC ATP ternary comp

moiety of the queuosine in the wobble position of the QUC anticodon

subunits

HAP)

o DNA

nthesis initiation begins

·eceptor directly interacting with Tat signal peptides

f purines, thymidylate, methionine, and other important biomolecules. Also exhibits THF- independent aldolase activity toward beta-hydroxyaminc

needed both before and after RbfA during the maturation of 16S rRNA. It has affinity for free ribosomal 30S subunits but not for 70S ribosomes

ole in the regulation of cell growth

sis of GTP during the formation of the 70S ribosomal complex

ɹrinic apyrimidinic) site. The AP-lyase activity cleaves the phosphodiester bond 3' to the AP site by a beta-elimination, leaving a 3'-terminal unsatu

ıed primers can be extended by PolIV. Exhibits no 3'-5' exonuclease (proofreading) activity. May be involved in translesional synthesis, in conjunctic

olism

ɔ and ATP as substrates and producing inorganic pyrophosphate

ins into lipoylated derivatives

, via interactions with LptC and LptD, thereby facilitating LPS transfer across the periplasm

ɔlex

ɨ 7, and are clamped together by SecE at the back. The channel is closed by both a pore ring composed of hydrophobic SecY resides and a short hel

ıine. Functions as a sulfur delivery protein for Fe-S cluster synthesis onto IscU, an Fe-S scaffold assembly protein, as well as other S acceptor prote

ɔf IGP and AICAR

s or polysomes). Required for efficient processing of 16S rRNA. May interact with the 5'-terminal helix region of 16S rRNA
e

. It interacts with LexA causing its activation and leading to its autocatalytic cleavage

uvAB is a helicase that mediates the Holliday junction migration by localized denaturation and reannealing. RuvA stimulates, in the presence of DN

ive threonylcarbamoyl-AMP (TC-AMP) as the acyladenylate intermediate, with the release of diphosphate

rase to acetyl-CoA to form malonyl-CoA

H subunit

ld NADP

:atalyzes the reverse reactions

e to acetyl-CoA to form malonyl- CoA

ıcoded in the rRNA operon. Processes pre- crRNA and tracrRNA of type II CRISPR loci if present in the organism
.,4-benzoquinol (DMQH2)

ıe polyisoprenoid side chain with PHB, generating the first membrane-bound Q intermediate 3- octaprenyl-4-hydroxybenzoate

ıergy coupling to the transport system

ruvAB is a helicase that mediates the Holliday junction migration by localized denaturation and reannealing

he general RNA quality control

:RISPR clusters contain spacers, sequences complementary to antecedent mobile elements, and target invading nucleic acids. CRISPR clusters are t

ıg strand to extend heteroduplex DNA faster. Binds ssDNA in the presence of ADP but not other nucleotides, has ATPase activity that is stimulated

:nting the misappropriation of this tRNA by the elongation apparatus

hosphopantotheine

reak via transesterification at a target site in duplex DNA. The scissile phosphodiester is attacked by the catalytic tyrosine of the enzyme, resulting

·eceptor directly interacting with Tat signal peptides. TatB may form an oligomeric binding site that transiently accommodates folded Tat precurso

BD) is responsible for energy generation

ıelic acid, an essential component of bacterial cell walls

hairpins. It also has a 5' single-strand endonuclease activity

ge

A and cis-3-enoyl-CoA as substrate

h epimers of NAD(P)HX, a damaged form of NAD(P)H that is a result of enzymatic or heat-dependent hydration

excision repair machinery to the damaged site

osome. The stimulation of RF- 1 and RF-2 is significantly reduced by GTP and GDP, but not by GMP
likely to be the physiological substrate

able complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex

late synthase (AS) provides the glutamine amidotransferase activity which generates ammonia as a substrate that, along with chorismate, is usec

yinosine triphosphate) and ITP. Seems to function as a house-cleaning enzyme that removes non-canonical purine nucleotides from the nucleotide

f the FtsZ ring is to recruit other cell division proteins to the septum to produce a new cell wall between the dividing cells. Binds GTP and shows G

glutaminyl-tRNA synthetases. The reaction takes place in the presence of glutamine and ATP through an activated phospho-Asp-tRNA(Asn) or phos

pass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as GreA or GreB allows the resump

which is responsible for energy generation. Confers resistance against macrolides

methyl group to a cysteine residue in the enzyme. This is a suicide reaction the enzyme is irreversibly inactivated

:A. The alpha subunit of the enzyme binds the substrates coenzyme A and phosphate, while succinate binding and nucleotide specificity is provided

ıte and process non-cognate amino acids such as alanine and cysteine, to avoid such errors it has two additional distinct editing activities against a
nslocated ribosomes. Back- translocation proceeds from a post-translocation (POST) complex to a pre-translocation (PRE) complex, thus giving elc

tamine and ATP through an activated gamma-phospho-Glu-tRNA(Gln)

ɛnting the misappropriation of this tRNA by the elongation apparatus

f precorrin-2 to yield sirohydrochlorin. Finally, it catalyzes the ferrochelation of sirohydrochlorin to yield siroheme

ɜs broad specificity at other positions

pid entry or exit of water in response to abrupt changes in osmolarity

uter membrane

until it encounters a Chi (crossover hotspot instigator) sequence from the 3' direction. Cuts ssDNA a few nucleotides 3' to the Chi site. The properti

the subunit. Circularly permuted GTPase that catalyzes slow GTP hydrolysis, GTPase activity is stimulated by the 30S ribosomal subunit

ıg channel of the Tat system

P pathway for isoprenoid precursor biosynthesis

glutaminyl-tRNA synthetases. The reaction takes place in the presence of glutamine and ATP through an activated phospho-Asp-tRNA(Asn) or phos

nanner freely and bidirectionally along dsDNA. Initially characterized for its ability to contact the catalytic subunit of DNA polymerase III (Pol III), a

es, displacing the stalled mRNA. The ribosome then switches to translate the ORF on the tmRNA

to 5'- polarity. Unwinds branched duplex DNA (Y-DNA)
ral outer membrane proteins. May act in both early periplasmic and late outer membrane-associated steps of protein maturation

intermediate II)

nds with high specificity to tRNAs

ıtly of the Sec translocase complex, as well as at least some lipoproteins. Aids folding of multispanning membrane proteins

acetate with ATP to form acetyl-adenylate (AcAMP) intermediate. In the second half reaction, it can then transfer the acetyl group from AcAMP to

:A. The beta subunit provides nucleotide specificity of the enzyme and binds the substrate succinate, while the binding sites for coenzyme A and pl

erythritol 2-phosphate (CDP-ME2P) to 2-C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-CPP) with a corresponding release of cytidine 5-monophos

ıe 5'-phosphate (PNP) and inorganic phosphate

NC). Interaction with SRP-RNC leads to the transfer of the RNC complex to the Sec translocase for insertion into the membrane, the hydrolysis of G

ɾeen N(2)-acetylornithine and glutamate

s needed for PGA export through the PgaA porin

ass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as GreA or GreB allows the resump

the wobble nucleotide

the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membr

ı-sensitive transpeptidase C-terminal domain (cross-linking of the peptide subunits)

ˀ, when it is trapped or immobilized on tightly supercoiled DNA. Does not activate transcription on linear DNA. Probably not involved in DNA repair

ucosamine-1-phosphate (GlcN-1-P) to produce N-acetylglucosamine-1-phosphate (GlcNAc-1-P), which is converted into UDP-GlcNAc by the transf

ysis of 10-formyl-tetrahydrofolate

;Z polymerization

reak via transesterification at a target site in duplex DNA. The scissile phosphodiester is attacked by the catalytic tyrosine of the enzyme, resulting

uctant in the reaction, yielding dihydrofolate (DHF) as a by-product. This enzymatic reaction provides an intracellular de novo source of dTMP, an e

substrate for the three terminal pathways of aromatic amino acid biosynthesis. This reaction introduces a second double bond into the aromatic ri

e SRP-RNC complex is then targeted to the cytoplasmic membrane where it interacts with the SRP receptor FtsY. Interaction with FtsY leads to the

as broad specificity at other positions

ntial for DNA replication and repair of damaged DNA

ll but it is not essential for cell division

nate), which tautomerizes to its imine form (iminobutyrate). Both intermediates are unstable and short- lived. The second step is the nonenzymat

until it encounters a Chi (crossover hotspot instigator) sequence from the 3' direction. Cuts ssDNA a few nucleotides 3' to the Chi site. The properti

lize SAM as an amino donor

ıd anhydro-N-acetylmuramic acid-linked peptides

eaction, S2AL is rearranged via a Mg-dependent methyl migration to produce 3- hydroxy-3-methyl-2-ketobutyrate (HMKB). In the reductase reactio

until it encounters a Chi (crossover hotspot instigator) sequence from the 3' direction. Cuts ssDNA a few nucleotides 3' to the Chi site. The properti

A(Ala) and Gly-tRNA(Ala) via its editing domain

nosome and loading of the major replicative helicase DnaB onto DNA

stream cell division proteins

nction in the homologous arms and leaves a 5'-terminal phosphate and a 3'-terminal hydroxyl group

tion state formed following C-C bond cleavage in the retro-aldol and decarboxylation reactions

he other activity is designated 'posttransfer' editing and involves deacylation of mischarged Val-tRNA(Ile)

rcoiling favors strand separation, and DNA replication, transcription, recombination and repair, all of which involve strand separation. Also able to

›lysis which occurs prior to release of AdoMet from the enzyme

either imported from the medium or derived from its own cell wall murein, and thus plays a role in cell wall recycling

3-oxoguanine (8-oxoG). Has AP (apurinic apyrimidinic) lyase activity and introduces nicks in the DNA strand. Cleaves the DNA backbone by beta-del

correct divisome assembly

specificity of the tRNA from methionine to isoleucine

s the potassium across the cytoplasmic membrane

embrane of the cell

ɔlex

ıg the membrane proton channel, linked together by a central stalk and a peripheral stalk. During catalysis, ATP synthesis in the catalytic domain o

rcoiling favors strand separation, and DNA replication, transcription, recombination and repair, all of which involve strand separation. Also able to

SecA

nbrane of the cell

primarily by regulation of HisG enzymatic activity

ıg the membrane proton channel, linked together by a central stalk and a peripheral stalk. During catalysis, ATP synthesis in the catalytic domain o

e, ribosome biogenesis and in those bacteria that undergo differentiation, in morphogenesis control

tum at the midpoint of the long axis of the cell

ne

:an be provided by H(2)S

C-C-A). Also appears to be involved in tRNA biosynthesis

SecA

s(2)U34, followed by the transfer of a methyl group from S-adenosyl-L-methionine to nm(5)s(2)U34, to form mnm(5)s(2)U34

ıt transfer of an adenylyl group from ATP to specific tyrosine residue of GlnA, thus reducing its activity. Conversely, when nitrogen levels are low, t

-His and -Tyr). Catalysis occurs through a double-displacement mechanism. The nucleophile active site attacks the C1' of nucleotide 34 to detach th

UPP is the precursor of glycosyl carrier lipid in the biosynthesis of bacterial cell wall polysaccharide components such as peptidoglycan and lipopol

ɔ-AMP and then transferred to the acceptor end of tRNA(Asp Asn)

taining compounds

atalyzes the conversion of the PII proteins and UTP to PII-UMP and PPi, while under higher glutamine levels, GlnD hydrolyzes PII-UMP to PII and UM

id A, a phosphorylated glycolipid that anchors the lipopolysaccharide to the outer membrane of the cell

ins into lipoylated derivatives

atic ring to yield 3- dehydroshikimate

ic mechanism

ent of the two tRNA molecules, the mRNA and conformational changes in the ribosome

ane), and thus conserves the redox energy in a proton gradient

ane), and thus conserves the redox energy in a proton gradient

ane), and thus conserves the redox energy in a proton gradient

ane), and thus conserves the redox energy in a proton gradient

ıo acids long. Binds to DNA in a double-stranded, site-specific manner

·e 70S translation initation complex

ane), and thus conserves the redox energy in a proton gradient. This subunit may bind ubiquinone

e chains across the membrane

ıcision complex is formed. This complex is subsequently bound by UvrC and the second UvrB is released. If no lesion is found, the DNA wraps arou

ane), and thus conserves the redox energy in a proton gradient

ɔuter membrane proteins

ɔlex

› acids, producing glycine and aldehydes, via a retro-aldol mechanism

rated sugar and a product with a terminal 5'-phosphate

ɔn with the beta clamp from PolIII

ix (helix 2A) on the extracellular side of the membrane which forms a plug. The plug probably moves laterally to allow the channel to open. The ri

eins

lA, the weak ATPase activity of RuvB

transcribed and processed into CRISPR RNA (crRNA). Acts as a dsDNA endonuclease. Involved in the integration of spacer DNA into the CRISPR cas

by ssDNA and various branched DNA structures, but inhibited by SSB. Does not have RecA's homology-searching function

in the formation of a DNA-(5'-phosphotyrosyl)-enzyme intermediate and the expulsion of a 3'-OH DNA strand. The free DNA strand then undergoe

ɔr proteins before their translocation

l in the second step, catalyzed by the large alpha subunit of AS (TrpE) to produce anthranilate. In the absence of TrpG, TrpE can synthesize anthran

e pool, thus preventing their incorporation into DNA RNA and avoiding chromosomal lesions

TPase activity

ɜpho-Glu-tRNA(Gln)

ɔtion of elongation from the new 3'terminus. GreB releases sequences of up to 9 nucleotides in length

d by the beta subunit

alanine. One activity is designated as 'pretransfer' editing and involves the tRNA(Pro)-independent hydrolysis of activated Ala-AMP. The other activ
ongation factor G a second chance to translocate the tRNAs correctly. Binds to ribosomes in a GTP-dependent manner

es and activities of the enzyme are changed at Chi. The Chi-altered holoenzyme produces a long 3'-ssDNA overhang and facilitates RecA-binding t

;pho-Glu-tRNA(Gln)

complex, multichain enzyme responsible for most of the replicative synthesis in bacteria

› the sulfhydryl group of CoA, forming the product AcCoA

nosphate are found in the alpha subunit

phate (CMP)

GTP by both Ffh and FtsY, and the dissociation of the SRP-FtsY complex into the individual components

ɔtion of elongation from the new 3'terminus. GreA releases sequences of 2 to 3 nucleotides

ane), and thus conserves the redox energy in a proton gradient

er of uridine 5- monophosphate (from uridine 5-triphosphate), a reaction catalyzed by the N-terminal domain

in the formation of a DNA-(5'-phosphotyrosyl)-enzyme intermediate and the expulsion of a 3'-OH DNA strand. The free DNA strand then undergoe

ssential precursor for DNA biosynthesis

ng system

e transfer of the RNC complex to the Sec translocase for insertion into the membrane, the hydrolysis of GTP by both Ffh and FtsY, and the dissocia

tic hydrolysis of the enamine imine intermediates to form 2-ketobutyrate and free ammonia. In the low water environment of the cell, the second

es and activities of the enzyme are changed at Chi. The Chi-altered holoenzyme produces a long 3'-ssDNA overhang and facilitates RecA-binding t

ɔn, this 2-ketoacid undergoes a metal-dependent reduction by NADPH to yield (R)-2,3-dihydroxy-isovalerate

es and activities of the enzyme are changed at Chi. The Chi-altered holoenzyme produces a long 3'-ssDNA overhang and facilitates RecA-binding to

catalyze the interconversion of other topological isomers of dsDNA rings, including catenanes and knotted rings. Type II topoisomerases break and

ta elimination to generate a single-strand break at the site of the removed base with both 3'- and 5'-phosphates

f F(1) is coupled via a rotary mechanism of the central stalk subunits to proton translocation

catalyze the interconversion of other topological isomers of dsDNA rings, including catenanes and knotted rings. Type II topoisomerases break and

f F(1) is coupled via a rotary mechanism of the central stalk subunits to proton translocation

he N-terminal adenylyl removase (AR) activates GlnA by removing the adenylyl group by phosphorolysis, increasing its activity. The regulatory regi

ıe guanine base from the RNA, forming a covalent enzyme-RNA intermediate. The proton acceptor active site deprotonates the incoming PreQ1, a

ysaccharide

MP (deuridylylation). Thus, controls uridylylation state and activity of the PII proteins, and plays an important role in the regulation of nitrogen

nd the other UvrB subunit that will check the other stand for damage

ŋg and the pore may move independently

sette

es passage around the unbroken strand, thus removing DNA supercoils. Finally, in the religation step, the DNA 3'-OH attacks the covalent intermedi

ılate directly from chorismate and high concentrations of ammonia

ity is designated 'posttransfer' editing and involves deacylation of mischarged Ala-tRNA(Pro). The misacylated Cys- tRNA(Pro) is not edited by Pro

ɔ the ssDNA for homologous DNA recombination and repair. Holoenzyme degrades any linearized DNA that is unable to undergo homologous recoı

es passage around the unbroken strand, thus removing DNA supercoils. Finally, in the religation step, the DNA 3'-OH attacks the covalent intermedi

tion of the SRP-FtsY complex into the individual components

step is accelerated by RidA

o the ssDNA for homologous DNA recombination and repair. Holoenzyme degrades any linearized DNA that is unable to undergo homologous reco

ɔ the ssDNA for homologous DNA recombination and repair. Holoenzyme degrades any linearized DNA that is unable to undergo homologous recoı

join 2 DNA strands simultaneously in an ATP-dependent manner

join 2 DNA strands simultaneously in an ATP-dependent manner

on of GlnE binds the signal transduction protein PII (GlnB) which indicates the nitrogen status of the cell

ıllowing a nucleophilic attack on the C1' of the ribose to form the product. After dissociation, two additional enzymatic reactions on the tRNA conv

iate to expel the active-site tyrosine and restore the DNA phosphodiester backbone

RS

mbination. In the holoenzyme this subunit contributes ATPase, 3'-5' helicase, exonuclease activity and loads RecA onto ssDNA

iate to expel the active-site tyrosine and restore the DNA phosphodiester backbone

mbination. In the holoenzyme this subunit has ssDNA-dependent ATPase and 5'-3' helicase activity. When added to pre-assembled RecBC greatly s

mbination. In the holoenzyme this subunit recognizes the wild- type Chi sequence, and when added to isolated RecB increases its ATP-dependent h

ert PreQ1 to queuine (Q), resulting in the hypermodified nucleoside queuosine (7-(((4,5-cis-dihydroxy-2- cyclopenten-1-yl)amino)methyl)-7-deazag

stimulates nuclease activity and augments holoenzyme processivity. Negatively regulates the RecA-loading ability of RecBCD

ıelicase processivity

;uanosine)